Risk-based Surveillance of Avian Influenza in Switzerland: Insights into Poultry Farm Determinants and Contact Networks

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LIST OF ABBREVIATIONS

AI	Avian influenza
AIV	Avian influenza virus
AGES	Austrian Agency for Health and Food Safety
AGIS	Agrarinformationssystem (agricultural information system)
AMLS	Animal movement licensing system
BE	Belgium
BFS	Bundesamt für Statistik (Switzerland) → FSO
BTB	Bovine tuberculosis
BVET	Bundesamt für Veterinärwesen (Switzerland) → FVO
CC	Clustering coefficient
CI	Confidence interval
CTS	Cattle tracing system
DB	Database
DBS	Database system
DBSM	Database management system
DCL	Data control language
DDL	Data definition language
DE	Germany
DEFRA	Department for Environment, Food and Rural Affairs (United Kingdom)
DML	Data manipulation language
DVG	Deutsche Veterinärmedizinische Gesellschaft (German Veterinarian Society)
EFSA	European Food Safety Authority
ERM	Entity relationship model
ETHZ	Eidgenössische Technische Hochschule Zürich
EU	European Union
FAO	Food and Agriculture Organization
FI	Finland
FMD	Foot-and-mouth disease
FSO	Swiss Federal Statistical Office → BFS
FVO	Swiss Federal Veterinary Office → BVET
FLI	Friedrich-Loeffler-Institute (Germany)
GBPR	Great Britain poultry register
H	Haemagglutinin
HIT	Herkunftsicherungs- und Informationssystem für Tiere (German animal register database)
HPAI	Highly pathogenic avian influenza
I	Infected and infectious
IED	Institute for Environmental Decisions (ETHZ)
ILT	Infectious laryngotracheitis
IQR	Inter-quartile range
IT	Italy
IVI	Institute of Virology and Immunoprophylaxis (Switzerland)
IVPI	Intravenous pathogenicity index
IVT	Institute for Transport Planning and Systems (ETHZ)

KM	Kilometer
LPAI	Low pathogenic avian influenza
M	Median
MRSA	Methicillin-resistant *Staphylococcus aureus*
N	Neuraminidase
NAI	Notifiable avian influenza
ND	Newcastle disease
NGO	Non-Governmental Organization
NO	Number
NS	Not significant
OFFLU	OIE-FAO network of expertise on influenza
OIE	World Organization for Animal Health
OR	Odds ratio
R	Removed or recovered
R_0	Basic reproductive ratio (basis reproductive number)
RNA	Ribonucleic acid
S	Susceptible
SAMS	Scottish animal movement system
SARS	Severe Acute Respiratory Syndrome
SAT	Schweizer Archiv für Tierheilkunde
SEIR	Susceptible-exposed-infected/infectious-recovered
SIR	Susceptible-infected/infectious-recovered
SIS	Susceptible-infected/infectious-susceptible
SNA	Social network analysis
SPS	Sanitary and Phytosanitary Agreement (WTO)
STI	Swiss Tropical Institute
SQL	Structured Query Language
TSV	Tierseuchenverordnung (Animal Health Decree of Switzerland)
TVD	Tierverkehrsdatendank (Swiss livestock movement register)
UK	United Kingdom
WHO	World Health Organization
WTO	World Trade Organization
WUV	„Wildvögel und Vogelgrippe“ project in Baden-Württemberg (Germany)

SUMMARY

Epidemic prevention and surveillance in human and animal populations are paramount to public health. Economic losses by highly pathogenic avian influenza (HPAI) in poultry flocks and human exposure to HPAI virus across Asia and parts of Africa and Europe are ongoing. This concern motivates also currently outbreak-free countries such as Switzerland to invest in epidemic preparedness planning and strengthening surveillance activities. Switzerland faces the two common risk scenarios: firstly, the introduction of HPAI to the poultry sector via wild birds and secondly, the introduction and further dissemination via poultry trade as well as via person movements and resources shared among poultry farms. The latter is widely determined by the attitude of poultry keepers and by farm characteristics, as well as by geographical and functional interrelations among farms, namely their contact networks.

To comply with national and international demands, epidemic surveillance activities and regulations must be based on scientific information and repeatable risk analyses. In Switzerland, it remains to be explored whether all poultry keepers are aware of HPAI and if they would contribute appropriately to passive HPAI surveillance by notifying a suspected disease. Country-specific information of demography and contact structures of the poultry farm population is needed to anticipate probable patterns of pathogen spread, and must be established prior to successful planning, implementation and evaluation of surveillance activities. Such data provide valuable inputs for epidemic models predicting epidemic dynamics and evaluating impacts of interventions. Mathematical models are increasingly important for decision making and epidemic preparedness planning in public health.

This dissertation aims to contribute to risk-based surveillance of HPAI in poultry in Switzerland by exploring, refining and organizing demographic and topological data and by providing evidence on poultry farms' vulnerability to HPAI (Part 1). It also aims to provide guidance on the issue of integrating a population's contact structures into epidemic models in general, and for the specific case of the poultry farm population in Switzerland (Part 2).

Part 1

Using a mixed methods research design, a countrywide cross-sectional survey was conducted among 3,978 poultry keepers, complemented by interviews with experts from the poultry industry from 2007 to 2009 in Switzerland.

Firstly, insights were gained into poultry farmers' disease awareness and their access to information concerning HPAI. In general, the risks perceived by the poultry keepers well reflected the officially communicated risks of HPAI introduction. Mass media was the main source and, especially at non-commercial farms, often the only source of HPAI-related information accessed by poultry keepers. From a scoring system from 0 to 8 (with 8 as maximum), poultry keepers reached an average knowledge level of 3.1. Having a non-commercial poultry farm was significantly associated with low knowledge scores. Commercial poultry farms gained information mostly from established consultation with companies they were affiliated to. A clear need was identified to enhance information exchange between non-commercial poultry keepers and cantonal and federal authorities.

Secondly, poultry farm topologically and epidemiologically relevant between-farm contacts were investigated and presented in maps. About 97% poultry farms had at least one neighboring poultry farm within one kilometer. Mapping poultry farm densities countrywide revealed areas with up to 8 poultry farms per square kilometer. Person movements and shared resources were identified in 78% of the 1,317 surveyed farms (93% among commercials, 67% among non-commercials). Poultry trading movements over extensive spatial ranges were reported in 65% of farms (79% among commercials, 55% among non-commercials). Movement frequencies depended on farm specialization and were higher for commercial than for non-commercial farms, except for poultry show visits. Estimates for the entire population revealed a 3.5 (CI 95%: 3.1 – 3.9) as high likelihood of reporting a poultry purchase, and a 14.6 (CI 95%: 9.9 – 22.2) as high likelihood of reporting exhibiting birds at poultry shows occurring in a given time by a small (mostly non-commercial) farm than by a larger (commercial) farm. The involvement of both commercial and non-commercial farms with remote between-farm contacts was in contrast to commonly presumed small poultry movement ranges in the non-commercial sector.

Thirdly, the need for a more flexible and consistent database format was identified while conducting the cross-sectional study based on decentralized registered poultry farm data.

Solutions, designed as entity relationship models (ERM), were provided to overcome three major constraints to flexible data storage: firstly, the current 1:1-relationship between poultry keeper and poultry farm; secondly, the impossibility of identifying whether one or more flocks or housing systems exist at one farm site; and thirdly, the lack of interfaces to data from other sources, such as poultry show attendance lists or diagnostic databases. The proposed ERM is suited for accessing person data separate from farm data, to account for poultry keepers having more than one farm site and to retrieve and link data quickly upon multi-criteria queries. A relational database format therefore is the tool of choice to organize demographic data and comply with epidemiological requests.

Part 2

The interplay was explored between a population's contact structure and its implication for epidemic modeling. Computer simulations were performed based on disease parameters from the available literature. The groundwork was established for a countrywide contact network model of the poultry farm population using the field data collected from Part 1.

Firstly, the objective was to provide guidance on when "contact repetition" and "clustering" (relevant social factors influencing the transmission of droplet or contact transmitted diseases), should be included in epidemic models. Results of two types of individual-based models were compared for the total outbreak size. The first model assumed a randomly mixed population without repetition of contacts; the second model assumed total stability of contacts, with and without clustering. Computer simulations under systematic parameter constellations revealed that random-mixing models provided acceptable estimates of the total outbreak size if the number of contacts per day is high or if the per-contact transmission probability is high. The same was true for diseases with very short infectious periods. If the number of daily contacts or the transmission probability is low, particular consideration should be given to the actual structure of potentially contagious contacts when designing the individual-based model.

Secondly, the contact network model of the poultry farm population was approached following evidence collected from the computer simulations and the knowledge that between-farm contacts were infrequent and stable. A step-wise approach of synthesizing census and local contact network data, as well as generating information on non-farm contact partners, was proposed. In the resulting synthetic poultry farm population, contact frequencies and the number of different contact partners per farm were highly skewed, with a majority of farms having no or one partner, and only 4% having 4 or more different contacts. Unexpectedly, only 20% of these highly connected farms were commercial poultry farms. For incoming contacts only 14%, and for outgoing contacts 40% were commercial farms. Further networks indices on the synthetic populations remain to explored. The preliminary findings reveal that show bird farms and mixed commercial farms might be more exposed to pathogen introduction via the considered contacts and that show bird farms and grower farms to have higher potential of enhancing disease transmission because of many outgoing contact partners.

This dissertation explored demographic data and poultry keeper- and farm-related determinants of HPAI risks in view of surveillance and epidemic modeling, with three major conclusions. *Issue of subpopulations*: Non-commercial farms do play an epidemiologically important role, as shown for poultry movements. Thus veterinary authorities must be particular vigilant in reaching non-commercial poultry farms with awareness training and information on epidemics to strengthen passive HPAI surveillance. *HPAI vulnerability*: Risk enhancing factors, such as “having many different contact partners” or “having limited access to information about HPAI”, and risk reducing factors, such as “poultry keepers well aware of HPAI risks” and “having stable and trustworthy trading partners” can occur in many combinations at the farm level. Instead of using single criterion HPAI risk indicators such as farm type or geographical position, surveillance intensity should be based on multiple criteria risk weighting and rating, and always be high in poultry and farm dense areas. *Contact network models*: Models at the between-farm level for HPAI or similarly transmitted poultry epidemics would ideally take the realistic arrangement of contacts into account. A contact network model for the Swiss poultry farm population is feasible although computationally and labor intensive.

Concluding, for epidemic modeling and for implementing surveillance strategies complete poultry registration data in a flexible database format are needed. This time could come up soon: While this dissertation was written the legal basis for a complete horse, poultry, bee and fish husbandry registry on a *federal* level has been created in Switzerland.

RÉSUMÉ

La surveillance et la prévention des épidémies dans les populations humaines et animales sont cruciales à la santé publique. Des pertes économiques causées par l'influenza aviaire hautement pathogène (IAHP) dans la volaille domestique, et l'exposition des humains à l'IAHP en Asie et dans certaines régions d'Europe et d'Afrique ne cessent pas. Cette préoccupation motive aussi les pays actuellement non affectés d'investir dans la planification et dans les activités renforcées de surveillance des épidémies. La Suisse se trouve confronté à deux scénarios de risque généralement admis : premièrement, l'introduction de l'IAHP par le biais des oiseaux sauvages, et deuxièmement, l'introduction et la propagation continue causées par les transports de volaille, par les déplacements des individus et par le partage des établissements par plusieurs fermes avicoles. Ce dernier est largement déterminé par l'attitude des aviculteurs et par les caractéristiques des fermes, et ainsi que les relations géographiques et fonctionnelles entre les fermes, notamment leurs réseaux de contacts.

Les activités de surveillance et la législation doivent suivre des demandes nationales et internationales : elles doivent être basées sur l'information scientifique et des analyses de risque reproductibles. En Suisse, il reste à determiner si tous les aviculteurs sont conscients de l'IAHP et s'ils contribueront d'une façon appropriée à la surveillance passive de l'IAHP en annonçant des cas suspects. L'information, spécifique d'un pays, sur la démographie et sur l'arrangement des contacts dans la population des fermes avicoles est nécessaire. Cette information permet d'anticiper le cours probable d'une épidemie et doit être établie préalablement à la plannification, à la mise en œuvre et à l'évaluation de la réussite des activités de surveillance. De telles données constituent des inputs valables pour les modèles de prévision de dynamique d'une épidémie et de l'impact des interventions. Les modèles mathématiques sont de plus en plus importants dans la santé publiqie pour la prise de décision et la planificaiton épidémiologique.

Cette thèse vise à contribuer à la surveillance de l'IAHP basée sur le risque en dépistant, amplifiant et organisant des donnés démographiques et topologiques et en évaluant la vulnérabilité des fermes avicoles face à l'IAHP (1ère partie). Le but est aussi de creuser dans la question de l'intégration des arrangements de contacts dans des modèles épidémiologiques en général, et au cas particulier de la population des fermes avicoles en Suisse (2ème partie).

1ère partie

Un plan de recherché mixte a été suivi, composé d'une enquête nationale transversale auprès de 3.978 aviculteurs, complétée par des interviews d'experts de l'industrie avicole en Suisse durant la période de 2007 à 2009.

Premièrement, de la connaissance a été gagnée sur la perception des risques par les aviculteurs et leur accès aux informations au sujet de l'IAHP. En général, les risques perçus par les aviculteurs reflétaient bien les risques d'introduction de l'IAHP officiellement communiqués. Les médias de masse repréntaient la première source, et surtout pour les détenteurs non commerciaux, souvent la seule source accédée. Sur une échelle de 0 à 8 (le maximum étant 8), les détenteurs de volaille atteignaient un moyen niveau de connaissance d'IAHP de 3,1. Le fait de posséder une ferme avicole non commerciale était associé de manière significative à des bas niveaux sur l'échelle de connaissance d'IAHP. Les fermes avicoles commerciales obtenaient des informations surtout par consultation des organisations de commercialisation auxquelles elles étaient affiliées. Le besoin de renforcer l'échange d'informations entre aviculteurs non commerciaux et les autorités cantonales et fédérales a été identifié.

Deuxièmement, les contacts entre fermes d'importance topologique et épidémiologique ont été repertoriés et présentés sur des cartes. Dans 97% des cas, moins d'un kilomètre séparait une ferme avicole de la suivante. En dressant des cartes de densité, des régions contenant jusqu'à 8 fermes avicoles sur un kilomètre carré ont été révélées. Des déplacements de personnes ont été identifiés chez 78% des 1.317 fermes participantes (93% chez des fermes commerciales, 67% chez des fermes non commerciales). Des mouvements de volaille à longue distance étaient rapportés par 65% de fermes (79% chez des fermes commerciales, 55% chez des fermes non commerciales). Les fréquences des mouvements dépendaient de la spécialisation des fermes, les fermes commerciales montrant des fréquences plus élevées que les fermes non commerciales avec l'exception des visites des expositions de volaille. Des projections sur la population entière révélait une chance 3,5 fois plus élevée (IC 95%: 3,1 – 3,9) qu'un achat de volaille soit reporté, et une chance 14,6 fois plus élevée (IC 95%: 9,9 – 22,2) qu'une exposition de volaille ait lieu dans une période de temps donnée due à une ferme petite (surtout non commerciale) que due à une grande exploitation de volaille (commerciale).

Les fermes avicoles commerciales et non-commerciales créaient des contacts à longue distance, contrairement à la supposition que les fermes avicoles non-commerciales n'étaient impliquées que dans des déplacements à courte distance.

Troisièmement, le besoin d'une base de données dans un format plus flexible et consistent a été identifié en conduisant l'étude transversale basée sur les registres des fermes avicoles décentralisées. Sous forme d'un modèle entité-association (ERM), des solutions pour surmonter les contraintes suivantes au niveau d'un enregistrement flexible ont été proposées : premièrement, l'actuel rapport 1:1 entre aviculteur et ferme avicole ; deuxièmement, l'impossibilité d'identifier si un ou plusieurs unités d'élevage ou poulaillers coexistent sur une site; et troisièmement l'absence d'interfaces avec des données d'une autre origine, par exemple des listes de participants aux expositions de volaille ou des bases des données diagnostiques. L'ERM proposé est adéquate pour l'accéssion aux données sur les personnes indépendamment des données sur les fermes, pour prenant en compte les aviculteurs travaillant sur plus d'un site d'exploitation, et d'affichant et liant les données sans délai suite à des recherches complexes. Une base de donnée relationnelle est ainsi idéale pour organiser les données démographiques conformément aux demandes épidémiologiques.

2ème partie

La relation entre les réseaux de contacts d'une population et son impact dans la modélisation des épidémies a été exploré. Des simulations sur ordinateurs ont été exécutées en se basant sur des paramètres des transmissions provenant de la littérature. La base d'un modèle de réseau de contact entre l'ensemble des fermes avicoles du pays a été établi en utilisant des donnés recensées dans la 1ère partie de l'étude.

Premièrement, l'objective était de déterminer quand est-ce qu'il fallait inclure la « répétition de contacts » et le « clustering » (deux facteurs sociaux agissant sur la transmission des maladies par des goutelettes ou par contact direct) dans les modèles d'épidémies. Les résultats de deux types de modèles basés sur les individus ont été comparés par rapport à la dimension totale de l'épidémie; le premier modèle supposant une population mixte aléatoire, le deuxième modèle soumis à l'hypothèse des contacts stables, avec ou sans clustering. Les simulations sur ordinateur définés par des paramètres systématiquement variées, ont révélé ceci : Des modèles supposant une population mixte aléatoire donnent des estimations acceptables pour la dimension totale de l'épidémie à condition d'un taux élevé de contacts quotidiens, ou une probabilité de transmission par contacte élevée. Ceci s'applique aux maladies de courte période infectieuse. Par contre, si le taux quotidien de contacts ou la probabilité de transmission sont bas, il est plus approprié de considérer l'arrangement actuel de contacts potentiellement contagieux dans la modélisation.

Deuxièmement, le modèle des réseaux de contacts de la population des fermes avicoles était envisagé, suite à l'évidence des simulations sur ordinateur et sachant que les contacts entre les fermes étaient plutôt peu fréquents et stables. Utilisant une approche par étapes, les données de recensement, des données locales sur les réseaux de contact, et l'information sur les acteurs en contact autres que des fermes avicoles ont été synthétisées. Dans la population synthétique des fermes avicoles, les fréquences des contacts et les nombres de différent partenaires de contact étaient fortement penchés à droite, la majorité des fermes n'ayant aucun ou qu'un partenaire de contact, et seulement 4% des fermes avaient 4 ontacts différents, ou plus. Inopinément, seulement 20% de fermes ayant beaucoup de contacts étaient des fermes avicoles commerciales. Considérant seulement les contacts entrants (achats) ou uniquement les contacts sortants (ventes), les fermes commerciales participaient à 14% et 40% des contacts, respectivement. D'autres indices restent à être déterminés. Les résultats intérmédiaires révèlent que les élevages de volaille de race et les exploitations commerciales mixtes sont plus exposés aux contacts examinés, et les élevages de volaille de race et élevages des produits finis ont plus de potentiel d'augmentaion de la diffusion de la transmission de maladies à cause des nombreux partenaires de contacts sortants.

En vue de surveillance et de modélisation des épidémies, ce travail a exploré des données démographiques et de déterminants de risque de l'IAHP liés aux aviculteurs et fermes avicoles. Trois aspects principaux ont été ceci. *L'aspect des sous populations* : Les fermes avicoles non commerciales jouent un rôle épidémiologique important, comme cela a été était montré pour les déplacements de volaille. Ainsi, les autorités vétérinaires sont invitées à être particulièrement vigilantes en transmettant les informations épidémiologiques et atteignant les fermes avicoles non commerciales afin de consolider la surveillance passive de l'IAHP. *La vulnérabilité face à l'IAHP*: Des facteurs accentuant le risque, comme « le maintien des contacts avec de multiples partenaires » ou « accès insuffisant aux informations sur l'IAHP », et des facteurs allégeant les risques, comme « la conscience du risque de l'IAHP de l'aviculteur » et « ayant stable et fiables

partenaires commerciaux » peuvent coexister au niveau des fermes en différentes combinaisons. Au lieu des indicateurs de risque de l'IAHP basé sur un seul critère de risque comme le type d'exploitation, ou le site géographique, l'intensité de surveillance serait dans l'idéal déterminée sur la base d'une évaluation et d'un classement de risque multicritère et toujours intense dans les régions de haute densité de fermes et de la volaille. *Les modèles de réseaux de contacts* : Au niveau des modèles (inter-ferme) pour l'IAHP et épidémies de volaille transmises de façon similaire, dans l'idéal les réseaux de contacts seraient pris en compte de manière réaliste. Un modèle de contact pour la population des fermes avicoles en Suisse n'est réalisable qu'avec l'aide de l'informatique et beaucoup de main d'œuvre.

En conclusion, la modélisation des épidémies, et la mise en place des stratégies de surveillance, nécessitent un registre des fermes avicoles dans un format flexible. Cela pourrait être bientôt réalisé : Pendant l'écriture de cette thèse, la base légale d'un enregistrement complet de l'entretien de chevaux, de la volaille, des abeilles et des poissons, sur un plan *fédéral*, a été crée en Suisse.

RIASSUNTO

La sorveglianza e la prevenzione epidemica nelle popolazioni umane e animali sono le fondamenta della salute pubblica. In questo periodo in Asia ed in alcune parti d'Africa ed Europa le popolazioni umane sono esposte al virus dell'influenza aviaria altamente patogena (IAAP) e le perdite economiche dovute a questo virus sono ingenti. Questa situazione motiva i Paesi quali la Svizzera, ancora non toccati dall'insorgere della malattia, ad investire nella pianificazione epidemica preventiva e a rafforzare le attività di sorveglianza. La Svizzera deve affrontare due scenari frequentemente incontrati in altri Paesi: primo, l'arrivo dell'IAAP negli allevamenti di pollame tramite gli uccelli selvatici e, secondo, l'introduzione e la successiva disseminazione del virus tramite il pollame infetto ed i movimenti di persone infette così come tramite i mezzi condivisi dai vari allevamenti di pollame. Questo ultimo punto é largamente influenzato dall'attitudine degli allevatori di pollame e dalle caratteristiche degli allevamenti, così come dai legami geografici e funzionali tra i vari allevamenti, ossia le loro reti di contatto.

Per conformarsi alle richieste nazionali e internazionali, le attività di sorveglianza epidemica ed i regolamenti devono basarsi su informazioni scientifiche ed analisi del rischio riproducibili. In Svizzera non è dato a sapere se tutti gli allevatori di pollame sono coscienti del rischio di IAAP e se ci sia, da parte loro, la disponibilità a contribuire in modo appropriato alla sorveglianza passiva del virus tramite la notifica di casi sospetti di malattia. Nel nostro Paese necessitiamo di un'informazione demografica dei vari allevamenti di pollame e delle strutture di contatto esistenti tra di essi, in modo da poter prevedere la diffusione spaziale e temporale del virus. Questa informazione è necessaria sia per una buona pianificazione sia per la valutazione e il miglioramento delle attività di sorveglianza. Questi dati inoltre contribuiscono alla creazione di modelli epidemici volti a predire le dinamiche epidemiche e a valutare l'efficacia degli interventi. I modelli matematici rivestono, infatti, un ruolo sempre più importante nella presa di decisioni e nella preparazione di piani d'intervento riguardanti la salute pubblica.

Questa dissertazione é volta a contribuire ad una sorveglianza basata sui fattori di rischio dell'IAAP nel pollame in Svizzera tramite l'esplorazione, la messa a punto e l'organizzazione dei dati demografici e topologici e la messa in evidenza della vulnerabilità degli allevamenti di pollame nei confronti dell'IAAP (Parte 1). Lo scopo di questo lavoro risiede anche nel fornire

delle linee guida per l'integrazione di strutture di contatto della popolazione in modelli epidemici in generale, e nel caso specifico negli allevamenti di pollame in Svizzera (Parte 2).

Parte 1

Tra il 2007 e il 2009, con l'ausilio di un disegno di studio basato su metodi misti, é stata svolta in Svizzera un'inchiesta trasversale a livello nazionale tra gli 3.978 allevatori di pollame, completata da interviste con esperti dell'industria del pollame.

In primo luogo si sono ottenute indicazioni riguardo alla consapevolezza degli allevatori di pollame nei confronti dell'IAAP e al loro accesso alle informazioni riguardanti questa malattia. In maniera generale, il rischio percepito dagli allevatori di pollame rifletteva quanto ufficialmente comunicato riguardante i rischi d'introduzione dell'IAAP nel nostro Paese. I mass media si sono rivelati essere le fonti principali d'informazione, ed in particolare per gli allevamenti non commerciali spesso questa fonte d'informazione era l'unica, relativa all'IAAP, alla quale gli allevatori di pollame facevano capo. In una classifica a punti, riguardante le conoscenze sull'IAAP, tra lo 0 e l'8 (con 8 quale punteggio massimo), gli allevatori di pollame raggiungevano il punteggio di 3,1. Il fatto di possedere un allevamento non commerciale era inoltre significativamente associato ad un minor punteggio nella classifica delle conoscenze. Gli allevamenti commerciali invece ricevevano le informazioni tramite le riunioni istituite dalle compagnie alle quali erano affiliati. Si è riscontrato un'evidente necessità di aumentare lo scambio d'informazioni tra gli allevatori non commerciali e le autorità cantonali e federali.

In secondo luogo, si sono indagati i contatti significativi a livello topologico ed epidemiologico tra gli allevamenti, e questi sono stati riportati su delle mappe. Circa il 97% degli allevamenti di pollame recensiti erano situati nel perimetro di 1km da un altro allevamento di pollame. La cartografia della densità degli allevamenti a livello nazionale ha rilevato delle aree nelle quali sono situati più di 8 allevamenti di pollame per chilometro quadrato. Inoltre nel 78% dei 1.317 allevamenti esaminati (93% commerciali, 67% non commerciali), è stato possibile raccogliere informazioni sui movimenti delle persone e delle risorse condivise tra i vari allevamenti. I movimenti commerciali di pollame su lunghe distanze sono stati documentati nel 65% degli allevamenti (79% commerciali, 55% non commerciali). Le frequenze degli scambi dipendevano dalla specializzazione dei vari allevamenti ed erano più alte per quelli commerciali che per quelli non commerciali, ad eccezione delle esposizioni di pollame. Stime sull'intera popolazione hanno rivelato che da parte dei piccoli allevamenti (spesso non commerciali) rispetto ai grandi allevamenti (commerciali) c'è una probabilità di 3,5 (CI 95%: 3,1 – 3,9) più alta di notificare una compera e di 14,6 (CI 95%: 9,9 – 22,2) più alta di segnalare una presenza ad una data esposizione di pollame. Contrariamente a quanto comunemente ritenuto riguardo agli spostamenti su brevi distanze del pollame nel settore non commerciale, dallo studio è risultato un coinvolgimento d'entrambi i tipi di allevamento, commerciale e non commerciale, nei contatti tra allevamenti geograficamente distanti.

Quale terzo punto, durante lo svolgimento dello studio trasversale basato sui dati registrati in modo decentralizzato riguardanti gli allevamenti di pollame è stata identificata la necessità di una creazione di una banca dati affidabile e flessibile. Le soluzioni, definite quali modelli a relazioni-identità (MRI), sono state suggerite per superare le 3 limitazioni principali dell'archiviazione di dati suscettibili di modifiche: primo, la relazione 1:1 tra gli allevatori di pollame e gli allevamenti; secondo, l'impossibilità di identificare se uno o più stormi di polli oppure diverse tipologie di allevamento erano presenti nello stesso stabilimento; e terzo, la mancanza di una connessione con i dati provenienti da altre fonti, come ad esempio la lista delle presenze alle esposizioni di pollame o banche dati sui risultati diagnostici. Quanto suggerito con l'MRI permette di accedere ai dati delle persone in modo indipendente dai dati sugli allevamenti, di considerare gli allevatori di pollame che gestiscono più allevamenti e di reperire e relazionare in modo rapido dati basati su delle richieste comprendenti diversi criteri. Una banca dati relazionale è quindi lo strumento ideale per organizzare i dati demografici e si conforma inoltre anche alle necessità epidemiologiche.

Parte 2

È stata studiata l'azione reciproca tra la struttura di contatto della popolazione investigata e la sua connessione con la modellizzazione epidemiologica. Sono state eseguite delle simulazioni al computer basate sui parametri ritrovati nella letteratura. La base per un modello di rete di contatto tra allevamenti di pollame è stata creata usando i dati raccolti sul terreno nella Parte 1.

In primo luogo, l'obiettivo era di fornire delle indicazioni sul quando il "raggruppamento" e la "ripetizione dei contatti" (fattori sociali importanti che influenzano la trasmissione di malattie via contatto o aerosol) dovevano essere inclusi nei modelli epidemiologici. Sono stati paragonati i risultati di due tipi di modelli basati sugli individui per investigare la taglia di popolazione necessaria all'insorgere dell'epidemia. Il primo modello assumeva una popolazione aleatoriamente mista senza ripetizione di contatti, il secondo modello assumeva una totale stabilità dei contatti, con e senza raggruppamenti. Le simulazioni al computer con una serie di parametri sistematici hanno rivelato che i modelli misti aleatori fornivano una stima accettabile della dimensione di popolazione necessaria per l'insorgere dell'epidemia nel caso in cui il numero di contatti giornalieri è alto oppure se la probabilità di trasmissione tramite contatto è alta. Lo stesso poteva essere applicato per le malattie con dei periodi di infezione molto bassi. Se il numero di contatti giornalieri o la probabilità di trasmissione dovessero essere bassi, quando si pianifica il modello basato sull'individuo bisognerebbe prestare particolare attenzione all'attuale struttura di contatti potenzialmente contagiosi.

In secondo luogo, il modello della rete di contatti degli allevamenti di pollame è stato affrontato basandosi sull'evidenza raccolta con le simulazioni al computer e la conoscenza che i contatti tra allevamenti erano poco frequenti e stabili. È stato suggerito un approccio graduale e progressivo nel sintetizzare i dati del censimento e della rete di contatti locali, così come nella creazione di informazioni sui contatti con soci non legati direttamente a degli allevamenti. Nella popolazione ideale di allevamenti di pollame investigata risultava che la frequenza dei contatti e il numero di soci con i quali questi entravano in contatto erano distribuiti asimmetricamente, con una maggioranza di allevamenti che avevano uno o nessun socio, e solo il 4% che aveva 4 o più diversi contatti. Inaspettatamente, solo il 20% degli allevamenti con molto connessioni nella rete di contatti, erano allevamenti commerciali. Per i contatti verso l'allevamento solo 14% e per i contatti dall'allevamento verso l'esterno 40%. Restano ancora da esplorare altri indici per la rete di contatti su popolazioni ideali. I risultati preliminari mostrano che allevamenti di razza e aziendi commerciale misto sono più esposti all'introduzione dell'agente patogeno tramite i contatti considerati nello studio e che allevamenti di razza e aziendi di allevemento hanno un più alto potenziale per contribuire alla trasmissione della malattia dovuto ai numerosi contatti verso soci esterni all'allevamento.

Questa dissertazione ha esplorato i dati demografici e i fattori determinanti per i rischi legati all'IAAP negli allevatori e negli allevamenti di pollame nell'ottica di una sorveglianza e di una modellizzazione epidemica, portando a tre conclusioni principali. *Esito nelle sotto-popolazioni*: Gli allevamenti non commerciali svolgono un ruolo epidemiologico importante, come mostrato dagli spostamenti di pollame. Le autorità federali devono quindi prestare particolare attenzione nel raggiungere gli allevamenti di pollame non commerciali in modo da fornire un'istruzione adeguata e delle informazioni sull'epidemia così da rafforzare la sorveglianza passiva dell'IAAP. *Vulnerabilità all'IAAP*: Fattori che accrescono il rischio, quali "avere diversi soci con i quali si sono istaurati dei contatti" oppure "avere un accesso limitato alle informazioni riguardanti l'IAAP", e fattori che riducono il rischio, quali "allevatori ben coscienti dei rischi legati all'IAAP" e "avere degli scambi commerciali con dei soci stabili e affidabili" possono presentarsi in varie combinazioni a livello degli allevamenti. Invece di utilizzare dei criteri singoli come indicatori del rischio da IAAP quali tipo di allevamento o posizione geografica, gli sforzi di sorveglianza dovrebbero basarsi su pesi e valutazioni multipli dei criteri di rischio ed essere sempre elevati nelle aree di alta densità di allevamenti di pollame. *Modelli della rete di contatti:* Nella creazione di modelli (al livello di relazioni tra allevamenti) sull'IAAP o altre malattie epidemiche del pollame trasmesse in modo simile è necessario tenere in considerazione la reale distribuzione dei contatti. Un modello per la rete di contatti degli allevamenti di pollame in Svizzera si è avverato fattibile anche se laborioso a livello di calcolo e di mole di lavoro.

In conclusione, è necessaria una registrazione completa dei dati relativi al pollame in una banca dati flessibile in modo da poter effettuare dei modelli epidemici ed implementare le strategie di sorveglianza. Questo potrebbe essere disponibile già nel prossimo futuro. Durante la redazione di questa dissertazione in Svizzera si sono create le basi legali per un registro completo a livello *federale* degli allevamenti di cavalli, polli, api e pesci.

ZUSAMMENFASSUNG

Die Überwachung und Vorbeugung von Epidemien in der Bevölkerung und in Tierpopulationen ist entscheidend für die öffentliche Gesundheit. Ausbrüche hochpathogener aviärer Influenza (HPAI, auch klassische Geflügelpest) in Geflügelhaltungen Asiens, Teilen Afrikas und Europas verursachen wirtschaftliche Schäden und gefährden Menschen. Auch in Ländern ohne aktuelle Ausbrüche, wie der Schweiz, ist es wichtig, in Bereitschaftsplanung und verbesserte Überwachungssysteme zu investieren. Für die Schweiz besteht die Gefahr eines HPAI-Eintrags in Geflügelbestände im Wesentlichen auf zwei Wegen: Einerseits eine Einschleppung über Wildvögel, und andererseits eine Einschleppung und Verbreitung durch Geflügelhandel, Personenverkehr und durch von mehreren Geflügelhaltungen genutzte Einrichtungen. Die Gefahr auf letzterem Wege wird durch das Verhalten der Geflügelhalter und durch Eigenschaften der Geflügelhaltungen bestimmt, sowie durch räumliche und operative Beziehungen, in denen Geflügelhaltungen zueinander stehen, nämlich ihre Kontaktnetzwerke.

Überwachungsaktivitäten und Rechtsvorschriften bedürfen einer wissenschaftlichen, auf wiederholbare Analysen gestützten Grundlage, um nationalen und internationalen Anforderungen gerecht zu werden. In der Schweiz gilt es herauszufinden, ob sich alle Geflügelhalter der Gefahr durch HPAI bewusst sind, ob sie Fälle klinisch erkennen würden und durch eine Verdachtsmeldung zur passiven HPAI-Überwachung beitrügen. Zur gezielten Planung, Durchführung und Evaluierung von Überwachungsaktivitäten in der Schweiz werden ausserdem demographische Information und Daten zu Kontakten zwischen Geflügelhaltungen benötigt. Diese sind zugleich wichtige Eingangsparameter für Epidemiemodelle zur Abschätzung der Ausbruchsdynamik und des Einflusses verschiedener Massnahmen. Solche mathematischen Modelle werden zunehmend herangezogen, um Entscheidungen zu stützen und vorbeugende Massnahmen im Gesundheitswesen zu gestalten.

Mit dieser Dissertation soll ein Beitrag zu einer risikobasierten HPAI-Überwachung Schweizerischer Geflügelbestände geleistet werden mittels einer Zusammenstellung und Ergänzung demographischer und räumlicher Daten, sowie der Erhebung neuer Daten, die Aussagen über die Gefährdung der Geflügelhaltungen durch HPAI erlauben (Teil 1). Ziel ist es ausserdem, eine Entscheidungsgrundlage dafür zu bieten, wann tatsächliche Kontaktstrukturen

einer Population im Allgemeinen und im besonderen Fall der Geflügelhaltungen in der Schweiz in Epidemiemodellen berücksichtigt werden sollten (Teil 2).

Teil 1

Im Zeitraum von 2007 bis 2009 wurden nach einem Mixed-Method-Studiendesign eine fragebogengestützte Querschnittstudie unter 3.978 Geflügelhaltern und Interviews mit Experten aus der Geflügelindustrie in der Schweiz durchgeführt.

Zuerst wurde untersucht, wie Geflügelhalter die Gefahr durch HPAI wahrnehmen und welchen Zugang sie zu entsprechenden Informationen haben. Die Einstufung verschiedener Gefahren durch die Geflügelhalter spiegelte insgesamt die offiziell kommunizierten Risiken einer HPAI-Einschleppung gut wider. Über HPAI informierten sich Geflügelhalter am häufigsten durch Massenmedien. Auf einer Skala von 0 bis 8 (Höchstpunktzahl) zur Beurteilung des Kenntnisstands erreichten sie durchschnittlich 3,1 Wissenspunkte. Befragte mit nichtgewerblichen Geflügelhaltungen hatten signifikant niedrigere Wissenspunktzahlen. Auf gewerblichen Geflügelhaltungen trug die Beratungstätigkeit von Vermarktungsorganisationen entscheidend zum Kenntnisstand bei. Der Bedarf eines intensiveren Austausches an Informationen zwischen nichtgewerblichen Geflügelhaltern und Behörden auf kantonaler und Bundesebene wurde festgestellt.

Desweiteren wurden die Verteilung von Betriebsstandorten und epidemiologisch bedeutsamen Kontakten unter Geflügelhaltungen untersucht und auf Karten dargestellt. Etwa 97% der Geflügelhaltungen hatten mindestens eine benachbarte andere Geflügelhaltung in einem Umkreis von 1km. Dichtekarten brachten Gegenden mit bis zu 8 Geflügelhaltungen pro Quadratkilometer zum Vorschein. Personenbewegungen und gemeinsam genutzte Einrichtungen kamen bei 78% der 1.317 Befragten, die hierzu Angaben machten, vor (93% bei gewerblichen, 67% bei nichtgewerblichen). Geflügelbewegungen über weite Entfernungen wurden von 65% Geflügelhaltern angegeben (79% bei gewerblichen, 55% bei nichtgewerblichen). Die Häufigkeit hing von der Nutzungsrichtung der Geflügelhaltung ab. Gewerbliche Geflügelhaltungen hatten im allgemeinen häufigere Tierbewegungen, ausser zu Ausstellungen. Hochrechnungen auf die Gesamtpopulation ergaben, dass in der Schweiz pro Zeiteinheit 3,5-mal (CI 95%: 3,1 – 3,9) so viele Geflügelzukäufe durch kleine (meist nichtgewerbliche) Haltungen wie durch (gewerbliche) Grossbetriebe anzunehmen sind. Für die Ausstellung von Geflügel war die

Wahrscheinlichkeit für kleine Haltungen 14,6-mal (CI 95%: 9,9 – 22,2) so hoch wie für Grossbetriebe. Eine solche Beteiligung nichtgewerblicher Geflügelhaltungen am Tierverkehr über weite Entfernungen steht im Gegensatz zur bisherigen Annahme, dass diese kleine Aktionsradien hätten.

Bei der Durchführung der Querschnittstudie, die auf dezentral erhobene Daten registrierter Geflügelhaltungen gestützt war, wurde ein Bedarf an einer flexiblen und einheitlichen Datenbank festgestellt. Anhand eines Entity-Relationship-Modells (ERM) wurde gezeigt, wie drei bestehende Einschränkungen der Datenspeicherung überwunden werden können: erstens, die momentane 1:1-Beziehung zwischen Personen- und Betriebsdaten, zweitens die bislang nicht mögliche Erfassung von mehr als einer Geflügelherde oder eines Haltungssystems an einem Betriebstandort, und drittens noch nicht vorhandene Schnittstellen zu Daten anderer Quellen, zum Beispiel Teilnehmerlisten von Geflügelausstellungen oder Diagnostikdatenbanken. Das vorgeschlagene ERM erlaubt einen separaten Zugriff auf Personen- und Betriebsdaten, die Zuordnung von Geflügelhaltenden zu mehren Betriebsstandorten, sowie multikriterielle Abfragen, bei denen Daten schnell aufgerufen und verknüpft werden können. Eine derartig gestaltete relationale Datenbank wäre geeignet, demographische Daten epidmiologischen Bedürfnissen entsprechend zu organisieren.

Teil 2

Zur Untersuchung, wie Kontaktstrukturen einer Population mit Epidemiemodellen in Beziehung stehen, wurden Computersimulationen mit Transmissionsparametern aus der Literatur durchgeführt. Unter Einbeziehung von in Teil 1 erhobenen Daten wurde zudem eine Grundlage für die Abbildung aller Geflügelhaltungen in einem Kontaktnetzwerkmodell geschaffen.

Zuerst sollte gezeigt werden, unter welchen Umständen es sinnvoll ist, „Kontaktwiederholung“ und „Clustering“ (soziale Faktoren, welche die Krankheitsübertragung per Tröpfcheninfektion und direkten Kontakt beeinflussen) in Epidemiemodellen zu berücksichtigen. Hierzu wurden zwei individuenbasierte Populationsmodelle, eines unter der Annahme einer Population mit zufällig verteilten Kontakten, das andere unter der Annahme stabiler Kontakte mit oder ohne Clustering, hinsichtlich des Endausmasses der Epidemie verglichen. Computersimulationen unter systematisch veränderten Parameterkonstellationen zeigten, dass mit dem Modell mit zufällig verteilten Kontakten annehmbare Schätzwerte für das Endausmass der Epidemie erreicht werden, wenn die Anzahl täglicher Kontakte oder die Ansteckungswahrscheinlichkeit pro Kontakt hoch ist. Dies gilt auch für Krankheiten mit einer sehr kurzen Ansteckungsdauer. Dagegen ist es bei einer geringen Anzahl täglicher Kontakte oder einer geringen Ansteckungswahrscheinlichkeit pro Kontakt angebracht, die tatsächliche Anordnung möglicherweise infektiöser Kontakte in ein individuenbasiertes Modell einzubeziehen.

Angesichts der Erkenntnisse aus den Computersimulationen und der Festellung, dass Kontakte zwischen Geflügelbetrieben meistens stabil und nicht häufig sind, wurde damit begonnen, ein Kontaktnetzwerkmodell für die Population der Geflügelhaltungen zu erstellen. Aus Zensusdaten, lokalen Kontaktdaten zu Geflügelhaltungen und Informationen über andere Kontaktpartner wurde schrittweise eine synthetische Population an Gelügelhaltungen aufgebaut. In dieser synthetischen Population waren die Kontakthäufigkeiten und die Anzahl verschiedener Kontaktpartner stark rechtsschief verteilt: die Mehrzahl der Geflügelhaltungen hatte keinen oder nur einen Kontaktpartner, und nur 4% der Geflügelhaltungen hatten vier oder mehr verschiedene Kontaktpartner. Nur 20% dieser kontaktreichen Haltungen waren gewerbliche Geflügelbetriebe. Wurden nur eingehende Kontakte (Zukäufe) betrachtet, waren 14% gewerbliche Geflügelhaltungen unter den kontaktreichen Geflügelhaltungen, und bei wegführenden Kontakten (Abgaben) alleine war ihr Anteil 40%. Die Untersuchung weiterer Kontakteigenschaften ist geplant. Die bisherigen Ergebnisse zeigen, dass Rassegeflügelhaltungen und gewerbliche Mehrzweckgeflügelbetriebe einem vergleichsweise grossen Risiko der Erregereinschleppung entlang der berücksichtigten Kontakte ausgesetzt sein dürften, und dass Rassegeflügelhaltungen und Aufzuchtbetriebe aufgrund zahlreicher Abnehmer ein grösseres Potenzial haben, zur Krankheitsausbreitung beizutragen.

In dieser Dissertation wurden demographische Daten und halter- und betriebsabhängige Einflussfaktoren auf das Risiko einer HPAI-Einschleppung und -Verbreitung untersucht. Im Hinblick auf Überwachungstätigkeiten und auf Epidemiemodelle wurden drei Schlussfolgerungen gezogen. *Besondere Populationsgruppen*: Auch nichtgewerbliche Geflügelhaltungen können eine wichtige epdiemiologische Rolle spielen, wie es anhand der Geflügelbewegungen gezeigt wurde. Seitens der Veterinärbehörden bedarf es daher einer besonderen Aufmerksamkeit und Anstrengung, nichtgewerbliche Geflügelhalter mit Aufklärungsarbeit und Informationen zu Seuchengefahren zu erreichen, und somit die passive HPAI-Überwachung zu stärken. *HPAI-Gefährdung*: Risikoverstärkende Faktoren, wie

„Kontakte zu vielen verschiedenen Partnern“ oder „schlechter Zugang zu Informationen über HPAI“, und risikomindernde Faktoren, wie „gute Kenntnisse Geflügelhaltender über HPAI“ und „vertrauenswürdige und stabile Handelspartner“, können in vielfältiger Weise auf der Ebene einer Geflügelhaltung zusammenkommen. Daher sollte die Überwachungsintensität nicht anhand eines einzelnen Merkmals wie der Art der Geflügelhaltung oder des geographischen Standorts festgelegt werden, sondern auf einer multikriteriellen Einstufung und Bewertung beruhen, sowie in Gebieten mit hoher Geflügelhaltungsdichte und Geflügeldichte hoch sein. *Kontaktnetzwerkmodelle*: Modelle zur Ausbreitung von HPAI (oder auf vergleichbarem Wege übertragbaren Geflügelkrankheiten) unter Geflügelhaltungen sollten tatsächliche Kontaktstrukturen in der Population berücksichtigen. Ein Kontaktmodell für die Population der Geflügelhaltungen in der Schweiz ist machbar, jedoch rechen- und arbeitsintensiv.

Für Epidemiemodelle, wie auch für die praktische Umsetzung der Überwachung von Epidemien, wird eine vollständige Registrierung von Geflügelhaltungen in einem flexiblen Datenbankformat benötigt. Diese könnte bald realisiert sein: Zeitgleich mit dieser Dissertation wurde in der Schweiz die Rechtsgrundlage für eine obligatorische Registrierung aller Pferde-, Fisch-, Bienen- und Geflügelhaltungen *auf Bundesebene* geschaffen.

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1 INTRODUCTION

This dissertation explores new potentials for a risk-based surveillance of highly pathogenic avian influenza (HPAI) in domestic poultry in an outbreak-free situation. The focus is on host population related risk factors and determinants of surveillance performance; namely poultry keepers' disease awareness, potential contagious contacts amongst poultry farms, and the issue of basic demographic data. Emphasis is placed on the interplay between population data, namely contact structures, and mathematical models of epidemics, in general, and on the specific case of the Swiss poultry population in particular.

Background is provided on the etiology and epidemiology of HPAI, on key features of HPAI surveillance, and on the poultry farm population as the concerned host population. Mathematical models and their use in infectious disease epidemiology are introduced, as well as network analysis, being a key method applied in this dissertation.

1.1 Avian influenza surveillance and poultry production

1.1.1 Avian influenza etiology and epidemiology

Highly pathogenic avian influenza (HPAI), also known as “bird flu” or “fowl plague”, has been noted for decades as an animal disease with a high economic impact. The term fowl plague was first used in Italy in 1878 (Perroncito, 1878). The viral etiology of influenza was discovered in 1930 in swine (Shope, 1931; Alexander, 2006). Although well documented and reported, HPAI received little public attention until 1997 when, human infections due to the H5N1 HPAI virus strain were confirmed for the first time (De Jong *et al.*, 1997; Abdel-Ghafar *et al.*, 2008). Beyond this zoonotic characteristic, the high degree of global public fear reflects the unpredictable pandemic potential of HPAI viruses (Horimoto and Kawaoka, 2001). Influenza pandemics (global outbreaks) were recorded in western history since the 17th century (Potter, 2001). During the 20th century three influenza pandemics occurred: an influenza A subtype H1N1 pandemic in 1918, a subtype H2N2 pandemic in 1957, and a subtype H3N2 pandemic in 1968 (Potter, 1998). The 1918 pandemic is estimated to have killed up to 50 million people worldwide and was one of the most fatal outbreaks of infectious disease in human history (Johnson and Mueller, 2002).

Since December 2003 HPAI H5N1 viruses have reached poultry populations across Asia and in parts of Africa and Europe. Significant outbreaks have occurred globally in domestic and wild birds (Alexander, 2007). A total of 440 human infections have been reported to date, of which 262 were fatal (WHO, 2009). Although the H5N1 virus fails so far to spread efficiently from human to human – and even though the 2009 influenza pandemic is caused by the H1N1 influenza A strain – H5N1 has high mortality in humans. Prevention, surveillance and control of the H5N1 strain in wild birds and domestic poultry remains essential for both animal and human health.

Avian influenza virus

Influenza viruses are single-stranded segmented RNA viruses of the family *Orthomyxoviridae.* They are classified according to major antigens as *Influenzavirus A, B,* or *C* (Webster *et al.*, 1992). The causative agents of avian influenza are genus A influenza virus strains, which are also responsible for pandemics. Most of the possible combinations of influenza A subtypes containing one haemagglutinin (H1–H16) and one neuraminidase (N1–N9) surface glycoprotein have been isolated from avian species (Cox and Subbarao, 1999; Fouchier *et al.,* 2005). Haemagglutin (H) allows for the virus attachment to the host cell by binding its sialic acid of glycoprotein surface receptors. Avian erythrocytes can be bound by the same mechanism, which is the basis for hemagglutination test diagnostics. Neuraminidase (N) is responsible for penetration of the host cell and the release of virus replicates by hydrolyzing the sialic acid receptor (Kayser *et al.*, 2005). Clinical observations in poultry, where only HPAI (always due to H5 or H7 strains) is characterized by sudden death or severe systemic syndromes, has lead to the differentiation of a low pathogenic (LPAI) and a highly pathogenic (HPAI) form of avian influenza (Alexander, 2006). Pathogenicity is related to tissue tropism and reflects diversity in the proteolytic cleavage site of heamagglutin; wheras LPAI viruses require specific proteases, for HPAI viruses unspecific proteases suffice (Kawaoka and Webster, 1988). Low pathogenic H5 and H7 viruses are also considered notifiable by the World Organization for Animal Health (OIE) as they have the potential for transformation into HPAI viruses (Capua and Alexander, 2006). The virus can also change gradually in nature of H or N expression due to mutation and selective pressure known as antigenic drift. Another process, known as antigenic shift, refers to a switch in H or N subtypes or both. This happens when a single cell is simultaneously infected with two or more influenza subtypes and gene segments exchange during one replication cycle, undergoing reassortment (Webster *et al.,* 1992).

Host species and clinical signs

Potential host species of H5N1, currently one of the most important avian influenza strains worldwide, are domestic or wild bird species. The disease has been reported first of all in food procuring birds such as chicken and turkey but also in guinea fowl, quail and ostrich as well as in pet birds (OIE, 2002). Clinical manifestations, mainly described for chicken, can be a mild form of the disease where only the respiratory system is affected or a decrease in egg production is noticed. Symptoms such as depression, shell-less eggs, swollen and congested wattles and comps, diarrhea, sneezing, coughing, hemorrhages and nervous signs can also be found. Disease is often severe when the virus affects multiple organs and tissues. In chicken populations a pattern whereby a few birds show moderate sign of infection for several days, followed by a sudden rise of mortality rates up to 100% within 48 hours in the entire flock has often been observed (OIE, 2007). Accordingly, diagnostics is clinical, but laboratory confirmation is always needed to confirm HPAI and identify the virus strain. Ducks, geese and wild bird species are generally regarded as asymptomatic virus carriers, but symptoms and death have also been observed in these species. Asymptomatic carriage might facilitate virus persistence in both domestic and wild aquatic birds (Olsen *et al.*, 2006). Mammal species such as pigs, cats, rats, mice, weasels and ferrets can be infected, in general unapparent (OIE, 2007; OIE, 2009b). H5N1 virus has also been isolated from a stone marten (Klopfleisch *et al.*, 2007) and from dogs (Butler, 2006). Human cases, mostly exhibiting respiratory symptoms, are rare, but the mortality rate is around 50 to 70% (Abdel-Ghafar *et al.,* 2008; WHO, 2009).

Transmission

Transmission of the H5N1 virus occurs after an incubation time of 3-5 up to 21 days (OIE, 2009b) in chicken. The virus can be transferred via faecal-oral, faecal-cloacal and respiratory route during direct contact with infected birds and indirectly via contaminated water, feed and material (Sturm-Ramirez *et al.*, 2004; OIE, 2007). Whether the virus intake occurs via digestive or respiratory system as well as the virus excretion routes, the virus charge and the immune status of a host are also important determinants for any influenza virus transmission. More research in this area is required, however. The particular role of pigs in the transmission is controversial. The observation that the trachea of pigs contains receptors for both avian and human influenza viruses (Ito *et al.*, 1998) lead to the hypothesis of the pig as a "mixing vessel" (Castrucci *et al.*, 1993). Avian influenza viruses prefer sialic acid receptors with an α-2,3-linkage to galactose, while human viruses have a preference for sialic acids with an α-2,6-linkage (Ito *et al.*, 1998). The N also has a preference for one of both types of sialic acid linkages and thus for humans or birds (Horimoto and Kawaoka, 2001). Pigs are clearly susceptible to infections with both LPAI and HPAI viruses under natural and experimental conditions, however they appear to replicate much less efficiently than the swine influenza virus. For an estimation of the virus' pandemic potential the ability to cross-species transmission per se is insufficient (Van Reeth, 2007). No virus transmission between experimentally inoculated and in-contact pigs has been shown. Avian viruses can, however, contribute genes in the generation of reassortants when co-infecting pigs with a swine influenza virus or human strains (Brown, 2000). The H5N1 virus infects humans without using the pig as an intermediary. It was discovered that humans also have receptors for both human and avian influenza viruses. These receptors predominate in the upper and lower respiratory tracts respectively. This fact suggests reassortment could occur in humans (Van Reeth, 2007). The H5N1 virus so far fails to spread efficiently from human to human; only singular cases have been described (Ungchusak *et al.*, 2005).

Virus tenacity

The resistance of the virus determines any transmission via vehicles and environmental contacts. In faeces, time-temperature couples of 7 days at 20°C and 35 days at 4°C at a pH 7 to 8 have been observed. In carcasses, 23 days at 4°C is considered to be the virus survival limit. Eggs laid in early disease stages may contain virus in the content and on the shell. Inactivation of the virus requires a temperature of 56°C for 3 hours or 60°C for 30 minutes, an acid pH or disinfectants such as formalin and iodine compounds (OIE, 2007; Brown *et al.*, 2007).

Outbreak situation

The current HPAI H5N1 virus strain was first found in a dead goose in the Guangdong Province in 1996 (Xu *et al.*, 1999). In 1997 H5N1 virus caused a major outbreak in domestic poultry as well as six fatal human cases (De Jong *et al.*, 1997). H5N1 was eliminated by a enormous stamping out campaign, but re-emerged in 2002 (Sturm-Ramirez *et al.*, 2004). Since 2003 outbreaks have spread starting from West and Southeast Asia and reached many wild bird and domestic populations in Central Asian, European and African countries. In many situations, this resulted in an endemic situation and human cases in which persons have been in close contact with infected birds (Alexander, 2006; Alexander, 2007). Accumulated outbreak data are presented in the WHO map (Figure 1.1).

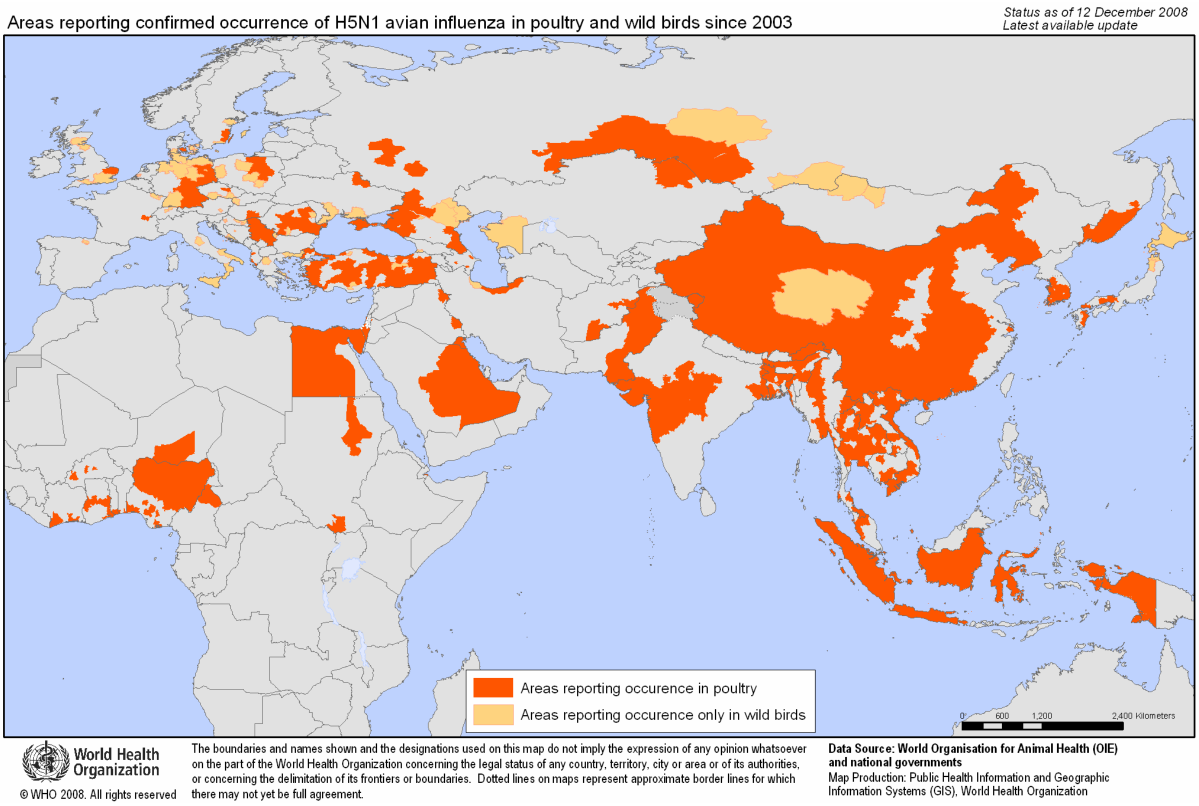

Figure 1.1 Areas reporting confirmed occurrence of H5N1 avian influenza in poultry (in red) and wild birds (in yellow) from 2003 up to 2008 (WHO, 2008)

Amongst 50 countries reporting H5N1 avian influenza in domestic poultry populations from 2005 up to 2009, outbreak numbers for countries being at least partly on the European continent were as follows (in ascending timeline referring to the initial outbreak): Russia (149), Kazakhstan (1), Romania (163) and Ukraine (42), from 2005 onwards; Turkey (219), France (1), Albania (3), Germany (8), Hungary (9), Sweden (1) and Serbia and Montenegro (1), from 2006 onwards; and United Kingdom (3); Czech Republic (4), Poland (10) and Denmark (1), from 2007 onwards. Outbreaks occurred in different poultry species and in both commercial and non-commercial flocks, including a case in a captive swan in the zoological garden of Dresden, Germany (OIE, 2009a).

Switzerland is free from HPAI in domestic poultry since 1931 (Bundesamt für Veterinärwesen, 2009a). However from February to April 2006, the HPAI H5N1 virus was confirmed in 34 out of 1,538 wild aquatic birds found dead (Rutz *et al.*, 2007). In March 2008 one common pochard (*Aythya ferina*), showing no signs of infection, was tested HPAI H5N1 positive in the frame of the national live bird HPAI monitoring program (OIE, 2009a).

Determinants of virus introduction into poultry farms and further dissemination

There has been an extensive debate on which the relevant pathways were for avian influenza virus spreading among countries. Scientific opinions, for instance of the World Organization for Animal Health (OIE, 2007), the European Food Safety Authority (EFSA, 2007), and the World Health Organization's working group on influenza research (WHO, 2006) agree widely on the following risks of HPAI introduction into European poultry farms:

- Infected wild birds that might come into direct or indirect contact with domestic birds are a primary risk factor;
- Infected live birds legally or illegally introduced into a poultry farm, when they are in their incubation period or infected with LPAI (and thus not clinically apparently infected), are another primary risk factor. The introduction of day old chicks and hatching eggs is regarded as less dangerous;
- Contaminated avian products, and contaminated farm equipment introduced into a poultry farm are also regarded as risk factor.

These pathways can be of varying relevance in different regions. Kilpatrick and colleagues (2006) calculated a number of "infectious bird days" for the pathways (i) migratory wild birds, (ii) poultry trade, and (iii) wild bird trade, by multiplying the estimated number of birds entering a country, the assumed prevalence of infection, and the assumed infectious period in days, to examine the past and future spread of H5N1 avian influenza for 52 countries. They concluded that in 20 out of 23 considered European countries, including Switzerland, H5N1 introduction was most likely through migratory birds.

The subsequent environmental and farm management factors are further considered to increase the risk of HPAI outbreaks in domestic poultry:

- A poultry farm's exposure to wild and domestic animals that are potential vectors for HPAI virus, for instance martens and domestic cats that are susceptible for H5N1 (Kuiken *et al.*, 2004; Klopfleisch *et al.*, 2007; OIE, 2007);
- High concentrations of poultry production, sometimes defined as more than 10,000 domestic birds kept on 1 km^2 and more than 3 poultry farms located within 1 km^2, are

assumed to raise infection pressure and allow for mutations from LPAI to HPAI virus strains (Grabkowsky, 2007; EFSA, 2007);

- A poultry farm's location close to habitats suitable for wild bird populations such as water reservoirs, which are particular frequented during by wild aquatic birds during hibernation (Hauser *et al.*, 2006b; Munster *et al.*, 2007);
- The poultry farm's flock composition, as, at least in Asian countries, keeping high proportions of domestic ducks has been shown to increase the risk of HPAI outbreaks (Bhopal, 2002; Hulse-Post *et al.*, 2005);
- Pigs kept on the same mixed farm with poultry has sometimes been stated as further risk factor for HPAI outbreaks in domestic poultry (Thomas *et al.*, 2005), which has, however, not been confirmed in the case of H5N1.

1.1.2 Surveillance of highly pathogenic avian influenza

Surveillance, prevention and control are public health and veterinary public health strategies that come into place prior to an outbreak (prevention), as a reaction to an outbreak (control), or are permanently in place (surveillance). The World Organization of Animal Health (OIE) as intergovernmental body for animal health provides surveillance standards in the Terrestrial Animal Health Code for diseases as "notifiable". Surveillance standards include notes on prevention and control strategies (OIE, 2009b).

Surveillance

Surveillance is the "*systematic ongoing collection, collation, and analysis of information related to (animal) health and the timely dissemination of information to those who need to know so that action can be taken*" (OIE, 2009b). Surveillance aims to demonstrate the absence of a disease or infection, to determine its occurrence or distribution and to monitor epidemic trends. Surveillance can be restricted to different units that are selected randomly for observation or can be undertaken in a targeted way. We can differenciate by means of data collection between *active* surveillance, which describes the periodic data collection by veterinary authorities and *passive* surveillance which describes the reporting of clinical observations by the livestock keeper (Lilienfeld and Stolley, 1994), which is mandatory for highly contagious diseases including HPAI. Whereas active surveillance can draw on many different sources of data including laboratory investigations and distributions of risk factors, passive surveillance is restricted to the detection of clinically manifest infections and depends on the livestock keepers' capability and willingness to notify the clinical observation (Lilienfeld and Stolley, 1994; Doherr and Audige, 2001).

Risk-based surveillance

Risk-based surveillance is targeted at subpopulations, defined geographical areas or time periods, in which disease is more likely to be introduced or found. The term risk describes the probability of an undesired event and its resulting damage. The detection and communication of risks can be expressed in narrative (qualitative risk analysis) or described in numerical values (quantitative risk analysis; OIE, 2004). Surveillance systems based on risk analysis aim to increase detection rates and cost-effectiveness in comparison with classic area-wide surveillance or random sampling. A condition prior to any risk-based surveillance is that risk factors are clearly defined (Stärk *et al.*, 2006). Risk analysis aims to identify hazards such as conditions, agents or activities leading to damages, to estimate the associated risks and to establish the measures needed to control the risk. Risk analysis is prescribed when decisions affect matters subject to international regulations, here by the OIE (2009b) and the Sanitary and Phytosanitary (SPS) Agreement of the World Trade Organization (WTO, 1995).

Avian influenza surveillance

Avian influenza caused by any avian influenza A virus of the H5 or H7 subtypes or with a pathogenicity greater than 1.2 proven by an intraveneous pathogenicity index (IVPI) or a mortality of at least 75% is notifiable to the OIE (NAI). The OIE therefore focuses on setting standards for defining a country's disease status related to domestic poultry and implements trading restrictions for countries experiencing outbreaks. The OIE has introduced the concept of zoning (geographical division) and compartmentalization (functional division by biosecurity measures) of a country. These concepts were introduced to allow unaffected parts or segments of larger countries to continue trading during an epidemic (Bruschke and Vallat, 2008; OIE, 2009b). To consolidate international expertise beyond these regulations a joint OIE-FAO network, OFFLU, has been established as veterinary counterpart to and collaborator of the WHO's influenza network. Its aims are to coordinate AI monitoring and control efforts of poultry and other bird species on an international level and to share biological material and data in view of early stages in the development of human pandemic vaccines (OFFLU, 2005). Each OIE member country has national laws to accomplish OIE requests and to implement surveillance strategies.

Avian influenza surveillance in Switzerland

In Switzerland both HPAI and LPAI surveillance is regulated in the Animal Health Act (Bundesversammlung der Schweizerischen Eidgenossenschaft, 2006). According to Art. 1, HPAI qualifies as a "highly contagious livestock disease" because of its transmission dynamics, its zoonotic potential, its sanitary, social and economic impact, its implications on animal trading and due to the fact that it cannot be entirely managed on the level of a single farm. The Directive for Notifiable Animal Diseases (TSV; Der Schweizerische Bundesrat, 1995) obliges each person keeping, guarding or handling poultry to report any suspected case to veterinary authorities (Art. 61). Additional regulatory statutes and technical instructions are in place, for instance immediate precautionary measures, which came into effect in 2005 when the first HPAI outbreaks occurred in Europe. They entailed mandatory registration of all poultry husbandries on a communal and cantonal level in Switzerland (Der Schweizerische Bundesrat, 2005). HPAI surveillance in domestic poultry is mainly passive. Active HPAI surveillance components include serological surveys of LPAI in mainly free-range domestic poultry (Wunderwald, 2007), wild bird monitoring of live and dead birds, as well as research-related targeted AI surveillance activities.

It is to note that vaccination against HPAI virus infections is possible and regulated by the OIE (2009b); it is implemented mostly in endemic situations for prevention and control in Asia, for instance in the form of ring-vaccination. In Switzerland and in most other European countries, vaccination against most of the highly contagious livestock diseases, including HPAI is prohibited (TSV Art. 81). The official HPAI control strategy is the implementation of control and surveillance zones around an infected premise and the culling of the poultry flock (TSV Art. 88, Art. 122a)

Switzerland pioneers the field of risk-based surveillance. To maintain an officially recognized outbreak-free status, countries have to scientifically prove that performed surveillance activities (e.g. serological surveys in sampled poultry flocks) are highly sensitive (OIE, 2009b). Therefore, in Switzerland the FVO makes increasingly use of the so-called

"Scenario-Tree" tool as analytical framework for evaluating complex surveillance systems and for defining sampling sizes according to desired surveillance sensitivity (Hadorn *et al.*, 2002; Cameron and Martin, 2006). In addition, risk assessments have been produced for the AI virus introduction into domestic poultry via wild birds (Hauser *et al.*, 2006a; Hauser *et al.*, 2006b). In addition, the daily amount of animals and animal products imported illegally into Switzerland and the related risk of virus introduction has been estimated (Läubli, 2009). An example of a risk-based decision was the federal strategy to prevent AI virus introduction into poultry farms via wild birds. In the winter season 2005/2006 the decree to confine all domestic poultry was put in place. This was motivated by regional H5N1 cases in wild birds and high densities of wild aquatic water birds during the winter time. H5N1 positive wild birds had only been found around lakes, which lead to confinement solely applied within one kilometer bands surrounding large water bodies in 2006/2007 (Bundesamt für Veterinärwesen, 2006). In the winter of 2007/2008 "high-risk zones" were only defined around the largest lakes and instead of strict confinement more specific rules for free-range poultry farms were applied. Feeding and drinking places should be indoors to avoid attracting wild birds, ponds had to be protected from wild bird visits and ratites and domestic water birds had to be kept separate from chicken. In these geographically and temporally defined risk zones poultry markets and shows were not allowed (Bundesamt für Veterinärwesen, 2007). New evaluations stating no temporality of outbreak patterns in Europe (EFSA, 2007) and country-specific data on potential wild bird-to-domestic poultry interactions (Saurina, 2009) lead to an abrogation of hibernal risk zones in Switzerland in 2008 (Bundesamt für Veterinärwesen, 2008).

1.1.3 Poultry production

Poultry production has a long tradition: In China, chicken were domesticated at latest around 6000 BC, gray geese and ducks around 2500 BC; in Mexico turkeys were domesticated around 200 AC (Heaton, 1976). The term poultry has been defined in many ways. In this dissertation it denotes the following species of the class *Aves*: domestic chicken (*Gallus gallus domesticus*), turkey (*Meleagris gallopavo*), duck (*Anas platyrhynchos domesticus* or *Cairina moschata*), goose (*Anser anser*), quail (*Coturnix coturnix*), guinea fowl (*Numida meleagris*), peafowl (*Pavo cristatus*), ostrich (*Struthio camelus*) or pigeon (*Columba livia*). In the avian influenza regulations of the OIE domestic birds, kept for purposes other than the production of food and commercial products and cock fighting, are not listed as poultry (OIE, 2009b).

Significance of poultry production

Commercial poultry production started in 1900 when artificial breeding became possible. It gained importance with the introduction of hybrid breeding in 1930. Since 1960 poultry production is highly industrialized and satisfies the high demands for low cost food of high hygienic quality and traceability of poultry products (Kaleta, 1997; Fallon, 2001). The annual production of chicken meat was 47 billion birds in 2004 (compared to 20 billion birds in 1984) and the annual production of laying hens was 5.4 billion in 2004 (compared to 3.1 billion in 1984; FAOSTAT, 2009). Poultry meat and eggs are valuable sources of animal protein in human nutrition in both developing and industrialized countries. Conditions for poultry production do for the most part not depend on climate zone and the cultural and religious background of societies (Steinfeld *et al.*, 2006). Other important poultry products are feathers and high-value fertilizer. Especially in developing countries, keeping poultry sustains the livelihood of many individuals and seems to promote gender equality and empower women. In some societies women cannot acquire land titles but can keep a small stock as an asset (LivestockNet, 2006).

Poultry production in Switzerland

In 2007, 46 million birds for meat production and 3 million laying hens were produced in Switzerland. Annual poultry meat consumption was 78,407 tons and egg consumption was 1,450 million eggs. Nearly half of the consumed products originated from domestic production (Aviforum, 2009). Official statistics for 2007 list a total of 15,550 poultry farms in Switzerland (Bundesamt für Statistik, 2007; Aviforum, 2009). In this dissertation figures 3.2 times as high as those of the official statistics were identified by collating poultry registration data of different sources. This issue is addressed in Chapters 6 and 7 and Appendix 1 of this thesis.

Commercial poultry farms in Switzerland usually operate with more than 500 chickens. Flock sizes rarely exceed 20,000 birds and are small compared to neighbor countries where often 100,000 birds are kept on one farm. Due to high animal welfare standards, cage systems on poultry farms are prohibited. Poultry is kept in litter-based floor systems and has often access to a covered veranda (winter garden) or a free-range area, which can make the poultry vulnerable to environmental factors and facilitates contact to vectors. Industrialized poultry production entails that each production step takes place at a different type of farm, namely growers, upbringing, layer and broiler farms, as well as at hatcheries (Fallon, 2001). There is no primary breeding company in Switzerland. Therefore elite breeds and sometimes hatching eggs and one-day chicken are imported. Most commercial farms are affiliated to industrial companies for egg or table poultry production.

Non-commercial poultry farms comprise all farms with smaller flock sizes. On these farms birds are kept for sideline production, subsistence farming or leisure. Backyard poultry, where the emphasis is on the production of table poultry or eggs for human consumption can be distinguished from show birds. Preservation of rare species is also reason to keep poultry. “Appenzeller cap” and “Appellenzeller barb” for instance are races kept on a small scale since the 15th century and the 19th century, respectively. Non-commercial farms are sometimes organized in breeding associations that also organize poultry shows.

Health issues in poultry

Domestic poultry is vulnerable to many health hazards; mainly to bacterial and parasitical infections, but also to diseases of non-infectious etiology for instance malnutrition and errors in poultry flock management (Surumay *et al.*, 1995; Kaleta, 1997). The *Salmonella gallinarum pullorum* plague in the 1930s created a need to establish poultry science as a branch of veterinary medicine (Siegmann and Neumann, 2005). Since then, disease management methods in poultry are highly developed in commercial production. Interventions are on the level of the flock, focus on prophylaxis and include vaccination feeding concepts and hygienic measures. Epidemic prophylaxis comprises also the breeding of more resistant lines and producing chicken with maternal antibodies in an attempt to create specific pathogen-free flocks. Farm surveillance is linked to mortality rates and production figures: for instance loss rates higher than 5% during the entire fattening period are suspicious (Siegmann and Neumann, 2005). Non-commercial farms are often assumed to be very different as to farming practices and hygienic measures depending on the keepers’ disease awareness and dedication.

Poultry diseases under surveillance in Switzerland are: Newcastle Disease (ND), classed as highly contagious (last case occurred in 1997), Infectious Laryngotracheitis of Chicken (ILT), classed as to control (ongoing), Salmonellosis, classed as to control (ongoing), and Campylobacteriosis, classed as to survey (ongoing). ND, ILT, Pneumovirus infections and

Avian Encephalomyelitis are considered as differential diagnosis of HPAI (Bundesamt für Veterinärwesen, 2009b).

1.2 Epidemiology of infectious diseases: tasks, tools and techniques

Infectious diseases are the clinical manifest of interactions between host organisms and infectious agents and sometimes vectors. The infectious agents are usually dependent on the host and the host suffering from the agent. Infectious agents include pathogenic multicellular parasites, protozoa, fungi, bacteria, virus, viroids, and aberrant proteins known as prions. The attributes communicable or contagious are used to denote transmission events from person to person or between other individuals or units under study upon direct or indirect contacts, respectively. Epidemiology is the science that studies the patterns of disease and health in populations and is driven by the aspiration to prevent, control or manage the problems under study, such as an infectious disease (Bhopal, 2002).

John Snow (1813 - 1858) is considered to be one of the fathers of epidemiology given his work on tracing the source of a cholera outbreak in London by entering case data and pump locations in a spot map and thus explaining outbreak patterns (Hamer, 1906). Similarly groundbreaking was the contribution of Ignaz Philipp Semmelweis (1818 - 1865), who investigated the causes of puerperal fever. Semmelweis made the link between medical students treating patients just after doing autopsies and a higher maternal mortality rate, which could be reduced when hand washing procedures were conscientiously followed by the medical students (Semmelweis, 1861).

There is evidence that the concept of contagious diseases was understood or guessed in the ancient world and addressed by a still valid prevention and control measure, namely social distancing. As an example, leprosy in India, named "kushta", was documented in a medical essay around 600 BC (Aufderheide *et al.*, 1998), and in the Old Testament (Levitikus). During medieval episodes of bubonic plague social distancing went to extremes as described in Boccaccio's Decameron (1353): *"Tedious were it to recount, how citizen avoided citizen, how among neighbors was scarce found any that shewed fellow-feeling for another, how kinsfolk held aloof, and never met […] that in the horror thereof, […] fathers and mothers were found to abandon their own children, untended, unvisited, to their fate, as if they had been strangers".*

Epidemiology is still concerned with both etiology of infectious diseases and mitigation strategies. Today, there are new tools to quantify epidemiological effects and the impact of interventions and to integrate qualitative predictions; a "modern science of mathematical epidemiology" as called by Matthews and Woolhouse (2005). This section addresses mathematical models of epidemics at a glance, and network analysis in particular as a technique to identify and quantify complex interaction patterns within a population as described by Bocaccio.

1.2.1 Mathematical models of epidemics

To save time and resources, simplifications of a system, such as a host-pathogen, or a host-host interaction, will sometimes be used to simulate its functioning in the real world. This representation is called a "model". A model usually consists of "theory" and "data". Theory explains the behavior of the system with the help of formal language of cause and effect logic or other. Main data sources include observations or other empirical data. Predictive values are generated, forming the output of the model. Models of epidemics assist with understanding disease ecology and predicting the impact of interventions. Of course *"The model that is simple enough to effectively analyze the transmission system but not so simple that realistic violation of simplifying assumptions will change an inference"* (Koopman, 2005) remains an ideal. Advances over the last decades have, however, lead to more and more detailed and thoroughly validated models of epidemics.

Classical models of epidemics

To reflect transmission of a disease at population level, often dynamic models that account for how systems change over time are chosen, for instance the compartmental "Susceptible-Infectious-Recovered" (SIR) model. This model construct can be mainly attributed to Kermack and McKendrick (1927; 1991) and their early predecessor Hamer (1906). Members of a population "N" are categorized into three compartments according to their current state of infection: "S" susceptible (not infected and susceptible to infection), "I" infectious (infected and infectious), and "R" recovered (not infected and usually immune).

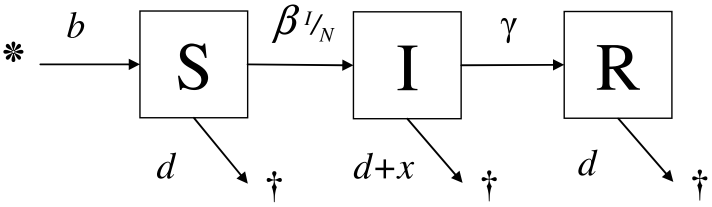

Figure 1.2 Schema of a compartmental SIR-type model

In the course of an epidemic, these compartments change in size over time dependent on the dynamics of the system. In its simplest form, the dynamics depend on disease specific transmission β, recovery γ, and diseased induced mortality rates x, as well as on demographic characteristics such as birth b, and death d rates. For diseases with short infectious periods a stable population size is often assumed and demographic characteristics are ignored. The compartmental SIR model described here is shown in Figure 1.2 and can be represented by a system of differential equations, namely

$$\frac{dS}{dt} = bN - \beta S \, {}^{I}\!/_{N} - dS \,, \tag{1}$$

$$\frac{dI}{dt} = \beta S \, {}^{I}\!/_{N} - \gamma I - (d + x)I \,, \tag{2}$$

$$\frac{dR}{dt} = \gamma I - dR \,. \tag{3}$$

Such a system allows one to derive epidemiologically relevant measures such as the "basic reproductive number" R_0, which gives the average number of secondary infections caused by one infectious individual (index case) in a fully susceptible population (Dietz and Hadeler, 1988; Anderson and May, 1991; Heesterbeek, 2002). For the above SIR model an epidemic occurs given a transmission rate β higher than the sum of the mortality rate $d + x$ and recovery rate γ. Here R_0 is defined as $\frac{\beta}{\gamma + (d + x)}$. In general, a basic reproduction number $R_0 < 1$ means that the disease will likely die out in the population and not lead to an epidemic (Dietz, 1993; Heffernan *et al.*, 2005). Conversely, $R_0 > 1$ implies introduced into the population will likely lead to an epidemic. Such models as an SIR model can either be deterministic, dealing with the average process of disease spread through a population, or stochastic. Stochastic models, also called probabilistic models, deal with the chance different events in transmission process occur. Such representation of transmission and output is assured to better represent underlying variabilities in biological processes (Matthews and Woolhouse, 2005).

Basic SIR-models have been extended to describe diseases with latency periods or particular immune responses (Anderson and May, 1979; Heffernan *et al.*, 2005). Chowell and colleagues (2006) investigated data from pandemic influenza in Geneva. They defined seven different compartments: “Susceptible”, “Latent”, “Infectious”, “Asymptomatic”, “Hospitalized”, “Recovered”, and “Dead”. Comparatively simple models are SIS-models, where infected individuals change back to S as no lasting immunity is developed. These models have been sometimes used to reflect recurrent outbreaks (Jacquez and Simon, 1993; Allen and Cormier, 1996; Zhou and Ma, 2009). Examples of successful adoptions and applications of deterministic and stochastic compartmental models are studies modeling outbreak dynamics and the effect of vaccination strategies, such as for measles outbreak in a university campus setting (Allen *et al.*, 1991), for the 2003 SARS outbreak in Beijing (Wang and Ruan, 2004), within the Garki project (Molineaux and Gramiccia, 1980), as well as for animal-human transmission of brucellosis in Mongolia (Zinsstag *et al.*, 2005) and for transmission of dog rabies in Chad (Zinsstag *et al.*, 2009).

An elementary assumption for most compartmental model of epidemics is that the susceptible population is entirely mixed and homogenous. Each member is equally likely to be in contact with all others and to pass on the infection upon contact. For some diseases, for instance sexually transmitted infections, this assumption leads possibly to the incorrect conclusion that the disease should not persist in the population (Pastor-Satorras and Vespignani, 2001). Such mixing assumption differs from societal reality (Morris, 1993; Klovdahl *et al.*, 1994; Altmann *et al.*, 1994). Moreover, in situations where members of a population are animals or units of higher orders, such as farms, inter-relational structures are found to be heterogeneous (Woolhouse *et al.*, 1997) and varying in space and time (Robinson and Christley, 2006).

In situations were the assumption of homogeneity does not hold, other model types or more complex compartmental models are required to adequately represent disease dynamics.

Extensions to compartment models to account for heterogeneity, such as different disease dynamics by age, are including multiple S, I, R compartments for each age group. To include spatial heterogeneity and movement, one example is a patch system model where the compartmental model is valid in each patch and movement into or out of each compartment in each patch, is also modeled as well as contacts between neighboring patches. One other example to include spatial or individual heterogeneity in movement and disease dynamics is the network or contact network model.

Network models

The term "network" or "contact network" is often used to describe a population's underlying contact structure; how members interact with each other. Models incorporating contact structures are individual or agent based. Agent based models consist of individual autonomous decision-making entities and their relationships result in complex behavior patterns (Bonabeau, 2002). For instance, network structures can result from the agents' rationality to raise their own position in a network to become more central (Shinoda *et al.*, 2007).

The SIR concept is not exclusively applicable to a compartmental model, but can also be used within agent based models. In such models the state S, I and R are then attributed to individual units as shown in Figure 1.3.

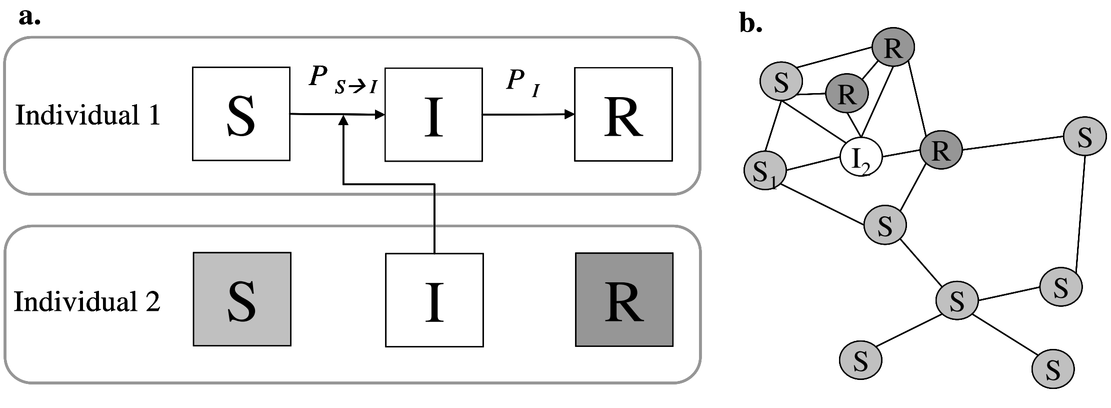

Figure 1.3 Schemata of (a) the SIR concept on individual level and (b) a graph representation of the individuals' position and their epidemic status (S, I or R) in a network. A state transition $S \rightarrow I$ requires at least one infected *individual 2* that interacts with the susceptible *individual 1* with a defined probability $P_{S\rightarrow I}$ of contagion per time step. Infected individuals change into a recovered state R with probability P_I per time step

Network prototypes

There are four prototypes that have been defined, which help to classify, to a large extent, the infinite possible network configurations: regular lattices, random graphs, small world networks and scale-free networks. Most interconnected systems in real world have characteristics resembling one or more of these prototypes. Networks are commonly presented in graphs consisting of dots (termed "nodes" or "vertices") representing actors such as individuals or other units for instance farms, and of lines representing contacts, as described in more detail below.

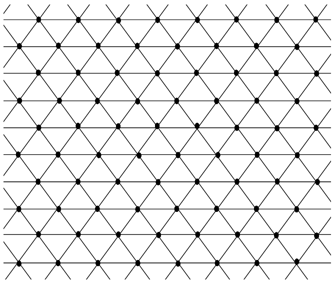

Figure 1.4 Detail (N=80) of a regular lattice network with an average of six contacts per individual

Regular lattices, also called regular grids, are the simplest two-dimensional theoretical network: Each vertex is only connected with its direct neighbors (Figure 1.4). Regular lattices are suited to describe populations with short movement ranges, such as wildlife population with a small habitat, human population groups where long distance transports are not available or used, or for instance livestock in tie-stalls. If potentially contagious contacts are arranged in a similar way, this often results in early expiration of the disease due to depletion of the local resources of susceptible individuals (Figure 1.8; Fiebig *et al.*, 2008). Looking at a longer time period, in population with regular lattices contact structure spread patterns are often wave-like spread patterns, similar to those observed for bubonic plague in 14th century Europe (Zietz and Dunkelberg, 2004; Christakos *et al.*, 2007) or the spread of rabies in Europe since the 1940s (Ou and Wu, 2006).

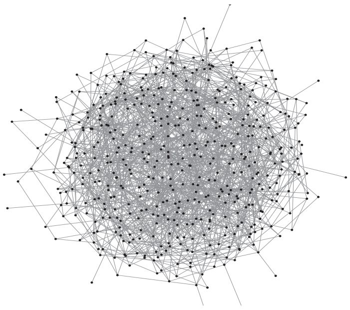

Figure 1.5 Random graph with N=500 and an average of six contacts per individual

Random graphs were subsequent network prototype developed by Erdős and Réyni (1960). In random graph construct, an algorithm chooses edges randomly and sequentially out of the entire set, which leads to the arrangement of homogenous mixed interrelating system (Figure 1.5). Random graphs are relatively simply to manage mathematically. Epidemiological models based on homogeneous random mixing, however, are often not suited to reflect a population where members differ in their partner selection choices, and where clustering (defined below) occurs. This leads to an overestimation of the size of an outbreak (Christley *et al.*, 2005; Keeling and Eames, 2005) or to an underestimation of the transmission probabilities if such a model is fitted to measured outbreak data.

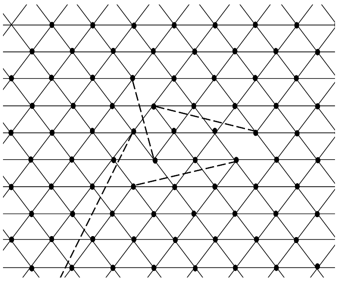

Figure 1.6 Detail (N=80) of a small-world network with an average of six contacts per individual; dashed lines are rewired links

Small world networks are basically structured networks similarly to regular lattices. A widely recognized representative of such a network is the *Watts-Strogatz model* (Watts and Strogatz, 1998). In contrast to a regular lattice, small world networks include some remote links all over the network that act as short cuts (Figure 1.6). The notion "small world" goes back to Milgram (1967), who hypothesized that each individual is connected to all other individuals over surprisingly short paths of contacts. There is evidence that many real-world contact networks have small world properties. Modern human societies, for instance have a fraction of highly mobile individuals (responsible for remote links) causing global spread patterns within short periods of time as seen for SARS and influenza outbreaks (Saramäki and Kaski, 2005). Small world properties have also been found for animal populations, for instance *Orcinus orca* societies (Guimarães *et al.*, 1990). The results of disease simulations based on small world networks depend vastly on the proportion of links randomly rewired. While a network with rewiring probability *p=0* equals exactly a regular lattice (i.e. a regular ring lattice in the case of the Watts-Strogatz model), *p=1* results in a random network with the respective disease spread characteristics. Small world networks have proportions of remote links between these two extremes; their disease spread behavior lies between random and regular networks (Figure 1.8). Even a small proportion of remote links leads to disease spread behavior comparably close to the random mixing assumption (Watts and Strogatz, 1998).

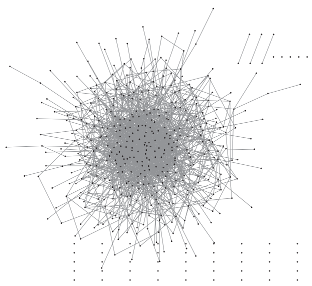

Figure 1.7 Scale-free graph with N=500 and an average of six contacts per individual

Scale-free networks, are among the most recent advances in describing complex network topologies and were introduced by Barabási and Albert eponymous for the widely used Barabási-Albert model (Barabási and Albert, 1999; Albert and Barabási, 2002). Scale-free networks consider the fact that in many real world networks, each individual does not have a typical number of contacts, but that many individuals have no or few potentially contagious contacts and few have an enormous number of such contacts (Figure 1.7). Liljeros and colleagues (2001) evidenced such structure for sexual networks in Sweden. In theory, Pastor-Satorras and Vespignani (2001) showed an underlying power-law distribution of number of contacts per actor in such networks. This leads to a situation in which a disease can persist *"at whatever spreading rate the epidemic agents possess"*, assuming that the individuals return to a susceptible state again after being infected. The disease either disappears before reaching a highly connected individual or spreads rapidly, if such a highly connected individual becomes infected early (Figure 1.8).

Examples of successful adoptions and applications of network based models in epidemiology are studies modeling control strategies of respiratory pathogens (Pourbohloul *et al.*, 2005), predicting outbreak diversity of SARS and the impact of transmission and contact interventions (Meyers *et al.*, 2005), evaluating influenza vaccination programs (Bansal *et al.*, 2006) or quantifying the impact of social distancing measures in the case of pandemic influenza (Glass *et al.,* 2006).

To visualize the impact of these four prototype network topologies on epidemiological models, Timo Smieszek simulated epidemic curves presented in Figure 1.8. All simulations are based on a population of N=500 with an average of six contacts per individual, birth and deaths not included, and an SIR-type model of disease spread. Transmission follows a stochastic process with a transmission probability of p=0.11 per time step. The infectious period has a length of three time steps. At time step one all individuals are susceptible except one individual infected. In Figure 1.8 the number of infected versus time of 50 simulation runs for each of the four network structures and the respective mean value of infectors per time step is shown.

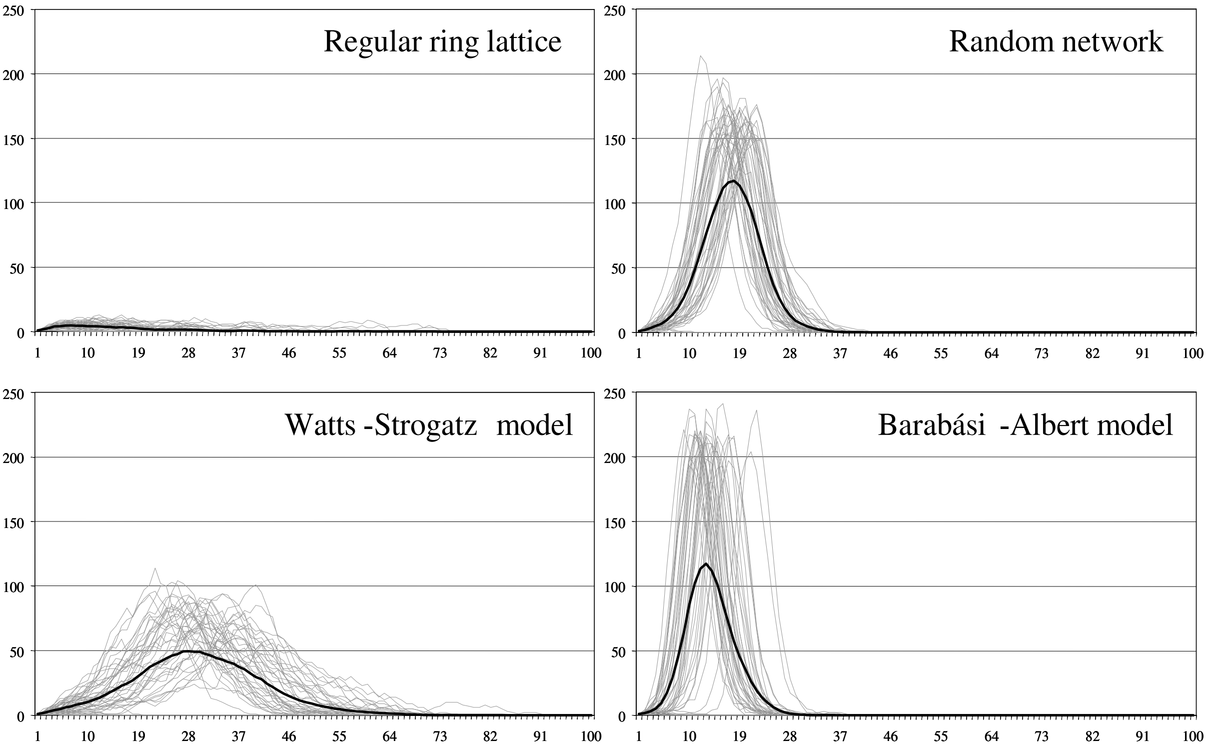

Figure 1.8 Number of infectors [y-axis] versus simulation time steps [x-axis] for four different network arrangements. Grey lines indicate one single simulation run. Bold, black lines give the average. Figure courtesy of T. Smieszek (Fiebig *et al.*, 2008)

Comparing simulation results, the random network lead to the highest peak of simultaneous disease cases. In the regular lattice network, clustering of contacts is high and recovered individuals cannot be infected once more, and there are too little resources for the disease to sustain itself under the model conditions. The Watts-Strogatz network, with a rewiring probability of 0.075, leads to an outbreak with an average peak between both extreme models and a more prolonged average duration of the epidemic period. Average epidemic curves of Barabási-Albert model appear similar compared to those of random networks. Looking at single simulation runs, disease either disappears at a very early stage in some cases; other curves have steep slopes of infected cases and reach highest peak values of all network models. Thus, with identical given transmission parameters and the same number of simulated individuals, and the same average number of contacts per individual in a population, epidemic curves vary vastly due to varying contact arrangements. To capture a real-world population's contact structure, or to fit model parameter to real world conditions, and thus realistically represent disease dynamics and quantify disease outbreaks, empirical datasets on the arrangement of contact are needed.

1.2.2 Analyzing networks

Network analysis is a technique to reveal, describe and quantify network structures. The term "network" can refer to any system of interconnected agents, for example individuals, groups, institutions, nations, or technical entities. Network analysis is therefore popular in many disciplines such as cybernetics, economics, history, biology, computer sciences and, since the rise of sociometry in the 1930s, in social science (Klovdahl, 2001). Social science coined the term "social network analysis" (SNA) to investigate individuals' social interactions within a group and the group's collective interaction behavior (Beshers and Laumann, 1967). This is directly transferable to infectious disease epidemiology (Laumann *et al.*, 1989). Here, the interactions of interest are those that can lead to the propagation of a specific infectious disease. The arrangement of potentially contagious contacts within a population, or the population's contact network, is of interest for modeling epidemics, as shown above. Certain contact network structures are also of direct interest for targeting disease surveillance, prevention and control.

Network terminology and network indices

Networks can be represented in at least three ways: (i) using mathematical notations, (ii) using adjacency matrices, and (iii) with the help graph theory (Figure 1.9). Graph theory, harkening back to a 1736 Leonard Euler talk entitled *"The Seven Bridges of Königsberg"* (Euler, 1741; Trudeau, 1993), provides the most intuitively understood illustration package and mathematical toolkit for network analysis in social sciences and epidemiology. A "graph" is determined by a set of actors ("vertices") and a set of contacts ("lines"). Lines can either be directed ("arcs") or undirected ("edges"). A "path" is the closed sequence of lines from one vertex to another vertex, respecting the directions of arcs and without passing the same vertex twice. In Figure 1.9, the path from vertex *g* to vertex *h* has the "path length" of two. This path is a "geodesic", the shortest possible path between two vertices. The path length allows for defining the set of vertices in certain distance *k* of an actor, so called "k-neighbors". These and other terms are widely standardized in the textbook *"Social network analysis: Methods and applications"* (Wasserman and Faust, 1994).

(i) G= {(g,i); (g,j); (h,g); (h,j); (i,h); (j,h)}

(ii)

$$\begin{array}{c|cccc} & g & h & i & j \\ \hline g & 0 & 0 & 1 & 1 \\ h & 1 & 0 & 0 & 1 \\ i & 0 & 1 & 0 & 0 \\ j & 0 & 1 & 0 & 0 \end{array}$$

(iii)

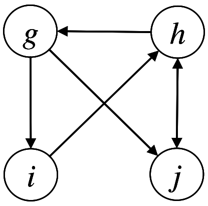

Figure 1.9 Three representations of a directed network of four vertices and, four arcs and one edge: (i) mathematical notation, (ii) adjacency matrix, and (iii) graph

A network is, however, more than a graph. It contains further information on actors, such as sex and age of individuals, or flock size of a farm. And it contains further information on lines, namely the qualities of contacts. The latter is sometimes expressed by a "weighted graph", where lines can have values other than 0 or 1. In addition, a network does not necessarily consist of only one set of actors. There are so-called "bi-partite" or "two-mode" networks which have a set of actors representing persons and another set representing the locations accessed by persons. There can also be multiple sets of different types of contacts represented by more than one set of lines, resulting in "multi-relational" networks.

Network indices are used to describe local positions and global configurations in networks. The aim is to identify important actors, where actors can also be groups (Everett and Borgatti, 1999). In epidemiology important actors such as individuals, communities, farms are those having high risk of getting infected or highly contributing to further dissemination of disease and hence, qualifying for being targeted with intervention strategies. In particular, centrality measures (Wasserman and Faust, 1994) have proven useful for identifying epidemiologically important actors:

- *Degree centrality* is the simplest centrality measure. An actor's (or vertex's) degree is the number of lines incident with it. A central actor is defined by a large degree and has potentially infectious contacts to a large number of other individuals. Degree centrality has proven to be a strong predictor for the risk of acquiring contagious diseases, in particular sexually transmitted diseases (Ghani and Garnett, 2000; Christley *et al.*, 2005). Distinguishing between "in-degree centrality", resulting from the number of an actor's in-coming arcs, and "out-degree centrality", only taking out-going arcs into account, can be relevant for describing highly exposed actors and actors being spreaders.

- *Closeness centrality* measures how short an actor's distances are to other actors in the network. "*The idea is that an actor is central if it can quickly interact with all others*" (Wasserman and Faust, 1994, p. 183). In epidemiology, closeness centrality proved to be significantly predictive for the risk of infection in a study done by Ghani and Garnett (2000). In a network of potentially infectious contacts, the length of the shortest path between two individuals is important. It indicates how many intermediate individuals have to be passed as a minimum until a disease is transmitted from any arbitrary index case to an individual of interest. The higher the closeness centrality of an individual is, the faster a disease can be transmitted to or from any other individual in the connected network. Accordingly, individuals with high closeness centrality are at high risk of getting and passing on a communicable disease early. Interventions that lead to a decrease of actor closeness centrality would possibly not only decrease the risk of infection for these individuals but for the entire network.
- *Betweenness centrality* describes an actor as central when it has control over many paths in the network. This is given for actors that lie on many geodesics in the network. Hence, they bridge different parts of a network that would be less well or not at all connected otherwise. Ghani and Garnett's (2000) proved betweenness centrality to be significantly related to the risk of infection. Betweenness measures are suitable to target interventions: monitoring, treating and immunizing central actors can help to mitigate the spread of a certain disease. If actors on "bridge" positions are no longer susceptible for instance due to vaccination, the paths, along which disease can spread, become considerable longer or are no more existent. Closeness and betweenness centrality are indices that are only applicable to an entirely described network.

Other concepts than centrality measures of epidemiological interest are "clustering" and "cohesiveness" assessing the level of a network's connectedness (Dubé *et al.*, 2009).

- The *clustering coefficient* is commonly defined as the ratio of "closed triplets" to "possible triplets" in a network (Ghani and Garnett, 2000). A closed triplet is defined as three actors having mutual contact. Possible triplets are all different combinations of three actors. Clustering describes the connectivity in the neighborhood of an actor. It deals with how many of an individual's contacts also have contact among each other. High clustering of contacts can lead to a rapid local depletion of susceptible individuals and thus result in flat epidemic curves as shown for the regular lattice network in Figure 1.8.

- *Cohesion* in the narrow sense denotes to which degree actors are directly connected within groups (every actor is directly tied to every other actor) or within "social circles". Social circles consider also actors that are indirectly tied to every other actor (Moody and White, 2003).
- *Fragmentation* is given by the proportion of pairs of vertices without a path between them. If fragmentation is zero, all actors are connected to all others, if it is one, all actors are isolated.

Additional indices are often purpose-specific defined in (veterinary) epidemiology, for instance in terms of livestock movements, as recently reviewed by Dubé and colleagues (2009) and in Table 1.1.

- *Cut-points* are defined as livestock operations, which, if removed, increase the level of fragmentation in the network (Dubé *et al.*, 2009).
- *Components* are defined as *"maximally connected subregions of a network in which all pairs of livestock operations are directly or indirectly linked"* (Robinson and Christley, 2007).
- *Farness* is defined as the sum of geodesics from a source livestock operation to all other reachable operations in the network (Christley *et al.*, 2005).

Network data collection

Network data consist of two nested data sets: data on individual actors and data on contacts (Wasserman and Faust, 1994). Prior to data collection, network boundaries and contacts have to be defined (Figure 1.10): What are the actors of interest? When are two actors related? Ideally, one would follow a so-called complete network design (Subfigure a), where each actor and all its contacts are known. Such a data set allows for direct calculation of all centrality indices. In many cases, however, the population of interest is larger than the group that can be realistically investigated in a given time and with given resources. Sampling becomes necessary. Useful sampling concepts have been developed (Granovetter, 1976). The most popular are local (egocentric) and partial network designs (Morris, 2004). The partial network design relies on cutting an intact interconnected subgroup out of the population (Subfigure b), for instance via snowball investigation. Snowballs start by collecting contacts of a small number of initial actors to identify their contacts. Then the contacts' contacts are investigated, up to a defined number of generations. A special case of partial networks are outbreak networks, which are defined through the actual spread pattern and include only diseased actors. The local network design is usually based on a random sample and provides profiles of single actors and knowledge about their direct contacts (Subfigure c).

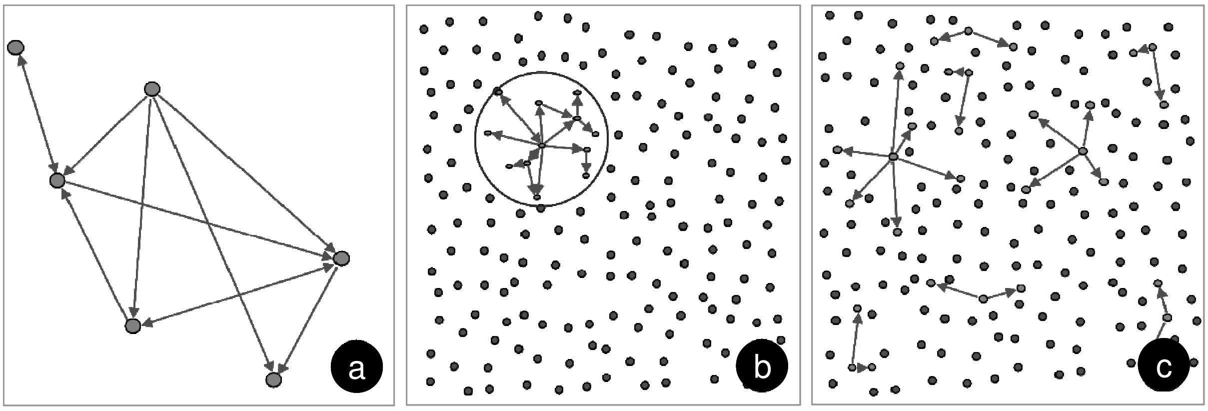

Figure 1.10 Schematic representation of complete, partial, and local network design: Subfigure a: completely interconnected study population of interest; Subfigure b: completely interconnected subgroup of the population of interest; Subfigure c: randomly selected individuals and their contacts

The choice between a partial and a local design impacts on the range of applicable statistical tests. With the partial design, global network properties can be applied to the investigated group and clustering and central actors can be calculated. Disadvantageous for the application of standard statistics are the interdependence of observations and the handling of the partial network's boundaries. The local design results in contact data of mostly random selected actors, also called egocentric network data. This does not allow for the calculation of network level indices, such as closeness and betweenness centrality. Egocentric data can, however, provide a basis for an extrapolated network.

Many data sources and survey instruments are suited to collect network data. Some of the most popular include:

- Archives, such as data from demographic surveillance systems or census data, as a basis for large scale network population models (Eubank, 2005); or, in the case of livestock populations, registers and movement databases for livestock movement networks (Bigras-Poulin *et al.*, 2006; Ortiz-Pelaez *et al.*, 2006; Lyytikäinen *et al.*, 2009; Lentz *et al.*, 2009);

- Face-to-face interviews, for instance for partner notification in the case of sexually transmitted diseases (Potterat *et al.*, 1990; Klovdahl *et al.*, 1994; Kretzschmar and Morris, 1996; Brewer and Garrett, 2001: Bell *et al.*, 2007);
- Participatory mapping of community structures for instance in focus group discussions (Greenwood *et al.*, 1993; Greenwood, 2009) often using the Venn diagram as a mapping tool (Thigpen and Drane, 1967; Kung and Harrison, 1984; Shamansky and Graham, 1999);
- Questionnaire surveys, for instance to collect data on events attended by participants (Webb, 2005);
- Contact diaries, for instance to collect individual activity and contact pattern over a whole day up to weeks (Mossong *et al.*, 2008, Smieszek, in press 2010);
- Technological devices including videotaping or sociometric badges (wearable transponders), often used in behavioral studies in both humans (Olguin *et al.*, 2009) and pets, aptly termed “petwork” (Contractor, 2007);
- Contact tracing via molecular typing (DNA finger print) for molecular epidemiological investigations, sometimes used in comparison to social contact tracing (Klovdahl, 2001).

Contact diaries and questionnaire surveys strongly depend on the capacity of the individual concerned to remember the relevant information (Brewer *et al.*, 1999), which is not the case for videotaping. Contact data from different sources and different inquiry tools are often combined to reduce response and recall biases and thus to increase validity and reliability of contact information.

Applications of network analysis in veterinary epidemiology

Network analysis has begun to play an increasingly important role in veterinary epidemiology. One of the first veterinary network analysis applications was in New Zealand in wild brushtail possums (*Trichosurus vulpecula*). There, individuals with higher centrality measures were found to be more often infected with *Mycobacterium bovis* (Corner *et al.*, 2003). The actual birth of veterinary epidemiology was subsequent to the 2001 Foot-and-Mouth disease (FMD) epidemic in the United Kingdom (UK) as recently reviewed by Dubé and colleagues (2009). The FMD control policy implemented by the veterinary authorities in 2001 was largely based on models assuming a homogenous mixing of the population and ignoring livestock movements over long distances (Woolhouse, 2003; Kao, 2002). Many farms in the vicinity of infected farms were preemptively culled with the intention of coming below an assumed epidemic threshold by eliminating susceptible actors. Shirley and Rushton (2005a) and Green and colleagues (2006) revisited data from the initial outbreak. They were able to show long distance livestock movements and contact patterns of infection, which resembled scale-free networks, and thus would miss an epidemic threshold of disease (Pastor-Satorras and Vespignani, 2001; Shirley and Rushton, 2005b). Numerous investigations analyzing cattle movements during the epidemic helped to identify highly connected farms and cattle markets, as well as high-risk movements, which qualify for being targeted with control measures including movement ban and more selective preemptive culling (Ortiz-Pelaez *et al.*, 2006; Robinson and Christley, 2007; Kao *et al.*, 2007). Since then, the demands for preemptive network investigations in livestock populations have become stronger (Martínez-Lopez *et al.*, 2009). This has resulted in network studies in different livestock populations including cattle (Brennan *et al.*, 2008; Turner *et al.*, 2008; Heath *et al.*, 2008; Natale *et al.*, 2009; Vernon and Keeling, 2009; Lentz *et al.*, 2009), sheep (Webb, 2005; Kiss *et al.*, 2006b; Kao *et al.*, 2007), pigs (Bigras-Poulin *et al.*, 2007; Ribbens *et al.*, 2009; Lyytikäinen *et al.*, 2009), poultry (Truscott *et al.*, 2007; Dent *et al.*, 2008), and fish farms (Green *et al.*, 2009). An overview of epidemiological network applications in different livestock populations is given in Table 1.1.

Table 1.1 Veterinary applications of network analysis in different livestock populations

Livestock population	Disease(s)	Country	Data collection	Network indices	Reference
Cattle	BTB, FMD cited	UK	survey	in-degree, out-degree	Woolhouse *et al.*, 2005
	FMD cited	DK	central livestock register, central husbandry register	in-degree, out-degree, path length, clustering coefficient	Bigras-Poulin *et al.*, 2006
	FMD	UK	CTS database	degree, strong components, week components	Robinson *et al.*, 2007
	FMD	UK	CTS database	in-degree, out-degree, betweenness	Robinson and Christley, 2007
	FMD cited	UK	survey	connectivity	Brennan *et al.*, 2008
	E.coli O157	UK	model of a typical cattle herd	in-degree, out-degree, cluster coefficient	Turner *et al.*, 2008
	FMD cited	UK	CTS database	density, components	Heath *et al.*, 2008
	FMD cited	UK	survey	density, largest component	Vernon and Keeling, 2009
	hypothetical disease	DE	HIT database	degree, closeness, betweenness	Lentz *et al.*, 2009
	hypothetical disease	IT	national bovine movement database	degree, closeness, betweenness, regular lattice, rewired lattice, scale-free, random network	Natale *et al.*, 2009
Cattle and sheep	FMD	UK	outbreak data DEFRA	degree, clustering, path length	Shirley and Rushton, 2005a
	FMD	UK	outbreak data DEFRA	regular grid, random, small-world, scale-free networks	Shirley and Rushton, 2005b
	FMD	UK	outbreak data DEFRA, CTS database	in-degree, out-degree, betweenness, nearest neighbors, hierarchical clustering	Ortiz-Pelaez *et al.*, 2006
Sheep	FMD	UK	show data, survey	Max. component, fragmentation	Webb, 2005
	FMD	UK	survey	in-degree, out-degree	Webb, 2006
	FMD	UK	AMLS, SAMS	inn-degree, out-degree, path length, strong component, clustering coefficient	Kiss *et al.*, 2006b
	FMD, Scrapies cited	UK	AMLS, SAMS	degree	Kao *et al.*, 2007

[AMLS=animal movement licensing system; BE=Belgium; BTB=bovine tuberculosis; CTS=cattle tracing system; DE=Germany, DEFRA=Department for Environment, Food and Rural Affairs; *E.coli* O157=*Escherichia coli* serotype O157:H7; FI=Finland; FMD=Foot-and-Mouth disease, GBPR=Great Britain poultry register; HIT=Herkunfstsicherungs- und Informationssystem für Tiere (German animal register database); IT=Italy, SAMS=Scottish animal movement system; SARS=Severe Acute Respiratory Syndrome]

Table 1.1 Veterinary applications of network analysis in different livestock populations (continued)

Livestock population	Disease(s)	Country	Data collection	Network indices	Reference
Swine	FMD cited	DK	industrial register of domestic swine movements	in-degree, out-degree, path length, clustering coefficient	Bigras-Poulin *et al.*, 2007
	FMD cited	FI	animal registry and movement databases	simulations on structured and random networks	Lyytikäinen *et al.*, 2009
		BE	survey	in-degree, out-degree	Ribbens *et al.*, 2009
Horse	Equine influenza cited	UK	survey	degree, path length, clustering coefficient, small-world and random networks	Christley and French, 2003
Poultry	AI	UK	DEFRA GBPR, survey	comparative simulations (spatial and network dependent)	Truscott *et al.*, 2007
	AI	UK	GBPR, DEFRA data collection exercise	degree, largest component	Dent *et al.*, 2008
Fish	diverse cited	UK	fish movement records for Scottland	in-degrees, out-degrees, centrality, betweenness	Green *et al.*, 2009
Diverse	HIV, BTB, FMD cited	diverse		degree, betweenness, clustering coefficient, assortativeness coefficient, farness, small-world and random networks	Christley *et al.*, 2005
	SARS, STD, FMD cited	diverse		degree, random and scale free networks	Kiss *et al.*, 2006c

[AMLS=animal movement licensing system; BE=Belgium; BTB=bovine tuberculosis; CTS=cattle tracing system; DE=Germany, DEFRA=Department for Environment, Food and Rural Affairs; *E.coli* O157=*Escherichia coli* serotype O157:H7; FI=Finland; FMD=Foot-and-Mouth disease, GBPR=Great Britain poultry register; HIT=Herkunftsicherungs- und Informationssystem für Tiere (German animal register database); IT=Italy, SAMS=Scottish animal movement system; SARS=Severe Acute Respiratory Syndrome]

2 RATIONALE, AIM AND SPECIFIC OBJECTIVES

2.1 Rationale

Epidemic prevention and surveillance in human and animal populations are paramount to public health. To comply with national and international demands, national authorities such as the Swiss Federal Veterinary Office in Switzerland, adapt epidemic surveillance activities and corresponding animal health regulations based on scientific information facts and repeatable risk analyses. In the context of the threat of highly pathogenic avian influenza (HPAI) for domestic poultry in Switzerland, the need arose to better understand the countrywide population of poultry farms and keepers, as well as population-related determinants of functioning epidemic surveillance. This is required prior to targeting poultry farms in the surveillance systems based on their risk of acquiring or transmitting HPAI. Mathematical simulation models have played an increasingly important role in supporting decision makers' choices among different surveillance, prevention and control strategies. An understanding of a population's composition and real contact structure, namely how poultry farms are connected amongst each other, is crucial prior to any model-based epidemic preparedness planning.

2.2 Aim

This dissertation aims to contribute to a risk-based surveillance of HPAI in poultry in Switzerland. It intends to provide evidence on poultry farms' vulnerability to HPAI, to explore, refine and organize demographic and topological data, and their integration into epidemic models for the target population, namely poultry farms.

2.3 Specific Objectives

The specific objectives and main research questions are:

1) to gain insights into poultry farmers' disease awareness, which impacts the poultry farms' vulnerability to HPAI (Chapter 5)

- What is the poultry keepers' level of knowledge?
- What information is accessed?

- How does the poultry industry contribute with information?
- What influences the level of knowledge possessed by poultry keepers?
- How are HPAI risks perceived?

2) to identify epidemiologically relevant between-farm contacts (Chapter 6)

- What is the poultry farm density distribution?
- What are farm specifics and neighborhood relations?
- Which poultry and person movements are performed?
- Which is the spatial dimension of poultry movements?
- How frequent are poultry movements?
- How many different partners are poultry moved to and from?

3) to propose a model for a relational poultry registration database (Chapter 7)

- How can demographic information be organized to comply with epidemiological requests?

4) to provide general guidance on when contact repetition and clustering should be included in epidemic models (Chapter 8)

- How does contact repetition affect the modeled total outbreak size?
- How does clustering affect the modeled total outbreak size?
- How do clustering *and* contact repetition affect the total outbreak size?
- How do effects vary under different disease parameter constellations?
- What are implications of the findings for different infectious diseases and population groups?

5) to suggest a countrywide contact network model of poultry farms (Chapter 9)

- How can demographic data and contact data sets be synthesized in a meaningful way?
- What are the demographic characteristics of the synthetic populationof poultry farms in Switzerland?
- Does the distribution of the number of contacts follow a power law?

3 STUDY DESIGN

The population of interest consists of all poultry farms in Switzerland. Poultry farms, including the respective poultry keeper, are the autonomous units of observation.

This dissertation follows a mixed method research design, drawing on different empirical research methods of natural and social sciences. The subsequent section gives an overview on the performed data collection and data analysis. Detailed descriptions are included in the respective chapters.

3.1 Data sources

- A *new poultry farm census for Switzerland* was built by merging all available federal livestock registers and cantonal poultry farm registration databases from 2005 up to 2007 as shown in Figure 3.1. The new census comprises 49,437 poultry farms.
- A *cross-sectional survey* was conducted among 3,978 (weighted) randomly selected poultry keepers. The survey instrument was a structured mail-out/mail-back questionnaire addressing the topics of (i) farm characteristics, (ii) knowledge on HPAI and risk perception, (iii) wild bird observations (Saurina, 2009), and (iv) poultry and person movements and shared resources. It was developed in German and translated to French and Italian languages (Appendix 2 [German]).
- Five *interviews with experts* from companies integrating poultry farms were conducted. Topics included (i) the company's efforts to inform poultry keepers on HPAI and (ii) poultry and person movements, as well as shared resources due to company affiliation. The interviews were conducted using guiding questions and a mapping tool (Appendix 3).
- A *literature review* was conducted on example diseases for the basic reproductive ratio (also R_0 or basic reproduction number), transmission period, and main contagious pathways. The transmission parameters were identified by literature searches of the Medline and Web of Science databases and biomedical textbooks without date restrictions up to February 2009.

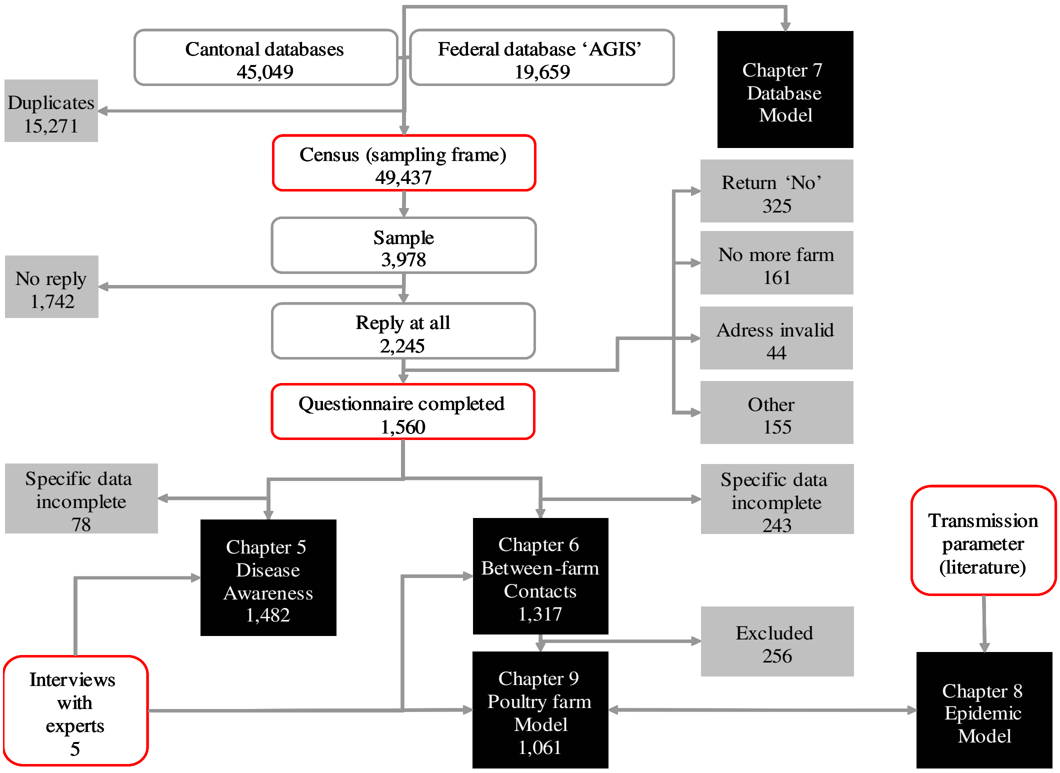

Figure 3.1 Data sources (red boxes) and their use in the dissertation chapters (black boxes)

3.2 Data analysis

Applied analytical approaches include:

- Descriptive and analytical statistics (generalized linear models) of ego-centric network data and other quantitative survey data using Stata (version 9.1, StataCorp LP, TX, USA) and R (version 2.7.2, the R Foundation for Statistical Computing);
- Spatial statistics with *maptools* and *spatstat* libraries in R, based on maps from Swisstopo 2008® and geo-referencing of all locations of poultry farms and their contacts;
- Transcription and qualitative content analysis of interview protocols according to Mayring (2003) and semi-quantitative analysis of narratives in the questionnaire;
- Relational database modeling using an entity-relationship model (Chen, 1976);
- Comparative epidemic simulations based on individual-based stochastic SIR-models of different architecture and under systematically varied transmission parameter constellations in Fortran language.

3.3 Concept of interplay between surveillance and epidemiological modeling

This dissertation is situated where surveillance and epidemiological modeling interplay. Decision making in epidemic surveillance, prevention and control draws increasingly on mathematical modeling. Mathematical simulation models are needed to make predictions on transmission dynamics and effects of different intervention options. This is challenging when case numbers are small, multiple population groups and dynamics of disease spread are highly variable. Matthews and Woolhouse (2005) provide a schematic of surveillance data qualifying as important input data for mathematical modeling. Surveillance components are classified into sources of demographic, epidemiological, and biological information, as well as of real-time data.

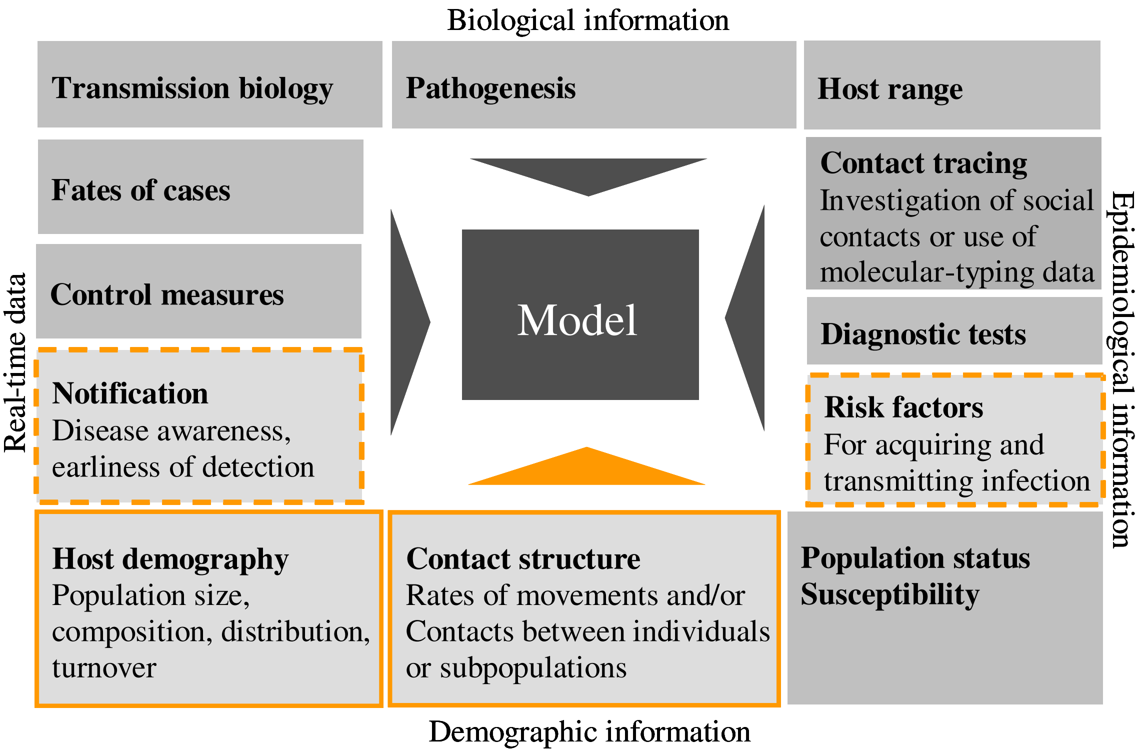

Figure 3.2 “From surveillance to modeling”. Components addressed in this dissertation are highlighted. This dissertation contributes to HPAI surveillance in Switzerland and respective models with input data (continuous orange borders) or with pre-outbreak assessments (dashed orange borders). Adoption of Figure 2 in Matthews and Woolhouse (2005); courtesy of L. Matthews

The advantage of drawing on defined schematics such as Figure 3.2 is the easy detection of gaps in surveillance and research. Defined schematics establish a basis for large-scale collaboration projects towards modeling of epidemiological effects, impact of interventions and their cost-effectiveness.

This dissertation draws on the provided schematic in the context of risk-based HPAI surveillance. Several components (highlighted in orange in Figure 3.2) are addressed; mainly demographic information and contact structure of the poultry sector are included. Given the HPAI outbreak-free situation in Switzerland, epidemiological information and real-time data are only partly addressed: firstly, by the inquiry of HPAI awareness of poultry keepers that is of predictive value for adequate and timely notification in case of an HPAI outbreak; secondly, by identifying presumptive risk factors. They include geographical location, flock composition, and, as part of a parallel dissertation, wild birds' access to poultry housing (Saurina, 2009). Biological factors and diagnostics are covered by different research projects in Switzerland (Chapter 4). The relationship between surveillance data and epidemic modeling is addressed for the demographic component. This comprised the conditioning and synthesizing of demographic data sets towards a contact network model of the poultry farms as a basis for epidemic modeling. Furthermore, this includes systematic comparison of structurally different models to better understand biological and demographic conditions under which detailed information on contact structure must be carefully surveyed.

3.4 Ethical considerations

Questionnaire survey and interviews with individuals were performed after informed consent was received. All data were handled using methods that precluded identification of individuals from the results or maps. Names of participants and research databases were kept separate from each other.

This dissertation involved no testing in humans or animals and was approved by the scientific committee of the STI.

4 COLLABORATION

4.1 Swiss Tropical Institute

The dissertation was embedded in the research project “Effectiveness of surveillance, prevention and control strategies of avian influenza in Switzerland” (project 1.07.05 BVET) and in the research project “Constanze” (project 1.07.01 BVET), funded by the Swiss Federal Veterinary Office and based at the Swiss Tropical Institute (STI). Two more thesis works have been performed within the same project framework:

- Dr. med. vet. Jennifer Saurina completed a Doctor of Veterinary Medicine thesis at the Vetsuisse Faculty in January 2009 entitled “Risk-based Surveillance of Avian Influenza in Switzerland: Wild Birds and Awareness”, supervised by Assistant Professor Dr. med. vet. PhD Dip. ECVPH Jakob Zinsstag (STI) and Professor Dr. med. vet. Ulrich Kihm (Vetsuisse);
- Msc. Biol. Thomas Kernen completed a Master of Science thesis in Infection Biology and Epidemiology at the University of Basel in Mai 2008 entitled “Survey among Swiss Poultry Holders in the Lake Constance Region in Relation to a potential Spread of Avian Influenza”, supervised by Assistant Professor Dr. med. vet. PhD Dip. ECVPH Jakob Zinsstag (STI).

These thesis works have been conducted in close cooperation with the present dissertation, drawing on common field data, in particular concerning Chapter 5. Dr. med. vet. PhD Esther Schelling supervised all project activities within the STI in the period of August 2008 to July 2009. PhD Jan Hattendorf has worked part-time within the project framework providing statistical support.

4.2 Swiss Federal Veterinary Office

This dissertation study was affiliated to the FVO Monitoring Department. The Department’s AI related activities involve risk analyses for the introduction of AI into domestic poultry (Hauser *et al.*, 2006b), serological LPAI surveillance in free-range poultry (Wunderwald, 2007), and for instance a risk assessment concerning the illegal import of animals and animal products and its implications for disease spread (Läubli *et al.*, 2008). In addition, the estimatation of the overall sensitivity of AI surveillance in domestic poultry in Switzerland has been approached (Hauser *et al.*, 2008). Dr. med. vet. PhD Martin Reist, head of the Monitoring Department, as well as many of his colleagues, supported the project activities at the STI scientifically and by facilitating the communication with cantonal veterinary authorities and experts of the poultry industry, as well as the poultry research, education and service centre “Aviforum”.

4.3 Research project Constanze

The three-year research project “Constanze” was launched in June 2006 to coordinate AI research around the Lake of Constanze. It involved German, Austrian and Swiss research institutions and veterinary authorities. The aim was to better understand transmission dynamics of AI and to assess surveillance activities in wild birds, namely passive surveillance, sentinel ponds and weirs, in a comparative way. To enhance passive AI surveillance on the level of poultry farms, a video entitled “Bird Flu: Prevent now!” (Bundesamt für Veterinärwesen, 2009c) was produced and distributed among a large part of the poultry keepers in Switzerland.

Main collaborators of the Constanze were:

- Friedrich-Loeffler-Institute (FLI) in Riems and Wusterhausen (Germany);
- Ornithological Station of the Max-Planck-Institute for Ornithology in Radolfzell (Germany);
- Agency for Health and Food Safety (AGES) in Bregenz and Graz (Austria);
- Institute of Virology and Immunoprophylaxis (IVI) in Mittelhäusern (Switzerland);
- Ornithological Station in Sempach (Switzerland);
- and the Swiss Tropical Institute (STI) in Basel (Switzerland).

Close links to AI research project “WuV” in Baden-Württemberg (Germany) were established.

Main project packages included:

- Ornithology;
- AI Surveillance in wild aquatic birds;
- AI Diagnosis;
- Experimental infections; and
- Risk modeling (mainly covered by the STI).

Assistant Professor Dr. med. vet. Christian Griot (IVI) was the project leader and Dr. med. vet. Iris Brunhart (BVET) was coordinating the project.

4.4 ETHZ

This dissertation was linked to research activities at the Institute for Environmental Decisions (IED) and the Institute for Transport Planning and Systems (IVT) of the ETHZ, Switzerland. The cooperation, in particular with Msc. ETH Timo Smieszek (IED), provided access to social contact networks and computing capacity.

- Msc. ETH Timo Smieszek is conducting a PhD thesis at the ETHZ entitled “Models of epidemics: How contact characteristics shape the spread of infectious diseases”, supervised by Professor Roland W. Scholz (IED), Assistant Professor Dr. med. vet. PhD Dip. ECVPH Jakob Zinsstag (STI), and Professor Dr. Ing. Kay W. Axhausen (IVT).

The dissertation project of Timo Smieszek is methodologically closely related to Part 2 and will contain Chapter 6 and 8 of the present thesis. Professor Dr. Ing. Kay W. Axhausen provided consult on the network study design and, together with his collaborator Veronika Killer, georeferenced all spatial data in this dissertation.

PART 1

POULTRY FARM DETERMINANTS

5 DISEASE AWARENESS OF THE POULTRY KEEPERS IN SWITZERLAND AND THEIR ACCESS TO INFORMATION CONCERNING HIGHLY PATHOGENIC AVIAN INFLUENZA

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5.1 Abstract

The passive surveillance of highly pathogenic avian influenza (HPAI) in domestic poultry (avian plague or fowl pest) is based essentially on the reporting of suspicious clinical cases by the poultry keepers to the veterinary services via a veterinarian. In the case of HPAI, there is a broad range of symptoms from high mortality to asymptomatic cases depending on the disease-causing virus strains and the affected host species. As little was known about HPAI disease awareness and the level of knowledge among Swiss poultry keepers, a cross-sectional study was conducted among poultry keepers in Switzerland from August to December 2007. To 3,978 poultry keepers, both non-commercial and commercial farms, a mail questionnaire was distributed. For data triangulation and complementary information, five interviews have been conducted with experts of poultry industry. The main information source used by the poultry keepers was mass media. Having a non-commercial poultry husbandry was significantly associated with lower knowledge scores. Non-commercial poultry keepers felt neglected by the veterinary authorities. Risks perceived by the poultry keepers reflected in general well the officially communicated risks for HPAI introduction.

These findings assist strategies to improve the knowledge on HPAI of all poultry keepers. By highlighting the needs, concerns and the knowledge level of the poultry keepers in Switzerland, we make recommendations with regard to more efficient information exchange between poultry keepers and cantonal and federal authorities. The main challenge will be to consistently integrate non-commercial poultry keepers in the formal information channels.

5.2 Résumé

La surveillance passive de l'influenza aviaire hautement pathogène (IAHP) chez la volaille (peste aviaire classique, grippe du poulet) consiste principalement en la notification des cas suspects par les détenteurs de volaille auprès des autorités vétérinaires par le biais des vétérinaires praticiens. En cas d'IAHP, de multiples manifestations sont possibles, variant d'une mortalité élevée à une forme clinique très modérée selon la souche pathogène et l'espèce infectée. Du fait que peu est connu sur la perception de l'IAHP ainsi que sur le niveau de connaissances des détenteurs de volaille en Suisse, une étude transversale a été conduite parmi les détenteurs de volaille en Suisse entre août et décembre 2007 ; 3.978 détenteurs de volaille, gérant de petites exploitations ou des fermes avicoles commerciales, ont reçu un questionnaire

par courrier postal. Pour une triangulation des données et afin de récolter des informations complémentaires, cinq interviews ont été conduites avec des experts d'organisations de commercialisation de volaille. Les médias se sont avérés comme la source et voie principale d'information consultée par les détenteurs de volaille. Le fait d'avoir une petite exploitation de volaille était significativement associé avec un score de niveau de connaissance inférieur. Les petits détenteurs de volaille interrogés se sentaient négligés par les autorités vétérinaires. En ce qui concerne la perception des risques, les estimations des participants correspondaient généralement avec les risques d'introduction de l'IAHP officiellement communiqués.

Ces résultats créent une base pour une amélioration des connaissances des détenteurs de volaille concernant l'IAHP. En considérant les besoins, les préoccupations et les connaissances des détenteurs de volaille en Suisse, nous recommandons de renforcer l'échange d'information entre les aviculteurs et les autorités vétérinaires cantonales et nationales. Le défi principal consistant en l'intégration continue des détenteurs de volaille non professionnels dans la voie d'information.

5. 3 Riassunto

La sorveglianza passiva dell'influenza aviaria altamente patogena (IAAP) nel pollame (peste aviaria classica, influenza del pollo) consiste principalmente nella notifica alle autorità veterinarie tramite gli studi veterinari dei casi sospetti segnalati dagli allevatori di pollame. Nel caso dell'IAAP le manifestazioni cliniche possibili sono molteplici, variando da una mortalità elevata fino ad una forma poco apparente, a seconda del ceppo patogeno e della specie ospite. Attualmente poco è noto circa la percezione dell'IAAP e il livello di conoscenze dei detentori di pollame in Svizzera, uno studio trasversale é stato condotto tra gli allevatori di pollame in Svizzera nel periodo compreso tra agosto e dicembre 2007. È stato inviato per posta un questionario a 3.978 allevatori, sia in piccole aziende che in allevamenti commerciali. È stata raggiunta una percentuale soddisfacente di risposte, ossia il 39%. Cinque ulteriori interviste con degli esperti di organizzazioni per il commercio del pollame sono state effettuate per avere una triangolazione dei dati e per ottenere informazioni complementari. I mass media si sono avverati essere le fonti e le vie principali di informazione consultate dagli allevatori di pollame. Il fatto di gestire un piccolo allevamento di pollame era significativamente associato ad un livello inferiore di conoscenze. I piccoli allevatori interrogati si sentivano trascurati dalle autorità federali. In generale, i rischi percepiti dagli allevatori riflettevano bene i rischi ufficialmente comunicati riguardanti l'introduzione dell'IAAP.

Questi risultati creano una base per un miglioramento delle conoscenze riguardanti l'IAAP da parte degli allevatori di pollame. Considerando i bisogni degli allevatori in Svizzera, le loro preoccupazioni e le loro conoscenze, raccomandiamo di rafforzare lo scambio di informazioni tra gli allevatori e i servizi veterinari cantonali e federali. La sfida principale consisterà nell'integrazione costante degli allevatori amatoriali nei canali di informazione ufficiali.

5.4 Zusammenfassung

Die passive Überwachung der hochpathogenen Aviären Influenza (HPAI) bei Nutzgeflügel (Klassische Geflügelpest) beruht vor allem auf der Meldung klinischer Verdachtsfälle durch Geflügelhaltende über einen Tierarzt an die Veterinärbehörden. Im Falle von HPAI können ganz unterschiedliche Krankheitsbilder vorkommen, die, je nach Erregerstamm und Wirtsspezies, von einer hohen Sterblichkeitsrate hin zu einer unscheinbaren Verlaufsform reichen können. Um vorschriftsgemäss handeln zu können, müssen Geflügelhalter die Krankheitserscheinungen gut genug kennen. Da wenig darüber bekannt ist, wie Geflügelhaltende in der Schweiz die HPAI-Gefahr wahrnehmen, und wie gut sie über die Krankheit Bescheid wissen, wurde eine Querschnittsstudie unter Geflügelhaltenden in der Schweiz im Zeitraum von August bis Dezember 2007 durchgeführt. Insgesamt 3.978 Geflügelhaltende, sowohl von nichtgewerblichen, als auch von gewerblichen Geflügelbetrieben, erhielten auf dem Postweg einen Fragebogen. Zur Datentriangulation und für weiterführende Informationen wurden fünf Interviews mit Experten von Geflügelvermarktungsorganisationen geführt. Es stellte sich heraus, dass Geflügelhalter hauptsächlich über Massenmedien Informationen erhalten. Telnehmende mit nichtgewerblichen Geflügelhaltungen hatten signifikant geringere Kenntnispunktzahlen und fühlten sich häufig von den Veterinärbehörden vernachlässigt. Was die Risikowahrnehmung betrifft, so deckten sich die Einschätzungen der Risiken durch die Geflügelhaltenden generell gut mit den offiziell kommunizierten Risiken für eine Einschleppung von HPAI.

Diese Ergebnisse sind wichtig für eine Verbesserung der Aufklärungsarbeit über HPAI. Auf der Grundlage der erfassten Bedürfnisse und Anliegen der Geflügelhaltenden, sowie der Einschätzung ihres Wissensstandes, wird insbesondere empfohlen, den Informationsaustausch zwischen Geflügelhaltern und zuständigen Veterinärbehörden auf kantonaler und nationaler Ebene zu fördern. Die hauptsächliche Herausforderung besteht darin, die nichtgewerblichen Geflügelhalter dauerhaft in offizielle Informationswege einzubinden.

5.5 Introduction

Highly pathogenic avian influenza (HPAI) in poultry, also known as fowl plague, is a viral disease with high economic impact (Davison *et al.*, 1999; Fasina *et al.*, 2008). Switzerland is declared free of AI in its domestic poultry population since 1931. In 1997, H5N1, a new highly pathogenic avian influenza virus having zoonotic potential, appeared in Hong Kong and spread subsequently since 2005 from Asia to Europe causing several outbreaks in poultry, for instance in England, Germany, France and Hungary (EFSA, 2007). These outbreaks in Europe occurred in different types of poultry husbandries with regard to location, production system, professionalism, and poultry species kept. To detect low and highly pathogenic avian influenza viruses early and to maintain the status of freedom from HPAI in domestic poultry, Switzerland is carrying out active monitoring programs and has a passive surveillance system in place (Bundesamt für Veterinärwesen, 2008). Passive surveillance relies essentially on livestock keepers reporting suspicious clinical signs in their poultry (Lilienfeld and Stolley, 1994). Prompt notification of suspicious cases of any OIE or nationally notifiable epidemic disease to the veterinary authorities, via a veterinarian, is mandatory for everyone keeping, handling, or treating animals (Der Schweizerische Bundesrat, 1995). The broad participation in a passive surveillance system facilitates a performance at rather low cost because it is continuously in place and operational wherever livestock is kept. However, its effectiveness strongly depends on the livestock keepers' disease awareness and whether they comply with their obligation of prompt reporting of suspicious cases to their veterinarian. Good disease awareness stands for having an adequate knowledge of the related clinical manifestations. This is particularly challenging in the case of HPAI where symptoms are manifold or even absent and differ between the disease-causing virus strains and the poultry species affected (Bundesamt für Veterinärwesen, 2008). Disease awareness further implies realistically assessing relevant pathways for pathogen introduction into poultry farms, avoiding risky behavior. Building and maintaining disease awareness for HPAI, which has not been emerging for decades in Switzerland, requires a specific information policy. The Swiss Federal Veterinary Office (FVO) names it a *"central and rewarding task"* to inform livestock keepers, veterinarians, and the general public on epidemics (Falk, 2005). Thus, the FVO provides free information material on HPAI, available on the FVO homepage and as print-outs in German, French, and Italian language (Bundesamt für Veterinärwesen, 2008). Further, H5N1, more popularly called “bird flu”, had high media attention. Many institutions, whether scientific or not, have made information available and affordable to anyone. However, not all information is adequate for all poultry keepers, and not all sources are regularly accessed by them.

Only few epidemiological investigations (for instance by Lovis *et al.*, 2008) focused on risk perception and disease awareness among livestock keepers in Switzerland. For poultry keepers, a complicating factor to set-up a study was the unknown number and diversity of poultry keepers in Switzerland, as non-commercial husbandries were only registered systematically since October 2005 (Der Schweizerische Bundesrat, 2006). Representative information on the poultry keepers’ HPAI awareness and their information sources accessed was not available. Data on these aspects are needed: One may assume that passive HPAI surveillance will remain crucial or even gain importance in Switzerland and internationally given its financial and strategic benefits. The present study aimed at identifying needs and gaps in the passive surveillance system for HPAI in Switzerland and at suggesting actions for improvement by 1) depicting the perceived information quality and the needs on information of poultry keepers, by 2) determining the sources of information accessed by the poultry keepers, by 3) assessing their level of knowledge on HPAI and its influencing factors, and by 4) providing an insight into the risk perception of the poultry keepers in Switzerland.

5.6 Material and methods

Study design

From August to December 2007 a cross-sectional study concerning avian influenza surveillance was conducted among poultry keepers in Switzerland. The sampling frame consisted of a total of 49,437 countrywide identified commercial and non-commercial poultry keepers. For the purpose of a single list of poultry keepers in Switzerland the so called AGIS database (agricultural information system) by the Federal Office for Agriculture and the cantonal agricultural offices (Bundesamt für Statistik, 2007) were aggregated with entries of poultry husbandries registered on a cantonal level (Kernen, 2008). A random sample of 3,978 keepers was drawn proportionally to the square root of the number of poultry kept on a farm, to ensure a sufficient number of the less numerous larger poultry farms.

A structured questionnaire with closed and open questions was developed together with epidemiologists, experts from the poultry sector and from the FVO, as well as ornithologists. The questions covered general characteristics of poultry husbandry, the observation of wild birds, trading contacts to other poultry farms, and, focus of the present article, the disease awareness of the poultry keepers and their access to relevant information as to avian influenza. Throughout the questionnaire the colloquial term “bird flu” was used to address the disease. The questionnaire was translated from German to French and Italian and was sent out to poultry keepers in all cantons of Switzerland. Data of the returned and completed questionnaires (39% response rate, n=1,560) were double-entered into Access (version 2003, Microsoft Corporation, Redmond, Washington, USA), compared and cleaned in EpiInfo (version 3.4.1, Centers for Disease Control and Prevention, Atlanta, Georgia, USA) and analyzed using Stata (version 9.1, StataCorp LP, TX, USA).

Further, five guided interviews have been conducted with experts of poultry marketing organizations (integrating companies) for checking the coherence of the collected data (data triangulation) and to complement information on information channels used within commercial poultry production.

Quantitative data

To assess the needs and concerns, the poultry keepers were asked whether they felt well informed or not and which further information they desired. A semi-quantitative analysis was performed by pooling similar narrative statements into three categories: sought information and needs, criticisms on accessed information and suggestions for improvements. The protocols taken during the interviews with experts from poultry marketing organizations were transcribed and underwent content analysis.

Scoring

A “knowledge score” and a “perceived risk score” have been introduced to rate the respondents’ answers on knowledge and their risk estimations for AI introduction into the Swiss poultry sector via different routes, respectively. The “knowledge score” was calculated based on four questions (Table 5.2) by giving 2 points for a correct answer, 1 or 0.5 points for a partly correct answer, 0 point for a wrong or an “I do not know” answer. Thus a maximum of 8 points could be obtained indicating highest level of knowledge. The “perceived risk score” of AI introduction in the poultry sector was assessed with participants’ estimations of the probability of 9 different routes of introduction qualified by “high”, “medium”, “small”, “insignificant”, or “I do not know”. Four points were assigned to “high”, 3 to “medium”, 2 to “small”, 1 to “insignificant” and 0 to “I do not know”,

Analysis of scores

The knowledge score was categorized into: category 1 if score ≤ 2, category 2 if score 2 < and ≤ 4, category 3 if score 4 < and ≤ 5 and category 4 if score > 5. These categories were introduced to show general trends rather than smooth differences. A multinomial model with the outcome of categorized scores was used to investigate the following explanatory variables: (i) the three language regions, (ii) the level of professionalism, (iii) the kept poultry and (iv) the information sources (Figure 5.1).

5.7 Results

Participants

In the general part of the questionnaire, 1,482 participants classified their husbandry into “commercial” 626 (42%) or “non-commercial” 856 (58%). This self-assessment referred basically to the number of poultry kept. Participants lived mainly in German speaking parts of Switzerland (1,167, 79%), but also in French (280, 19%) and Italian speaking parts (35, 2%). Further details on the participants’ characteristics are shown in Table 5.1 and in an analysis report for poultry keepers (Appendix 4).

Perceived information quality and needs on information

Eighty one percent of the respondents stated being well-informed about “bird flu”, 14% felt that they were not well enough informed and 5% replied that they did not know whether they were sufficiently informed. No significant differences in perceived information level were seen between commercial and non-commercial keepers, the language regions and the different information sources (data not shown).

Out of a total of 134 respondents, who did not feel well-informed, two-thirds provided narratives. More than 55% were classified as needs, close to 20% as criticisms and more than 16% as suggestions for improvement. Nine percent could not be classified.

Table 5.1 Participant groups (commercial and non-commercial) and their characteristics (language of participant, number of poultry kept, flock composition)

	Commercial	**Non-commercial**	**Total**
	n=626 (42.2%)	n=856 (57.8%)	n=1,482 (100%)
Language of participant			
German	494 (78.9%)	670 (78.6%)	1,167 (78.7%)
French	130 (20.8%)	150 (17.5%)	280 (18.9%)
Italian	2 (0.3%)	33(3.9%)	35 (2.4%)
Number of poultry kept			
Median [IQR[1]]	4,500 [6,992]	15 [22]	40 [3,838]
Flock composition	relating to n= 621:	relating to n=849:	relating to n=1,470:
No water bird kept	585 (94.2%)	670 (78.9%)	1,255 (85.4%)
Pure water bird flock	0 (0%)	20 (2.4%)	20 (1.4%)
Mixed flock with water birds	36 (5.8%)	159 (18.7%)	195 (13.3%)

[[1]IQR : Interquartile range]

Needs

The respondents asked for detailed information about the infectious agent, its survival strategies, its transmission pathways and in particular (47% of all comments) the symptoms in the different poultry species. More than 15% of the respondents wanted more information on protection and preventive measures, which can be implemented by laypersons. Results of risk analyses done by the veterinary services and the success of preventive measures in place were requested by another 5%. Further, some poultry keepers were interested in receiving more information on the number of birds that died in Switzerland due to “bird flu” and the number of poultry slaughtered because keepers were unable to confine their animals. Close to 3% of respondents stated that there was too little information about the danger for humans and about risk of AI introduction via wild birds.

Critics

Media in particular but also veterinary authorities were criticized by respondents' as shown in the following remarks:

"[The poultry keepers] do not know whom to trust and which information is distorted by the media"; *"If something marginal happened, it will be exaggerated by the media"*; *"[The poultry keepers learn] too much from the mass media and too little from the FVO and the cantonal veterinary offices"*; *"[The poultry keepers would like] more objectiveness and less hysteria"*.

Suggestions

Main proposition of the respondents was a more coordinated information strategy. They made suggestions for an optimized communication such as *"Information from one center and targeted at the professionals [would be beneficial]"*. This central office should update the keepers on a regular basis on the current situation in the region, either by e-mail, personal communication, or the professional journal (e.g., „Schweizerische Geflügelzeitung“) as pointed out in the following citations: *"[Poultry keepers want] regular reports as to where the risk is the highest"*; *"Half-yearly situation reports from the cantonal veterinary office [are desired]"*.

Sources of information accessed by the poultry keepers

The main source of information for Swiss poultry keepers was the mass media for 68% and 88% of commercial and non-commercial poultry keepers, respectively. In contrast to non-commercial poultry keepers, the second most used source of information for commercials was the commercial associations (virtually all commercial farms were integrated in poultry marketing organizations) and commercial journals. Twenty-two percent and 31% of respondents received information from the federal and the cantonal veterinary office, respectively (Figure 5.1).

Professional associations played an exceptional role among the information sources. In contrast to other sources, counseling from commercial associations requires membership and a consistent mutual commitment of poultry keepers and associations. The interviews with experts showed that the associations were actively and regularly informing their members on HPAI and other relevant topics of poultry health. The frequency of updates depended on the epidemiological situation in Switzerland and surrounding countries, but was always more frequent than once per year. All associations have used more than one channel for disseminating the information. Mostly, newsletters were sent by mail and/or delivered together with the accounts to egg producers. Annual producer meetings were optional, but well attended. Consultants and/or veterinarians from the associations were visiting all member farms regularly (several times per year), and additional visits were organized on the poultry keepers' request. Experts were available to the members by telephone all day or even around the clock. With regard to the content of information, the experts were drawing on own experiences, on legal texts, and on recent and scientific publications. Their professional network involved cantonal and federal veterinary services, Swiss and international poultry experts and the Aviforum, the Swiss aviculture education, research, and service centre. All experts affirmed that with all their member farms at least a baseline information exchange on HPAI was guaranteed.

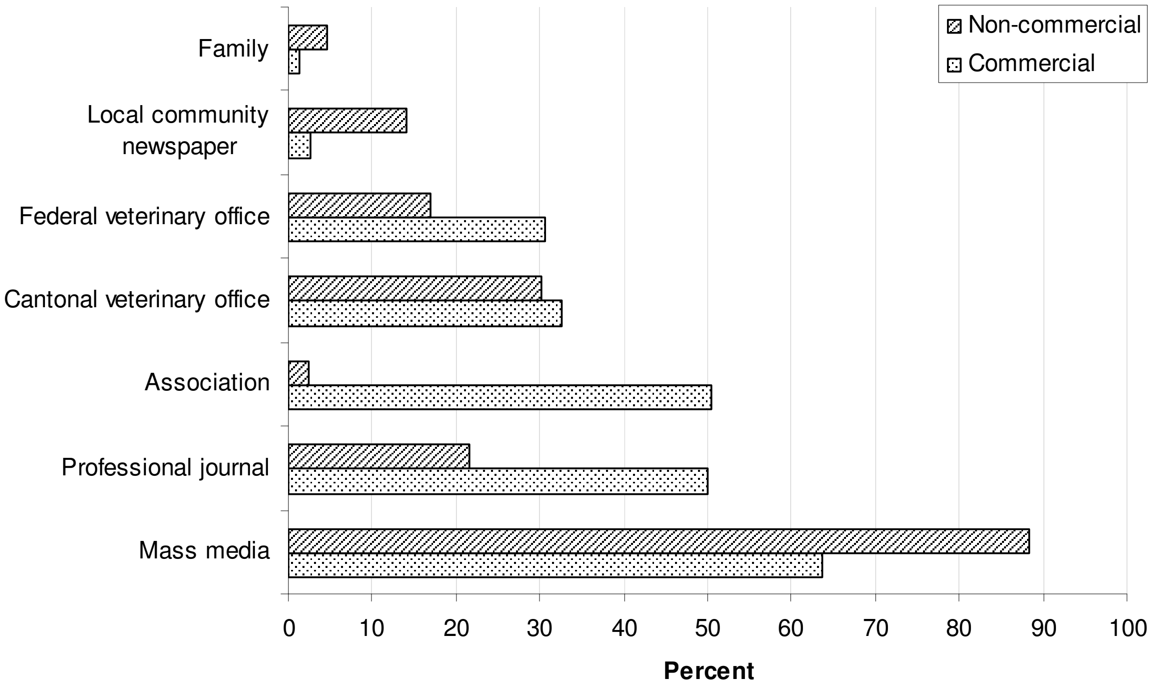

Figure 5.1 Source of information according to degree of professionalism: Proportion (in %) of commercial and non-commercial poultry keepers getting information from different sources

Level of knowledge on HPAI and its influencing factors

The mean score of the knowledge level was 3.1 with a minimum of 0.5 and a maximum of 8 points. This distribution of participants' score results has been taken into account for the categorization. Multinomial regression analyses resulted in "living in the French speaking region", being a "commercial keeper", "keeping only chicken" and getting information from "professional journals" and "affiliation to marketing organization" being explanatory variables which were significantly associated with a higher knowledge level (category 2-4) of respondents. The French speaking region being associated with higher knowledge scores when compared to the German and Italian speaking regions could not be explained by a different distribution neither of professionalism nor of information sources. The questions asked on HPAI and detailed results are provided in Table 5.2.

Table 5.2 Distribution of the answers given to the four questions and allocated points used to calculate the knowledge score

Question		Number	Percent	Points
Please assess: bird flu and... ..		n=1158		
... flow plague …	are the same	143	12%	2
	are similar	201	17%	0
	are different	343	30%	0
	I do not know	471	41%	0
... Newcastle disease …	are the same	2	<1%	0
	are similar	75	6%	0
	are different	324	28%	2
	I do not know	757	65%	0
... the yearly human flu …	are the same	7	1%	0
	are similar	224	19%	1
	are different	607	52%	2
	I do not know	320	29%	0
Bird flu situation in Switzerland:		n=1486		
In the past 5 years did any case occur in commercial poultry?	Yes	239	16%	0
	No	1057	71%	2
	I do not know	190	13%	0

Table 5.2 (continued) Distribution of the answers given to the four questions and allocated points used to calculate the knowledge score

Question			Number	Percent	Points
Symptoms:			n=1418		
	Which of the following symptoms make you suspecting a bird flu infection in chicken?				
		Coughing	143	9%	a
		Poor eating and drinking	403	28%	a
		Scrubby plumage	217	14%	a
		Lameness	156	10%	a
		Loss of coordination	185	12%	a
		Abnormal eggshells	54	4%	a
		Cannibalism	5	<1%	a
		Diarrhea	166	11%	a
		Unexplained death of several animals	1321	87%	a
		Vomiting	22	1%	a
		Sneezing	87	6%	a
		Decrease of egg production	179	11%	a
		Decrease of growth	37	2%	a
		Swollen head and crest	185	12%	a
		Paralysis	164	11%	a
		Abnormal movement of the head	125	8%	a
		I do not know	143	9%	0
	Which poultry species do(es) not show any obvious and typical symptoms?				
		All poultry species show obvious symptoms	752	53%	b
		Chicken	32	2%	b
		Duck	52	4%	b
		Quail	19	1%	b
		Turkey hen	12	1%	b
		Partridge	20	1%	b
		Guinea fowl	18	1%	b
		Ostrich	63	4%	b
		Goose	37	3%	b
		I do not know	550	39%	b

a		
5 and more symptoms checked	198 (13%)	2
3-4 symptoms checked	328 (21%)	1
1-2 symptoms checked	892 (58%)	0.5
No symptom checked	8%	0

b		
If duck and goose	29 (2%)	2
If duck or goose + and others	37 (3%)	1
If one other	1361 (95%)	0

Risk perception of poultry keepers

The respondents probability weighting for nine different routes of AI introduction resulted in highest perceived risk scores (possible from 0 to 4) for “Migratory birds” between 2.9–3.3 (overall mean 3.1) and for “Live poultry” between 3.0–3.4 (overall mean 3.2) with non significant differences between types of professionalism and the region (Table 5.3).

Table 5.3 The mean of the “perceived risk score” is shown for type of professionalism level and language region with the rank in brackets. The minimum possible score was 0 and the maximum 4. Because of the too few data from the Italian speaking region, no summary statistics were done

		Live poultry	Migratory birds	Tourism	Poultry product	Animal feed	Bio-terrorism	Other animal species	Wind	Other options
	All keepers	3.2 [1]	3.1 [2]	2.4 [3]	2.3 [4]	2.1 [5]	1.4 [6]	1.4 [6]	1.4 [6]	0.9 [9]
mean risk (0-4)	Commercial	3.4 [1]	3.3 [2]	2.8 [3]	2.4 [4]	2.0 [5]	1.6 [6]	1.6 [6]	1.6 [6]	1.2 [9]
	Non-commercial	3.0 [1]	2.9 [2]	2.1 [4]	2.2 [3]	2.1 [4]	1.4 [6]	1.2 [8]	1.3 [7]	0.6 [9]
	German speaking	3.2 [1]	3.0 [2]	2.4 [3]	2.3 [4]	2.1 [5]	1.5 [6]	1.4 [7]	1.4 [7]	1.0 [9]
	French speaking	3.1 [2]	3.3 [1]	2.3 [3]	2.1 [4]	2.0 [5]	1.3 [6]	1.2 [8]	1.3 [6]	0.3 [9]

5.8 Discussion and conclusions

This is the first large-scale study addressing the disease awareness of the poultry keepers in Switzerland and their access to information concerning HPAI with the overall goal to identify needs and gaps in the passive surveillance system for HPAI in Switzerland. The investigation of the poultry keepers’ perceived information quality, their stated needs, and the sources of information they access basically confirmed that there were various information sources available. Access to comprehensive and high quality information differed between respondent groups. Commercial poultry keepers were integrated in the information policy of their marketing organization whereas non-commercial poultry keepers mostly had mass media as principal information source and were not affiliated to a marketing organization.

The investigations related to the poultry keepers’ disease awareness highlighted both an adequate knowledge level of the participants for several HPAI related topics, and gaps on other topics. Good knowledge was evident in the part on risk perception. The outcome that “migratory birds” and “live poultry” were determined as most probable pathways for HPAI introduction went in line with official risk assessments. This supported a successful risk communication on that topic. The need for enhanced awareness training and communication on topics such as clinical manifestations of HPAI in different poultry species and on preventive measures was identified in the written statements and by the knowledge questions. Non-commercial poultry keepers had comparatively lower knowledge score outcomes than commercial poultry keepers which can partly be explained by their presumed training background and by the limited information sources accessed. Interestingly, the majority of the respondents felt to be well-informed, whereas the results of the analysis of the knowledge level did not generally support this self-concept. One can therefore not assume that every poultry keeper would actively and specifically search for further information.

The presented study was done to obtain an overview among all types of poultry holdings. It could be assessed that respondents and non-respondents did not differ significantly with regard to geographical region, flocks size, and poultry kept. The questions used for the knowledge score were posed in a simplistic way and might have been ambiguous to very well informed participants. Furthermore, it was not possible to validate if keepers used external help while completing the questionnaire and thus achieving a higher knowledge score result. However, for the purpose of this study, it did not matter if keepers knew where to look or whom to ask. For an in-depth understanding of single items and their influencing factors, complementary qualitative investigations among poultry keepers would be an asset.

A close collaboration between authorities, veterinarians, and livestock keepers is essential for rapid reporting (OIE, 2004) and requires the continuous exchange of concerns and opinions. Those benefiting from a well functioning disease surveillance, namely poultry keepers, commercial organizations, veterinarians, federal and cantonal veterinary authorities, should share knowledge intensively, and communicate proactively with members of the media to provide effective and coordinated information to the public and more specifically to the poultry keepers (Abbate *et al.*, 2006). This can help to avoid both inattentiveness and panic mongering.

Needs and gaps identified in the present study can impinge upon the current performance of passive HPAI surveillance in Switzerland and should therefore be addressed by veterinary authorities. First, it is essential to record all poultry keepers in an updated database, useful for the surveillance and control of any poultry related and zoonotic disease. Only then high quality and well tailored information material such as the produced and already distributed video "Bird Flu: Prevent now!" (Bundesamt für Veterinärwesen, 2009c) can reach poultry keepers all over Switzerland without delay. A particular challenge for veterinary services remains to fully integrate non-commercial poultry keepers in the information channel which they might highly appreciate.

5.9 Acknowledgements

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5.10 Authors' contributions

JS designed the study, was responsible for the data collection, analysis and interpretation and wrote the article. LF participated in the study design, conducted and analyzed the expert interviews and wrote the article. JZ participated in the survey design and paper editing. ES participated in the analysis and paper editing. All authors read and approved this manuscript.

6 CONTACTS BETWEEN POULTRY FARMS, THEIR SPATIAL DIMENSION AND THEIR RELEVANCE FOR AVIAN INFLUENZA PREPAREDNESS

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6.1 Abstract

Ongoing economic losses by and exposure of humans to highly pathogenic avian influenza (HPAI) in poultry flocks across Asia and parts of Africa and Europe motivate also outbreak-free countries such as Switzerland to invest in preparedness planning. Country-specific population data on between-farm contacts are required to anticipate probable patterns of pathogen spread. Information is scarce; in particular on how strongly small, non-commercial poultry farms are involved in between-farm contacts. We aimed to identify between-farm contacts of interest for HPAI spread at both commercial and non-commercial farms in a non-outbreak situation: whether or not commercial and non-commercial farms were involved in poultry and person movements and shared resources by company integration. Focus was on poultry movements for the purpose of purchase, sale and poultry show visits, their spatial dimension, their frequencies and the farm types they connected. Of the total 49,437 recorded poultry farms in Switzerland, 95% had less than 500 birds. The farm number resulted in densities of up to 8 poultry farms per km^2 and a median number of 47 neighbour farms within a 3 km radius around the farms. Person movements and shared resources were identified in 78% of the surveyed farms (93% among commercials, 67% among non-commercials). Poultry trading movements over extensive spatial ranges were stated at 65% (79% among commercials, 55% among non-commercials). Movement frequencies depended on farm specialization and were higher for commercial than for non-commercial farms except for poultry show visits. Estimates however for the entire population revealed 3.5 times higher chances of a poultry purchase, and 14.6 times higher chances of exhibiting birds at poultry shows occurring in a given time by a farm smaller than 500 birds (non-commercial farm) than by a larger (commercial) farm. These findings indicate that both commercial and non-commercial farms are involved in neighbourhood and remote between-farm contacts relevant to HPAI spread. It is necessary to include all poultry farms, irrespective of their size and purpose in both livestock registration and disease surveillance systems, as well as in transmission models for poultry and zoonotic diseases.

6.2 Introduction

Highly pathogenic avian influenza (HPAI) has been noted for decades as an animal disease with high economic impact. Although well documented and reported, HPAI received little public attention until 1997 when, for the first time, human infections due to the H5N1 HPAI virus strain were confirmed (De Jong *et al.*, 1997) and caused 262 confirmed fatal human cases to date (WHO, 2009). Since December 2003, HPAI viruses, mainly H5N1, have reached poultry populations across Asia and parts of Africa and Europe causing high economic losses (Koppinen, 2005; Webster *et al.*, 2006; Dent *et al.*, 2008; Fasina *et al.*, 2008). Switzerland has been free from HPAI in domestic poultry since the 1930s but in early 2006, 34 cases of H5N1 HPAI-infected dead water fowl were identified (Hofmann *et al.*, 2008). Both wild birds (Kilpatrick *et al.*, 2006) and the import of poultry and poultry products represent a certain risk of HPAI virus introduction into the Swiss poultry sector (Hauser *et al.*, 2006b). HPAI virus transmission to susceptible birds occurs by direct contact with excretions and secretions from infected birds and indirectly via contaminated water, feed and equipment used on a farm. Between-farm transmission can occur through direct bird-to-bird contact when subclinically infected poultry is traded or exhibited at poultry shows. Other animals such as wild birds, martens, or domestic cats are known to potentially act as vectors (OIE, 2002; Normile, 2005; Klopfleisch *et al.*, 2007). People can contribute to virus spread by introducing contaminated fomites into a susceptible flock. Such between-farm contacts are also depending on the organization of the local structure of poultry industry (Capua *et al.*, 2002a). It is known from post-outbreak investigations that such potentially contagious contacts, in particular livestock movements amongst farms, strongly influence the course of epidemics (Shirley and Rushton, 2005). The distribution of number of contacts (degree distribution) among the members of a population (here poultry farms) was shown to be relevant for identifying members with high probabilities of being infected early in a course of epidemic because of having many incoming contacts. Members having many outgoing contacts were causing high numbers of secondary cases (Woolhouse *et al.*, 1997; Bell *et al.*, 1999; Bansal *et al.*, 2007). Furthermore, it was shown that high dispersions of degree distributions lowered the epidemic threshold, and thus were an important factor to consider when predicting epidemic dynamics (Hethcote and Yorke, 1984; Anderson and May, 1991; Pastor-Satorras and Vespignani, 2001; Duerr *et al.*, 2007). Clustering, describing how many of a member's contact partners have contact amongst one another, and other structural properties such as the stability of contacts further influence the spread of disease. To assume that all members have equal numbers of contacts and that they randomly chose contact partners, changing them continuously as is often done in transmission models, is known to overestimate the size of an outbreak for many infectious diseases (Zaric, 2002; Lyytikäinen *et al.*, 2009; Smieszek *et al.*, 2009).

Only rarely detailed contact information in its spatial context has been systematically integrated in models for HPAI transmission and used for the planning of preparedness and control strategies. Boender and colleagues (2007) performed a spatial analysis of the HPAI outbreak that occurred in 2003 in the Netherlands. They modeled HPAI transmission from infected to uninfected farms as a function of inter-farm distance and farm density. Resulting risk maps help to define areas where preemptive culling is advisable. Truscott and colleagues (2007) showed that transmission models taking both density-dependent spatial transmission and periodic network contacts into account were particularly suitable to reflect HPAI spread within the Great Britain poultry flock. Other countries, especially those not yet experiencing HPAI outbreaks can draw on these findings in their own preparedness planning. Country-specific information on the spatial distribution, structural composition and the connectedness of the poultry sector is required to develop transmission models properly. In particular it has to be clarified to what extent non-commercial poultry farms should be considered. Their role in between-farm transmission is controversial. Often non-commercial farms were defined by small flock sizes and were assumed to have small poultry movement distances. However, Garber and colleagues (2007) investigated destination locations for “birds sold or given away” by non-commercial farms in the USA and found movements beyond the State and beyond the USA borders. Capua and colleagues (2002a) suggested defining non-commercial backyard poultry farms not only by small flock size but primarily by the absence of functional connection to commercial poultry production systems. Such definition would imply that specific information on the interconnectedness of the poultry sector is available. Boender and colleagues (2007) considered only commercial flocks in their model. In Great Britain, only farms with 50 or more birds kept have to be registered, and are thus included in models. Distant contacts were only taken into account for farms keeping 500 or more birds (Truscott *et al.*, 2007) or 1,000 and more birds (Dent *et al.*, 2008). This makes it difficult to judge the actual role of non-commercial poultry husbandries in between-farm transmission scenarios.

This study was aimed to identify between-farm contacts of interest for HPAI spread at both commercial and non-commercial farms in a non-outbreak situation. We took advantage of available data in Switzerland where registration of poultry farms irrespective of size and purpose has been introduced in 2005 on a communal and cantonal level (Der Schweizerische Bundesrat, 2005). We georeferenced the locations of poultry farms to understand where occasional between-farm contacts within a neighbourhood were most probable. We then identified in a cross-sectional study whether commercial and non-commercial farms were involved in person movements, such as employees shared by two farms, and shared resources by company integration (affiliation to poultry marketing organizations). Of particular interest were poultry movements for the purpose of purchase, sale and poultry show visits, their spatial dimensions, their frequencies and the farm types they connected. This was to inform the discussion on whether at all, and under what circumstances poultry farms, and non-commercial farms in particular, play a role in the sector's connectedness and how they should be considered in the HPAI surveillance system and in pertinent transmission models.

6.3 Material and methods

Study population and density of poultry farms

The population investigated in this study are the poultry farms of Switzerland. By poultry farm we understand all sites where one or more domestic chicken (*Gallus gallus domesticus*), turkey (*Meleagris gallopavo*), duck (*Anas platyrhynchos domesticus* or *Cairina moschata*), goose (*Anser anser*), quail (*Coturnix coturnix*), guinea fowl (*Numida meleagris*), peafowl (*Pavo cristatus*), ostrich (*Struthio camelus*) or pigeon (*Columba livia*) are kept.

We established a single list of all recorded poultry keepers and farms (data from 2005 to 2007) in Switzerland out of 23 registers maintained by the 26 Swiss cantons (some cantons cooperate), and the federal livestock register database "Agrar information system" (AGIS) from 2005 (Bundesamt für Landwirtschaft, 2007). The AGIS contains only farms receiving direct government subsidy. The cantons recorded either all their poultry farms or only those not included in AGIS. Therefore data from all sources had to be merged and duplicates to be eliminated electronically privileging the more recent cantonal records. This lead to a single list subsequently called "census" containing a total of 49,437 countrywide identified poultry keepers. Captured attributes included farm address and total number of birds kept. Further farm details were provided in the original registers, however not in a standardized way. Manual checks revealed similar entries of farms under different names. Thus, the census might still contain some duplicates. The address data from the census were georeferenced and read into a base map from Swisstopo 2008®. An accuracy of exact localization was reached for 78% of the farms. For 6% and for 15% only precision on the street level and on the postal code level could be achieved, respectively. The census was used to investigate the density distributions of poultry farms and birds kept for the entire country and to depict them in density maps.

Survey design

The investigation of the between-farm contacts and their determinants followed a mixed methods research design. First a quantitative cross-sectional study among poultry keepers was conducted. In addition five experts from companies integrating commercial poultry farms (poultry and egg marketing organizations) were interviewed (qualitative part).

Cross-sectional study among poultry keepers

The census was used as sampling frame of which a random sample of 3,978 poultry keepers was drawn. The poultry keepers' probability of being selected for the cross-sectional study was proportional to the square root of the number of birds kept on their farm (farm size), to ensure a sufficient number of the less numerous larger poultry farms. A mail-out/mail-back survey among the 3,978 selected poultry keepers was conducted between August and December 2007. As survey instrument a structured questionnaire was developed in the German language and translated into French and Italian; national languages of Switzerland. Topics covered between-farm contacts, a self-assessment of the farm type by the respondent, a section on disease awareness, and one on wild bird observations in the poultry free-range area if existing. The two latter topics are presented elsewhere (Saurina, 2009; Saurina *et al.*, in press 2010).

Defining relevant contacts

Between-farm contacts potentially relevant for HPAI transmission were identified based on available literature (OIE, 2002; Thomas *et al.*, 2005; WHO, 2006; DEFRA, 2007; Grabkowsky, 2007) and based on consultation with poultry experts. The investigated contact relations included farm neighbourhood and neighbourhood-related contacts. Farm neighbourhoods are commonly considered to allow for casual contacts between the poultry keepers and overlapping movement ranges of potential vectors such as sparrows and freely moving domestic animals such as cats being potential vectors for HPAI viruses (Reed *et al.*, 2003; Kuiken *et al.*, 2004). This is reflected in the implementation of control and surveillance zones with 3 km and 10 km radii as a HPAI control measurement regulated in the Animal Health Act (Bundesversammlung der Schweizerischen Eidgenossenschaft, 2006) and 1 km bands for risk zones in other appraisals (Hauser *et al.*, 2006a). Therefore, the number of the participants' neighbour farms within all 1, 3 and 10 km radii was based on the addresses given in the poultry farm census. Contacts surpassing a 10 km radius were defined as remote contacts. Investigated contact relations beyond neighbourhoods included human movements, shared resources and poultry movements (Table 6.1). Poultry movements for the purpose of "purchase" and "sale" had one direction; those for "exhibiting birds at poultry shows" were bidirectional. The questionnaire allowed specifying of up to six different contact partners for each purchase, sale and show visits. Date (month/year), site (postal code) and types of contacts (hatchery, other farm or abattoir/butcher) or name of poultry show were inquired. The frequency of poultry trade and show visits was captured in "x times per year" and "less than once a year" which was coded as 0.5 times per year in the analyses. The term poultry included here live birds of the species described above, one-day chicks and also hatching eggs.

Data processing and analysis

Data of the returned and completed questionnaires were double-entered into a database, compared and cleaned. Presented analyses rely on data of 1,317 (33%) questionnaires that contained valid contact information. Spatial data were collected for all poultry movements, "show visits" and "coworking" in the form of the postal code of the contact partner or event. Postal codes were georeferenced. Maximum air-line distances in km between respondents and contacts were calculated for each contact relation if the postal code was given. Map presentations were completed using the *maptools* and *spatstat* libraries in R (version 2.7.2, the R Foundation for Statistical Computing) and base maps from Swisstopo 2008®. Two participant groups were formed based on the respondents' self-description in the questionnaire: "commercial" and "non-commercial" poultry farms. Further information on these groups is provided in Box 6.1.

Multinomial models with poultry movement distances as an outcome were used to investigate the following explanatory variables: number of birds kept (farm size), the respondent's farm type, and flock composition. Estimates and confidence intervals for the poultry movement frequency of the entire poultry sector were constructed using Bootstrap resampling with 2,000 replications.

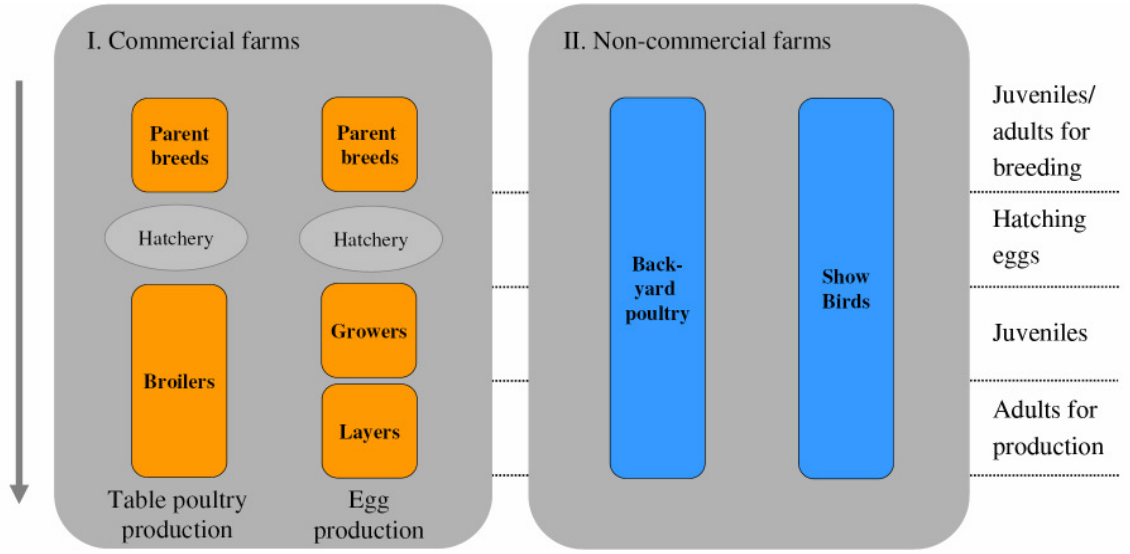
Interviews with experts from poultry industry

For the purpose of data triangulation and complementary information on between-farm contacts, interviews with experts from the poultry industry were conducted in addition to the survey. Five companies integrating commercial poultry farms in Switzerland were selected for interviews. The selection was based on whether the companies were frequently named by the survey participants and in order to include different areas of the poultry industry, including broiler and egg production. Company I and II, integrating about 400 farms each, covered the entire broiler production line from the hatchery to the abattoir. Companies III to V were involved in egg production; company III contracted about 100 farms with laying hens, company IV regrouped 110 organic farms on different levels. Company V covered around 60 farms levels plus one hatchery. All together the experts represented about one-half of the some 2,000 commercial poultry farms in Switzerland.

Main topics of the interview were between-farm contacts among the company's integrated farms, contacts to outsiders and shared resources. The experts were asked to describe production cycles, numbers, and specifics of their integrated farms. An interview guideline was used to systematically probe on issues not mentioned spontaneously by the experts. Information on poultry trade and shared resources was depicted by expert and interviewer together on paper (mapping tool; Appendix 3). Here, different colors were used to draw the studied contact relations (Table 6.1) amongst the company's farms, and to outsider farms. The interview protocols including notes from experts and the interviewer were transcribed and underwent qualitative content analysis according to Mayring (2003).

Table 6.1 Overview on contact relations under study

Contact relation	Vector	Connection through	Source of information
NEIGHBORHOOD			
Neighborhood to other poultry farms within 1, 3, and 10 km	Human and animal vectors	Proximity	Poultry farm census
PERSON MOVEMENTS AND SHARED RESOURCES			
Poultry show (visiting only)	Person	Co-attending show	Questionnaire
Co-working	Person, equipment	Staff and equipment	Questionnaire/interviews
Dead stock collection	Person, equipment	Co-accessing communal dead stock collection point	Questionnaire/interviews
Company integration	Person, equipment	Staff and shared resources	Questionnaire/interviews
POULTRY MOVEMENTS			
Poultry purchase	Live birds/hatching eggs	Transport (unidirectional)	Questionnaire/interviews
Poultry sale	Live birds/hatching eggs	Transport (unidirectional)	Questionnaire/interviews
Poultry show (exhibiting birds)	Live birds	Co-attending show	Questionnaire



Poultry is kept in different livestock production systems for different purposes and on different professional levels that is in different farm types. Legal definitions for these farms types differ between countries or are missing. It is commonly understood that commercial poultry farms (I) add essentially to earning a living and are operating with more than 500 and up to tens of thousands of birds. These farms, represented by orange boxes, typically cover only one step in either the table poultry production line or the egg production line. The arrow indicates the general direction of production. In Switzerland, parent breeds (F1) are imported from few global companies. Imports of breeding eggs by hatcheries and of one-day chicks by producers supplement the domestic production. Hatcheries don not keep live birds and are not considered as farms. Non-commercial poultry farms (II), represented by blue boxes, comprise all farms with smaller flock-sizes. Birds are kept for sideline production, subsistence farming and/or leisure. We distinguish between backyard poultry, when the emphasis is on the production of table poultry and/or eggs for human consumption, and show birds, when fancy birds or rare species are kept for breeding and preservation.

Box 6.1 Overview of the poultry sector composition

6.4 Results

Poultry farm density and neighborhood

The identified number of poultry farms in Switzerland was 49,437 until May 2007. The largest poultry flock comprised of 47,300 birds and the smallest had 1 bird; 95% of the farms had less than 500 birds, and 90% had less than 50 birds. The poultry farm density differed amongst regions. High density areas with more than 8 farms per km^2 were presented in purple, areas with moderate farm density in yellow and with very low farm density and no farms in grey. Light areas were congruent with high altitudes in the Alps in southern Switzerland (Figure 6.1). The distribution of the number of birds kept per km^2 resembled roughly the farm density distribution with low densities in the Alps. Maxima with more than 2,500 birds per km^2 were, however, more in the west of the country between Berne and Lausanne reflecting the location of several large commercial farms (Figure 6.2). South of Bellinzona farm density was at a maximum, but low numbers of birds were kept per km^2 reflecting the sparsity of large commercial farms in that area.

In the sample of 1,317 poultry farms, 543 were self-described as commercial farms and 783 as non-commercial farms. Similar group sizes were due to the weighted sampling privileging the less frequent large farms. The median total number of birds kept was 4,500 for commercial farms and 15 for non-commercial farms (Table 6.2). The threshold between both farm groups was roughly around 500 birds. 97% of farms had other farms within 1 km of the farm. Equal median numbers of neighbour farms representing potential contacts were found for both commercial and non-commercial farms with a median of 11 poultry farms within 1 km, 47 within 3 km and 283 within 10 km (Table 6.2).

Potential human and animal vectors (cats) were found on commercial and non-commercial farms. In both groups a median of 3 people were, on average, present on the farm during a normal working day. These persons were mostly described as “staff” at commercial farms and as “residents” and “guests” on non-commercial farms. One or more cats were kept on 65% of the farms without significant difference between commercial and non-commercial farms (unpublished data).

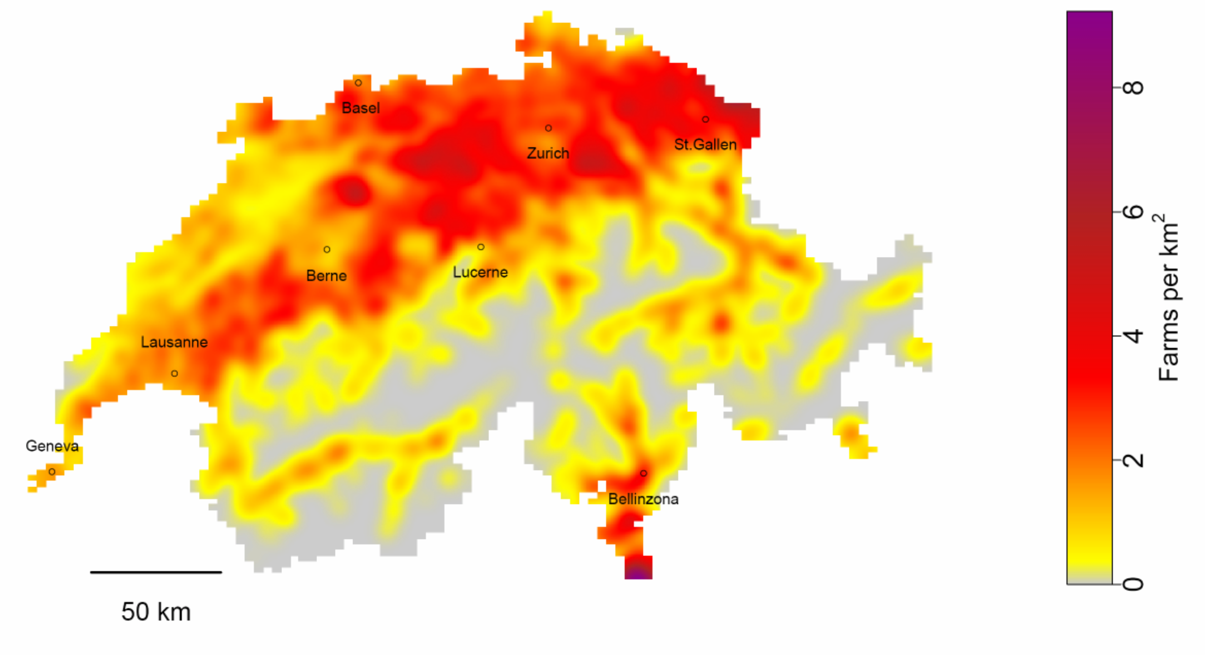


Figure 6.1 Density distribution of poultry farms in Switzerland (in farms per km^2). Locations of important cities of Switzerland are given for orientation

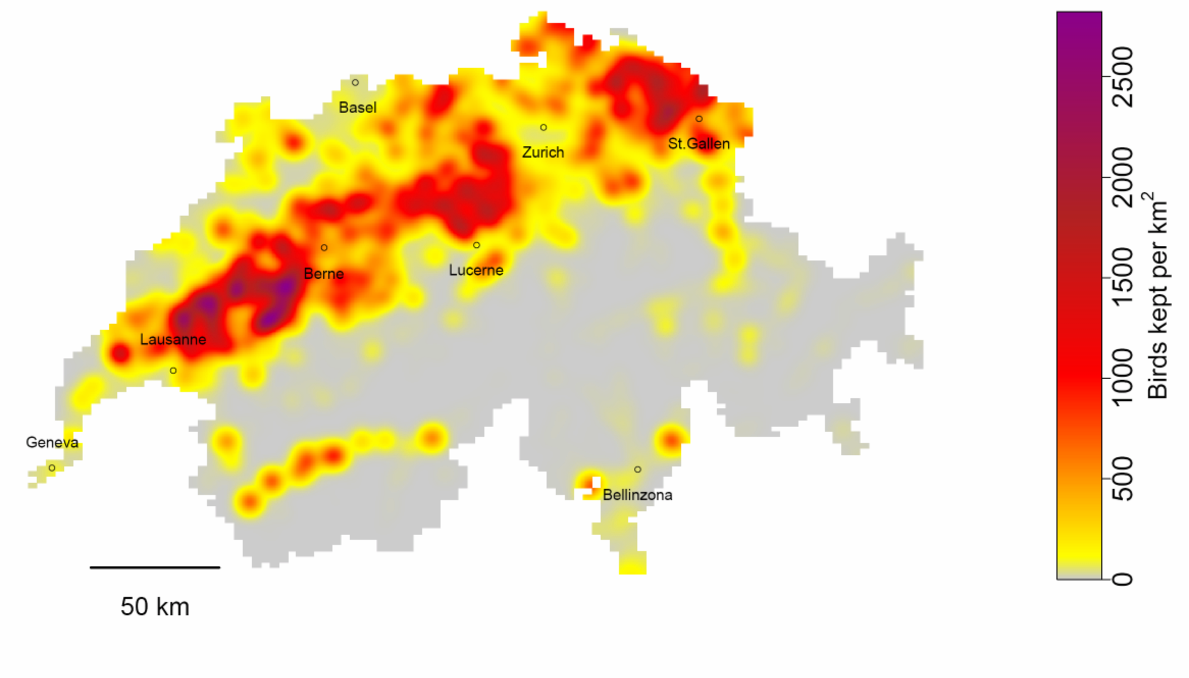


Figure 6.2 Density distribution of birds kept in Switzerland (in birds kept per km^2). Locations of important cities of Switzerland are given for orientation

Person movements and shared resources

At least one incident of human movement and shared resources was present at 78% of the participating farms (93% for commercial and 67% for non-commercial farms). “Use of dead stock collection points” was the most frequent response with 75%, “company integration” was stated by 30%, “poultry shows (visiting only)” by 7% and “coworking” on other farms by 4% of the respondents. “Use of dead stock collection points”, “company integration” and “co-working” on another poultry farm were more common among commercial farms. Non-commercial farms were virtually non-integrated into companies and visited more often poultry shows (Table 6.3). Median distances were available for “poultry shows (visiting only)” and “co-working”. Visited poultry shows were in a median distance of 12 km from the farm, with 27 km for the commercial and 8 km for non-commercial farms. This difference was explained by the commercial farm group mostly indicating visits to national agricultural expositions, and the non-commercial group mostly indicating visits to local shows and markets. “Co-working” on other farm was mainly indicated by the commercial farm group (Table 6.3). Between farms sharing employees a median distance of 2 km was identified. Thus sharing employees happened within a neighbourhood and should not be classified as a remote contact.

Poultry movements

Poultry movements were identified for 65% of the participating farms, with 79% among commercial and 55% among non-commercial farms. Purchase of poultry occurred more often (61%) than sale (25%) and exhibiting birds at poultry shows (3%), with a higher contribution of commercial farms except for poultry shows (Table 6.4). Geo-mapping of the air-line distances showed a geographical overlap of all poultry movements by commercial and non-commercial farms in farm dense areas. Itemizing poultry movements by type of origin and destination contact revealed characteristic patterns. Purchase from hatcheries (Figure 6.3a) and sale to abattoirs/butchers (Figure 6.3a) by commercial farms was focused. The foci were the same for farms integrated into the same company, confirmed by the interviewed experts. Commercial farms were not always affiliated to the company whose hatchery and abattoir were closest to the farm. Each of the companies had contract farms in up to 19 of the 26 Swiss cantons. That implies same suppliers, consulters and veterinarians serve contract farms over large parts of the country. Commercial farms’ purchases from other farms were mainly identified as laying farms buying laying hens from growers. Non-commercial farms had essentially other farms as contact partners, clear centers in the overall pattern were not identified (Figures 6.3a-6.6a).

The air-line distances of poultry purchase increased significantly with increasing farm size. For purchases from hatcheries, the increase was estimated as 0.75 km per farm size increase by 1000 birds ($p=0.026$; Figure 6.3b), for purchases from other farms the increase was 1.80 km ($p < 0.001$) (Figure 6.4b). Sales to abattoirs/butchers ($p=0.378$), to other farms ($p=0.718$), and distances to poultry shows where a farm's own birds were exhibited ($p=0.582$) did not depend on the farm size (Figure 6.5b-6.7b). Comparison of median distances between participant groups revealed poultry purchase (25 km median distance) being more than twice as distant for commercial farms (40 km) than for non-commercials (16 km). Median poultry sale distances (20 km) were 25 km for commercial farms and 10 km for non-commercials, explained by the commercials' longer journeys to abattoirs (31 km). In contrast to distances for "poultry shows (visiting only)", distances to poultry shows where owned birds were exhibited were about equal for commercial (median distance of 28 km) and non-commercial farms (27 km; Table 6.4). Within the non-commercial group show participation was mainly attributed to farms self-described as "show bird breeders" (odds ratio = 8.0; 95% confidence interval (CI) = 4.9-13.2, n = 783). Among the commercial farms, 6 out of 9 responses were attributable to self-described "layer farms".

Poultry movements across the farm groups

Commercial and non-commercial farms were directly connected by between-farm poultry movements. Out of a total of 767 specified purchases and sales between farms, 212 (28%) contacts were within the commercial farm group only, and 198 (26%) within the non-commercial farm group only. Across group contacts were mainly from commercial to non-commercial (347; 45%) and 10 times (1%) from non-commercial to commercial farm types. Commercial to non-commercial contacts were mainly identified to be from grower and layer farms to backyard poultry farms. The experts from Companies III, IV and V confirmed that some grower farms produced an excess of laying hens knowing the market opportunity to supply non-commercial farmers. Several layer farms were known to sell their hens, sorted out after one year of production, at low price to non-commercial farmers rather than disposing of them or supplying them to soup-hen production. Non-commercial to commercial farm contacts were attributed to several commercial farms keeping small flocks in a hen house separate from the commercial production although this was not recommended by the companies. Further connections were found through the access to the same hatcheries in 4 cases (Figure 6.3a) and the same poultry shows in 2 cases (Figure 6.7a) by both commercial and the non-commercial farms. The "use of dead stock collection point", the officially recommended practice for the disposal of dead livestock and pets, created a further link (although not through live poultry movement) as commercial and non-commercial farms share the same facilities.

Number of different contact partners

Only one contact partner per each origin (hatchery and other farm) and destination (hatchery, abattoir/butcher and other farm) contact relation was found in most cases. Exceptions were observed in the few specialized farms. Grower farms supplied up to hundreds of commercial layer farms with laying hens. The experts confirmed that this distribution of the number of contact partners (degree distribution) was highly skewed and that the contacts were mostly stable over time.

Frequency of poultry movements

Movement frequencies were higher at commercial farms compared to non-commercial farms. Higher figures for commercial farms were explained by 6 to 8 transactions a year at broiler farms for purchase and sale, one purchase and sale by layer farms, and up to 80 purchases per year and daily sales by the few specialized farms (parents or grower farms cf. Box 6.1, or farms having more than one production level). Non-commercial farms had purchases and sales one time or less per year. If owned birds exhibited at poultry shows, this was commonly done twice a year for both commercial and non-commercial farms. Both groups had outliers with 20 to 30 show attendances per year.

Data extrapolation to the entire poultry sector in Switzerland

Contact data were collected on a sample where the poultry keepers' probability of being selected was proportional to farm size, to ensure a sufficient number of the less numerous larger poultry farms. To provide contact estimates for the entire poultry sector, contact data were extrapolated on the entire poultry sector taking the sampling weight into account. Except for contact relations uncommon among non-commercial farms (such as sales to abattoirs/butchers), the extrapolated values were in the same range as in the non-commercial farm group (right column of Tables 6.2-6.5).

Estimates of the median number of poultry movements per month in Switzerland were calculated, ignoring seasonal variations of layer farms. Accordingly, 488 (95% CI: 443-538) purchases per month would be performed by farms with 500 or more birds kept (basically commercial farms), and 1,686 (95% CI: 1,665-1,707), 3.5 (95% CI: 3.1-3.9) as many, by farms smaller than 500 birds (basically non-commercial) farms. Poultry sales would be in the same range with 1,092 (95% CI: 880-1,327) for large and 1,018 (95% CI: 925-1,116) for small farms. Poultry movements to poultry shows would be 45 (95% CI: 31-63) by large, and 655 (95% CI: 624-687), 14.6 (95% CI: 9.9-22.2) times as many transactions, by small farms.

Table 6.2 Farm specifics and neighborhood of the commercial and non-commercial farm group and data extrapolation to the entire Swiss poultry sector

	Commercial	**Non-commercial**	**All**	**Extrapolation to CH*** poultry sector**
No. of birds kept per farm	*n=534*	*n=783*	*n=1317*	*n=1317*
(m* [IQR**])	4500 [2000-8610]	15 [7-30]	37 [12-3807]	11 [6-23]
Fraction of farms having neighbor farms in radii of	*n=532*	*n=780*	*n=1312*	*n=1312*
1 km	98 %	96 %	97 %	97 %
3 km	100 %	99.7 %	99.8 %	99.4 %
10 km	100 %	100 %	100 %	100 %
No. of neighbor farms in radii of				
1 km (m [IQR])	11 [7-18]	11 [6-19]	11 [7-19]	11 [6-19]
3 km (m [IQR])	47 [29-75.5]	47.5 [25-74.5]	47 [28-75]	46 [25-73]
10 km (m [IQR])	289 [162.5-402]	279 [142-381]	283 [152-393]	277 [144-386]

[*m=median; **IQR=inter-quartile range; ***CH=Switzerland]

Table 6.3 Prevalence of contact relations under study among the commercial and non-commercial farm group and data extrapolation to the entire Swiss poultry sector

	Commercial	**Non-commercial**	**All**	**Extrapolation to CH*** poultry sector**
Poultry show (visiting only)	*n=518*	*n=754*	*n=1272*	*n=1272*
	7 %	9 %	9 %	8 %
Co-working	*n=534*	*n=782*	*n=1316*	*n=1316*
	10 %	1 %	4 %	1 %
Dead stock collection points	*n=533*	*n=782*	*n=1315*	*n=1315*
	92 %	63 %	75 %	62 %
Company integration	*n=534*	*n=783*	*n=1317*	*n=1317*
	73 %	0.3 %	30 %	3 %
Fraction of farms having one or more of above incidents	*n=517*	*n=752*	*n=1269*	*n=1269*
	93 %	67 %	78 %	65 %
DISTANCES				
Poultry show (visiting only)	*n=22*	*n=51*	*n=73*	*n=73*
km (m* [IQR**])	27 [9-37]	8 [5-27]	12 [6-34]	8 [6-34]
Co-working	*n=44*	*n=5*	*n=49*	*n=49*
km (m [IQR])	2 [1-4]	3 [2-3]	2 [1-4]	2 [2-4]

[*m=median; **IQR=inter-quartile range; ***CH=Switzerland]

Table 6.4 Contact relations and median maximum distances to contact partners in km by the commercial and the non-commercial farm group and data extrapolation to the entire Swiss poultry sector

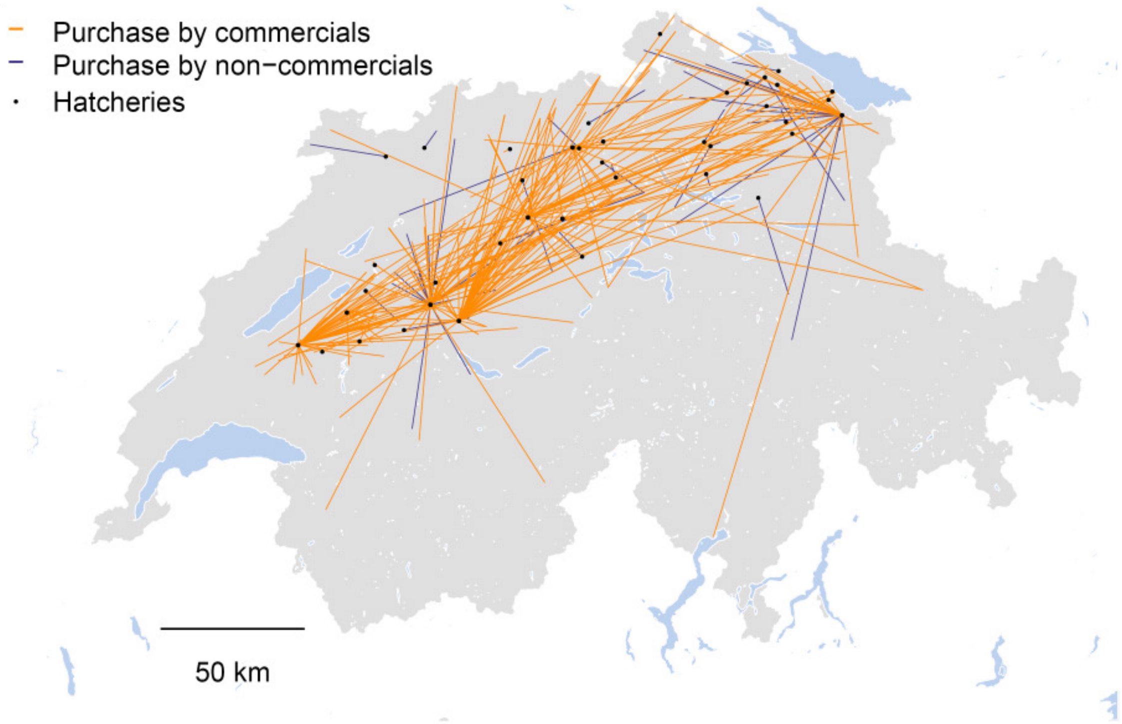
	Commercial	**Non-commercial**	**All**	**Extrapolation to CH*** poultry sector**
Purchase (total)	*n=534*	*n=783*	*n=1317*	*n=1317*
	75 %	52 %	61 %	50 %
Sale (total)	*n=534*	*n=783*	*n=1317*	*n=1317*
	50 %	8 %	25 %	8 %
Poultry show (exhibiting birds)	*n=518*	*n=754*	*n=1272*	*n=1272*
	2 %	4 %	3 %	3 %
Fraction of farms having one	*n=518*	*n=754*	*n=1272*	*n=1272*
or more of above incidents	79 %	55 %	65 %	52 %
DISTANCES				
Purchase of poultry (total)	*n=337*	*n=337*	*n=674*	*n=674*
km (m* [IQR**])	40 [23-74]	16 [8-29]	25 [12-51]	16 [8-32]
Purchase from hatchery	*n=223*	*n=46*	*n=269*	*n=269*
	37 [23-74]	23 [13-37]	36 [22-68]	26 [16-51]
Purchase from other farm	*n=134*	*n=311*	*n=445*	*n=445*
	37 [18-67]	15 [7-28]	18 [8-40]	15 [7-28]
Sale of poultry (total)	*n=148*	*n=40*	*n=188*	*n=188*
km (m [IQR])	25 [13-60]	10 [2-17]	20 [9-51]	10 [3-21]
Sale to hatchery	*n=6*	*n=2*	*n=8*	*n=8*
	18 [6-25]	9 [7-12]	12 [6-24]	12 [7-12]
Sale to abattoir/butcher	*n=119*	*n=2*	*n=121*	*n=121*
	31 [15-72]	18 [15-21]	30 [15-71]	29 [15-64]
Sale to other farm	*n=27*	*n=38*	*n=65*	*n=65*
	9 [3-19]	10 [2-17]	10 [2-17]	9 [2-17]
Poultry show (exhibiting birds)	*n=9*	*n=25*	*n=34*	*n=34*
km (m [IQR])	28 [16-44]	27 [9-56]	28 [12-48]	18 [9-45]

[*m=median; **IQR= inter-quartile range; ***CH=Switzerland]

Table 6.5 Frequency of poultry movements in times per year by the commercial and non-commercial farm group and data extrapolation to the entire Swiss poultry sector

	Commercial	**Non-commercial**	**All**	**Extrapolation to CH*** poultry sector**
Purchase (total)	*n=395*	*n=405*	*n=800*	*n=800*
times per year (m* [IQR**])	5 [1-7]	1 [0.5-1]	1 [0.75-5]	1 [0.5-1]
Sale (total)	*n=262*	*n=62*	*n=324*	*n=324*
times per year (m [IQR])	6 [2-7]	1 [0.5-2]	6 [2-7]	2 [0.5-3]
Poultry show (exhibiting birds)	*n=9*	*n=27*	*n=36*	*n=36*
times per year (m [IQR])	2 [1-10]	2 [1-3]	2 [1-3]	2 [1-3]

[*m=median; **IQR= inter-quartile range; ***CH=Switzerland]



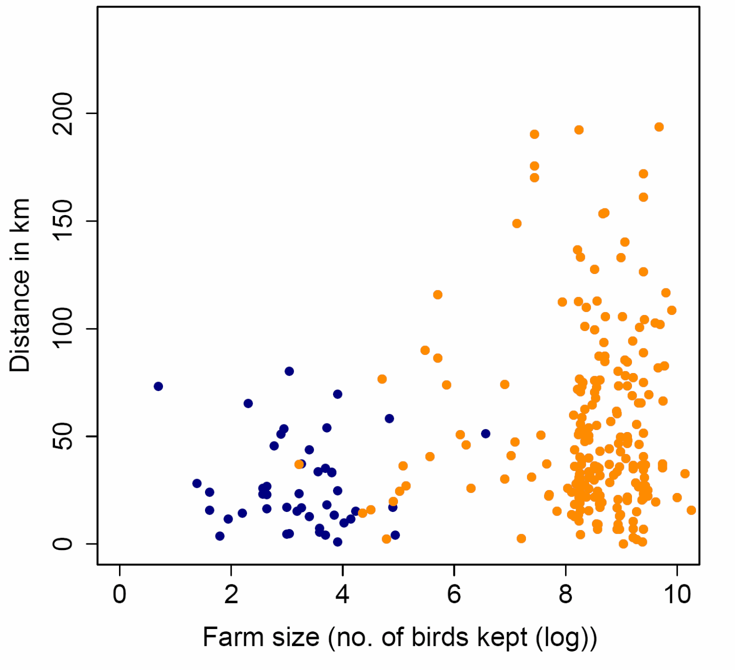
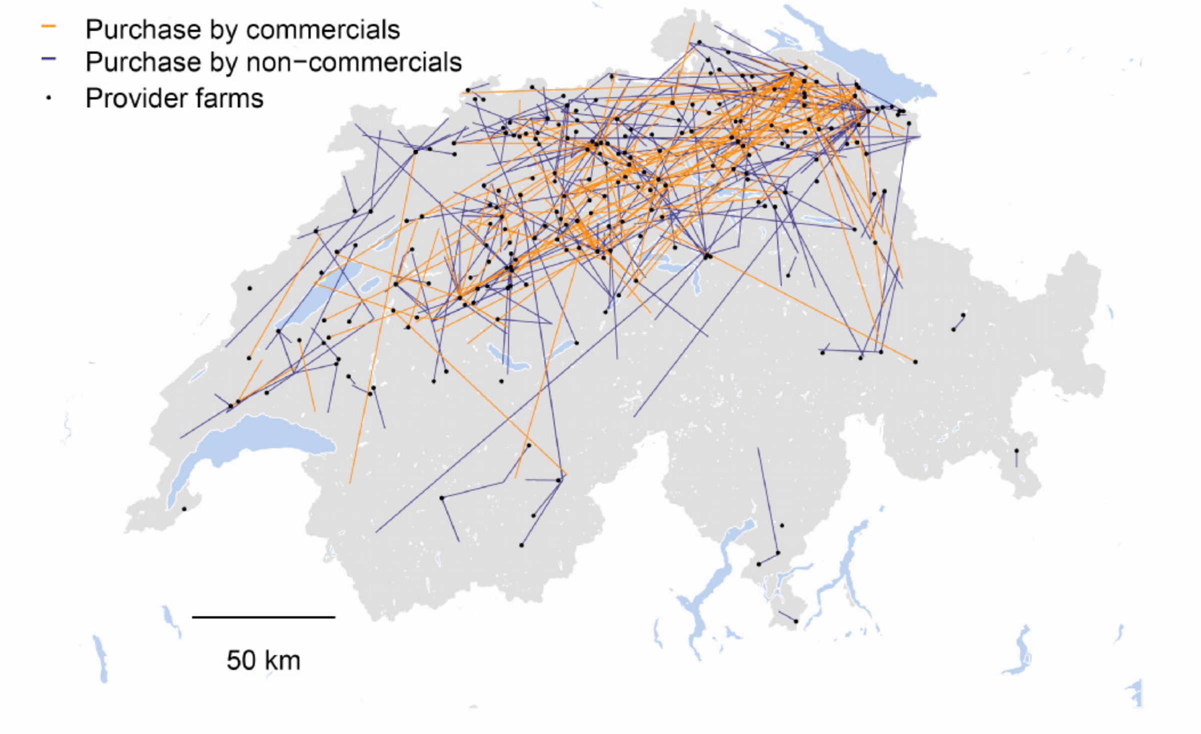


Figure 6.3 Poultry movements. The map indicates airline distances for purchase from hatcheries (black dots) by commercial (orange lines) and non-commercial farms (blue lines). In the scatter plot correlation between farm size (log) and airline distances is shown. Non-commercial farms are represented by blue dots, commercial farms by orange dots



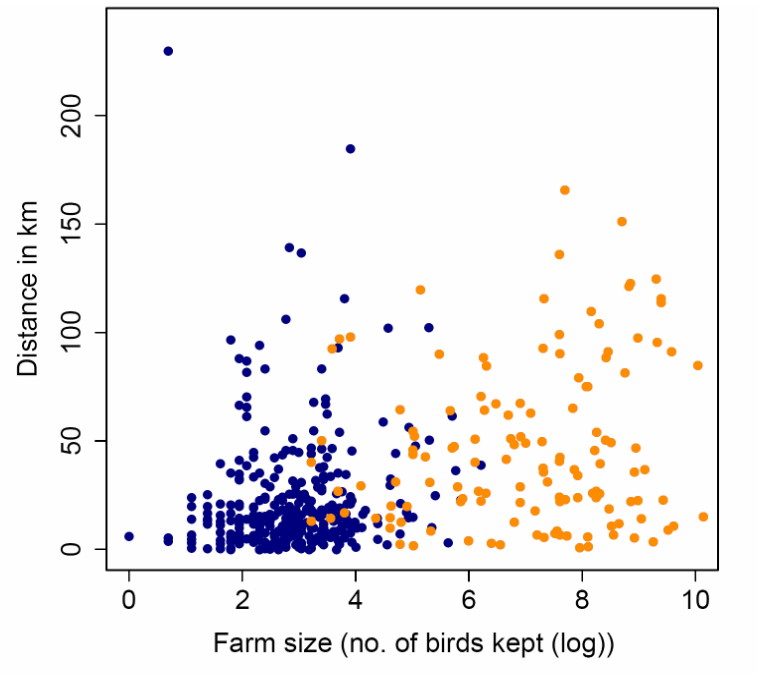
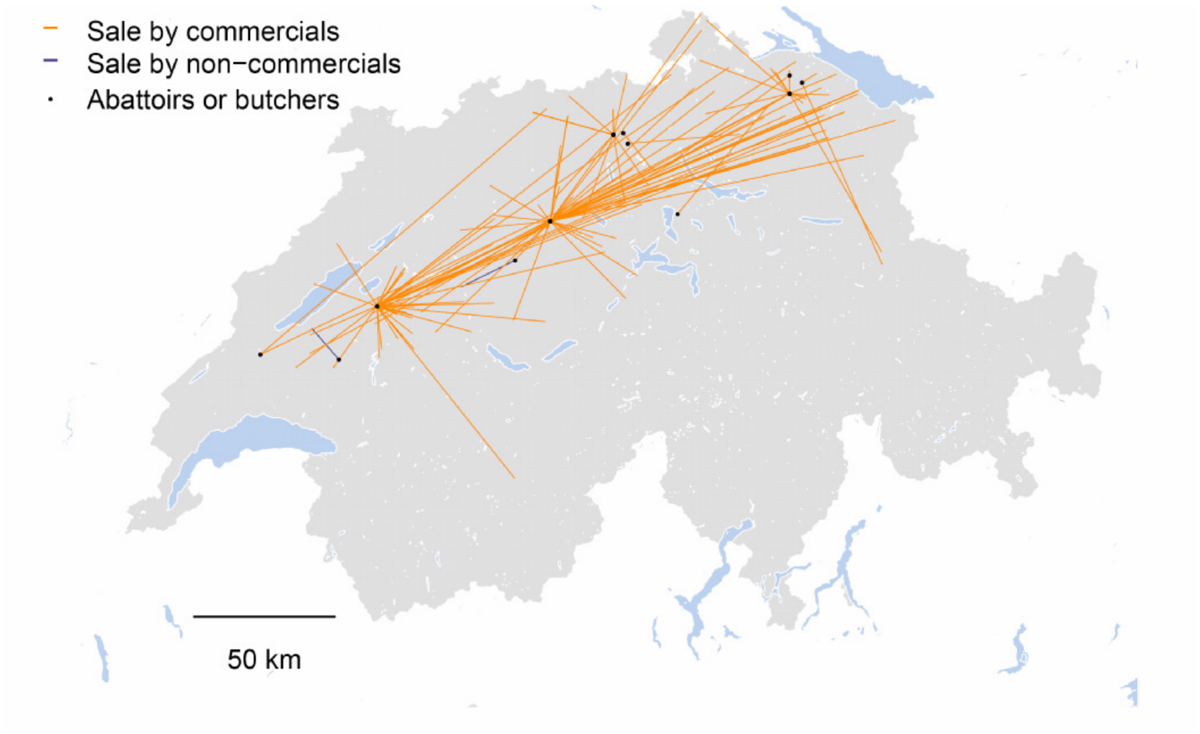


Figure 6.4 Poultry movements. The map indicates airline distances for purchase from other farms (black dots) by commercial (orange lines) and non-commercial farms (blue lines). In the scatter plot correlation between farm size (log) and airline distances is shown. Non-commercial farms are represented by blue dots, commercial farms by orange dots



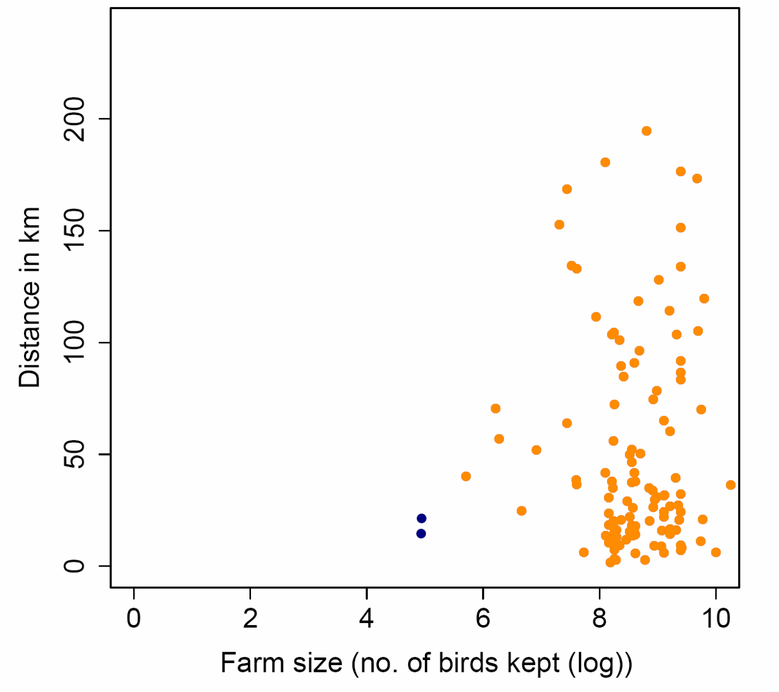


Figure 6.5 Poultry movements. The map indicates airline distances for sales to abattoirs or butchers (black dots) by commercial (orange lines) and non-commercial farms (blue lines). No significant correlation between farm size (log) and airline distances was found (scatter plot). Non-commercial farms are represented by blue dots, commercial farms by orange dots

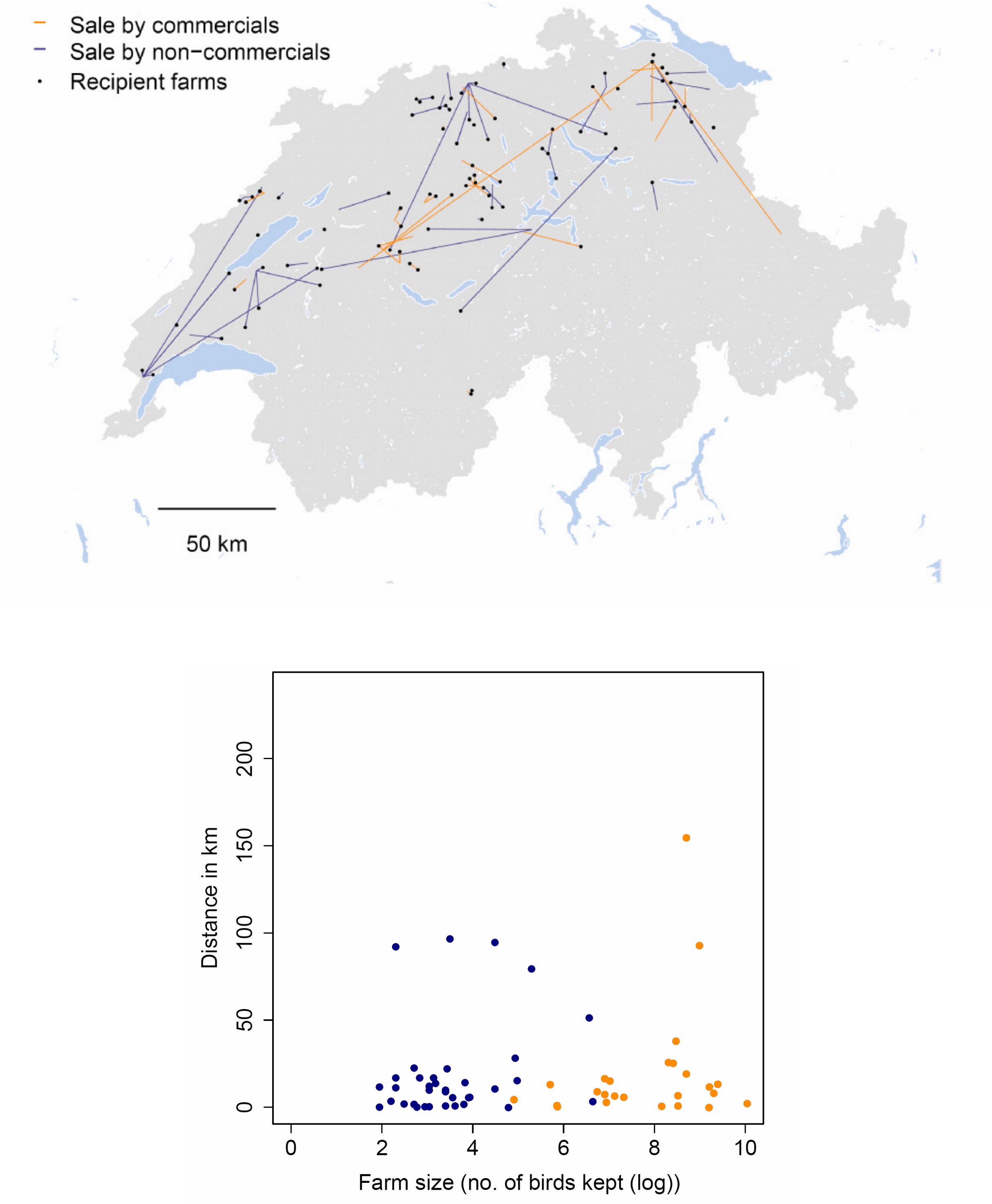
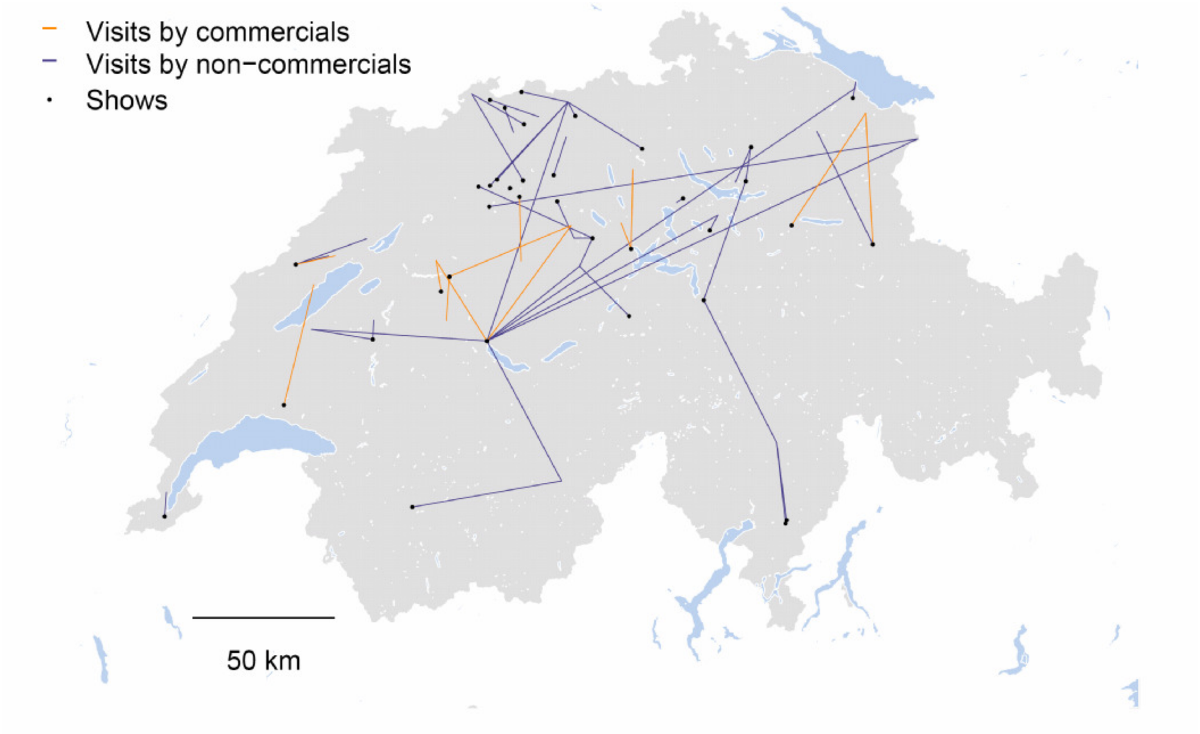


Figure 6.6 Poultry movements. The map indicates airline distances for sales to other farms (black dots) by commercial (orange lines) and non-commercial farms (blue lines). No significant correlation between farm size (log) and airline distances was found (scatter plot). Non-commercial farms are represented by blue dots, commercial farms by orange dots



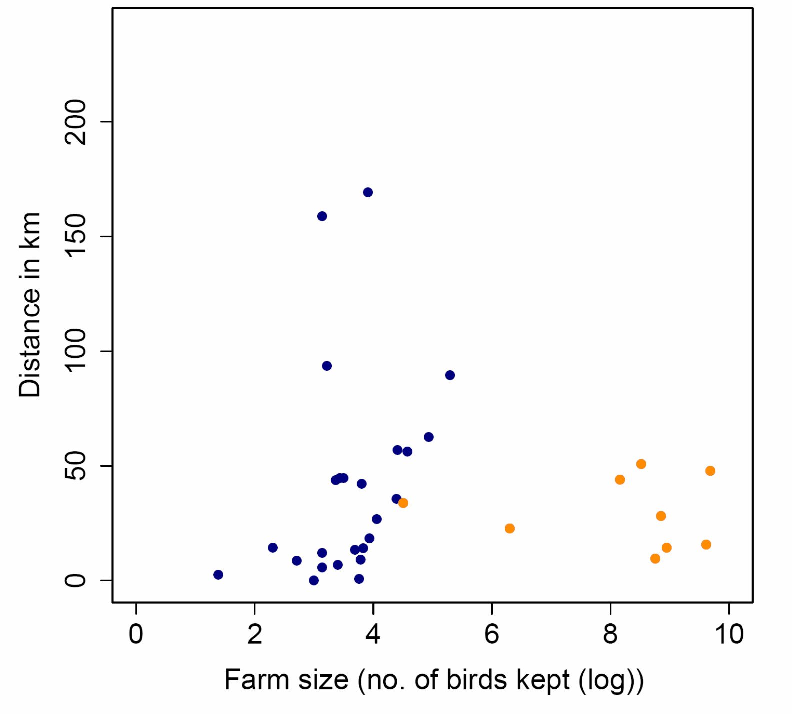


Figure 6.7 Poultry movements. The map indicates airline distances for poultry show visits where own birds were exhibited (black dots) by commercial (orange lines) and non-commercial farms (blue lines). No significant correlation between farm size (log) and airline distances was found (scatter plot). Non-commercial farms are represented by blue dots, commercial farms by orange dots

6.5 Discussion

We aimed to identify between-farm contacts potentially allowing for HPAI to be spread between and amongst poultry farms in Switzerland. At the completion of this study, countrywide density maps for both poultry farms and birds kept were produced for the first time for Switzerland. Both density maps provided complementary information. Bird density is an import factor to assess infection pressure. Farm density is relevant to HPAI control measurements such as the implementation of control and surveillance zones around farms. When only commercial poultry farms are included in farm density maps it might be concluded that areas such as south of Bellinzona have a very low farm density and thus are of minor importance for HPAI surveillance. In fact, the area south of Bellinzona is the densest for poultry farms in Switzerland with more than 8 poultry farms per km^2 when non-commercial farms are included in the dataset. Our findings support the concept of "farm neighbourhood" as a potential contact in poultry farm population models. The two participant groups, poultry keepers with commercial (large) and non-commercial (small) farms were found to have equal neighbourhood characteristics: (i) the number of other poultry farms in the neighbourhood, and (ii) the potential human and animal vectors such as cats and small birds (unpublished data) present on the farms. Free-range systems, facilitating vectors' access to domestic poultry and thus the risk of HPAI virus dissemination, were more common among non-commercial farms (92%) compared to commercial farms (61%; unpublished data). Sharing employees within a neighbourhood was, in contrast, more common among commercial (10%) compared to non-commercial farms (1%). This could increase the risk of HPAI virus dissemination amongst commercial farms, in the case where hygiene measurements are deficient.

The majority of farms were involved in human movements and shared resources (78%) or poultry movements (65%). The fraction was higher among commercial farms and distances were larger compared to non-commercial farms, except for those that exhibited birds at poultry shows. The number of different contact partners and poultry movement frequencies had skewed distributions. Few specialized grower and parent farms had high rates, mainly of outgoing contacts. The majority had low rates or no contacts at all. Highly connected farms are critical for a rapid spread of an epidemic (Bell *et al.*, 1999). These farms must therefore be well surveyed by veterinary authorities. The operating companies and producer must be particular vigilant at maintaining good farm hygiene management practices. Poultry movement frequencies were higher at commercial farms compared to non-commercial farms. Estimates however for the entire population of poultry farms revealed 3.5 times as high chances of a poultry purchase, and 14.6 times as high chances of exhibiting birds at poultry shows occurring in a given time by a farm smaller 500 than birds (non-commercial farm) as by a larger (commercial) farm. This is because 95% of poultry farms in Switzerland keep less than 500 birds. The common assumption of a closed circuit of the commercial poultry production without connections to non-commercial farms does not entirely hold true. Commercial and non-commercial farms were functionally connected through direct purchase and sale interactions (mainly from commercial to non-commercial), access to the same dead stock collection points and hatcheries and visits of the same poultry shows.

The pattern of contacts between poultry farms has been investigated in terms of whether or not contact incidents were present. This was ignoring the strength of contacts (e.g. number of birds moved per transaction) and hygiene precautions taken by the poultry keepers. Contact partners were identified on a postal code level for data protection and the respondent's convenience resulting in only approximate air-line distances. Knowledge on effective transport routes may identify potential critical control points for remote contacts. We assume a slight under-reporting of contacts in the questionnaire: in follow-up interviews with 28 of the non-commercial respondents, it was sporadically explained that respondents had received birds as a gift that they had not declared in the postal questionnaire (Kernen, 2008). Interviews with experts from poultry industry indicated that commercial broiler producers do not always own the flock but raise birds on contract. This may explain why only 77% of the broiler subgroup indicated "purchase of poultry/hatching eggs".

There is a need to better understand why and under what conditions non-commercial keepers trade over long distances even though they have many other poultry farms in their direct neighbourhood. The identified structural properties of the poultry sector must be complemented with data of biological factors for sound predictions of outbreak dynamics. For instance, HPAI susceptibilities could be flock specific depending on virus strain and species kept, as described for the H7N7 outbreak in the Netherlands in 2003 (Stegeman *et al.*, 2004). Our findings have both local and global implications; for instance on zoning (geographical division) and compartmentalization (functional division by biosecurity measures). These are strategies introduced by the World Organization of Animal Health (OIE) to allow unaffected parts or segments of larger countries to continue trading during an epidemic (Bruschke and Vallat, 2008). Geographical and functional connections between commercial and non-commercial poultry farm subpopulations, as found in Switzerland, might also exist in larger countries. Geographical separations might be especially difficult to establish and maintain when poultry farm density is high over larger areas. Further, the present study helps to strengthen awareness for the importance of comprehensive and well organized epidemiological baseline data on the poultry population. The legislative basis for a mandatory notification of all poultry on a federal level has been created in Switzerland (Der Schweizerische Bundesrat, 2009). The future federal poultry register would, ideally, be entirely georeferenced, maintained in a relational database format, and linked up with data on poultry movements and data on presence of wild birds and waterfowl as main reservoirs. Regarding other livestock species, movement databases for cattle have shown to capture spatio-temporal data in nearly real-time (Robinson and Christley, 2006). Such data support authorities in the timely prevention, surveillance and control of HPAI and any other poultry epidemic or zoonotic disease. Maps are a well-proven utility for combined presentations of data on agricultural, wildlife and ecosystem factors in preventive (East *et al.*, 2008a; East *et al.*, 2008b) and post-outbreak investigations concerning HPAI (Ward *et al.*, 2008).

As for models for HPAI transmission, the study results indicate that contact patterns are far from random given close neighbourhood, farm type-specific long distance contacts and strong influence of the farms' affiliation to companies. To reflect the population's contact characteristics the combination of diffusion models (to reflect neighbourhood contacts) and network models (to reflect long distance poultry movement contacts) as suggested by Truscott and colleagues (2007) should be considered. However, this should not only be done for commercial farms but also for non-commercial farms. Our findings indicate that both commercial and non-commercial farms are involved in neighbourhood and remote between-farm contacts relevant to HPAI spread. It is necessary to include all poultry farms, irrespective of their size and purpose in both livestock registration and disease surveillance systems, as well as in transmission models for poultry and zoonotic diseases.

6.6 Acknowledgements

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6.7 Authors’ contributions

LF planned, conducted, and analyzed the quantitative and qualitative parts of the study, and drafted the manuscript as the lead writer. TS participated in the survey design, the analytical framework, and helped to draft the manuscript. JS planned and conducted the quantitative study part, and helped to draft the manuscript. JH provided support for data management, for the quantitative analyses, and for preparing the maps. JZ supervised the project, participated in the study design, and helped to draft the manuscript. All authors have read and approved the final manuscript.

7 A RELATIONAL DATABASE MODEL FOR THE POULTRY SECTOR

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7.1 Abstract

While conducting a study on highly pathogenic avian influenza surveillance (HPAI) in the Swiss poultry sector we noticed a need to improve the decentralized poultry registration system. Apart from database maintenance issues there are three constraints to flexible data storage in particular which have to be overcome. First, the current registration system only allows for one poultry keeper to own or work on one poultry farm site. Second, it is not possible to retrieve information as to whether birds on one farm are kept within the same housing system or in separate units. Third, the possibility of creating interfaces for the exchange of data that is potentially relevant does not exist yet.

A conceptual representation of a relational database is developed for poultry farm and poultry keeper registration in Switzerland. An entity-relationship model (ERM) is presented for the basic storage of demographic data. In addition, four examples of extensions are provided, namely links to: (i) private companies' member lists, (ii) poultry show attendance lists, (iii) diagnostic databases. The fourth extension (iv) consists of a way of integrating data on poultry trading movements between farms.

The resulting ERM for a poultry registration database and its extensions is suited to overcome all identified limitations. It allows for special poultry farm settings where the "one poultry keeper equals one farm site equals one flock" assumption does not hold. The proposed format is devised for quick multi criteria queries as typically needed in disease surveillance applications. The presented ERM provides an ideal basis for discussion amongst poultry experts, user groups and programmers in view of a modern poultry registration database.

We conclude that for the purpose of poultry registration in Switzerland a relational database would be well suited and a necessary prerequisite prior to any effective planning of surveillance activities for health-related issue in the target population.

7.2 Introduction

The availability of demographic baseline data are a prerequisite prior to any successful planning, implementation and evaluation of epidemiological studies and health interventions in both human (de Savigny *et al.*, 1999; Setel *et al.*, 2007; Weibel *et al.*, 2008) and animal populations (Zessin *et al.*, 1985; Mindekem *et al.*, 2005). In epidemiological research comprehensive demographic baseline data help to minimize selection biases and thus to comply with "Good Epidemiological Practice" demands (Zeltner, 2005; International epidemiological association, 2007).

In the context of highly pathogenic avian influenza (HPAI) surveillance, a cross-sectional study survey among poultry keepers was conducted in Switzerland in 2007. This gave rise to an intensive investigation of poultry registration data. In contrast to (aspired) individual identification of humans and for instance cattle populations (Wismans, 1999), official poultry registration happens on a farm level. Poultry farms are registered in the national agricultural information system AGIS, comprising all farms that receive direct government subsidies (Bundesamt für Landwirtschaft, 2008). Driven by the HPAI threat, compulsory registration of all husbandries irrespective of purpose and size was introduced in October 2005 (Der Schweizerische Bundesrat, 2005). These registration data were collected in the communes and compiled on cantonal level resulting in 23 poultry registers using different templates and software. For the conducted study poultry farm registers were merged into a single list with duplicates eliminated electronically. This list is subsequently referred to as census. Two types of disadvantages were identified the current decentralized poultry farm registration system. First, there are general data management issues such as

- A unique identifier for all poultry farms is missing. Used farm registration and identification numbers differ amongst lists.
- Variables describing farm specifics are inconsistent or absent (in canton Ticino).
- Variables to specify poultry species are inconsistent or are missing (in canton Zurich).
- Number of birds kept on a farm are given in exact numbers, except in canton Solothurn, where there is a distinction between small farms with less than 50 birds and farms with 50 birds and more.
- Missing values were sometimes not distinguishable from variables for "not present".

This type of disadvantages can be overcome by using a standard register template provided for instance by the project “Kodavet” anchored in the Swiss Animal Health Act (Bundesversammlung der Schweizerischen Eidgenossenschaft, 2006).

Second, there are real-world observations that are difficult to compress in the format of a single table.

1) Single tables, as currently used, only allow for a 1:1-relation between poultry keeper and poultry farm. There is evidence that in some cases farmers run more than one farm site and that one farm can be run by more than one farmer or by entire cooperatives.
2) Single tables allow for the recording of farm specifics. It is difficult, however, to specify whether or not all birds belong to one flock and whether they are all kept in the same housing system. There is evidence that some commercial farms have a unit for their commercial flock and separate units (that are not part of the same housing system) where poultry is kept for leisure.
3) There is more than one database containing potentially relevant information to the poultry sector such as member lists maintained by companies and poultry breeder associations as well as diagnostic databases. It would be in the mutual interest of all parties involved to create interfaces from federal poultry register to such lists. Merging data into a single table poultry register is not an efficient solution, however.

To address these issues, a more flexible database format is needed. A relational database, based on multiple relations, represented by sets of tables instead of a single fixed table, seems therefore appropriate. Relational databases have proven useful in many contexts including epidemiological applications: In a multi-institutional project relating clinical patient data to data collected in experimental laboratories they helped to overcome inconsistency and fragmentation of data (Wang *et al.*, 2009). In an Italian Poison Centre a relational database was introduced to store phone calls in a harmonized way including details of the phone call, patient data, symptom description files and lists of substances (Barelli *et al.*, 2006).

This paper aims at drafting a relational database for poultry farm and keeper registration in Switzerland. The conceptual representation is made using an entity relationship model. Beyond a base model for storing demographic data, four examples of extensions, i.e. links to: (i) member lists of private companies, (ii) poultry show attendance lists, (iii) diagnostic databases; and (iv) a way of integrating data on poultry trading movements between farms, are provided.

7.3 Material and methods

Population of interest

The population of interest on which the database is modelled, is the total of poultry farms in Switzerland. By poultry farm we understand all sites where one or more domestic chicken (*Gallus gallus domesticus*), turkey (*Meleagris gallopavo*), duck (*Anas platyrhynchos domesticus* or *Cairina moschata*), goose (*Anser anser*), quail (*Coturnix coturnix*), guinea fowl (*Numida meleagris*), peafowl (*Pavo cristatus*), ostrich (*Struthio camelus*) or pigeon (*Columba livia*) are kept. By poultry keeper we understand each individual person owning or being in charge of a poultry farm. Prior information on the population of interest originates from our review of the federal farm register AGIS (Bundesamt für Landwirtschaft, 2007) and cantonal poultry farm registers. All examples relating to poultry farm/poultry keeper data or to other content are only of a general type without providing specific details on companies' records, laboratories diagnostic databases, or documentation of poultry shows.

Database format

The proposed database is developed using an entity relationship model (ERM). A general introduction to database systems and to standard terminology of ERMs is provided.

A database is any record of data in a structured way, usually in the form of a table. By data we understand computer-readable information. In situations where large amounts of data have to be stored in a persistent way and accessed in parallel more advanced systems than collections of plain files are needed. A general configuration of a modern database is shown in Figure 7.1.

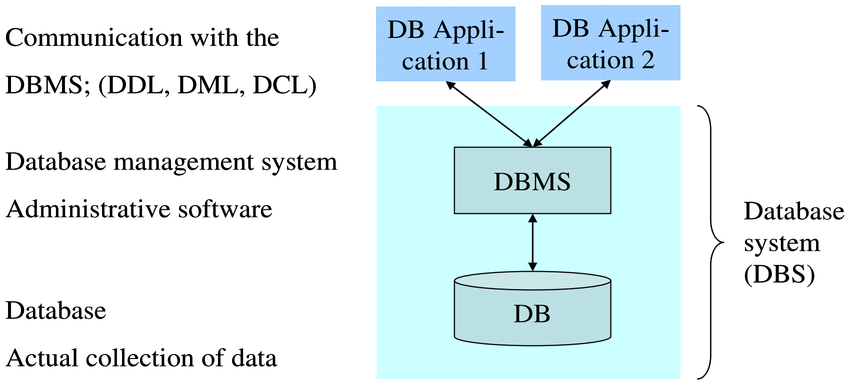


Figure 7.1 General configuration of professional databases

A database system (DBS) consists of the physical level, which is the actual collection of data stored on hardware (DB), the logical level, which is the database management system (DBSM) which is congruent with the database scheme (intentional level) and the actual content (extensional level). A database language such as SQL (Structured Query Language) is the interface between user applications and the DBMS. The purpose of user-database communication includes defining data (by using DDL-Data Definition Language), manipulating data (by using DML-Data Manipulation Language), or checking data integrity, creating formula editors, reports and menus (by using DCL-Data Control Language). Main tasks of a DBS are the description, storage and maintenance of huge amounts of data, which can be retrieved by different user programs (Kemper and Eickler, 2006). As claimed by the originator of relational databases, Edgar F. Codd, the DBS must ensure the integrity of data by means of avoiding redundancy, performing consistency checks and cascading of changes. Furthermore a DBS has to provide operations for storage, search and data manipulation as well as a data dictionary (catalog) and user interfaces with access control (authority) and synchronization of queries (Codd, 1970; Codd, 1982; Codd, 1990).

Relational database models are the most popular models to describe a database scheme that conforms to the demands above. In relational databases information is organized in a set of tables. Each data point is stored in only one location to avoid redundancy. At the moment of a query all relevant tables are accessed and all matching entries are presented in a temporary result table.

ERM, originated by Peter P. Chen (1976), are the most popular abstract data models for the conceptual representation of a database. The purpose of such a conceptual representation is to support the transformation of a real world context into a computer-aided database scheme as shown in Figure 7.2.

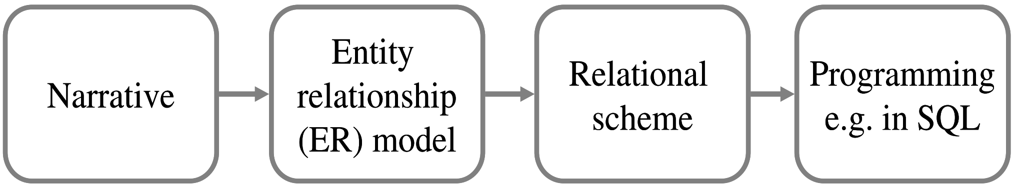
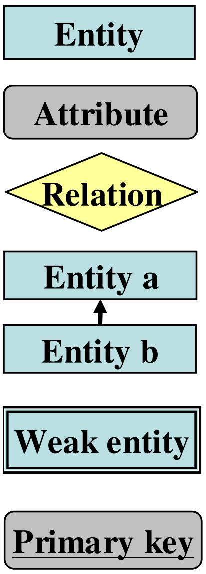


Figure 7.2 Process showing the following steps: a verbalized actual situation (narrative), its conceptual representation (ER model), the semi-automatic transformation into a relational scheme and finally the programming of the database scheme in a specific software language such as SQL

Basic components of the ERM are “entities” and their “attributes” and “relations” to other entities. Standard symbols and definitions of the basic components are introduced in Figure 7.3.



Entities are basic units of an ERM. Entities are types of objects and are defined sets of attributes. They correspond to tables in the final database.

Attributes are characteristics of the entity. They correspond to variables (column names) of a table in the final database.

Relation define the type of connection between entities which is quantified by cardinalities.

Generalization and specification of entities is possible, indicated by an arrow, where **a** is a generalization of **b**, and **b** is a specification of **a**. **b** inherits all attributes from **a**. This allows for representing hierarchical structures.

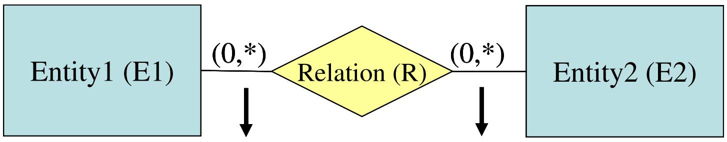
Weak entity types do never occur alone, they are always dependent on another entity (such as a room always depends on a building) they depicted with a double border.

Primary keys are unique identifiers of objects of an entity. Primary keys can be a single attribute such as a id number, or a combination of attributes.

Figure 7.3 Symbols used in an entity-relationship diagram

Entity types are types of objects such as persons in the database, characterized by attributes such as name of person: they correspond to variables (column names) of a table. The attribute or the set of attributes uniquely identifying a tuple (are row in a table) is called a primary key. Generalization, specification and weak entities are concepts to express permanent dependencies between entities. Relations define the connection between entity types by verbal expressions such as “has” or “visits” and with the help of “cardinalities” (relationship types) specifying ratios. Relations can also have their own attributes.

Figure 7.4 provides an overview of cardinalities for four principle types of relations according to the ISO-Min-Max notification (Abrial, 1974). The first number in brackets denotes the minimum cardinality. That means that entity 1 (E1) must appear at least never $(0,X_{1,*})$ or once $(1,X_{1,*})$ in the relation to entity 2 (E2). The second number in brackets is the maximum cardinality. E1 can therefore appear once $(X_{0,1},1)$, for instance in a 1:1- or a N:1-relationship or indefinitely often $(X_{0,1},*)$ for instance in a 1:N- or M:N-relationship in the relation to E2. In a similar way, E2's perspective in R has to be specified and labeled.



Type of relation R between E1 and E2	Cardinality of E1 in R	Cardinality of E2 in R
1) 1:1 – relation	(0,1) or (1,1)	(0,1) or (1,1)
2) 1:N - relation	(0,*) or (1,*)	(0,1) or (1,1)
3) N:1 - relation	(0,1) or (1,1)	(0,*) or (1,*)
4) M:N - relation	(0,*) or (1,*)	(0,*) or (1,*)

Figure 7.4 Cardinalities characterizing a relation (ISO-Min-Max notification (Abrial, 1974))

7.4 Results and discussion

Base model

The ERM developed for a poultry registration database in Switzerland is presented in Figure 7.5. The chosen entity types are "Poultry keeper", "Address and canton" and "Poultry farm". "Farm unit", "Housing system", and "Poultry flock" are weak entity types depending on the entity type "Poultry farm".

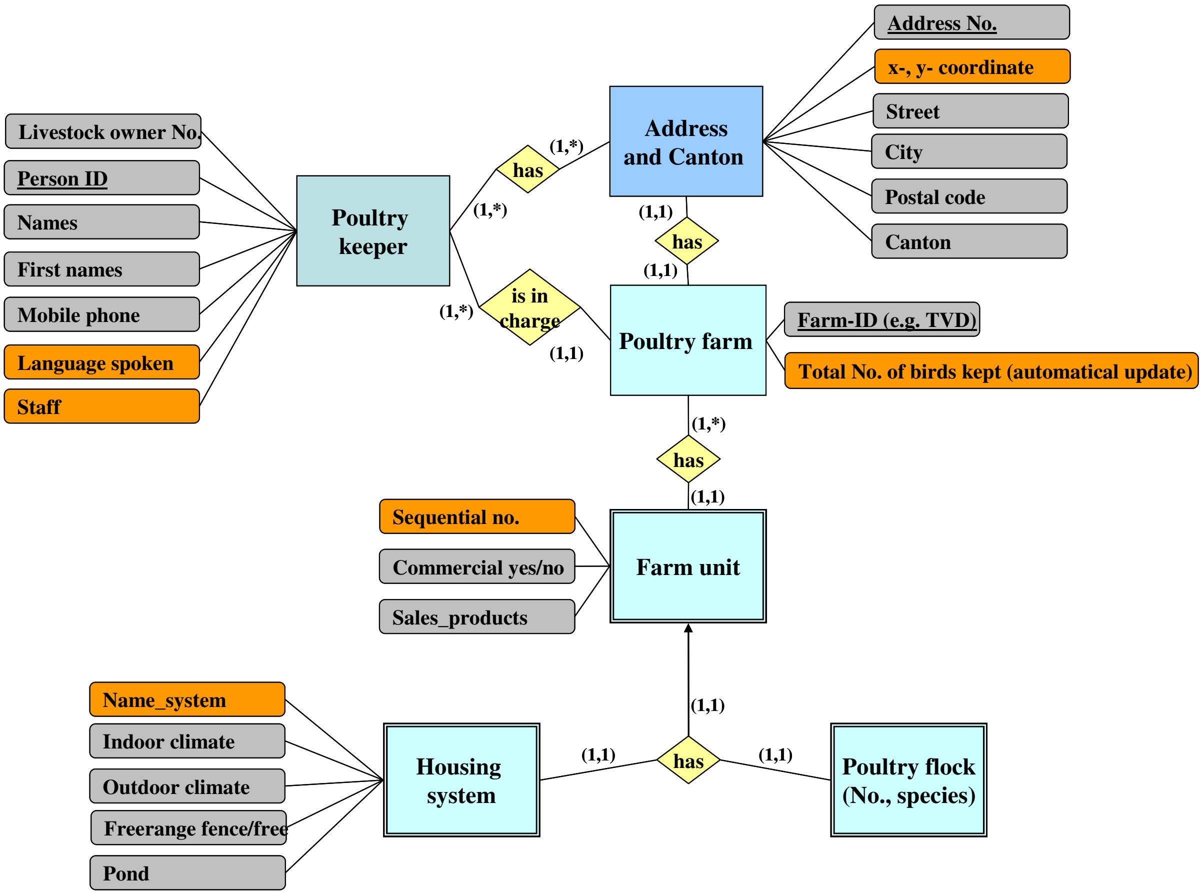


Figure 7.5 ERM for a poultry registration database in Switzerland. Attributes newly added (not existing in available registers) are highlighted in orange

In the ERM a poultry farm is defined as a site consisting of one up to a (theoretically) infinite number of farm units. Important attributes include a unique identification number (primary key) and the total number of birds kept on the farm. The farm number of the existing animal traffic database (TVD) could serve as a unique identifier if the database is extended to include non-commercial farms and if it is only used for one site. The total number of birds kept on a poultry farm is calculated from the number of birds per farm unit and is updated automatically.

The entity type “Farm unit” is well-defined by having exactly one “Poultry flock” and one “housing system”. The entity type “Poultry flock” is a simple list of number of birds per species (details not shown). The entity type “Housing system” is specified by the new attribute “Name_system”, for which several terminologies are available. Additional attributes denote if there is “Indoor”, or “Outdoor” climate in the housing system and whether or not a fenced or unfenced “free-range” area is present. For other epidemiologically relevant specifics of a housing system, attributes such as “Pond” are of interest (Saurina, 2009).

The entity type “Poultry keeper” contains data of the person in charge of the poultry farm. A 1:N-relation to the poultry farm, named “is in charge” is chosen. Therefore one person can be in charge of more than one farm site. More than one person working on the poultry farm can be recorded in the attribute “Staff”. We prefer this solution compared to a M:N-relation between personal and farm data, as for administrative purposes it is practical to have one defined legal contact person. The poultry keeper’s attributes are the “Person ID” number and a “Livestock owner number”. The combination of both is used as primary key. Attributes further include the persons’ “Names”, “First names” and “Mobile phone” numbers. We suggest adding the attribute “Language spoken”. This ensures that the persons can be contacted appropriately and without delay in a country with multiple national languages.

The entity type “Address and canton” is created in common for both poultry farms’ and poultry keepers’ addresses. The attribute “Address number” is introduced as primary key; it indicates whether the address refers to a farm or person. Further attributes include “Street” with street number, “City” and “Postal code” and, newly added, the “x-/y-geo-coordinate” attribute ideally on a street number level. This attribute can be used for producing geo-data maps and calculating air-line distances directly. The inclusion of “Canton” is important. In Switzerland as a federal state, partial lists for the administrative region “Canton” will be needed. Persons can have secondary residences, and one address can be the same for different poultry keepers and the poultry farm. Thus, we introduce a M:N-relation between the entity types “Address and Canton” and “Poultry keeper”. A “Poultry farm” has by definition one location and therefore a 1:1-relation to the entity type “Address and Canton”.

The proposed model addresses the first two issues pointed out in the introduction. First, it overcomes the 1:1-relation between poultry keeper and poultry farm that existed before. Second, the database model accounts for the case of more than one flock being kept on a poultry farm by introducing the concept “Farm unit”. The improvements are evident: so far poultry farms were sometimes listed twice under different persons’ names and assumedly identical persons were listed more than once with different farm addresses and details.

Model extensions

Four proposals for the extension of the model are subsequently presented to address the issue of database interfaces mentioned in the introduction. To improve the readability of the following diagrams (Figures 7.6-7.9), attributes and the entities "Address and Canton", "Housing system" and "Poultry flock" from the base model (Figure 7.5) are not shown.

I. Creating a link to producer lists of private companies

In Switzerland private companies (poultry marketing organizations) integrate commercial poultry farms for production and marketing of table poultry and eggs for human consumption. They keep an account of their member farms and production data. The farms' company affiliation is also of epidemiological interest as discussed in Chapters 5 and 6. Thus an interface allowing the retrieval of a poultry farm's company affiliation is presented in Figure 7.6.

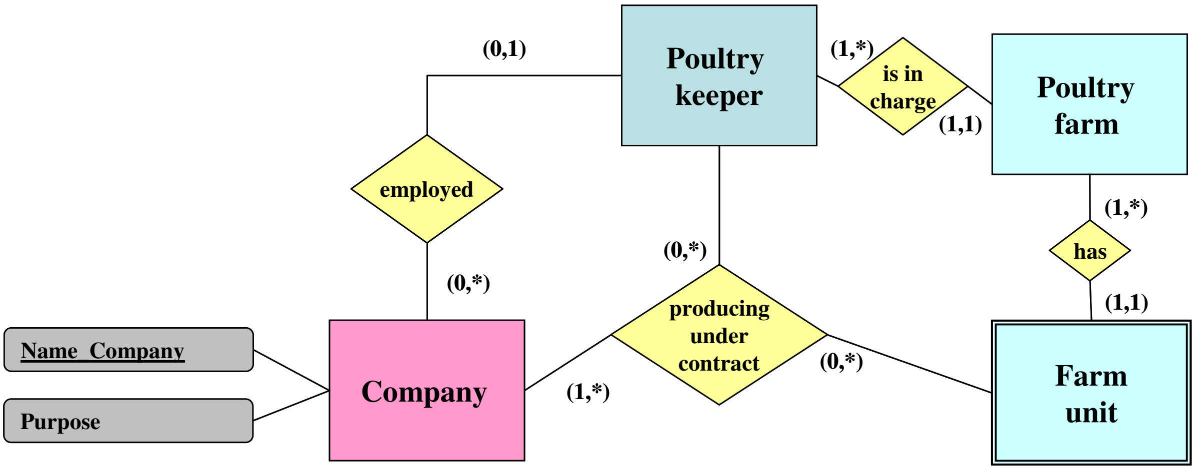


Figure 7.6 Extended base ERM showing new relations to the new entity type "Company" and its attributes

The entity type "Company" is described by the unique attribute "Name_Company" acting as primary key and the "Purpose" attribute. All additional company related data are ignored in our model. The relation "producing under contract" involves a "Poultry keeper", a "Farm unit" and the entity type "Company". One poultry keeper can produce for one or more companies (normally only one). "Farm unit" rather than "Poultry farm" is the entity type of choice in a case where only a part of the farm is under contract. This case is not desired by companies, but it cannot be excluded. A company by definition requires at least one poultry keeper and one farm unit under contract. Theoretically there is no upper limit to the number of farm affiliations, although typical numbers are between 50 and 450 farms affiliated to one company. A second relation "employed" is created to take the possibility into account that a poultry keeper can work for one company, for instance as a consultant, and that the company in turn has employees being poultry keepers themselves.

II. Creating a link to show attendance lists

Up to a few hundred local, cantonal, national and international poultry shows take place in Switzerland every year. They attract both poultry keepers who exhibit their own birds and visitors who attend the show.

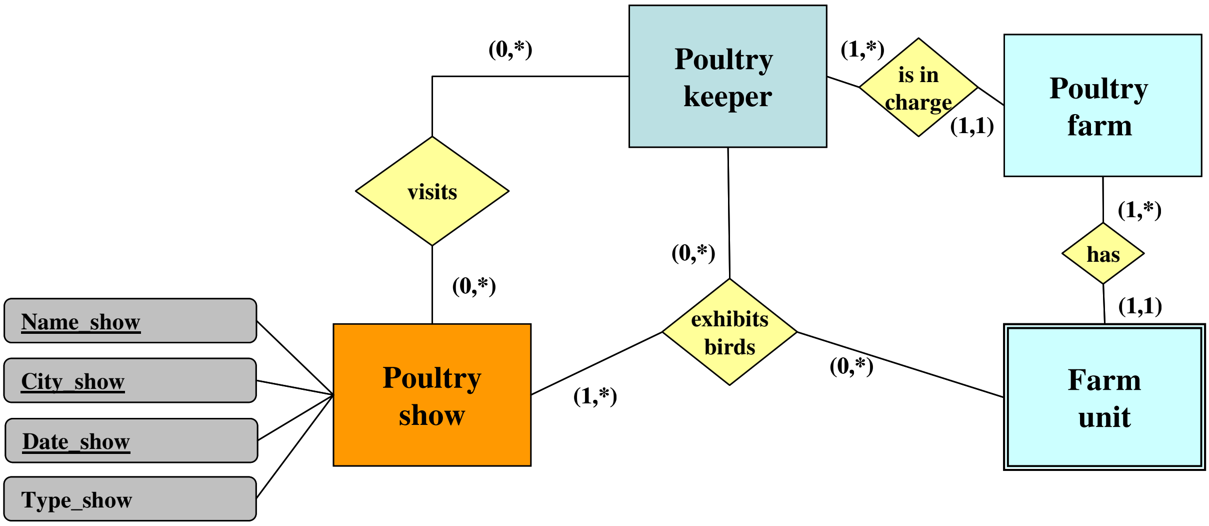


Figure 7.7 Extended base ERM with new relations to the new entity type "Poultry show"

The "Poultry show" extension of the base model is analog to the company example (Figure 7.7). Poultry shows are temporary events that can be repeated periodically. For this reason, their primary key includes the attributes "Name_show", "City_show" and "Date_show". The attribute "Type_show" allows for adding show specifics, for instance whether the show is cantonal and focuses on squabs exclusively. The relation "exhibits birds" involves the entity types "Poultry keeper", "Farm unit" and "Poultry show". One poultry keeper can exhibit birds at one or multiple shows. "Farm unit" is the farm entity type of choice in a case where only one farm unit exhibits birds at shows. For poultry shows to take place there has to be at least one participating poultry keeper with at least one farm unit involved. A second relation "Visit" is introduced to account for numerous poultry keepers visiting shows without exhibiting their own birds (Chapter 6). There is no system, however, to register these visitors systematically. A poultry keeper can visit one or more poultry shows. A poultry show can have visitors who are poultry keepers themselves.

III. Creating a link to diagnostic databases

Diagnostic tests in poultry flocks are performed in the context of *Salmonella spp.* monitoring programs or as clinical surveys of not apparent low pathogenic avian influenza (LPAI) virus infections. We provide an example of how diagnostic test records can be linked to the base model (Figure 7.8).

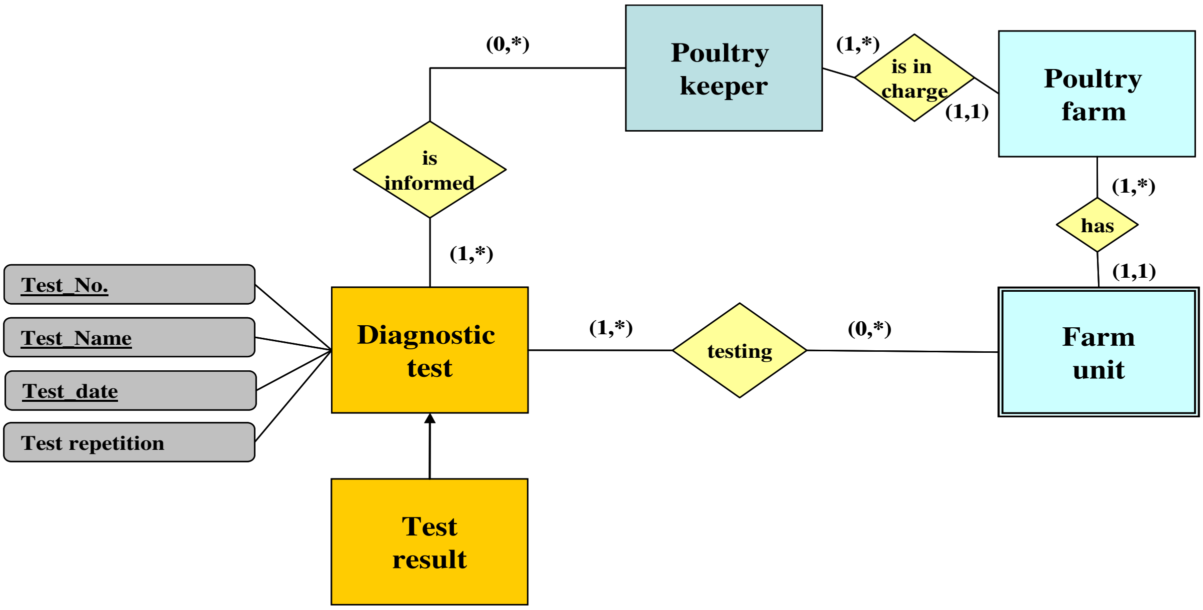


Figure 7.8 Extended base ERM with new relations to the new entity types “Diagnostic tests” and “Test result”

The entity type “Diagnostic test” is introduced. Important attributes are “Test_Number”, “Test_Name”, “Test_date” together forming the primary key. Some tests have to be repeated, especially when results are ambiguous. To document this, the attribute “Test repetition” is useful. Assuming that comprehensive test results can include several pathogen parameters, host antibodies or hemograms, we prefer to introduce an entity type “Test results” rather than a simple attribute. The entity type “Test results” is employed as a specification of the entity type “Diagnostic test”. Thus all attributes are inherited and the test result is clearly attributed to a unique test realization. The relation “testing” involves the entity types “Diagnostic test” and “Farm unit”. The 1:N-relation from “Diagnostic test” to

“Farm unit” allows for many tests on one farm unit or the same type of test on multiple farm units to be conducted. The relation “is informed” is introduced to trace the communication with poultry keepers, e.g. by informing poultry keepers prior to each testing and discussing the test results with them.

IV. Integrating data on poultry trading movements between poultry farms

In the poultry industry farms are often highly specialized in performing one step of the production process (for instance the upbringing of squabs). Therefore poultry must be moved between farms. Non-commercial farms are also involved in poultry movements as shown in Chapter 6.

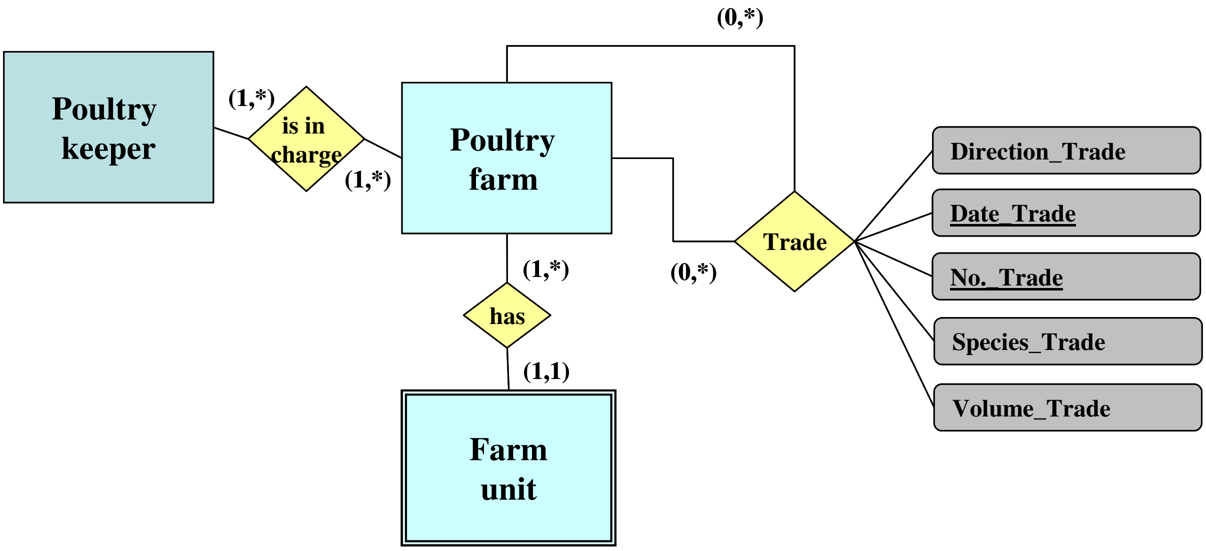


Figure 7.9 Extended base ERM with new relation “Trade” and its attributes to record poultry movements between farms

The relation “Trade”, which is used as a connector between poultry farms, is introduced to illustrate animal movement between farms. Useful attributes to describe animal movements are “Date_Trade” and a unique attribute “Number_Trade” transaction code as the primary key. Trade has a direction; one farm acts as provider the other as purchaser. Attributes such as “Species_Trade” and the number of birds traded are epidemiologically relevant details to assess the risk of virus spread amongst farms for instance (Chapter 6). The introduced M:N-relation allows for none up to many purchasing and selling transactions in both directions. Alternatively, the relation “Trade” can also be added on the level of “Farm unit” or on the

“Poultry keeper” level as trading is a transaction initiated by persons. We opt for the farm level because this allows for a direct calculation of trading distances between farms using the farms’ x-/y-geo-coordinates. For a complete picture of poultry movements, the entity types “Abattoir”, “Butcher”, “Hatchery” and others including their corresponding relations need to be introduced.

Identified needs

The present work summarizes experiences from the investigation of poultry registration data. It captures a selected real world context. The conceptual database representation provides a basis for discussion. Prior to an actual implementation of a new database model, it is strongly recommended that a mixed team of future user groups, experts from veterinary services, private companies and other interest groups such as breeding associations revise the model. This helps to add important criteria and to simplify structures that prove to be of minor practical relevance and to streamline the database in a comprehensive but clearly arranged way. At this point also data protection issues have to be addressed and agreements on sharing data between public authorities and private companies and associations have to be made.

Communication with computer scientists, programmers and data administrators is important in order to identify appropriate software that fulfills all demands and for which long-term support is guaranteed. It is also crucial to design practical and intuitive data entry masks and to clarify users’ authorities and access rights. Given that an increasing group of commercial farmers maintain livestock data electronically (Fallon, 2001), the option of designing interfaces for exchanging data collected on the level of the farm and registration data collected by veterinary and agricultural authorities should be addressed.

Poultry experts should work out clear, non-overlapping and unambiguous definitions for entities, attributes and relations, and create guidelines for data collection and entry. This is particular challenging in a multilingual country such as Switzerland. A major obstacle might be that a unique and legal definition for “commercial and non-commercial” poultry farm is missing. Available definitions in Switzerland are purpose-specific such as for *Salmonella spp.* surveillance (Der Schweizerische Bundesrat, 1995) or the decree on direct governmental subsidies (Der Schweizerische Bundesrat, 1998). This issue might result in a multi-criteria definition. Definitions only based on the number of birds kept on a farm, must take into account that typical flock sizes differ amongst species for instance commercial chicken and commercial ostrich farms (Capua *et al.*, 2002).

Finally, the quality of the database strongly depends on regular updates such as adding new data and changing or deleting old entries. In the conducted cross-sectional survey, about 8% of returned questionnaires stated that birds were no longer kept (unpublished data). Often the HPAI threat and its legal implications such as mandatory confinement of poultry were stated. Keeping changes up to date is particularly important in situations when the database is used as a crisis management tool (Kroschewski *et al.*, 2006).

New database systems are known to be costly in the development and introduction stages, but they are often very profitable for different user groups in the long term (Disney *et al.*, 2001). The cost-benefits of the suggest database format need to be assessed.

Outlook

The presented database model allows for any easy and quick processing of complex queries: Queries of interest to cantonal veterinary services could be *"Display all poultry keepers who have their residence in the canton Fribourg and who are German speaking"* or *"Display all layer farms located in the canton of Geneva"*. Queries can also be performed on a federal level and can address housing systems and kept species, e.g. *"Display all poultry farms keeping chicken in an unfenced free-range area"*. A query on poultry movements could, e.g., be *"Display all poultry farms being connected via trade in the period from 2nd October until 20th October 2009"*. The query *"Display all poultry farms that use free-range systems and are located in a band of 1 km around defined large water bodies and then retrieve the addresses of the poultry keepers"* would have been an application of interest in winter 2006/2007 and 2007/2008 when geographical risk areas in which poultry had to be kept inside had to be defined.

The proposed separation of person (poultry keeper) and farm data is of particular importance for practical purposes. For the implementation of epidemic prevention and control measures the farm site within its geographical context and population density must be known. For all targeted information policy as suggested in other parts of the study (Chapter 5) the keepers' addresses must be directly accessible and the national language spoken by the keeper must be recorded so that keepers can be approached without delay.

Recently, the legal basis for a complete horse, poultry, bee and fish husbandry registration on a *federal* level has been created, coming into effect in January 2010 (Der Schweizerische Bundesrat, 2009). This is an important step towards an improved data situation of livestock populations and subpopulations that have been neglected so far such as, e.g., non-commercial poultry flocks.

7.5 Conclusion

With the proposed base model for poultry registration data and its extensions three major constraints of previous registers can be overcome. We provide a flexible a format allowing for other than 1:1-relations between poultry keepers and poultry farms. Our format can account for more complex and exceptional farm structures where more than one flock is kept. Interfaces to other data sets of interest can be easily created. Our proposed format allows for secure storage of existing data and flexible query options providing quick access to epidemiologically relevant data. We conclude that a relational database is an ideal solution for organizing demographic baseline and surveillance data for epidemiological purposes.

7.6 Acknowledgements

We would like to thank Heiko Schuldt, professor in the Database and Information Systems Group, and Nadine Fröhlich, computer scientist at the Computer Science Department of the University of Basel, for their lecture on relational databases and for their advice on the proposed entity relationship models. We acknowledge Tom Jung for the English proofreading of this article.

7.7 Authors' contributions

LF designed the database models and wrote the manuscript as the lead writer. JH provided support for database models and helped to draft the manuscript. JZ supervised the project and helped to draft the manuscript.

PART 2

CONTACT NETWORKS

8 MODELS OF EPIDEMICS: WHEN CONTACT REPETITION AND CLUSTERING SHOULD BE INCLUDED

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8.1 Abstract

The spread of infectious disease is determined by biological factors, e.g. the duration of the infectious period, and social factors, e.g. the arrangement of potentially contagious contacts. Repetitiveness and clustering of contacts are known to be relevant factors influencing the transmission of droplet or contact transmitted diseases. However, we do not yet completely know under what conditions repetitiveness and clustering should be included for realistically modelling disease spread.

We compare two different types of individual-based models: one assumes random mixing without repetition of contacts, whereas the other assumes that the same contacts repeat day-by-day. The latter exists in two variants, with and without clustering. We systematically test and compare how the total size of an outbreak differs between these model types depending on the key parameters transmission probability, number of contacts per day, duration of the infectious period, different levels of clustering and varying proportions of repetitive contacts.

The simulation runs under different parameter constellations provide the following results: The difference between both model types is highest for low numbers of contacts per day and low transmission probabilities. The number of contacts and the transmission probability have a higher influence on this difference than the duration of the infectious period. Even when only minor parts of the daily contacts are repetitive and clustered can there be relevant differences compared to a purely random mixing model.

We show that random mixing models provide acceptable estimates of the total outbreak size if the number of contacts per day is high or if the per-contact transmission probability is high, as seen in typical childhood diseases such as measles. In the case of very short infectious periods, for instance, as in Norovirus, models assuming repeating contacts will also behave similarly as random mixing models. If the number of daily contacts or the transmission probability is low, as assumed for MRSA or Ebola, particular consideration should be given to the actual structure of potentially contagious contacts when designing the model.

8.2 Introduction

The spread of infectious disease is determined by an interplay of biological and social factors (Koopman, 2005). Biological factors are, among others, the virulence of an infectious agent, pre-existing immunity and the pathways of transmission. A major social factor influencing disease spread is the arrangement of potentially contagious contacts between hosts. For instance, the distribution of contacts among the members of a population (degree distribution) strongly impacts population spread patterns: Highly connected individuals become infected very early in the course of an epidemic, while those that are nearly isolated become infected very late, if at all (Hethcote and Yorke, 1984; Anderson and May, 1991). For a high dispersion of the degree distribution, the transmission probability above which diseases spread is lower than for a low dispersion (Hethcote and Yorke, 1984; Anderson and May, 1991; Duerr *et al.*, 2007). If the degree distribution follows a power law, the transmission probability necessary to sustain a disease even tends to zero (Pastor-Satorras and Vespignani, 2001; Keeling and Eames, 2005; Kiss *et al.*, 2006b).

Another important structural property influencing the spread of diseases is the clustering of contacts. Clustering deals with how many of an individual's contacts also have contact among each other. High clustering of contacts means more local spread (within cliques) and thus a rapid local depletion of susceptible individuals. In extreme cases, infections get trapped within highly cohesive clusters. Random mixing is known to overestimate the size of an outbreak (Zaric, 2002), whereas the local depletion caused by clustering remarkably lowers the rates of disease spread (Keeling, 1999; Eames, 2008): Clustering results in polynomial instead of exponential growth, which can be expected for unclustered contact structures (Szendrói and Csányi, 2004).

For most of the diseases transmitted by droplet particles or through close physical contact, the number of contacts that can be realistically made within the infectious period has a clear upper limit. The mean value of potentially contagious contacts can be interpreted in a meaningful way, since the distribution of daily contacts is unimodal with a clear "typical" number of contacts (Edmunds *et al.*, 1997; Beutels *et al.*, 2006; Mossong *et al.*, 2008; Mikolajczyk *et al.*, 2008). Potentially dominant properties of the underlying contact structure are the clustering of such contacts and their repetitiveness, i.e., whether contacts repeat within the infectious period or not.

A recent study combining a survey and modelling showed that the repetition of contacts plays a relevant role in the spread of diseases transmitted via close physical contact. Contrarily, the impact of repetitiveness seems to be negligible in case of conversational contacts (Read *et al.*, 2008). However, the generality of these findings is limited, as they are based on a small, unrepresentative sample and as the specific patterns of such contacts vary depending on the national and cultural context (Mossong *et al.*, 2008). A more theoretical work showed that the dampening effect of contact repetition is further increased by contact clustering and is more pronounced if the number of contacts per day is low (Eames, 2008).

The aim of this paper is to better understand the conditions under which the inclusion of contact repetition and clustering is relevant in models of disease spread compared to a reference case assuming random mixing. This is pertinent, as many researchers still use the random mixing assumption without thoroughly discussing its adequacy for the respective case study (Gani and Leach, 2001; Sertsou *et al.*, 2006; Ray *et al.*, 2007; Nagelkerke *et al.*, 2007; Nishiura *et al.*, 2008). In particular, we test and discuss the influence of transmission probability, number of contacts per day, duration of the infectious period, clustering and proportion of repetitive contacts on the total outbreak size of a disease. This helps modelers and epidemiologists make informed decisions on whether the simplifying random mixing assumption provides adequate results for a particular public health problem.

8.3 Material and methods

Stochastic SIR models

We assess the influence of repetitive contacts and clustering on the total outbreak size I_{tot} (number of new infections over simulation time) for a simple SIR structure (Kermack and McKendrick, 1927; Anderson and May, 1991) under which every individual is either fully susceptible or infectious or recovered (immune; Figure 8.1a). We construct two different types of individual-based models: one assuming random mixing (i.e., contacts are unique and not clustered), the other assuming complete contact repetitiveness (i.e., the set of contacts of a specific individual is identical for every simulation day) and allowing for clustering. Both model types can be blended in varying proportions. In our models, every infectious individual infects susceptible contacts at a daily probability β, which is equal for all infectious-susceptible pairs. Individuals remain infectious for an infectious period τ, which is exactly defined and not stochastic in its duration. Infectious individuals turn into the recovered state as soon as the infectious period passed by. We assume that infection confers full immunity for the time scale of the simulation. Hence, recovered individuals cannot be reinfected by further contacts with infectious persons. There are no birth or death processes: hence, the population size is constant. All possible state transitions are delineated in Figure 8.1a.

Under the random mixing assumption (in mathematical terms denoted by index ran), n contacts are randomly chosen out of the whole population (including susceptible, infectious and recovered individuals) for every individual and every day. There is neither contact repetition nor clustering, as our algorithm ensures, that no contact partner is picked twice by the same individual.

In fact, clustering is neither properly defined nor is it a reasonable concept under the random mixing assumption for theoretical and practical reasons: In this paper we refer to the common definition that the clustering coefficient CC is the ratio of closed triplets to possible triplets (Watts and Strogatz, 1998), where a closed triplet is defined as three individuals with mutual contact. This definition is based on static networks. As in random mixing models contacts change daily, different clustering coefficients could be calculated for every single simulation time step. However, no epidemiologically relevant effect of such clusters could be observed, because any new infection comes into effect only in the following time step when contacts are already rearranged. As a consequence, there is no local depletion of susceptible individuals observable under this definition, even for high clustering coefficients. If clustering would be defined for an extended time interval (e.g., the infectious period), an enormous amount of closed triplets would be necessary to attain only slight clustering coefficients as the total number of contacts over such a long time is very high. For such huge cliques, there is no meaningful interpretation and no analogy in the real world.

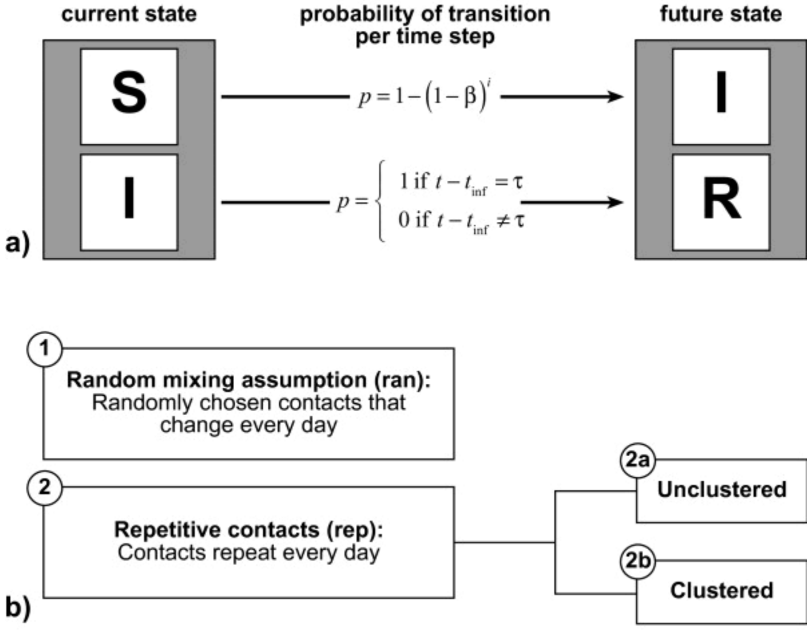


Figure 8.1 State transitions and contact structures: Subfigure a: Two transitions are allowed between three different states an individual can take: (S)usceptible to (I)nfectious and (I)nfectious to (R)ecovered. β denotes the transmission probability of one susceptible-infectious pair per time step. i stands for the number of infectious contacts that a specific susceptible individual has at the current time step. t gives the current simulation time, whereas t_{inf} gives the time step at which the individual was infected. τ is the infectious period. Subfigure b: We compare two model types: the contacts in the first type change daily while those in the second type are constant over time. The second model type assuming repetitive contacts exists in the two variants 2a and 2b

Repetitive contacts (in mathematical terms denoted by index rep) are implemented by generating a static network with n links for every individual. The links of this network represent stable, mutual, daily contacts between individuals. As mentioned, the model type assuming repetitive contacts exists in two variants. For the variant without clustering, individuals are linked completely at random. Nonetheless, for repetitive contacts, clustering is a meaningful concept as contacts are static and as clusters correspond to observable entities in the real world: family or work contacts, for instance, are usually clustered and tend to be highly repetitive. In this paper, predefined average clustering coefficients are achieved by alternately generating random links and triplet closures, as suggested by Eames (2008), until the clustering aim is achieved in average for the whole population. When the target value of closed triplets is reached, the network is filled up with random contacts until all individuals have n contacts.

This paper compares most parameter settings for a model assuming either full random mixing or perfect repetitiveness of contacts. This comparison allows for estimating the maximal possible difference between both antipodal simplifications of reality. However, real world dynamics of networks are far more complicated; therein some contacts are repeated daily, others on certain days of the week and others only once in a while. In order to investigate the effect of different proportions of repetitive contacts, we vary the fractions of repetitive contacts.

Parameter space to be tested

In the following section, we describe some important factors in the spread of infectious diseases that will be systematically tested for their influence on the difference between the random mixing model and the model assuming repetitiveness (with and without clustering). Important biological factors influencing the spread of infectious diseases are the duration of the infectious period τ and the per-contact transmission probability β.

The *infectious period* τ stands for the number of days (simulation time steps) a newly infected individual will remain infectious. The effect of repetitive contacts is tested for diseases with τ values between 2 and 14 days (see τ values given for various diseases in Table 8.1).

Table 8.1 Key transmission parameters of selected diseases

Disease	R_0	τ **[d]**	**Transmission pathways**[3]
Chickenpox (Varicella)	7-12[1]	10-11[1]	Direct contact, airborne, droplet, contact with infectious material
Ebola	1.34[11a] 1.79[12] 1.83[11 b] 2.13[12 c,a] 3.07[12 c,b]	14[12]	Direct contact, contact with infectious material, monkey-to-person
Influenza	1.3; 1.8; 3.1[2 d] 1.39[16] 1.58; 2.52; 3.41[17 e] 1.7–2.0[18] 2–3[19 f] 3.77[20]	2-3[1] 2.27[20] 3-7[21]	Direct contact, airborne, droplet[22]
Measles	5-18[1] 7.17-45.41[4 g,h] 7.7[5] 15-17[3] 16.32[4 g]	6-7[1]	Direct contact, airborne, droplet, contact with infectious secretions
MRSA[i]	1.2[23 j]	as long as purulent lesions continue to drain[1]	Direct contact, contact with infectious material[10]
Mumps	7-14[1] 4.4[6 h] 10-12[3]	4-8[1]	Direct contact, airborne, droplet, contact with infectious secretions
Norovirus	3.74[7 j]	1.8[7 j]	Direct contact, droplet (vomiting), contaminated food[8,9]
SARS[k]	1.43[12 l] 1.5[12 m] 1.6[13] 2.2-3.7[14] >2.37[15]	4[15] 5[12]	Close direct contact
Whooping cough (Pertussis)	10-18[1] 15-17[3]	7-10[1]	Direct contact, airborne, droplet, contact with infectious secretion

[Abbreviations, data sources and methods for the calculation of R_0, as far as known: [a]outbreak Uganda 2000 (Oyok *et al.*, 2001); [b]outbreak Congo 1995 (Khan *et al.*, 1999); [c]regression estimates; [d]1918 pandemic data from an institutional setting in New Zealand (Sertsou *et al.*, 2006); [e]1918 pandemic data from Prussia; assuming serial intervals of 1, 3 and 5 days (Nishiura, 2007); [f]1918 pandemic data from 45 cities of the United States (Mills *et al.*, 2004); [g]data from six Western European countries (Wallinga *et al.*, 2001); [h]age structured homogenous mixing model; [i]MRSA, Methicillin-resistant *Staphylococcus aureus*; [j]hospital outbreaks; [k]SARS, Severe Acute Respiratory Syndrome; [l]outbreak Singapore 2003 and [m]outbreak Hong Kong 2003 (WHO, 2003) Further literature sources: [1]Anderson and May, 1991b; [2] Sertsou *et al.*, 2006; [3] Heymann, 2004; [4] Wallinga *et al.*, 2001; [5]Mossong and Muller, 2000; [6]Edmunds *et al.*, 2000; [7]Vanderpasa *et al.*, 2009; [8] Duizer and Koopmans, 2006; [9] Evans *et al.*, 2002; [10]Public Health Agency of Canada, 2001; [11]Chowell *et al.*, 2004; [12]Ferrari *et al.*, 2005; [13] Meyers, 2007; [14] Riley *et al.*, 2003; [15]Wang *et al.*, 2006; [16]Gani *et al.,* 2005; [17]Nishiura, 2007 [18]Ferguson *et al.*, 2006; [19]Mills *et al.*, 2004; [20]Wearing *et al.*, 2005; [21]Davis *et al.*, 1980; [22]Brankston *et al.*, 2007, [23]Bootsma *et al.*, 2006]

The *transmission probability* β is defined as the probability that an infectious-susceptible pair results in disease transmission within one single time step of the simulation. β is equal for every infectious-susceptible pair. The effect of β on the impact of repetitive contacts compared to the reference case (without repetitive contacts) is analyzed via systematic variation.

In the results section, we show all results for $\beta \cdot n \cdot \tau$ values instead of pure β values to assure comparability of the outcomes: $\beta \cdot n \cdot \tau$ equals the basic reproduction number R_0 for the random mixing model and thus models with the same $\beta \cdot n \cdot \tau$ result in a similar total outbreak size. Referring to $\beta \cdot n \cdot \tau$ values assures that model comparisons are always made for a relevant range of β. The effect of repetitive contacts is tested for $\beta \cdot n \cdot \tau$ values between 1.2 and 4.0 in increments of 0.2. The epidemic threshold of random mixing models is $\beta \cdot n \cdot \tau = 1.0$. As we are only interested in diseases that can cause an epidemic, we set the lower boundary to 1.2. The upper boundary is chosen arbitrarily.

Social factors considered in this paper are the number of contacts per day n, the proportion of repetitive contacts and the clustering coefficient.

For every single simulation run, the *number of contacts per day* n is constant and equal for all individuals. n counts every contact an individual has within one simulation step, regardless of the alter’s infection status (susceptible, infectious or recovered) and regardless of whether the contact is repetitive. The effect of repetitive contacts on the simulation outcome is tested for n values between 4 and 20 with a step width of 2 (mean values for conversational contacts lie in this range (Mossong *et al.*, 2008)).

In order to investigate the effect of varying *fractions of repetitive contacts*, we simulate the total outbreak size for 0%, 25%, 50%, 75% and 100% repetitive contacts. Thereby, 25% repetitive contacts means that one fourth of all contacts on a given day repeat daily but that three fourth of the contacts on a given day are unique.

In the case of repetitive contacts, *clustering coefficients* between $CC = 0.0$ and 0.6 with a step width of 0.2 are accounted for. This span covers a wide range of existing transmission systems from highly infectious diseases with high number of contacts per day and with clustering coefficients close to zero to highly structured settings with a considerable proportion of clustered contacts like in hospitals (Liljeros *et al.*, 2007).

For all runs of the simulation model, the total population N was fixed to 20000 individuals. As initial seed 15 randomly chosen individuals are set to infectious every simulation run. For each combination of model parameters 350 runs were performed to achieve stable mean values of the outcome variables. A simulation run was terminated when no infectious individual was left.

Overview on performed analyses

We test the influence of the abovementioned parameters on the difference between the model typed in three distinct analyses. First, we show how strongly the total outbreak sizes $I_{tot,ran}$ and $I_{tot,rep}$ differ depending on τ, n and β. In the second analysis we vary n and β and the clustering coefficient CC for the case of repetitive contacts. Thirdly, we show how the total outbreak size changes under various n, β and CC, when repetitive and random contacts are mixed in varying proportions. Details for the three analyses are given in Table 8.2. In addition to the total outbreak size, we present further epidemiologically relevant indicators in the additional files (Smieszek *et al.*, 2009).

Table 8.2 Parameter settings of the analyses

	n	τ [d]	$\beta \cdot n \cdot \tau$	CC	**Proportion repetitive contacts**
Analysis 1					
a	4 – 20; 2	2 – 14; 1	1.6	.0	.0 vs. 1.0
b	4 – 20; 2	14	1.2 – 4.0; .2	.0	.0 vs. 1.0
c	4	2 –14; 1	1.2 – 4.0; .2	.0	.0 vs. 1.0
Analysis 2	4 – 20; 2	14	1.2 – 4.0; .2	.0 – .6; .2	.0 vs. 1.0
Analysis 3	8 – 20; 4	14	1.2 – 3.0; .6	.0 – .6; .2	.0 – 1.0; .25

[Parameter ranges are given before the semicolon; the increment is given after the semicolon. Single numbers stand for fixed values]

8.4 Results and discussion

Analysis 1: The effect of contact repetition depending on τ*,* n *and* β

As described in the methods section, τ, n and $\beta \cdot n \cdot \tau$ have been varied systematically to investigate the difference between the mean values of the outbreak sizes $\overline{I}_{tot,rep}$ and $\overline{I}_{tot,ran}$ under different parameter constellations. Figures 8.2a-c show three contour plots in which the difference between both model types $\left(\overline{I}_{tot,ran} - \overline{I}_{tot,rep}\right)/N$ is given for various τ, n and β values. Figure 8.2a gives $\left(\overline{I}_{tot,ran} - \overline{I}_{tot,rep}\right)/N$ depending on $4 \le n \le 20$ and $2 \le \tau \le 14$ with a fixed $\beta \cdot n \cdot \tau = 1.6$. The total outbreak size depends strongly on the number of contacts per day n but only slightly on the infectious period τ. In case of an infectious period between two and four days, there is a considerable change of $\left(\overline{I}_{tot,ran} - \overline{I}_{tot,rep}\right)/N$ with $\Delta\tau$; for $4 < \tau \le 8$, slight changes are observable; in case of infectious periods over eight days, the difference between both models depends mainly on n. Figure 8.2b gives $\left(\overline{I}_{tot,ran} - \overline{I}_{tot,rep}\right)/N$ depending on $4 \le n \le 20$ and $1.2 \le \beta \cdot n \cdot \tau \le 4.0$ with a fixed $\tau = 14$. It shows that the difference between both models depends strongly on both parameters, the number of daily contacts n and the transmission probability β. Differences are large for a small n or small β but negligible for a large n when β is large at the same time. Figure 8.2c, showing $\left(\overline{I}_{tot,ran} - \overline{I}_{tot,rep}\right)/N$ for $1.2 \le \beta \cdot n \cdot \tau \le 4.0$, $2 \le \tau \le 14$ and $n = 4$, is consistent with the observations made for the other two figures.

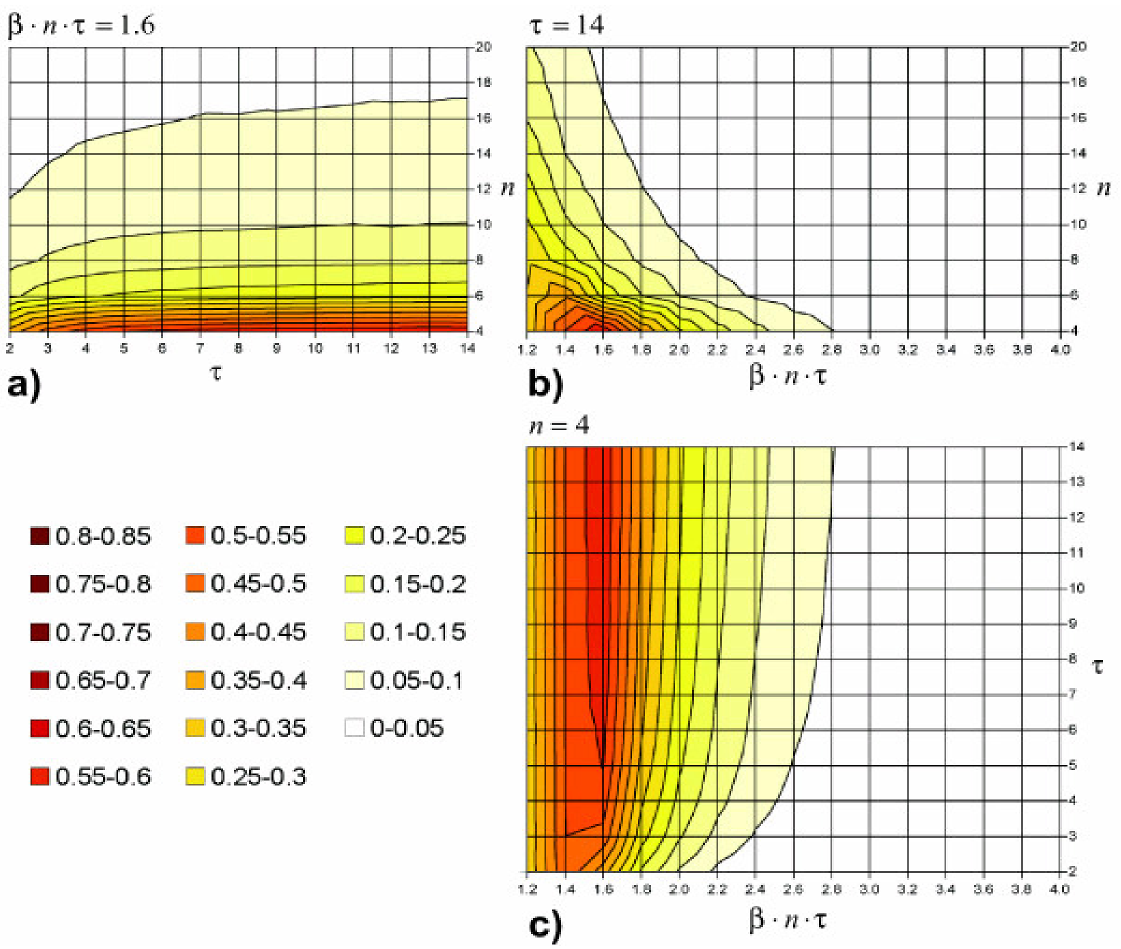


Figure 8.2 Model differences depending on τ, n and β: Subfigures a-c show the difference in the total outbreak size between a pure random mixing model and a model assuming complete repetitiveness (without clustering) relative to the population size N. Contour plots are interpolated from a grid of measurement points using Excel (version 11, Microsoft Corporation, Redmond, Washington, USA). (a) infectious period: $2 \le \tau \le 14$, step width (sw): $\text{sw} = 1$; daily number of contacts: $4 \le n \le 20$, $\text{sw} = 2$; per-contact transmission probability: $\beta \cdot n \cdot \tau = 1.6$. (b) $1.2 \le \beta \cdot n \cdot \tau \le 4.0$, $\text{sw} = .2$; $4 \le n \le 20$, $\text{sw} = 2$; $\tau = 14$. (c) $1.2 \le \beta \cdot n \cdot \tau \le 4.0$, $\text{sw} = .2$; $2 \le \tau \le 14$, $\text{sw} = 1$; $n = 4$

Effect of contact number: The increasing difference between $\bar{I}_{tot,rep}$ and $\bar{I}_{tot,ran}$ with decreasing n can be explained by two lines of reasoning.

First, in the case of contact repetition, there is always at least one out of the n contacts per day that is already infected (and thus not available for new infection): As contacts are stable over time, the infector of a susceptible individual is included in the subsequent contact list of that individual even when said individual has changed to the infectious state. Thus, at the least, the contact that originally transmitted the infection is not susceptible. In contrast, contacts change in every time step under the random mixing assumption: hence, the infector is not more likely to appear in the contact set than any other individual. This difference between $\overline{I}_{tot,rep}$ and $\overline{I}_{tot,ran}$ is more pronounced for small n because one non-susceptible individual out of a small set of contacts means a relatively higher decrease in local resources than does one out of a large set of contacts.

Secondly, any new infection means that the infector will have one susceptible contact less for all subsequent time steps. This local depletion of resources is more pronounced for small n for the same reason as in the first argument. Further, stochasticity acts stronger in small local environments than in large ones (Keeling and Grenfell, 2000).

Both effects can also be seen in the equation 1, which gives $R_{0,rep}$ as a function of $R_{0,ran}$, n and τ (see also Figure 8.3a)

$$R_{0,rep} \cong (n-1) \cdot \left[1 - \left(1 - \frac{R_{0,ran}}{n \cdot \tau} \right)^{\tau} \right] \quad (1)$$

In this equation the number of susceptible individuals in the local environment is reduced by 1 compared to the random mixing case, as we assume that every contact except the one that originally transmitted the infection is susceptible. This number of susceptible individuals $(n-1)$ is multiplied by the probability that such an individual becomes infected during the infectious period τ. As $(n-1)$ is smaller than n and $\left\lfloor 1-(1-\beta)^{\tau} \right\rfloor$ is smaller (or equal for $\tau = 1$) than $\beta \cdot \tau$, the expected number of secondary cases caused by an infectious individual in a population with a huge number of susceptible and few infected ones is always smaller in the repetitive case.

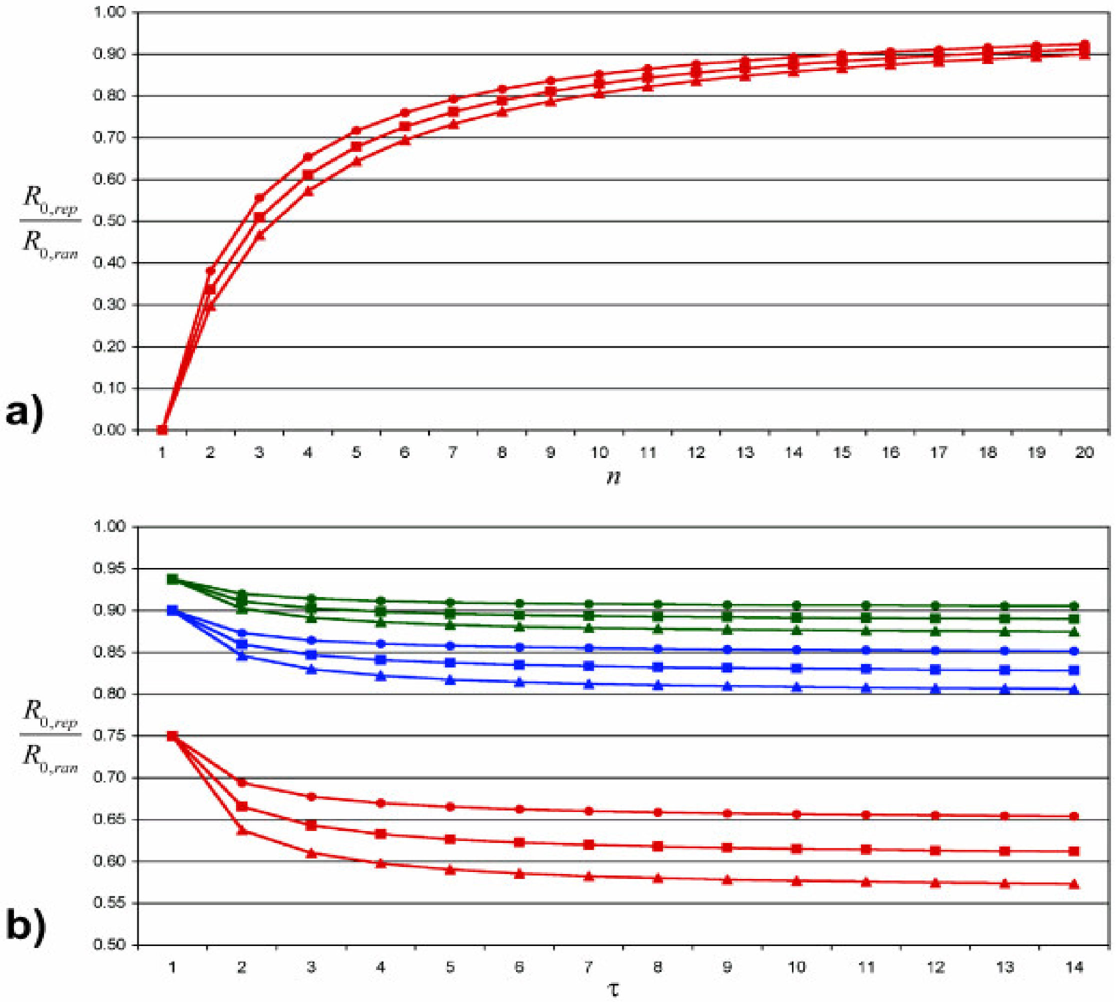


Figure 8.3 Ratio of the basic reproduction numbers: Subfigure a shows the ratio $R_{0,rep}/R_{0,ran}$ (as defined in equation 1) for $1 \leq n \leq 20$ (number of daily contacts) and $\tau = 14$ (infectious period). Triangles stand for $\beta \cdot n \cdot \tau = R_{0,ran} = 2.4$, squares for $R_{0,ran} = 1.8$ and circles for $R_{0,ran} = 1.2$. Subfigure b gives $R_{0,rep}/R_{0,ran}$ depending on the infectious period τ. Red lines and symbols are for $n = 4$, and blue lines stand for $n = 10$, whereas green lines represent $n = 16$. The meaning of the symbols is identical as in subfigure a

Effect of the per-contact transmission probability: The difference between $\bar{I}_{tot,rep}$ and $\bar{I}_{tot,ran}$ decreases rapidly with increasing β. The reason is that practically every individual will be reached and infected in case of large transmission probabilities, regardless of the underlying contact structure. Differences between both models may appear in the shape of the outbreak curve, but in terms of I_{tot} both models are equivalent. In case of small transmission probabilities, differences in the effective number of secondary cases generated by an infectious individual can become visible, as only a fraction of the whole population will be infected under both assumptions.

Effect of the infectious period: As expected, the difference between $\bar{I}_{tot,rep}$ and $\bar{I}_{tot,ran}$ increases with increasing τ. However, the change in difference is largest for $\Delta\tau$ in a range of low τ values, but is almost irrelevant for high values of τ. This observation is explained by the τ-dependence of $R_{0,rep}$ (equation 1, see also Figure 8.3b): The longer the infectious period, the smaller the chances for a specific contact to remain uninfected. However, this increase in individual infection probability is partly compensated by a lower per-day transmission probability, which is needed to achieve constant $R_{0,ran}$. The interaction of these antagonistic effects results in a stabilization of $R_{0,rep}/R_{0,ran}$ for a large τ.

Analysis 2: The effect of contact repetition combined with clustering depending on n and β

The results presented previously show that $\left(\bar{I}_{tot,ran} - \bar{I}_{tot,rep}\right)/N$ depends mainly on n and β. In a second step, we investigate how the difference between model type 1 and 2 changes, if clustering is introduced in the latter. Figures 11.1.4a-d show the difference between both model types for clustering coefficients CC between 0.0 and 0.6 when τ is fixed to 14 days and when n and $\beta \cdot n \cdot \tau$ vary in the ranges mentioned above. As expected, clustering results in an increased difference between both model assumptions. This increase is most pronounced for small numbers of contacts per day. The peak of $\left(\bar{I}_{tot,ran} - \bar{I}_{tot,rep}\right)/N$ is constantly at $n = 4$ but shows a right shift on the $\beta \cdot n \cdot \tau$ axis for increasing CC.

The further dampening of disease spread by clustering can be explained by increased locality of resources: While repetition limits the number of available susceptible individuals by keeping previously infected ones in the set of contacts, clustering reduces the number of susceptible contacts because there is a higher likelihood that contacts of an infector have already become infected by others during the infectious period, as infections spread rapidly within cliques. The reason why this effect is more pronounced for small n rather than for large n is the same as in the case of unclustered, pure contact repetition: Any reduction of susceptible individuals in the set of contacts weights relatively stronger in the case of few contacts than in the case of many. The right shift of the peak of $\left(\bar{I}_{tot,ran} - \bar{I}_{tot,rep}\right)$ can be explained by the increased transmission probability β needed to pass the epidemic threshold under increased clustering compared to the constantly low levels of β necessary under the random mixing assumption (Aparicio and Pascual, 2007).

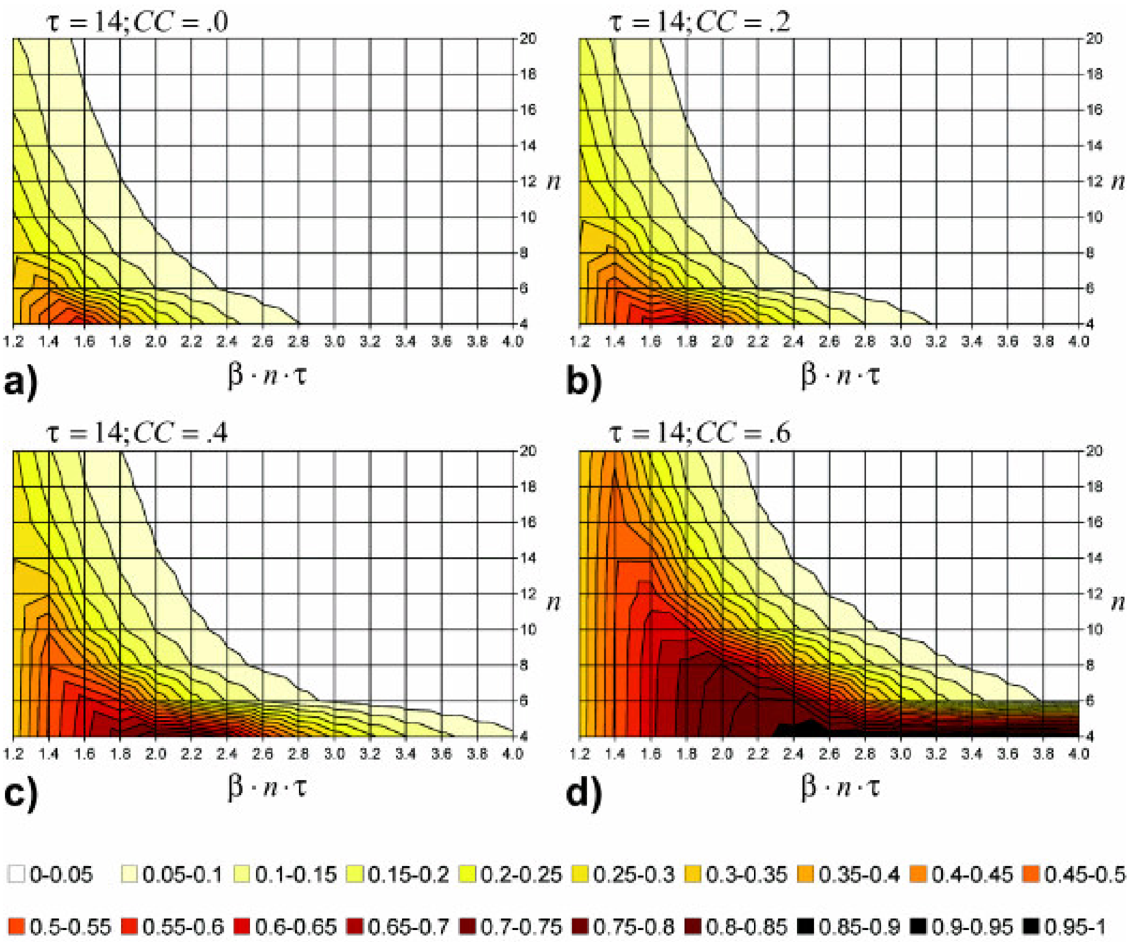
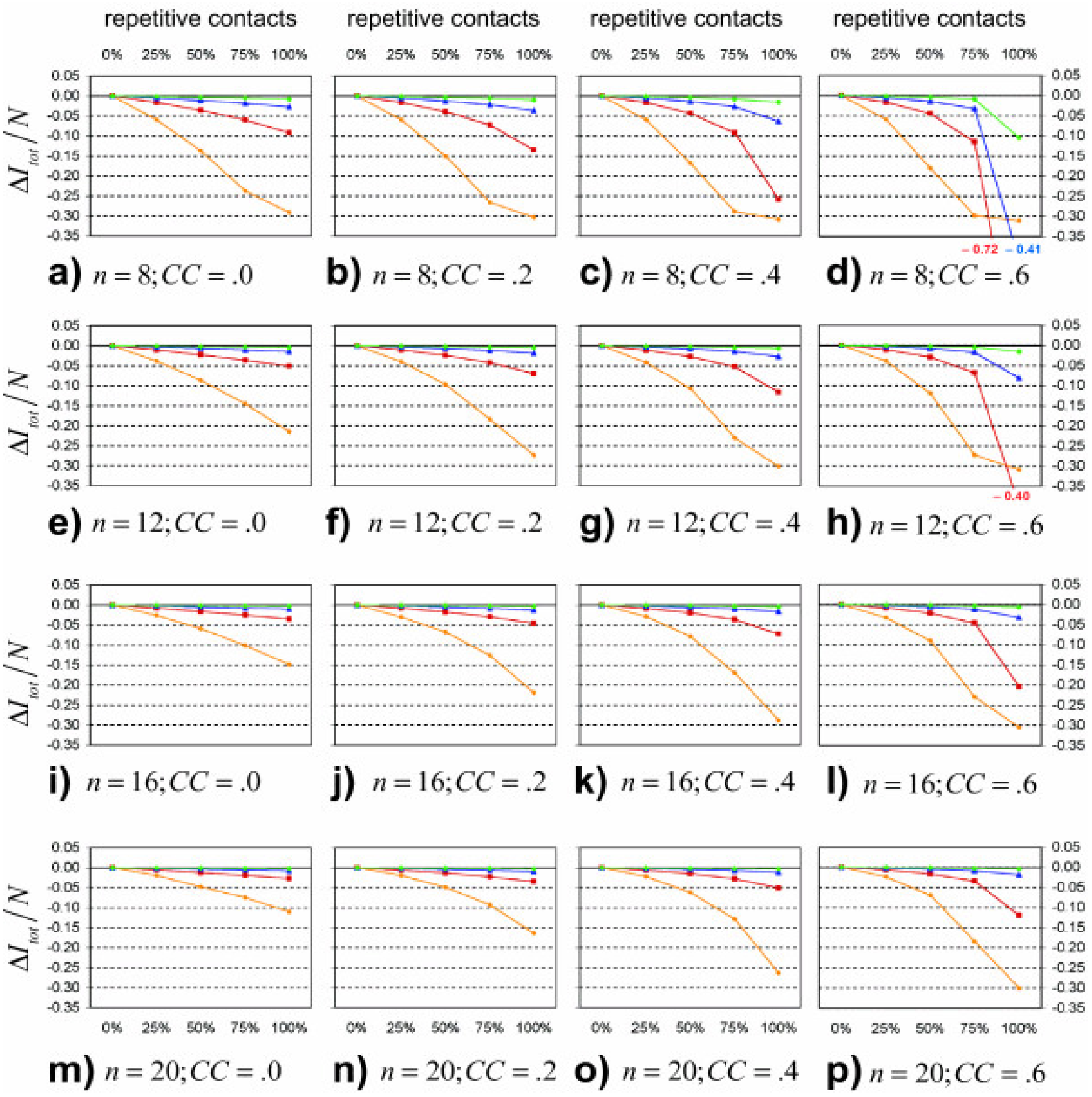


Figure 8.4 Dampening effect of clustering: Subfigures a-d show the difference in the total outbreak size between a pure random mixing model and a model assuming complete repetitiveness (with different levels of clustering) relative to the population size N for $4 \le n \le 20$, $1.2 \le \beta \cdot n \cdot \tau \le 4.0$ and $\tau = 14$. Subfigure a is identical with subfigure b. The clustering coefficient CC is increased picture-wise in steps of .2

Analysis 3: Varying proportions of contact repetition, clustering and β

We simulated the difference between both model assumptions for all possible combinations of $n = 8$, 12, 16 and 20, $\beta \cdot n \cdot \tau = 1.2$, 1.8, 2.4 and 3.0, $\tau = 14$ and $CC = 0.0$, 0.2, 0.4 and 0.6. The simulation results are shown in Figures 8.5a-p. The relation between the proportion of repetitive contacts per day and the average difference between this mixed model and a model assuming purely random mixing is approximately linear in the absence of clustering (for all tested cases, linear regressions between the proportion of repetitive contacts per day and the deviation of $\overline{I}_{tot}$ from the purely random mixing model achieve $R^2 > .98$). However, the deviation from the random mixing model increases disproportionately with the fraction of repetitive contacts when clustering is introduced (cf. to Figures 8.5b-d, 8.5f-h, 8.5j-l and 8.5n-p).



a) $n = 8; CC = .0$ **b)** $n = 8; CC = .2$ **c)** $n = 8; CC = .4$ **d)** $n = 8; CC = .6$

e) $n = 12; CC = .0$ **f)** $n = 12; CC = .2$ **g)** $n = 12; CC = .4$ **h)** $n = 12; CC = .6$

i) $n = 16; CC = .0$ **j)** $n = 16; CC = .2$ **k)** $n = 16; CC = .4$ **l)** $n = 16; CC = .6$

m) $n = 20; CC = .0$ **n)** $n = 20; CC = .2$ **o)** $n = 20; CC = .4$ **p)** $n = 20; CC = .6$

Figure 8.5 Mixed models: Subfigures a-p show the decrease of the total outbreak size relative to the size of the total population when the fraction of repetitive and clustered contacts is increased. 25% rep means that one fourth of all contacts on a given day repeat every day but that three fourths of the contacts on a given day are unique. Clustering coefficients CC are only defined and calculated for the repetitive fraction of the contacts. All simulations were calculated for an infectious period of 14 days. Orange circles stand for $\beta \cdot n \cdot \tau = 1.2$, red squares for $\beta \cdot n \cdot \tau = 1.8$, blue triangles for $\beta \cdot n \cdot \tau = 2.4$ and green rhombi for $\beta \cdot n \cdot \tau = 3.0$. The number of daily contacts n increases in steps of 4 per line of the subfigures, beginning with $n = 8$ in the first line. The first column of the subfigures shows $CC = .0$, the second column $CC = .2$, the third column $CC = .4$ and the fourth column $CC = .6$

One mechanism driving this non-linear relation when clustering is present is the local depletion of resources. Repetitive contacts of an infector have a much higher chance of becoming infected than do non-repetitive contacts. Moreover, if these repetitive contacts are also highly clustered, it is likely that the disease will become trapped in those cohesive social subgroups. However, if only a few non-repetitive, non-clustered contacts are added per day, the chances of spreading the disease between otherwise unrelated regions of the social network greatly increase.

Limitations

This paper systematically investigates a variety of epidemiologically relevant parameters needed to describe real-world transmission systems of diseases spread by droplet particles or direct physical contact. However, real-world social and biological processes involved in the transmission of infectious diseases are far more complex than captured by the archetypical model structures presented. Conceptual decisions and simplifications which could have potentially influenced the results are critically discussed in the following:

Model structure: We designed our two model types as SIR models, assuming that every individual is either susceptible, infectious or immune with respect to a certain disease. Transitions are only allowed from susceptible to infectious or from infectious to immune. The SIR structure is a fairly good representation for many diseases which lead to full immunity after recovery (e.g., measles). However, many diseases require other representations, as relevant intermediate states need to be covered, e.g., as with a long latency period in SEIR (Susceptible-Exposed-Infectious-Recovered) models. Another common deviation from the SIR structure arises, when recovery confers only partial or no immunity. In such cases, SIS (Susceptible-Infectious-Susceptible) representations are often chosen. In SIR or SEIR models, a total outbreak size can be defined (because the disease fades out at the end of an epidemic), whereas SIS models typically achieve an equilibrium $I(t)$ in the long run, but the disease does not die out. Despite all the differences in model behaviour, we expect the rough picture to be the same for SIR, SEIR and SIS models, as the mechanisms behind the observed differences for SIR models that we discussed also apply to SIS and SEIR models. Thus, the general conclusions derived in this paper should also hold true for these model types.

Degree distribution: The number of daily contacts n is fixed and equal for the entire population in both modelling approaches presented. This is a reasonable simplification for the purpose of this paper, as it keeps the investigated number of interactions manageable. However, in real world systems, the number of daily contacts appears to follow a negative binomial distribution (Mossong *et al.*, 2008; Mikolajczyk *et al.*, 2008), with some people having a relatively high number of contacts and others being almost isolated. It is known that the variance of the degree distribution impacts the spread of infectious disease, for instance, by decreasing the transmission probability needed to cause an epidemic (Bansal *et al.*, 2007). Particularly relevant for the difference between random mixing models and models accounting for contact repetition and clustering are the correlations between the number of contacts per day and contact repetition and clustering, respectively. It is plausible to assume that individuals with many contacts tend to also have many unrepeated contacts, whereas individuals with few contacts tend to have disproportionately high levels of repetitive contacts. If the proportion of repetitive contacts and clustering is correlated with the number of contacts, individuals with few contacts are likely to be dead-end streets for infectious diseases. In contrast, highly connected individuals could be structurally more important than expected, as they bridge distinct cliques.

Occasional contact repetition: In our simulations, contacts repeat either daily or never. Intermediate states between both extremes of complete random mixing and complete contact repetition have been investigated by combining both models in defined proportions. However, in reality, specific persons can be met at any frequency between never and daily. It is plausible to assume that intermediate frequencies reduce the effect of repetitiveness depending on the duration of the infectious period τ: For short infectious periods, those with low contact frequencies might appear as unrepeated contacts whereas they unfold their full dampening potential for long infectious periods.

Contact intensity and duration: In our models all contacts between an infector and a susceptible individual are equally likely to result in the transmission of the infectious disease. This simplification is not a good representation of the real world: The transmission probability depends on the amount of infectious material ingested by a susceptible person (Wells, 1955; Haas *et al.*, 1999). The uptake correlates with contact duration and intensity. Contact duration is long for highly repetitive contacts, while unrepeated contacts tend to have short duration (unpublished data). Accordingly, it can be expected that the interaction of clustering, contact repetitiveness and contact duration leads to a rapid infection of all closely tied clusters (primarily families, then workgroups and cliques at school and childcare institutions), leaving behind the people connected via mainly short, unclustered, occasional contacts.

Distribution of infectious period: The infectious period τ is fixed in our model, which contrasts to the design of classical mean-field models assuming exponentially distributed infectious periods (Kermack and McKendrick, 1927; Anderson and May, 1991). Keeling and Grenfell argue that R_0 is smaller for exponential period models than for fixed period models under otherwise identical conditions, because individuals with a long τ rapidly exhaust the susceptible in their local neighbourhood and, therefore, cannot compensate for the large majority of individuals with extremely short infectious periods (Keeling and Grenfell, 1997; Keeling and Grenfell, 2000). However, the often assumed exponential distribution is highly unrealistic, as observed infectious periods tend to be closely centred around a mean period and are thus less dispersed (Lloyd, 2001). Thus, assuming a fixed infectious period is a reasonable simplification of the reality that is not likely to have a major influence on $\bar{I}_{tot}$ as only very few individuals will use up their local susceptible resources during the infectious period in most cases. Moreover, if the infection probability is high enough to exploit almost the entire local environment (such that deviations of τ could affect the individual reproduction ratio), $\bar{I}_{tot}$ will reach the order of magnitude of the population size in either the fixed or the exponential case.

Implications for some exemplar diseases

Information on the per-contact transmission rate β and the number of potentially contagious contacts n is often not easily accessible or available and has to be measured (or fitted) if included in models of disease spread. However, rough estimates of both variables can be obtained when R_0 estimates are available and when the possible pathways of transmission are known, because β and n are linked to the basic reproduction number by $R_{0,ran} = \beta \cdot n \cdot \tau$ and the possible pathways reveal information on the possible number and structure of contacts at risk: At one extreme there is transmission via close physical contacts, which correlate mostly with intense social relations and are typically rare, repetitive and highly clustered. The other extreme is airborne transmission via tiny droplet nuclei that remain suspended indoors for a long time. In this case, vast numbers of persons can potentially be exposed, and such casual contacts are neither highly repetitive nor strongly clustered.

Table 8.1 provides information about the infectious period τ, R_0 estimates and the possible pathways of transmission for a variety of infectious diseases. The implications of clustering and contact repetition for models of the diseases listed in this table are discussed below.

Typical childhood diseases like mumps, measles, pertussis (whopping cough) or chickenpox have comparatively high R_0 estimates (Anderson and May, 1991; Mossong and Muller, 2000; Edmunds *et al.*, 2000; Wallinga *et al.*, 2001; Heymann, 2004), which means that one infector generates many secondary cases if a sufficient number of susceptible contact partners are available. These diseases are highly communicable – in fact, measles is one of the most highly communicable diseases in the world (Moss and Griffin, 2006) – and thus, very short and non-intense contacts have the potential to confer infection. Accordingly, both the number of contacts per day n and the per-contact transmission probability β are very high. We further assume that a high proportion of the contacts are casual contacts, because the threshold for a contact to be potentially contagious is very low with respect to duration and intensity. Consequently, the levels of repetitiveness and clustering are low, which means that the contact patterns for such childhood diseases are structurally similar to random mixing. Considering, that high numbers of daily contacts n make both types of models that we discussed behave similarly and considering, that under high transmission probabilities β almost every individual will be reached, random mixing models achieve almost the same results as more elaborate models including a certain amount of contact repetition and clustering.

Also in case of Norovirus, the difference $\left(\bar{I}_{tot,ran} - \bar{I}_{tot,rep}\right)$ is probably small, as the infectious period of this infectious agent is very short (Vanderpasa *et al.*, 2009) and as at the same time the basic reproduction number is comparatively high (Vanderpasa *et al.*, 2009; because the disease is easily communicable (Evans *et al.*, 2002; Duizer and Koopmans, 2006).

On the other side, there are diseases with comparatively low R_0 estimates and typically low numbers of contacts that still qualify for potential transmission. Methicillin-resistant *Staphylococcus aureus* (MRSA), for instance, is an infectious agent mostly transmitted in health care and nursing institutions. It needs close physical contact for transmission (Public Health Agency of Canada, 2001) and R_0 estimates given in the literature are close to the epidemic threshold (Bootsma *et al.*, 2006). Accordingly, both β and n are low. At the same time, health care settings tend to be highly structured regarding who cares for whom and who shares a room with whom. Hence, high levels of contact repetitiveness and clustering can be assumed (Liljeros *et al.*, 2007). Modelling MRSA under the random mixing assumption is likely to overestimate the total number of cases for given n, β and τ. If, in contrast, a random mixing model is fitted to measured data from an outbreak, either the infectivity or the number of potentially infectious contacts will be underestimated to meet the measured outbreak size. A similar argumentation applies to Ebola, which is transmitted via direct contact with infected blood, secretions, organs or semen (thus, n is rather low) and seems to be only moderately infectious (Khan *et al.*, 1999; Oyok *et al.*, 2001; Chowell *et al.*, 2004; Ferrari *et al.*, 2005). As a consequence, random mixing models of Ebola (Legrand *et al.*, 2007) are of limited validity.

Finally, there are some diseases not easily attributable to one or the other class. Severe Acute Respiratory Syndrome (SARS) and Influenza, for instance, have a range of R_0 estimates between 1.43 and 3.7 (WHO, 2003; Riley *et al.*, 2003; Ferrari *et al.*, 2005; Wang *et al.*, 2006; Meyers, 2007) and between 1.3 and 3.77 (Davis *et al.*, 1980; Mills *et al.*, 2004; Wearing *et al.*, 2005; Gani *et al.*, 2005; Ferguson *et al.*, 2006; Sertsou *et al.*, 2006; Nishiura, 2007), respectively. No definite consensus has been reached on whether Influenza is transmitted predominantly by large droplets and close contact or by very small droplets that disseminate quickly and stay suspended in indoor air for a long time (Brankston *et al.*, 2007). In the latter case, a large amount of people would be at risk of infection, so random mixing would be a reasonable approximation of the real contact patterns. In the case of transmission by close contact and large droplets (that fall out quickly), the mean number of potentially contagious contacts per day lies between 8 and 18, depending on the national and cultural context (Mossong *et al.*, 2008). Considering, that not all contacts are equally likely to transmit influenza, but that long and intense contacts (such as household contacts (Ferguson *et al.*, 2005)) are more prone to do so and that such contacts also tend to be more repetitive and clustered, it is likely that random mixing models also overestimate the outbreak size for given n, β and τ. However, problems will definitely arise when the impact of social distancing measures (decrease of n) or of antiviral treatment (decrease of β) are estimated under the random mixing assumption: both interventions will be much more effective in a more elaborate model than in a random mixing model when n, β and τ are the same for both model types. This argumentation is consistent with recent findings on the impact of other network properties on influenza spread: Heterogeneity in degree distribution does not influence the outbreak size in case of highly contagious influenza strains, but does so for moderately contagious strains; however, it does influence the total outbreak size when interventions are simulated – even in case of highly contagious strains (Duerr *et al.*, 2007).

8.5 Conclusions

Real-world contact patterns are complex. They typically show all kinds of intermediate states ranging from contacts repeating on a daily basis to and never again. There are various clearly defined, cohesive groups with typically high intra-group clustering coefficients (e.g. households, workgroups, peer groups at school) and, at the same time, random contacts, e.g., in a leisure setting. Moreover, contacts differ in intensity and duration, which further complicates the dynamics of disease spread in such settings. This paper simplifies these complex patterns to a manageable model and parameter space that can be investigated systematically. Our research applies to diseases transmitted via conversational or direct contact, for which a typical number of contacts per day can be defined. For such diseases, our findings can help modellers judge whether a specific transmission system consisting of a specific infectious agent and a specific human system at risk can be represented by a simple random mixing model or if more elaborate models are necessary.

Random mixing models result in acceptable estimates of the total outbreak size $\bar{I}_{tot}$ even if the real world contacts are highly repetitive and clustered

- if the number of potentially infectious contacts per day is high and
- if the transmission probability for a single infectious-susceptible pair is high and
- particularly, if the infectious period is just one to three days.

If the number of contacts per day or the transmission probability is low, particular consideration should be given to the actual structure of potentially contagious contacts in designing the model.

8.6 Acknowledgements

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8.7 Authors' contributions

TS carried out the majority of the model design, implemented the model, computed the analyses and prepared the manuscript as the lead writer. LF participated in the model design, contributed to the epidemiological interpretation of the model results, reviewed the literature on model parameters for specific diseases and helped to draft the manuscript. RWS participated in the model design and helped to draft the manuscript.
All authors read and approved the final manuscript.

9 BUILDING A COUNTRYWIDE CONTACT NETWORK MODEL OF POULTRY FARMS: GROUNDWORK FOR ANTICIPATING POULTRY EPIDEMICS

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9.1 Abstract

Network based transmission models are more adequate in many settings to predict the course and the final outbreak size of an epidemic compared to models assuming random mixing and to identify targets for preventive and control measures. Truly relevant contacts for disease spread often only become evident during or following an outbreak. However, one would like to know the target population's rough contact network characteristics prior to an outbreak and employ them in prediction models. In Switzerland, the highly pathogenic avian influenza (HPAI) threat created the need to preemptively understand potential transmission pathways between poultry farms (free from HPAI to date). Here, we present a step-by-step approach to building a countrywide contact network of poultry farms.

Data were retrieved and collected from different sources: a poultry farm census was established from all poultry registration data. Data on poultry movements and contact partners (farms, hatcheries, abattoirs/butchers, poultry shows) were collected by a survey among 3,978 sampled poultry keepers and by interviewing five experts from companies integrating poultry farms, and by reviewing literature. In all, 1,061 valid contact survey datasets were extrapolated on the farm census. From this synthetic poultry farm population, distributions of numbers of different contact partners (degree distributions) and contact frequencies were calculated.

The synthetic poultry farm population had highly right skewed distributions of contact frequency, as well as of a varying number of different contact partners per farm; a majority of farms had no or one partner, and only about 4% of the poultry farms had 4 or more different contacts. Unexpectedly, only 20% of these highly connected farms were commercial poultry farms. For incoming contacts only 14% and for outgoing contacts 40% were commercial farms. Further networks indices on the synthetic populations remain to be explored. The preliminary findings reveal "show bird farms" and "mixed commercial farms" to be more exposed to pathogen introduction via the contacts considered and show bird farms and upbringing farms to have a higher potential of encouraging disease transmission because of larger number of outgoing contact partners.

9.2 Introduction

Network analysis has begun to play an increasingly important role in infectious disease epidemiology. Network analysis offers, for the first time, an analytical framework to study contact patterns amongst members of a given population and to quantify the mere effect of the arrangements of potentially contagious contacts on pathogen spread within a population. In many settings, network based epidemic models reflect the course and final outbreak sizes more realistically than more traditional models which assume randomly mixed host populations (Zaric, 2002; Wallinga *et al.*, 2006; Eames, 2008; Lyytikäinen *et al.*, 2009). Network analysis further provides defined indices to describe the individuals' network positions within a population. Network indices help to identify central actors (individuals, farms etc.) that are at greatest risk of becoming infected or of passing on infection (Bell *et al.*, 1999). This is valuable information for defining targets in risk-based surveillance systems and for planning prevention and control measures.

Our population of interest is the Swiss poultry sector in view of highly pathogenic avian influenza (HPAI) epidemics. Although free from HPAI since 1931 (Bundesamt für Veterinärwesen, 2009b), poultry farms face the potential risk of HPAI virus introduction from wild birds (Kilpatrick *et al.*, 2006; Hauser *et al.*, 2006a) and through the legal and illegal trade of poultry and poultry products (Hauser *et al.*, 2006b; Läubli, 2009). Moving infected poultry, which is not obviously diseased (for instance during the incubation period), amongst farms and other facilities is assumed to be relevant for HPAI virus dissemination within the country (Thomas *et al.*, 2005; Truscott *et al.*, 2007; EFSA, 2007; Dent *et al.*, 2008). Information on such determinants of HPAI spread and their distribution within the host population is important in order to plan and target epidemic surveillance. For this purpose, mathematical models predicting transmission dynamics and the impacts of interventions are increasingly used. But how would poultry farms including their poultry movement interactions be adequately reflected in such model?

The choice of an epidemic model depends on the constellation of different biological parameters, mainly the infectious period and the contagiousness, and of population-related determinants, such as the number of different contact partners of the population members, the stability of contacts, and clustering of contacts within the population.

Smieszek and colleagues (2009) found that considering the underlying contact structure of a population was particular important when the number of daily contacts was small, the transmission probability low or the infectious period long.

Transmission parameters for farm-to-farm spread of HPAI are not available for Switzerland. For the 1999-2000 H7N1 outbreak in Northern Italy, reproductive ratios (number of new infected farms originating per infected farm in one day) of 0.6 to 1.8 have been calculated, and infectious periods on the farm level from 10.9 to 14.3 days have been described for commercial farms. Basic reproductive rates were highest in the first month of the outbreak (Mannelli *et al.*, 2007). For the same outbreak Garske and colleagues (2007) estimated a mean basic reproductive ratio of 2.2 and an infectious period of 5 days. For the 2003 H7N7 outbreak in the Netherlands they generated mean basic reproductive ratios of 2.9 and 3.3 in two different regions, and infectious periods of 1.9 and 3.4 days, respectively. For the Netherlands outbreak, there were also reports of average infectious periods of 6 days, especially at the onset of the epidemic (Stegeman *et al.*, 2004; Le Menach *et al.*, 2006). Informed by experimental data from individual turkeys and chicken, Truscott and colleagues (2007) extrapolated on the farm-to-farm spread level and generated basic reproductive rates of 1.5 and 3.0 and infectious periods of 4 days for farm-to-farm spread H5N1 in the UK. These studies suggest relatively low inter-farm transmission probabilities and varying infectious periods.

Several population-related determinants including between-farm poultry movements were described for a sample of both commercial and non-commercial poultry farms in Switzerland (Chapter 6). Poultry movements were shown to be mostly stable (for instance, always to the same abattoir) and of low frequency with median numbers of 1 poultry purchase movement, 2 poultry sale movements and 2 show visit movements per annum if poultry was moved at all. The available biological and contact information suggests that the integration of data on contact structures might attach value to models reflecting the poultry farm population in Switzerland.

We present an approach to build a poultry farm population model integrating information on contact structures from different sources. Our data sets include: (i) poultry farm registration data, (ii) survey data on between-farm contacts, and (iii) interview data on farms' affiliations to private companies. We describe the extrapolation of the contact data collected on the population census and present distributions of and numbers of different contact partners and contact frequencies in the synthesized population. That adds to the identification of farm types, which are highly connected and thus might particular contribute to contribute to HPAI spread.

9.3 Material and methods

Population of interest

The population to be reflected in the model consists of all poultry farms of Switzerland. By poultry farm we understand all sites where one or more domestic chicken (*Gallus gallus domesticus*), turkey (*Meleagris gallopavo*), duck (*Anas platyrhynchos domesticus* or *Cairina moschata*), goose (*Anser anser*), quail (*Coturnix coturnix*), guinea fowl (*Numida meleagris*), peafowl (*Pavo cristatus*), ostrich (*Struthio camelus*) or pigeon (*Columba livia*) are kept. To account for indirect contact between poultry farms, three other sets of actors are considered, including hatcheries, abattoirs/butchers and poultry shows.

Conceptual framework

The study design consists of three major steps as illustrated in Figure 9.1. *Step 1* involves collecting original data. In *Step 2* a recombinant dataset is established, which combines contact information from different sources and adds newly identified actors. *Step 3* contains the development of a contact generation and optimization algorithm to complete a network out of information from Steps 1 and 2.

Step 1: Sets of original data

Census data (data set 1): All available poultry registration data from cantonal veterinary services and federal livestock register database AGIS were merged and duplicates electronically eliminated, thereby privileging the more recent cantonal records. This lead to a single list, henceforth called "census" in this article, containing a total of 49,437 poultry keepers and farms identified countrywide. Attributes include farm address he and total number of birds kept and subsequently added geo-coordinates (Chapter 6).

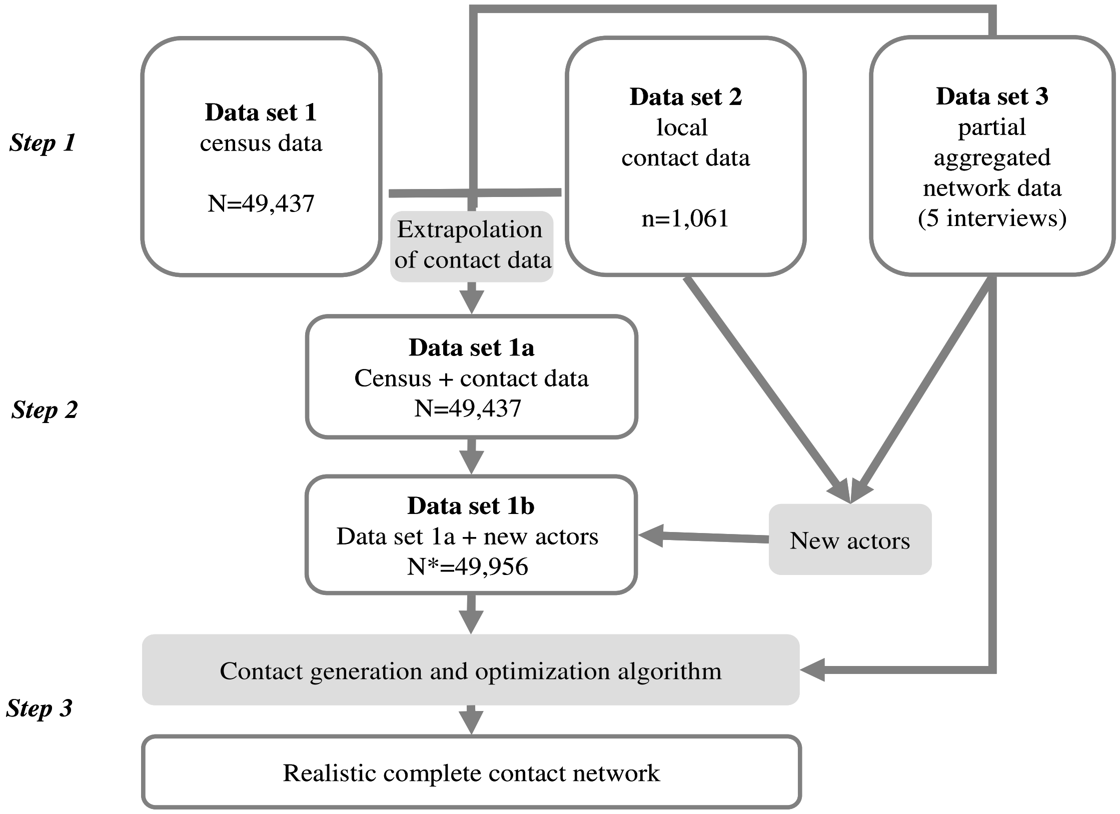

Figure 9.1 The conceptual framework of the study

Ego-centric contact data (data set 2): Poultry movement data were collected in a mail-out/mail-back survey in 2007 addressed to 3,987 poultry keepers selected randomly from the census. The poultry keepers' probability of being selected was proportional to the square root of the number of birds kept on their farm (farm size) to ensure a sufficient number of the less numerous larger poultry farms were included. Three types of poultry movement contacts were defined: poultry purchase, poultry sale, and exhibiting poultry at poultry shows. The term poultry here included live birds of the species described above, one-day old chicks as well as hatching eggs. Poultry movements for the purpose of purchase and sale were unidirectional: incoming for purchase and outgoing for sale. Those for exhibiting birds at poultry shows were bidirectional. The frequencies of all movement types were collected in “x times per year” and “less than once a year” (coded as 0.5 times per year in the analyses). Up to six different contact partners could be specified for each type of movement type, with date (month/year) of transaction, as well as site (postal code) and type (hatchery, other farm, or abattoir/butcher, show name) of contact partner.

Data of the returned and completed questionnaires were anonymized, double-entered into a database, compared and cleaned. Entries were excluded for this study when no poultry movement was stated AND no juvenile birds/hatching eggs were present AND the farm was not self-described as hatchery or upbringing or parent farms (multiple choices were possible). The expert interviewed (see below) supported the assumption that the excluded entries were incomplete as farms either have to raise juveniles or must purchase poultry sometime. The resulting 1,061 remaining entries (21% of the questionnaires distributed) are subsequently also called contact profiles. They consist of farm characteristics (number of birds kept, company integration, organic farm, dead stock disposal, free range area and the poultry species composition) and the above described contact information including calculated airline distances to the contact partners above described.

Partial network data (data set 3): Interviews were conducted with experts from five companies integrating commercial poultry farms in Switzerland. Company selection was based on whether a company was frequently named by the survey participants and in order to include different areas of the poultry industry, including broiler (companies I and II) and egg production (companies III to V). The aim of the interviews was to better understand the interactions amongst the subsets of poultry farms integrated into the same company. Therefore the experts were asked to describe production cycles, numbers, and specifics of their integrated farms. In particular, poultry movements, their frequencies and directions both amongst member farms and involving outsider farms were discussed following an interview guideline and depicted in a drawing by the expert and interviewer together on paper (Appendix 3). The interview protocols, including notes from experts and the interviewer, were transcribed and underwent qualitative content analysis (Mayring, 2003).

Other sets of actors: For actors other than poultry farms, namely hatcheries, abattoirs/butcher and poultry shows, no complete registers were available. The questionnaire was used as name generator (Milardo, 1992), to identify a maximum of these non-farm actors. To complement the actor list, literature and mercantile directories were reviewed and the experts were consulted. A calendar of events of the show bird umbrella organization helped to retrieve all the declared poultry shows in the inquiry period from May 2006 to August 2007 (Schweizerischer Rassegeflügelzuchtverband, 2009).

International contacts: Only poultry keepers in Switzerland were included in the questionnaire survey. The questionnaire allowed country to be specified for contact partners outside of Switzerland. All foreign contacts were found to be situated in the European Union (EU). In the subsequent steps, all EU nominations are considered to be different actors. Data on EU actor specifics and precise location are not available.

Step 2: Recombinant data set

A cluster analysis was performed with data set 2. Farm attributes, namely the number of birds kept (log), company integration, show birds kept, chicken kept, turkeys kept, aquatic birds kept and other poultry species kept, and the numbers of different contact partners (hatcheries, abattoirs/butchers, poultry shows) were used. The resulting groups corresponded to the farm groups build upon self-assessment in the survey: commercial farms (layer, upbringing, parent, broiler, and other/mixed) and non-commercial farms (backyard and show bird), attribute values of one farm were therefore considered as interdependent observations.

Contact data extrapolation: Contact profiles from data set 2 were extrapolated. In both data sets 1 and 2 the same 7 farm size categories were built. To each farm of data set 1 one contact profile was matched. The matching was random within the respective farm size category: A farm in the census (data set 1) could, only receive a contact profile from a surveyed farm (data set 2) of the same farm size category. At this point, the weighted sampling procedure was inversed: More copies from small farms' contact profiles were needed to supply the numerous small farms in the census that were underrepresented in the survey data set 2. This extrapolation step resulted in a synthetic poultry farm population, the recombinant data set 1a. Analyses presented in this article are based on this data set.

Merging all actor sets: Data set 1a was complemented with all identified hatchery, abattoir/butcher and poultry show actors and their geo-coordinates (except for actors in the EU) and date (for poultry shows). The resulting data set 1b comprises a total of 49,956 actors belonging to four different sets.

Step 3: Connecting actors

A *contact generation and optimization algorithm*: In data set 1a all 49,437 farm actors in Switzerland have a contact profile. This defines to which types of actors, to how many different actors and within which preferred airline distance links should exist. Each connection has an associated weight that stands for the approximate frequency of the contact. Further connection criteria include the requirement that connections are preferential between farm actors that are both organic farms and between actors if at least one poultry species is identical. To model the connection rules and build a complete interrelated network, an algorithm in analogy to Read and colleagues (2008) is needed. Data set 1b is the used input file with all farm actors in Switzerland having contact profiles. At the beginning all contacts are contacts to nowhere (Read and colleagues call them "stubs"). The algorithm joins these contacts to nowhere under the following conditions in the connection rules: To be joined, two actors must both have at least one matching interaction (one farm purchasing, the other selling), contact frequency needs to be respected, and actors must mutually accept the other type as a contact partner. The algorithm goes through all actors to connect them. Its termination rule is that all actors have realized their contacts accordance with the contact profiles and have no more contacts to nowhere (at a predefined level of accuracy), or that no more meaningful contact can be made. The resulting complete network will be one out of several possible static network manifestation *(work in process).*

Analysis of the recombinant data set

Firstly, the recombinant data set 1a is described in its general actor composition. Distributions of farm actor attributes are given, such as contact frequency distributions.

Secondly, the *actor degree centrality* is calculated, because this index is applicable on the yet unconnected data set 1a (Wassermann and Faust, 1994). The actor degree centrality describes the number of incoming contacts (*in-degree*) or outgoing contacts (*out-degree*) of an actor in a directed network (here poultry purchasing and selling transactions) and the degree in undirected networks (here exhibiting poultry at shows). The degree distribution is the distribution curve of all actors' degree centrality. Actor degree centrality is calculated according to Proctor and Loomis (1951) by

$$C_D(n_i) = d(n_i) = \sum_j x_{ij} \qquad (1)$$

where x_{ij} are the elements of the adjacency matrix $\mathbf{X}$ describing the network of defined contacts, here poultry movements.

Thirdly, it is examined whether degree distributions follow a *power law*. A distribution follows a power law *"when the probability of measuring a value of the distribution varies inversely as a power of that value"* (Newman, 2005) and is characterized by a histogram that follows closely a straight line with a negative slope when both horizontal and vertical axes are plotted logarithmically (Auerbach, 1913; Zipf, 1950; Newman, 2005). The slope of the line is described by

$$P(x) = Cx^{-\alpha} \qquad (2)$$

where C is a constant and α is the exponent of the power law, which takes often values of $2 \le \alpha \le 3$ in power law distributions occurring in nature (Newman, 2005). In a population, where number of contacts is distributed in such way, there are many individuals with no or few of contacts and few with an enormous number of contacts.

9.4 Results

Composition of the synthetic poultry farm population

The synthesized poultry farm population consists of a total of 49,956 actors. They belong to four different sets: the set of poultry farms (1), the set of hatcheries (2), of abattoirs/butchers (3) and of poultry shows in the inquiry period (4). The identified number of actors in each set is specified in Table 9.1.

Table 9.1 Number of identified actors of all sets

Set of actors	Poultry farms (1)	Hatcheries (2)	Abattoirs/ butchers (3)	Poultry shows (4)
In Switzerland	49,437	34	13	277
EU countries	177	36	-	2
Total no.	49,604	70	13	279

[no. = number]

Set 1, the poultry farms, is at the center of interest. The synthetic farm population consists of about 8% of commercial farms and 92% of non-commercial farms. The distribution of farm types (based on self-description in the questionnaire survey) within these groups is given in Table 9.2.

Table 9.2 Number of poultry farms of different types in the synthetic population (only the 49,437 poultry farms in Switzerland are considered)

Type of farms	Sub-groups	Frequency (%)	Total	Frequency (%)
Commercial farms				
Broilers	1212	*2.5*	3,835	*7.8*
Layers	2053	*4.2*		
Upbringing	218	*0.4*		
Parents	145	*0.3*		
Other/mixed	207	*0.4*		
Non-commercial farms				
Backyard	36645	*74.1*	45,602	*92.2*
Show birds	8957	*18.1*		

Degree distribution

Overall, 23% of poultry farms in the synthetic population have 2 or more different contacts and make up at least 63 % of all identified contacts. The distributions of the farms' degree centrality (numbers of contact partners), called degree distributions, are highly right skewed and are therefore presented in plots with both axes logarithmically scaled (Figures 9.2 and 9.3). The all-degree distribution considers contact partners of all types. The degree distribution resembles a straight line representing a power law distribution with $\alpha=2.35$). The observations in the lower part (more than 5 contacts) are below the line (Figure 9.2). It should be noted that for each type of poultry movement a maximum of 6 different contact partners could be specified in the questionnaire. That resulted in a maximum actors' all-degree centrality of 16 different contact partners. The distribution plotted in Figure 9.2 refers to the 64% of population members that have contact partners at all (Table 9.3).

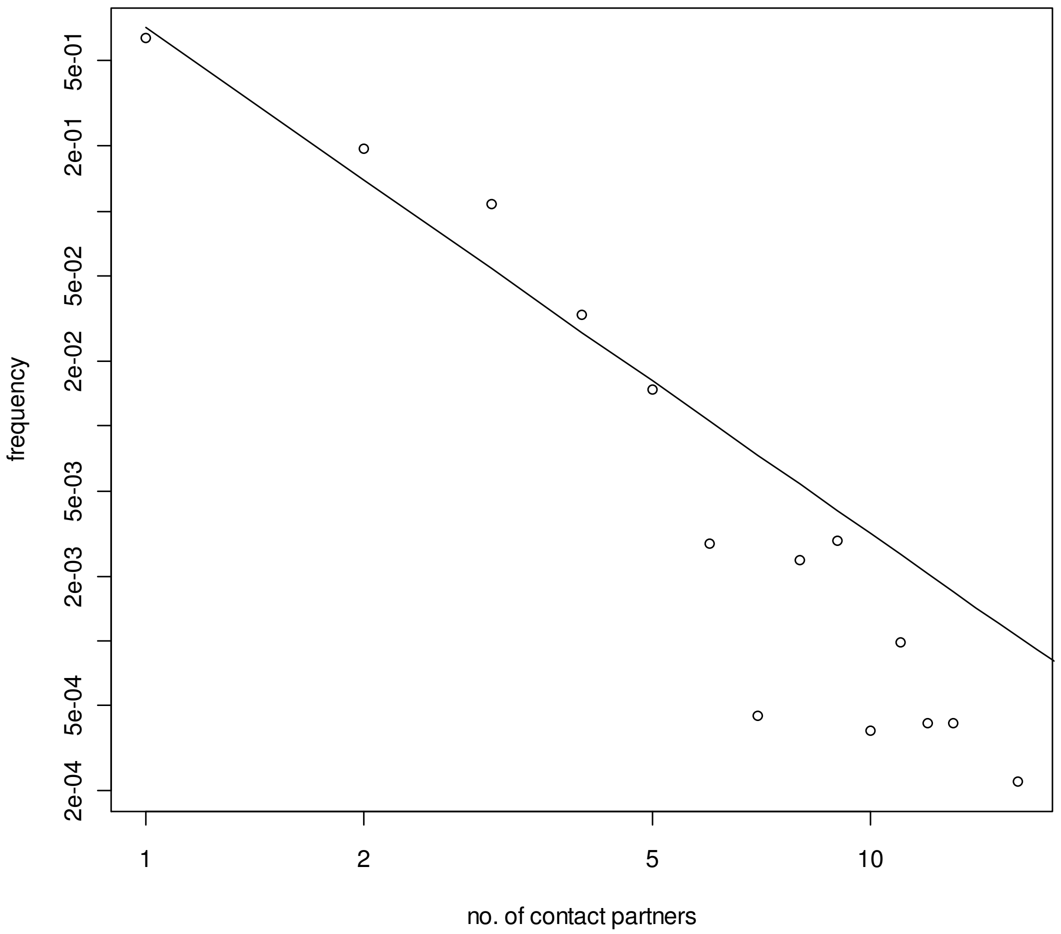

Figure 9.2 All-degree distribution; both axes are scaled logarithmically

Table 9.3 Proportion of the population (data set 1b; n=49,437) considered in the actors degree centrality distributions

	All	**Purchase**	**Sale**	**Show visit**
No. of obs. > 0	31491	31288	8243	1647
Fraction (%) of synthetic population	63.7	63.3	16.7	3.3
Maximum no. of different contacts	16	6	6	6

[no. = number]

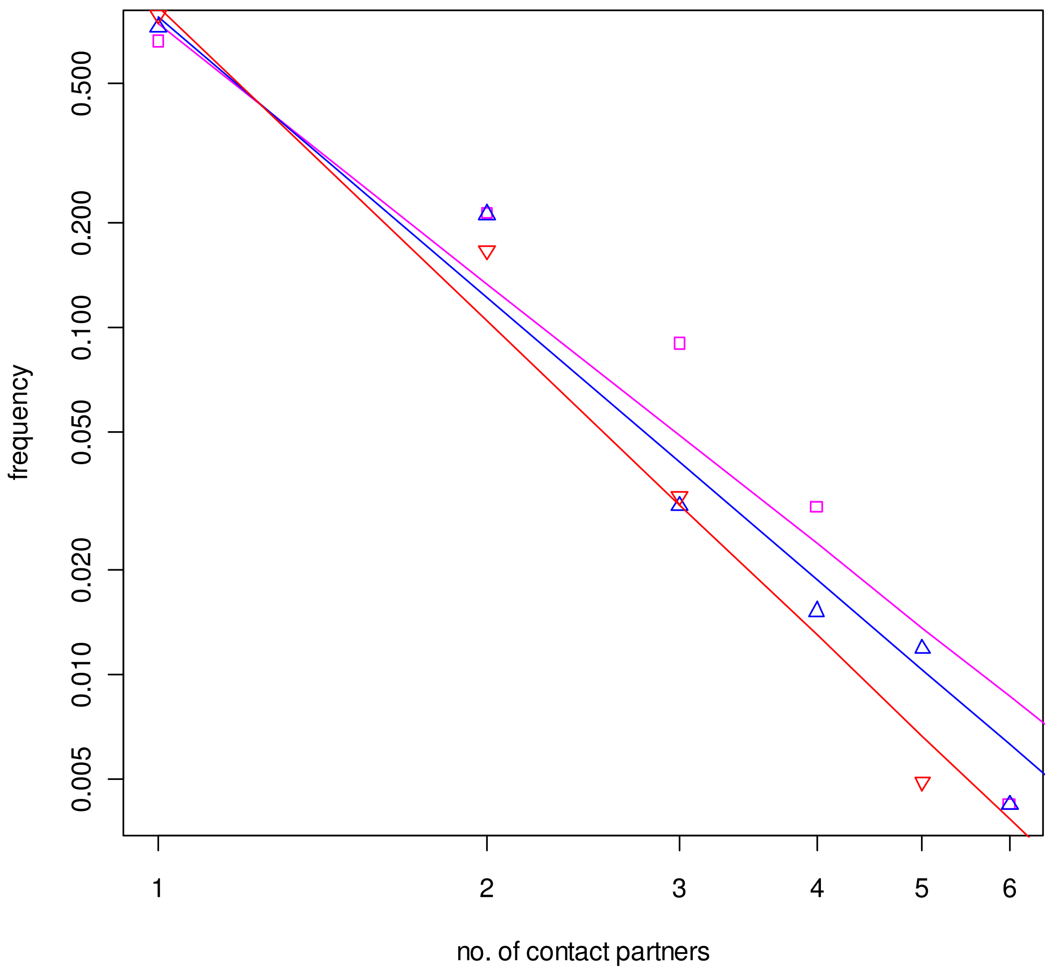

Figure 9.3 Degree distributions for poultry purchase (in-degree; in red), poultry sale (out-degree; in blue) and poultry show visits (bidirectional; in pink); both axes are scaled logarithmically

In Figure 9.3, the distribution of poultry movements is given for poultry purchases as incoming poultry movements, poultry sales as outgoing poultry movements, and poultry show attendance as bidirectional poultry movements. The power law distributions fitted to the observations have slopes of α= 2.35 for purchases; α= 2.69 for sales and α= 2.48 for poultry show visits. The fit for all relations separately are better than for the all-degree distribution, in particular for in- and out-degrees. Figure 9.3 refers to the 64% of poultry farms for purchase, the 63% for sale and the 3% for poultry show visits that have at least on contact partner of the respective type (Table 9.3).

Highly connected poultry farms

Poultry farms that have a total of 4 or more different contact partners were defined as highly connected farms “high-alls”. They constitute 1844 (4%) of the poultry farms in the synthetic population. In addition, highly connected poultry farms were also defined according to the different types of poultry movements. Poultry farms with 4 or more different contact partners only of one specific type numbered 283 (0.6%) for purchase “high-ins”, 277 (0.6%) for sale “high-outs”, and 57 (0.1%) for poultry show attendance “high-shows”. Figure 9.4 shows how the groups of commercial and non-commercial keepers are represented within these highly connected groups. As to all-degrees (left column), only 412 out of 1844 (22%) of the high-all are commercial farms. Only 40 out of 283 farms (14%) among the high-ins are commercial farms, and 110 out of 167 farms (40%) are commercial farms. The high-shows only consist of non-commercial farms.

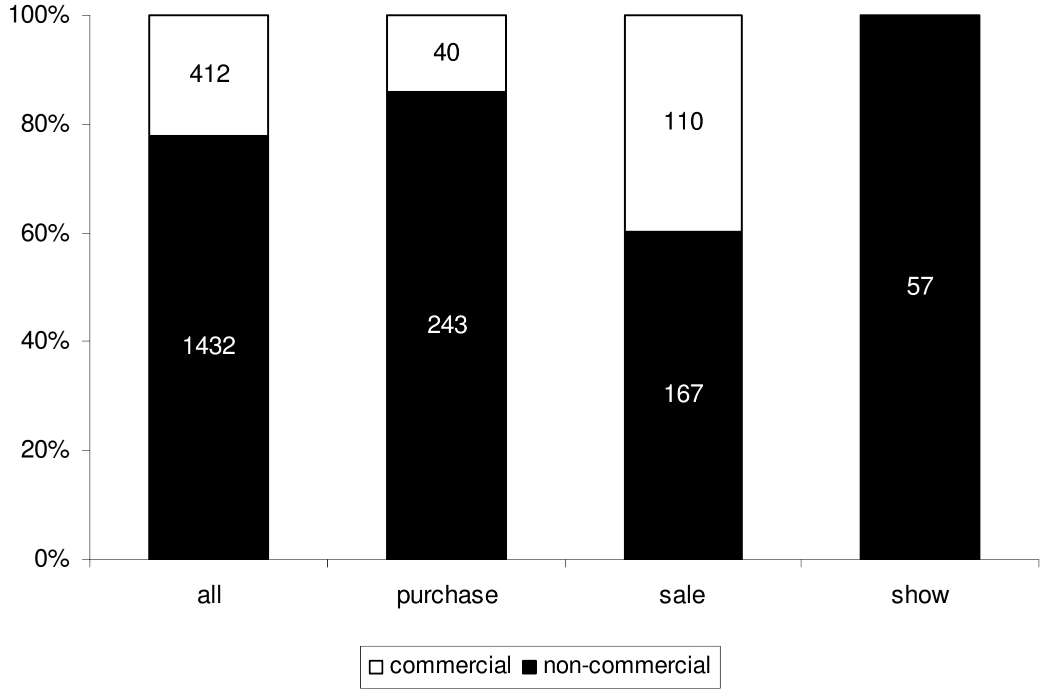

Figure 9.4 The percentages of commercial and non-commercial farms within highly connect groups as to all-degree (all), and specifically in-degrees (purchase), out-degrees (sale) and show-degrees (show)

Non-commercial farms are more frequent in the synthetic population (Table 9.2). Therefore, in Figure 9.5 we show how both commercial and non-commercial farms are represented among the highly connected farms in proportion to their number in the population. Except for high-shows, commercial farms are proportionally higher represented than non-commercial farms.

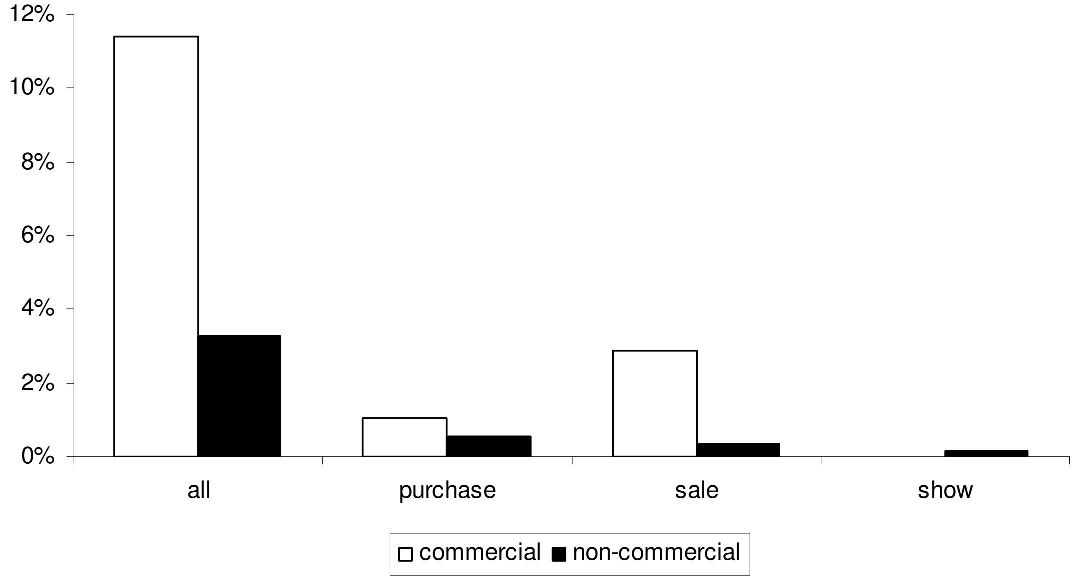

Figure 9.5 Commercial and non-commercial farms among highly connected farms, proportional to the their number in the population; shown for all-degree (all), in-degrees (purchase), out-degrees (sale) and show-degrees (show)

Commercial and non-commercial farms are further specified into specific farm types (Table 9.2). These farm types differ in the number of contact partners they have. Show bird farms contribute most (42%) to the high-alls. Other/mixed commercial farms have, however, the highest per-farm contribution of 30%. Show bird farms contribute most (44%) to the high-ins. Other/mixed commercial farms have the highest proportion among high-ins (3%). Most high-outs are show bird farms (57%). Upbringing farms have the highest per farm rate (12%). As to the contact relation poultry show, show bird farms are the only farm type that has at least 4 different contacts (Table 9.4).

Table 9.4 Occurrence of different farm types in the highly connected groups

		Commercial					*Non-commercial*	
		Broiler	**Layer**	**Up-bringing**	**Parents**	**Other / mixed**	**Back-yard**	**Show birds**
All-degree	row[1] (%)	8.2	7.3	3.4	-	3.4	35.9	**41.8**
	col[2] (%)	*12.5*	*6.5*	*28.9*	-	***30.4***	*1.8*	*8.6*
In-degree	row (%)	11.7	-	-	-	2.5	41.7	**44.2**
	col (%)	*2.7*	-	-	-	***3.4***	*0.3*	*1.4*
Out-degree	row (%)	21.3	6.1	9.7	-	2.5	2.9	**57.4**
	col (%)	*4.9*	*0.8*	***12.4***	-	*3.4*	*0.0*	*1.8*
Show-degrees	row (%)	-	-	-	-	-	-	**100.0**
	col (%)	-	-	-	-	-	-	***0.6***

[[1]denotes the percentage of farm types present among the highly connected ones. [2]the rate of poultry farms of a specific type that is among the highly connected ones. In bold: highest value per line]

Distributions of poultry movement frequencies

The frequency distributions of poultry movements are highly right skewed and therefore presented in plots with logarithmically transformed horizontal and vertical axes. The total movement frequency reaches a maximum of 410 single transactions per year. Figure 9.6 shows the power law distribution with a slope of α=2.13 fitted to the observations. The observations are dispersed on both sides of the line. All 31,829 (65%) observations with a total movement frequency greater than zero are considered (Table 9.5).

Table 9.5 Proportion of the population (data set 1b; n=49437) considered in the frequency distributions

	All	**Purchase**	**Sale**	**Show visit**
No. of obs. > 0	31829	31555	5184	1645
Fraction (%) of synthetic population	64.4	63.8	10.5	3.3
Maximum no. of transactions per year	410	80	356	30

[no. = number]

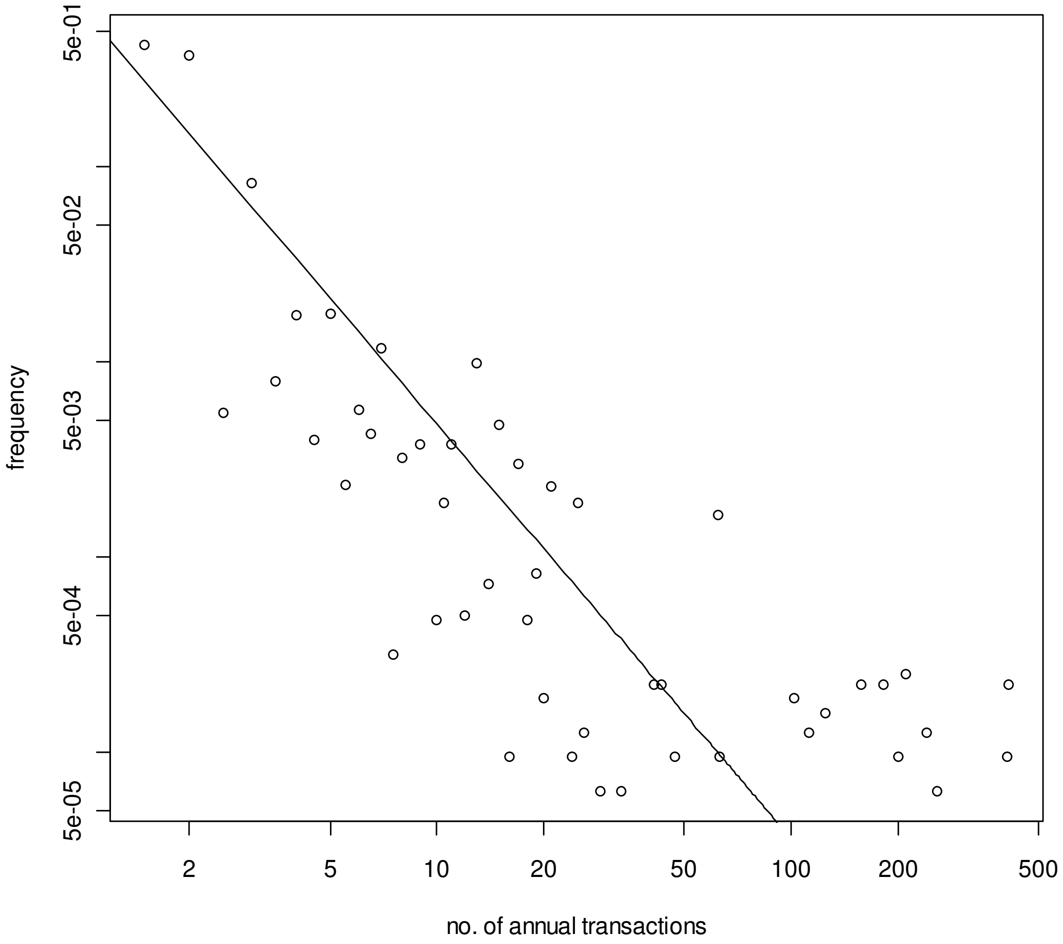

Figure 9.6 Frequency distribution of the total of poultry movements; both axes are scaled logarithmically

Looking at the different poultry movement transactions separately leads to slightly better fits of the power law distributions for purchase (in red; α=2.61), sale (in blue; α=1.65), and poultry show visits (pink; α=1.94; Figure 9.7). Out of all poultry farms in the synthetic population, about 66% have a purchase frequency, and 64% a sale frequency greater than zero, and only about 3% have a poultry show visit frequency greater than zero, and are considered in the distribution (Table 9.5).

Poultry movement frequencies of the highly connected commercial and non-commercial farms are given in Table 9.6. Commercial farms have about 3.5 as high frequencies as non-commercials farms.

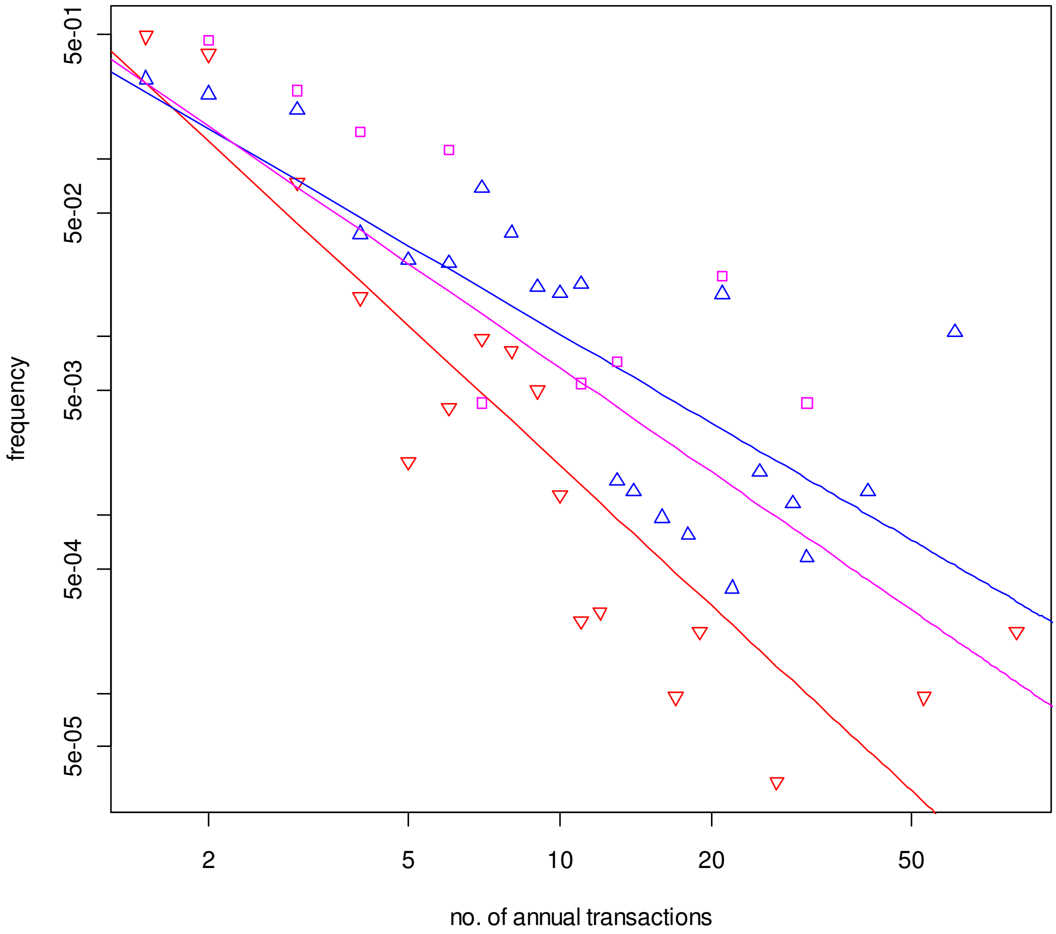

Figure 9.7 Frequency distributions of poultry movements for the purpose of purchase (red), sale (blue), and poultry show visits; both axes are scaled logarithmically

Table 9.6 Poultry movement frequencies for poultry farms among the highly connected ones, shown for the commercial and non-commercial farm group. Frequency is given in poultry movements per year, 0.5 denotes "less than once a year".

Frequency for highly connected groups as to	***Commercial***	***Non-commercial***
All-degree (median [IQR])	7 [3.5 - 16]	2 [1 - 4.5]
In-degree (median [IQR])	6 [6 - 7]	1 [0.5 - 3]
Out-degree (median [IQR])	3 [1 - 6]	1 [0.5 - 20]
Show-degree (median [IQR]	0	5 [5 - 5]

[IQR = Inter-quartile range]

9.5 Discussion

This study has demonstrated how different data sets can be combined to estimate and explore contact structures of a large population, namely the 49,437 poultry farms in Switzerland. A synthetic poultry farm with complete information on the individual farms' contact profiles was created, and supplementary actors other than Swiss poultry farms were identified, namely contact farms abroad, as well as hatcheries and abattoirs/butchers resulting in a total of 49,956 actors.

About 23% of poultry farms in the synthetic population have at least 63% of all identified contacts - and probably more: the questionnaire allowed only for stating six different contact partners for purchase, sale and poultry shows, respectively. The distributions of in-degrees (purchase) and out-degrees were found to be approximately similar to power law distributions when both axes were scaled logarithmically, even though the maximum degrees were unknown. This could suggest that the topology of the network of poultry movements is similar to a so-called scale-free network. Scale-free networks are defined by in- and out-degree distributions that fit a power law distribution (Barabási and Albert, 1999). This is of epidemiological relevance: It is argued that the scale-free properties of the UK cattle network lead to spread patterns during the 2001 FMD epidemic and the difficulties in controlling it (Woolhouse, 2003; Shirley and Rushton, 2005; Ortiz-Pelaez *et al.*, 2006). Scale-free networks miss an epidemic threshold for diseases. This means that disease can either disappear before reaching highly connected actors or spread rapidly once a highly connected actor is involved (Pastor-Satorras and Vespignani, 2001; Kiss *et al.*, 2006b).

About 4% of poultry farms were found to have at least 4 different contact partners as concerns poultry movements. Unexpectedly, only about 20% of them were commercial farms, while 80% were non-commercial farms. This reveals that contact structures of non-commercial farms matter not only as to their spatial dimension (Chapter 6), but also in terms of degree centrality, although their poultry movements were mostly less frequent. It is of interest to identify farms with high degrees prior to outbreaks. Woolhouse and colleagues (2005) have shown for 55 Scottish cattle farms that few farms had more than 100 cattle movements while most farms had a small number. They determined the contribution of individual farms to the basic reproductive ratio and found that 20% of farms contribute to 80% of the R_0 and therefore qualify as targets for surveillance, and also for control in order to decrease the number of new infected farms due to one infected farm.

Furthermore, the direction of contacts matters. For sexually transmitted diseases (Ghani and Garnett, 2000), and other epidemics in humans and livestock (Woolhouse *et al.*, 2005; Christley *et al.*, 2005), it has been shown, that actors with high in-degrees were highly exposed, and actors with high out-degrees are at high risk of passing on infections. We found that poultry farms with 4 or more in-degrees were mostly show bird farms (45%). These also contributed most (57%) to the group of farms with at least 4 out-degrees. The proportion of poultry farms with high in-degrees was greatest for other/mixed commercial farms (3%). The proportion of poultry farms with high out-degrees was greatest for upbringing farms (12%). About 30% of other/mixed farms had all-degrees of 4 or more. Accordingly, farm types at higher risk concerning actor degree centrality are non-commercial show bird farms and commercial upbringing and other/mixed commercial farms. This is only a rough estimate. Variation within farm types need to be better understood.

Whether a farm is central, and therefore to be targeted in a surveillance system, is not only determined by the actors' degree centrality. Closeness and betweenness centrality are also relevant. Closeness centrality denotes the distance any given actor has to all other actors in the network. Betweenness centrality describes an actor as central when it has control over many paths in the network, thus actors bridging different parts of a network that would otherwise be less well or not at all connected (Wassermann and Faust, 1994). The calculation of these indices, however, requires an entirely connected network, which has been aspired to in this study. Connecting all poultry farm actors to a realistically interrelated network is labor intensive and computationally demanding, including in terms of the central processing unit time needed. A test algorithm according to Read and colleagues (2008) suggests feasibility (*work in process*). Data extrapolation and combination of different data sets, as done to build the synthetic poultry farm population, can be a source of errors due to unnoticed selection and respondent biases. In the process of contact generation, all contacts that could not captured by the investigations will be ignored. In the resulting model, they will be replaced by randomly selected linkages. A constructed complete model, as is aspired to in this study, will therefore have a topology between the real contact network and random network.

The study was restricted to the contact relation “poultry movement”. As shown in Chapter 6, there are other epidemiologically relevant contacts that need to be integrated in our future work. These include contacts through direct farm neighborhood (cf. Boender *et al.*, 2007, and Truscott *et al.*, 2007), person movements, shared resources and any visit to poultry shows or markets. Weighting contacts is also important; according to their specific frequency, to the number of birds moved, according to the means of transport employed, precautionary measures in place, for instance quarantine, and the type of contact partners involved. Contacts can further be weighted according to the type of contact partner. Poultry movements to abattoirs/butchers are, for instance, dead-end movements. Little is known about affiliations other than to industrial companies, which, for instance, show how show bird-breeding associations impact on poultry movement contact structures.

Despite the multiplicity of constraints, this study has contributed to a better understanding of the poultry movement contact structure of the Swiss poultry farm populations. Findings, such as upbringing poultry farm having proportionally greatest out-degrees, may not surprise a poultry expert: By definition, upbringing farms have the purpose of delivering laying hens to many layer farms. For the first time, however, this study allows the contact structures of commercial farms and non-commercial farms countrywide to be compared. This provides important input parameters for risk assessments and promotes the need to equally integrate non-commercial farms in the surveillance of poultry epidemics.

In the case of HPAI in domestic poultry, even an approximate contact network model might improve model predictions and the targeting of surveillance. Its construction will therefore be pursued further.

9.6 Acknowledgements

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The authors acknowledge all study participants and the interviewed experts for their valuable information and time.

9.7 Authors’ contributions

LF designed and carried out the study, conducted the interviews and analyses, and drafted the manuscript as the lead writer. TS is developing the algorithm, participated in the study design and helped to draft the manuscript. JH provided support for data management, for the quantitative analyses, and for the data extrapolation. JZ supervised the project and participated in the study design.

10 CONCLUSIONS

The findings of this dissertation emphasize that poultry keeping is more widespread in Switzerland than previously thought, and that the population to consider in highly pathogenic avian influenza (HPAI) surveillance comprises of about 49,437 poultry farms and the respective keepers (as to 2007).

This dissertation explored demographic data and poultry keeper- and farm-related determinants of HPAI risks in view of surveillance and epidemic modeling, with three major conclusions.

Issue of subpopulations: Non-commercial farms do play an epidemiologically important role, as shown in particular for poultry movements. It is, however, not assured that small-scale poultry keepers are well informed about HPAI risks, and that they would suspect and notify potential HPAI cases without delay.

Poultry farms' HPAI vulnerability: Risk enhancing factors, such as "having many different contact partners" or "having limited access to information about HPAI", and risk reducing factors, such as "poultry keepers well aware of HPAI risks" and "having stable and trustworthy trading partners" can occur in many combinations at the farm level. Instead of using single criterion HPAI risk indicators such as farm type, geographic location or season, surveillance intensity should be based on multiple criteria risk weighting and rating.

Contact network models: Contact arrangements amongst poultry farms identified by applying network analysis techniques, by performing comparative computer simulations, and HPAI transmission parameters described in literature strongly suggest that models at the between-farm level for HPAI or similarly transmitted poultry epidemics would ideally take the realistic arrangement of contacts into account. A contact network model for the Swiss poultry farm population is feasible but computationally and labor intensive.

The outcomes of this dissertation impact directly on risk-based HPAI surveillance activities in domestic poultry in Switzerland.

Scenario-Tree Analysis: The conducted research has significantly contributed to a Scenario-Tree for HPAI surveillance in domestic poultry, namely with detailed demographic data and with new evidence on probabilities of different hazards including “between-farm contact rates” and “probability that suspected HPAI cases will be reported”.

Risk maps: Although risk-based surveillance is complex, a simplified statement can be made: high prevelences of HPAI risk factors are high in areas where farm and poultry density is high. As evident from the provided geo-maps, this applies to the Mitteland, reaching from Lake Constance to Lake Geneva and bordered by the Alpes in the South and the Jura in the North of Switzerland, as well as for the area south of Bellinzona. Specific maps produced for poultry and farm density and poultry trading facilitate the strategic planning of HPAI surveillance, and shall encourage inter-cantonal cooperation of veterinary services, in particular in the Mittelland.

Risk-based passive HPAI surveillance: The term “risk-based passive surveillenace” seems contradictory. Passive disease surveillance is per definition are-wide and involvs all livestock keepers and veterinarians, as well as the general public reporting wild bird cadavers. This dissertation claims that targets can also be set within passive surveillance: they consist of “poultry keepers at risk”, which are those that are not yet entirely reached with official information on HPAI.

Above all, for implementing surveillance strategies and epidemic modeling complete poultry registration data are needed, preferentially in a flexible database format as proposed. This is to avoid a *petitio principii*: It is practically impossible to prove impacts and address needs of population groups, here small-scale poultry keepers, under the premise of selective registration privileging units with higher economic and (assumed) epidemiological relevance. Switzerland could take a lead on a more equitable consideration of livestock husbandries: While this dissertation was written the legal basis for a complete horse, poultry, bee and fish husbandry registry on a *federal* level has been created in Switzerland.

10.1 International relevance of findings

Decision makers and researchers from other countries are encouraged to resume and adapt inputs given by this dissertation. The findings of this dissertation are specific for the poultry sector and the HPAI outbreak-free situation in Switzerland. Prevention, surveillance and control priorities might differ among regions. Nevertheless, there is potential for knowledge transfer:

- The suggested relational database model provides a basis for discussion wherever the implementation or modification of a livestock register is intended.
- The identified between-farm contact activities of non-commercial poultry farms might encourage also veterinary authorities in other countries to integrate small-scale poultry farms into livestock identification and movement registers and to consider them in research.
- Although depending on cultural and educational factors, and on the current AI outbreak situation in a region, the disease awareness of poultry keepers is everywhere crucial for epidemic surveillance. In contexts, where complete poultry registers and active surveillance cannot be afforded, veterinary authorities are particularly encouraged to invest in awareness training via facilitators, for instance para-veterinarians, and by using popular information channels such as local broadcast.
- The affiliation of a poultry farm to a marketing organization was associated with a relatively high disease awareness of the poultry keeper. The disease awareness of small-scale poultry keepers could possibly be enhanced by market driven approaches. If unique selling points are created for certified production, poultry keepers would have a direct incentive for complying with hygiene practices and awareness training. A pilot program for certified small-scale poultry keeper supply chains in Vietnam highlights that market driven approaches are promising (Roland-Holst *et al.*, 2006).

10.2 Prospects of future research

On the collected contact data

Centrality and cohesiveness measures remain to be calculated for the synthetic poultry farm population, once the connections amongst all members are established in the model. These measures will help to identify even better poultry farms at epidemiologically relevant network positions, and to highlight how well the network resists fragmentation, for instance by movement control measures. Further research based on this model, e.g. in collaboration with the FVO, would ideally include validity checks by simulating existing similarly transmitted poultry epidemics, for instance ILT, based on the contact network model. The FVO is currently refining disease reporting data and presenting them in maps including retrospective data (Bundesamt für Veterinärwesen, 2009a). The comparison of these existing outbreak maps with simulated spread pattern outcomes based on the contact network model remains to be explored. Finally, HPAI outbreak scenarios and the impact of different control measures should be explored using transmission parameters from literature, based on the continuously refined contact network model for the poultry farm population, initiated in this dissertation.

Additional qualitative information

Future qualitative research is recommended to gain in-depth information on non-commercial poultry keepers' attitudes and specifics of their farms. In many of the performed analyses all non-commercial farms were pooled, knowing well that this subpopulation is very large and heterogeneous. Face-to-face interviews and focus-group discussions with different small-scale poultry keepers, as well as members of poultry breeding associations are suggested. Pertinent questions are: What motivates small-scale poultry keepers to purchase and sale poultry from and to remote places? How intensive are between-farm contacts within direct neighborhood? What are precautionary measures taken by the poultry keepers to make person and poultry movements save? Gained insights would help to improve the weighting of contact in the network model according to the newly defined risk potential. As to disease awareness, a crucial question to answer would be: What are factors impairing access to official HPAI information? This issue would ideally be addressed in a formalized way, for instance in the style of the "Access to health care" framework (Obrist *et al.*, 2007). Studying access to information by differentiating among availability, accessibility, affordability, adequacy, and acceptability of different information sources, would help to direct information campaigns by veterinary authorities in a differentiated and efficient way.

Co-evolution of between-farm contact networks and communication networks

Not only epidemics spread along network structures: There exists a large body of research on the spread of information (Kossinets *et al.*, 2008), on the spread of rumors (Kawachi *et al.*, 2008), and of innovations (Valente, 2005) amongst individuals or institutions. This dissertation has shown that poultry marketing organizations had influence on both the dissemination of information amongst members, and on the arrangement of poultry movement contacts and resources shared by their affiliated poultry farms. It would be exciting to explore whether pathways of communication amongst poultry keepers and between-farm contacts are correlated. If the dissemination of disease-specific information evolves similar to epidemiologically relevant contacts, central actors would in the best case have both: many potentially contagious contacts but also the ability to put precautionary measures in place. Wrong perceptions of disease risks could be disseminated along contact structures. Exploring such potentially co-evolutionary processes along network structures might improve the weighting of risks related to contacts and the identification of "targets for information" at central positions of the communication network, for instance poultry shows. To note, some pathways of communication, such as e-mail correspondence, are not directly related to epidemiologically relevant contacts and need to be distinguished from face-to-face communication.

Network analysis in research on zoonotic diseases

There is a high demand for assessments of public health risks associated to livestock and pets, e.g., of whether human-to-animal contacts play a crucial role in pathogen transmission in specific settings. A pertinent question is if pets should be admitted or not in nursing homes. This issue is addressed in a current case-control study within the HAH group (project 1.06.12 BVET, PhD cand. Paola Decristophoris) examining the prevalence of multi-resistant *Staphylococcus aureus* strains in humans and pets. There are prospects for enhanced research on human-to-human, human-to-animal, and possibly animal-to-animal contacts, and for the comparison of epidemiological links and data on pathogen evolution gained by molecular typing. Such comparative approach is considered to be superior in revealing infection chains compared to one approach alone.

Similar studies would be interesting in all settings where human population groups live closely together with animal populations. New insights would be gained into diseases emerging from animal reservoirs. The practicability and potential of network analysis in research on zoonotic diseases might be great in well-defined settings where complete network data can be collected, for instance in nursing homes, and everywhere where network data are directly available, for instance in a livestock movement database. Well-established research collaborations of social scientists, microbiologists, epidemiologists and mathematical modelers would be a particular asset to compile data on different social and biological factors and to integrate them into transmission models.

10.3 Recommendations

- *Veterinary and agricultural authorities* need to implement the upcoming federal poultry register database carefully. The format should be flexible and in compliance with all general database management demands. Both demographic and epidemiological factors should be entered thoroughly. Regular updates are important because of the poultry sector's dynamics, in particular as to small-scale poultry husbandries. A well designed and maintained database is a condition prior to area-wide and timely (risk) communication and surveillance.
- *Veterinary authorities* are recommended to maintain, and further enhance disease awareness training for non-commercial poultry keepers. This will help to strengthen the monetary and operationally beneficial passive disease surveillance. The poultry keepers are a heterogeneous group. For instance, not all poultry keepers have access to information on the internet. A large variety of information channels should be

used, including articles in official gazettes, postal correspondence, TV-spots, information desks at poultry show events and possibly to conduct also HPAI simulation exercises that involve small-scale poultry farms. Veterinarian services are encouraged to enhance inter-cantonal coordination while preparedness planning, performing disease surveillance activities and epidemiological investigations. This is particular relevant in the Mittelland with its high poultry and farm densities and strong poultry movement activities.

- *Poultry keepers* are reminded to fulfill their responsibilities as livestock owners. They have to ensure animal husbandry according to animal welfare and general hygiene standards, and to report suspected cases of HPAI and other notifiable diseases without delay to a veterinarian. If poultry keepers are uncertain about signs of diseases, they are strongly encouraged to contact a veterinarian or the local veterinary service for advice. Poultry keepers are recommended to increase the protection level of their farm by limiting wild animals' access to the poultry housing system, by keeping different poultry species separately from each other, by restricting animal movements to a minimum, and by well documenting production and mortality rates in their flock, as well as animal movements. If poultry keepers comply with these demands and recommendations, they have no reason to render a poultry farm because of the epidemic threat.
- *Poultry associations and companies'* support will be further needed to maintain databases and agreeing on database interfaces to facilitate the distribution of information on HPAI, and to mediate between the poultry keepers' needs and national and international animal health requests.
- *Public health and veterinary authorities* that intend to develop or to commission epidemic models for decision making in epidemic surveillance are encouraged to make use of the guidance on model choice provided in this dissertation. Due consideration of biological and social factors might help to obtain valid models for an appropriate investment in time and resources.

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APPENDICES

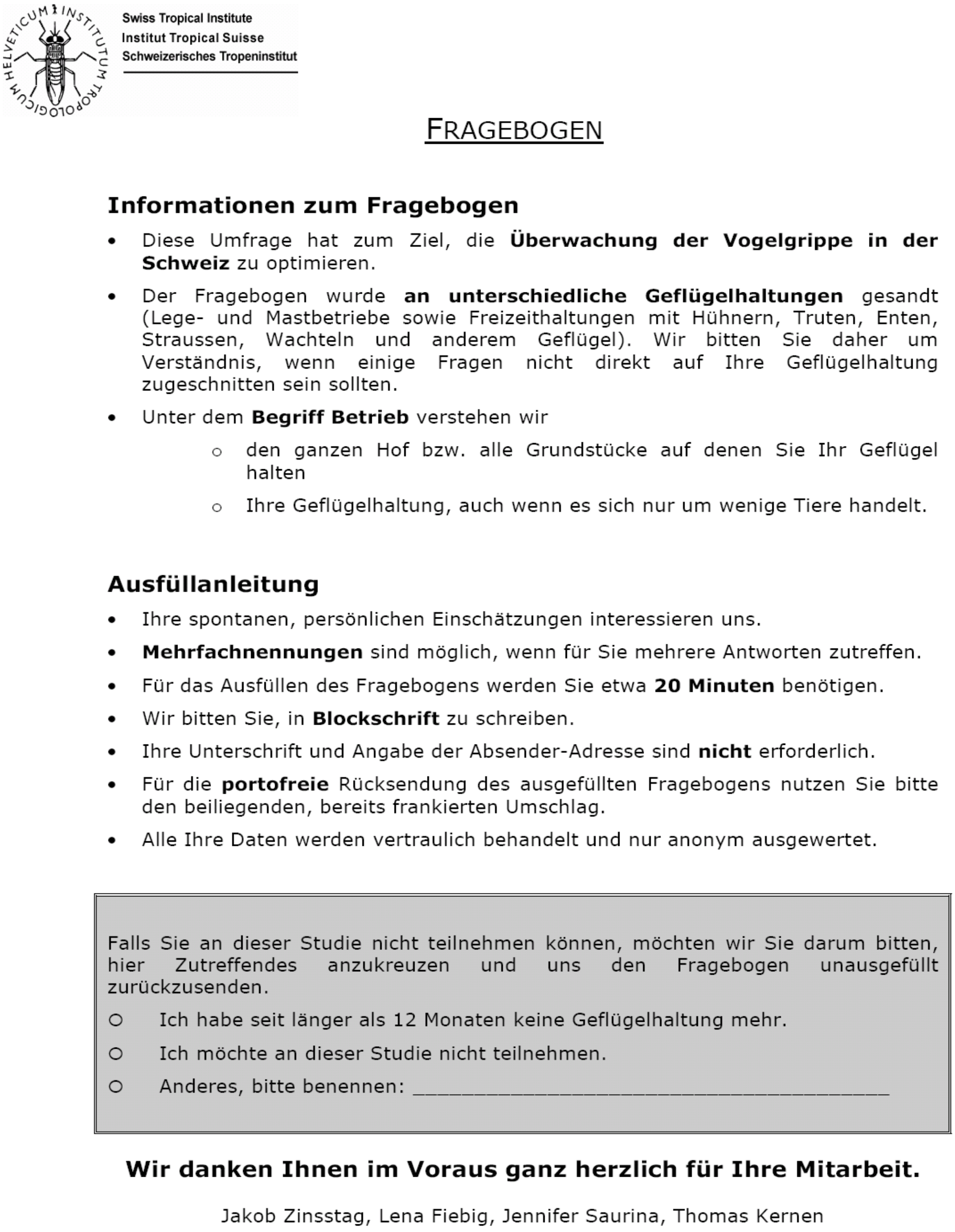
APPENDIX 1: Comparison of databases

Comparison of demographic data of official statistics of 2007 (Aviforum/Swiss Federal Statistical Office (FSO)) and newly collected data compiled by the Swiss Tropical Institute (STI)

Canton	Farms			Birds		
	No. (FSO)	**No. (STI)**	**Ratio STI:FSO**	**No. (FSO)**	**No. (STI)**	**Ratio STI:FSO**
Zurich	1'150	5'005	4.4	371'700	482'499	1.3
Berne	4'100	5'725	1.4	1'381'500	1'570'009	1.1
Lucerne	1'530	3'641	2.4	963'800	1'084'499	1.1
Uri	140	352	2.5	3'800	6'265	1.6
Schwyz	460	878	1.9	92'500	92'314	1.0
Obwalden	110	311	2.8	41'800	48'528	1.2
Nidwalden	140	257	1.8	33'800	35'545	1.1
Glarus	130	313	2.4	8'300	21'511	2.6
Zug	210	467	2.2	56'600	72'959	1.3
Fribourg	700	3'328	4.8	1'313'900	1'604'094	1.2
Solothurn	550	2'281	4.1	172'500	248'457	1.4
Basel-Stadt	10	62	6.2	300	1'039	3.5
Basel-Land	430	1'543	3.6	97'800	121'119	1.2
Schaffhausen	160	550	3.4	168'100	187'137	1.1
Appenzell Ausserrhoden	260	688	2.6	35'600	44'579	1.3
Appenzell Innerrhoden	140	244	1.7	131'300	147'322	1.1
St. Gallen	1'110	3'897	3.5	627'100	720'153	1.1
Graubünden	780	2'683	3.4	41'500	119'039	2.9
Aargau	1'110	4'644	4.2	745'700	820'656	1.1
Thurgau	860	2'939	3.4	783'000	879'246	1.1
Ticino	160	2'803	17.5	35'100	66'587	1.9
Vaud	750	3'036	4.0	732'000	1'027'882	1.4
Valais	130	1'398	10.8	64'700	275'417	4.3
Neuchâtel	90	845	9.4	86'600	110'527	1.3
Geneva	70	363	5.2	10'100	18'376	1.8
Jura	270	1'184	4.4	102'600	153'608	1.5
Switzerland	*15'550*	*49'437*	*3.2*	*8'101'700*	*9'959'367*	*1.2*

[no. = number]

APPENDIX 2: Questionnaire



Swiss Tropical Institute
Institut Tropical Suisse
Schweizerisches Tropeninstitut

FRAGEBOGEN

Informationen zum Fragebogen

- Diese Umfrage hat zum Ziel, die **Überwachung der Vogelgrippe in der Schweiz** zu optimieren.
- Der Fragebogen wurde **an unterschiedliche Geflügelhaltungen** gesandt (Lege- und Mastbetriebe sowie Freizeithaltungen mit Hühnern, Truten, Enten, Straussen, Wachteln und anderem Geflügel). Wir bitten Sie daher um Verständnis, wenn einige Fragen nicht direkt auf Ihre Geflügelhaltung zugeschnitten sein sollten.
- Unter dem **Begriff Betrieb** verstehen wir
    - den ganzen Hof bzw. alle Grundstücke auf denen Sie Ihr Geflügel halten
    - Ihre Geflügelhaltung, auch wenn es sich nur um wenige Tiere handelt.

Ausfüllanleitung

- Ihre spontanen, persönlichen Einschätzungen interessieren uns.
- **Mehrfachnennungen** sind möglich, wenn für Sie mehrere Antworten zutreffen.
- Für das Ausfüllen des Fragebogens werden Sie etwa **20 Minuten** benötigen.
- Wir bitten Sie, in **Blockschrift** zu schreiben.
- Ihre Unterschrift und Angabe der Absender-Adresse sind **nicht** erforderlich.
- Für die **portofreie** Rücksendung des ausgefüllten Fragebogens nutzen Sie bitte den beiliegenden, bereits frankierten Umschlag.
- Alle Ihre Daten werden vertraulich behandelt und nur anonym ausgewertet.

Falls Sie an dieser Studie nicht teilnehmen können, möchten wir Sie darum bitten, hier Zutreffendes anzukreuzen und uns den Fragebogen unausgefüllt zurückzusenden.

○ Ich habe seit länger als 12 Monaten keine Geflügelhaltung mehr.
○ Ich möchte an dieser Studie nicht teilnehmen.
○ Anderes, bitte benennen: ____

Wir danken Ihnen im Voraus ganz herzlich für Ihre Mitarbeit.

Jakob Zinsstag, Lena Fiebig, Jennifer Saurina, Thomas Kernen

Swiss Tropical Institute
Institut Tropical Suisse
Schweizerisches Tropeninstitut

I. Ihr Betrieb und Ihre Tätigkeitsbereiche

1. Wie viele der genannten Tiere halten Sie momentan auf Ihrem Betrieb?

Bitte tragen Sie die entsprechende Anzahl in die Kästchen ein. z.B. für 345 Legehennen, wie folgt

		3	4	5	Legehennen

a. Hühner

					Rassehühner und –hähne
					Legeküken und Junghennen
					Legehennen
					Hähne
					Mastpoulets
					Andere, bitte benennen:____

b. Andere Geflügelarten

					Truthühner
					Wachteln
					Enten
					Perlhühner
					Gänse
					Strausse
					Rebhühner
					Andere, bitte benennen:____

c. Andere Tiere

					Katzen
					Hunde
					Schweine
					Rinder
					Schafe/Ziegen
					Pferde/Esel
					Ziervögel (Papageien, Sittiche, …)
					Andere, bitte benennen:____

2. Welche Bezeichnungen beschreiben Ihre Geflügelhaltung am besten?

	Professionell	Als Nebenaktivität/ Hobby	Weiss nicht	*Trifft nicht zu*
Rassegeflügelzucht	○	○	○	○
Legebetrieb	○	○	○	○
Mastbetrieb	○	○	○	○
Vermehrungsbetrieb	○	○	○	○
Brüterei	○	○	○	○
Aufzuchtbetrieb	○	○	○	○
Anderes:________________	○	○	○	○

3. Welche Bestandteile hat Ihre Geflügelhaltung?

○ Stall
○ Wintergarten bzw. Aussenklimabereich
○ Freilandbereich
○ Weiss nicht
○ Anderes, bitte benennen:____

Wenn Sie keine Freilandhaltung haben, machen Sie bitte direkt mit Frage 4 weiter.

Angaben zum Geflügel – Freilandbereich:

a. Wie viele Quadratmeter umfasst Ihr Freilandbereich?

○ ________________m^2
○ Weiss nicht

b. Welche der folgenden Elemente hat Ihr Freilandbereich?

○ Wiese/Erdboden
○ Sandbad
○ Futterstellen
○ Tränken
○ Teich
○ Bach
○ Misthaufen
○ Komposthaufen
○ Bäume
○ Sträucher
○ Mobiler Schattenspender
○ Dachgitter/-Netz
○ Weiss nicht
○ Anderes, bitte benennen:____

c. Befand sich Ihr Betrieb im Winter 2006/2007 in einem Gebiet mit Aufstallungspflicht (Freilandverbot)?

○ Ja
○ Ja, mit Ausnahmegenehmigung
○ Nein
○ Weiss nicht
○ Anderes, bitte benennen:____

4. Welche Gewässer gibt es in einem 1 km-Umkreis um Ihren Betrieb?

○ keine
○ Bach
○ Fluss
○ Teich
○ See
○ Offenes Wasserreservoir/Zisterne
○ Weiss nicht
○ Anderes, bitte benennen:____

5. Wohin wird auf Ihrem Betrieb totes Geflügel gebracht?

○ Kadaverbehälter
○ Tiefkühltruhe
○ Misthaufen
○ Gülleloch
○ In den Wald (für die Füchse)
○ Verfüttert an Schweine
○ Direkt zur Sammelstelle
○ Vergraben im Erdboden
○ Abgabe an Tierarzt/zur Sektion
○ Weiss nicht
○ Anderes, bitte benennen:____

6. Haben Sie in den letzten zwölf Monaten Tätigkeiten in den folgenden Bereichen ausgeübt (siehe Tabelle)?
(z.B. im Haupt-, Neben-, Zusatzerwerb, bzw. als freiwilliger Helfer)

○ Ja	*(Bitte füllen Sie die Tabelle weiter aus.)*
○ Nein	*(Bitte machen Sie mit Frage 7 weiter.)*
○ Weiss nicht	*(Bitte machen Sie mit Frage 7 weiter.)*

Bereich	Ort	
Wildhüter/ Jäger	(PLZ/ Ortsname) ☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________
Schlachthof/ Metzgerei	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________
Anderer Geflügelbetrieb	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________
Eisammelstelle bzw. Eipackstelle	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________
Transport von Geflügel/ Geflügelprodukten	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________

Ausfüllbeispiel

Bereich	Ort	
Wildhüter/ Jäger	(PLZ/ Ortsname) **4 0 5 7 BASEL**	● Kanton: **B S** ○ Ausland: ______________

II. Vogelgrippe: Ihre Einschätzung

7. Bitte schätzen Sie ein: Die Vogelgrippe und ...

	sind genau dasselbe	sind ähnlich	sind völlig verschieden	weiss nicht
... die Klassische Geflügelpest	○	○	○	○
... die Newcastle-Krankheit	○	○	○	○
... die alljährliche Grippe beim Menschen	○	○	○	○

8. Gab es in den letzten 5 Jahren Vogelgrippe-Fälle bei Hausgeflügel in der Schweiz?

○ Ja
○ Nein
○ Weiss nicht

9. Angenommen, es käme zum Vogelgrippe-Ausbruch in einem Schweizerischen Geflügelstall. Wie hoch schätzen Sie die Wahrscheinlichkeit folgender Einschleppungswege ein?

	gross	mittel	gering	vernachläs-sigbar	weiss nicht
Durch Zugvögel	○	○	○	○	○
Durch Windübertragung	○	○	○	○	○
Durch Reisende	○	○	○	○	○
Durch Einfuhr von Geflügel	○	○	○	○	○
Durch Einfuhr von Geflügelprodukten	○	○	○	○	○
Durch Einfuhr von Futtermitteln	○	○	○	○	○
Durch Bioterrorismus	○	○	○	○	○
Durch andere Tierarten	○	○	○	○	○
Auf anderen Wegen:_____________	○	○	○	○	○

10. Bei welchen Krankheitsanzeichen <u>bei Hühnern</u> würden Sie besonders an Vogelgrippe denken?

○ Husten
○ Fress- und Trinkunlust
○ Struppiges Federkleid
○ Lahmheit
○ Koordinationsverlust
○ Abnormale Eierschale
○ Kannibalismus
○ Durchfall
○ Ungeklärter plötzlicher Tod von mehreren Tieren
○ Erbrechen
○ Niesen
○ Verminderte Eierproduktion
○ Verzögertes Wachstum
○ Geschwollener Kopf und Kamm
○ Lähmungen
○ Abnormale Kopfbewegungen
○ Bei keinem dieser Krankheitsanzeichen
○ Weiss nicht
○ Andere, bitte benennen:____

11. Bei welchen Geflügelarten erwarten Sie keine Krankheitsanzeichen bei einer Vogelgrippe-Ansteckung?

○ Alle Geflügel zeigen sehr deutliche Krankheitsanzeichen
○ Hühner
○ Enten
○ Wachteln
○ Truthühner
○ Rebhühner
○ Perlhühner
○ Strausse
○ Gänse
○ Weiss nicht

12. Bei einem Verdacht auf Vogelgrippe bei Ihrem Geflügel, wen würden Sie als erstes kontaktieren?

○ Bundesamt für Veterinärwesen (BVET)
○ Kantonales Veterinäramt
○ Geflügel-Lieferant
○ Verband / Vermarktungsorganisation
○ Untersuchungsstelle für Geflügel- und Kaninchenkrankheiten der Universität Zürich
○ Rassengeflügelzuchtverband
○ Aviforum
○ Entsorgungsfirma
○ Tierarzt
○ Tierheilpraktiker
○ Schlachthof
○ Weiss nicht
○ Anderes, bitte benennen: ____

13. Für wie sinnvoll halten Sie eine Aufstallungspflicht in Risikogebieten (Bsp.: Schutzmassnahme im Winter 2006/2007)?

○ Sehr sinnvoll
○ Eher sinnvoll
○ Eher nicht sinnvoll
○ Nicht sinnvoll
○ Weiss nicht

14. Woher erhalten Sie hauptsächlich Informationen über die Vogelgrippe?

○ Nachrichten (Zeitung, Fernsehen, Radio)
○ Bundesamt für Veterinärwesen (BVET)
○ Kantonales Veterinäramt
○ Verband / Vermarktungsorganisation
○ Fachzeitschriften
○ Gemeindeblatt
○ Internet
○ Familie und Bekannte
○ Weiss nicht
○ Anderes, bitte benennen:____

15. Fühlen Sie sich gut informiert über die Vogelgrippe?

○ Ja
○ Nein, mehr Information würde ich mir wünschen zu: ________________________
____
____
○ Weiss nicht

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III. Wildvögelbeobachtung

16. Wie sehr interessieren Sie sich für Wildvögel?

○ Sehr
○ Ein wenig
○ Kaum
○ Gar nicht
○ Weiss nicht

17. Beobachten Sie Wildvögel in Ihrem Geflügel-Freilandbereich?

○ Ja *(Bitte füllen Sie die Fragen a. bis d. weiter aus.)*
○ Nein *(Bitte machen Sie direkt mit Frage 18 weiter.)*
○ Kein Freilandbereich vorhanden *(Bitte machen Sie direkt mit Frage 18 weiter.)*

a. Welche Wildvögel werden beobachtet?

	Enten	Schwäne	Gänse	Bläss-/ Teichhühner	Kleinvögel (Spatzen, Schwalben,...)	Raben, Krähen	Greifvögel (Bussarde, Falken, ...)	Eulen	Reiher	Störche	Tauben	Möwen	Andere
Bitte ankreuzen													

b. Wann werden diese oben (Abschnitt 17a.) angekreuzten Wildvögel beobachtet?

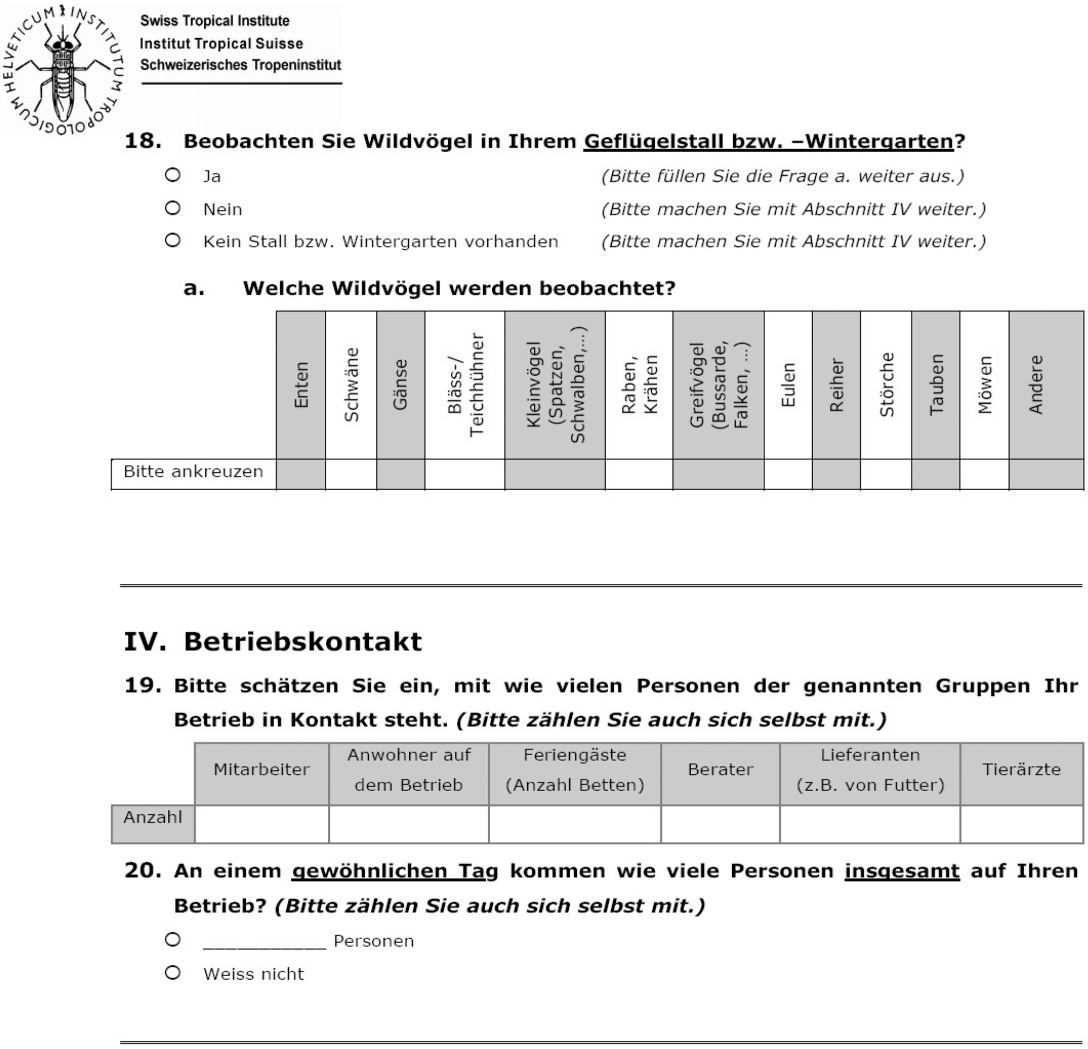
Ganzes Jahr													
Mai-September													
Oktober-April													
Weiss nicht													

c. Wie oft kommen diese oben angekreuzten Wildvögel?

Täglich													
Wöchentlich													
Monatlich													
Weiss nicht													

d. Kommen die oben angekreuzten Wildvögel einzeln/im Paar oder im Schwarm?

Einzeln/Paar													
Schwarm													
Weiss nicht													



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18. Beobachten Sie Wildvögel in Ihrem <u>Geflügelstall bzw. –Wintergarten</u>?

○ Ja	*(Bitte füllen Sie die Frage a. weiter aus.)*
○ Nein	*(Bitte machen Sie mit Abschnitt IV weiter.)*
○ Kein Stall bzw. Wintergarten vorhanden	*(Bitte machen Sie mit Abschnitt IV weiter.)*

a. Welche Wildvögel werden beobachtet?

	Enten	Schwäne	Gänse	Bläss-/ Teichhühner	Kleinvögel (Spatzen, Schwalben,...)	Raben, Krähen	Greifvögel (Bussarde, Falken, ...)	Eulen	Reiher	Störche	Tauben	Möwen	Andere
Bitte ankreuzen													

IV. Betriebskontakt

19. Bitte schätzen Sie ein, mit wie vielen Personen der genannten Gruppen Ihr Betrieb in Kontakt steht. *(Bitte zählen Sie auch sich selbst mit.)*

	Mitarbeiter	Anwohner auf dem Betrieb	Feriengäste (Anzahl Betten)	Berater	Lieferanten (z.B. von Futter)	Tierärzte
Anzahl						

20. An einem <u>gewöhnlichen Tag</u> kommen wie viele Personen <u>insgesamt</u> auf Ihren Betrieb? *(Bitte zählen Sie auch sich selbst mit.)*

○ ___________ Personen

○ Weiss nicht

V. Zukauf und Abgabe

21. Dient Ihr Geflügel der Lebensmittelproduktion (Eier, Fleisch)?

- ○ Ja *(Bitte füllen Sie die Fragen a. bis c. weiter aus.)*
- ○ Nein *(Bitte machen Sie mit Frage 22 weiter.)*
- ○ Weiss nicht *(Bitte machen Sie mit Frage 22 weiter.)*

a. Wird das Geflügel geschlachtet?

- ○ Ja, und zwar:
  - ○ Hausschlachtung
  - ○ Metzger
  - ○ Schlachthof
  - ○ Weiss nicht
  - ○ Anderes, bitte benennen:____
- ○ Nein
- ○ Weiss nicht

b. Werden Eier bzw. Fleisch verwendet oder abgegeben?

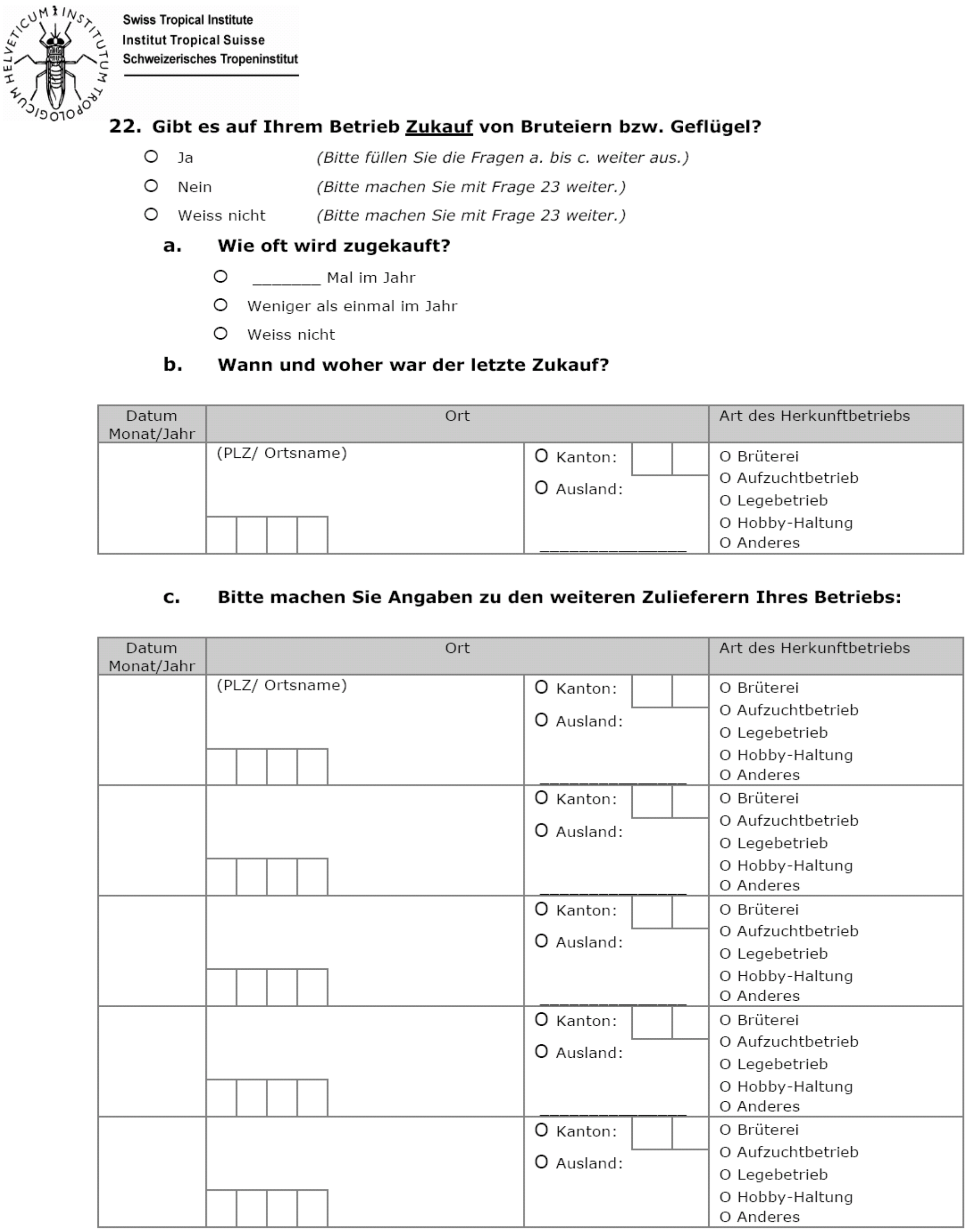
- ○ Ja, wie folgt:

	Eigen-bedarf	Ab-Hof-Verkauf	Markt-verkauf	Grossab-nehmer	Post-versand	Anderes: ________
Eier	○	○	○	○	○	○
Fleisch	○	○	○	○	○	○

- ○ Nein
- ○ Weiss nicht

c. Ist Ihr Betrieb einem Label bzw. einer Vermarktungsorganisation angeschlossen?

- ○ Ja, und zwar:
  - ○ Eico
  - ○ EiAG
  - ○ Lüchinger & Schmid
  - ○ Eier Hungerbühler
  - ○ Hosberg
  - ○ Micarna
  - ○ Bell
  - ○ Kneuss
  - ○ Frifag
  - ○ Favorit
  - ○ Lehnherr
  - ○ Fournier Frères
  - ○ Proviande
  - ○ Gallo Suisse
  - ○ Coop Naturaplan
  - ○ Coop Naturafarm
  - ○ M-Engagement
  - ○ BTS
  - ○ Raus
  - ○ BIO
  - ○ Anderes , bitte benennen:____
- ○ Nein
- ○ Weiss nicht



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22. Gibt es auf Ihrem Betrieb <u>Zukauf</u> von Bruteiern bzw. Geflügel?

○ Ja *(Bitte füllen Sie die Fragen a. bis c. weiter aus.)*
○ Nein *(Bitte machen Sie mit Frage 23 weiter.)*
○ Weiss nicht *(Bitte machen Sie mit Frage 23 weiter.)*

a. Wie oft wird zugekauft?

○ _______ Mal im Jahr
○ Weniger als einmal im Jahr
○ Weiss nicht

b. Wann und woher war der letzte Zukauf?

Datum Monat/Jahr	Ort		Art des Herkunftbetriebs
	(PLZ/ Ortsname) ☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Anderes

c. Bitte machen Sie Angaben zu den weiteren Zulieferern Ihres Betriebs:

Datum Monat/Jahr	Ort		Art des Herkunftbetriebs
	(PLZ/ Ortsname) ☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Anderes
	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Anderes
	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Anderes
	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Anderes
	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland:	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Anderes

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23. Werden von Ihrem Betrieb Bruteier bzw. lebendes Geflügel abgegeben?

○ Ja *(Bitte füllen Sie die Fragen a. bis c. weiter aus.)*
○ Nein *(Bitte machen Sie mit Frage 24 weiter.)*
○ Weiss nicht *(Bitte machen Sie mit Frage 24 weiter.)*

a. Wie oft im Jahr wird abgegeben?

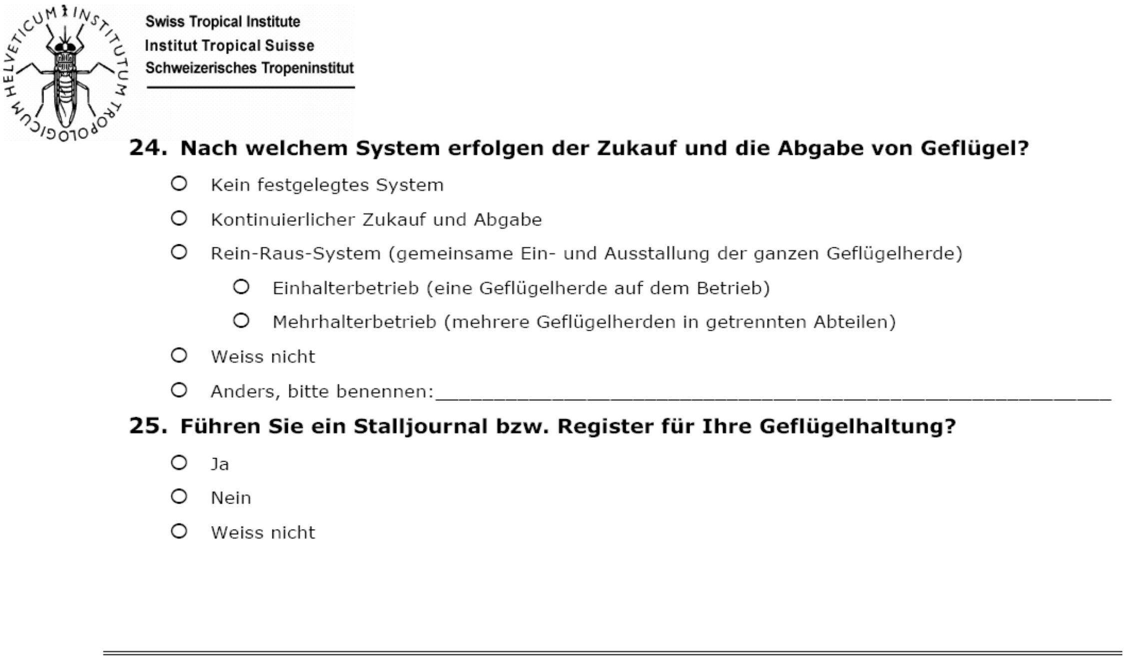
○ _______Mal im Jahr
○ Weniger als einmal im Jahr
○ Weiss nicht

b. Wann und wohin wurde das letzte Mal abgegeben?

Datum Monat/Jahr	Ort		Art des Abnehmerbetriebs
	(PLZ/ Ortsname) ☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Schlachthof/Metzger ○ Anderes

c. Bitte machen Sie Angaben zu den weiteren Abnehmern:

Datum Monat/Jahr	Ort		Art des Abnehmerbetriebs
	(PLZ/ Ortsname) ☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Schlachthof/Metzger ○ Anderes
	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Schlachthof/Metzger ○ Anderes
	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Schlachthof/Metzger ○ Anderes
	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: ______________	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Schlachthof/Metzger ○ Anderes
	☐☐☐☐	○ Kanton: ☐☐ ○ Ausland:	○ Brüterei ○ Aufzuchtbetrieb ○ Legebetrieb ○ Hobby-Haltung ○ Schlachthof/Metzger ○ Anderes



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24. Nach welchem System erfolgen der Zukauf und die Abgabe von Geflügel?

- ○ Kein festgelegtes System
- ○ Kontinuierlicher Zukauf und Abgabe
- ○ Rein-Raus-System (gemeinsame Ein- und Ausstallung der ganzen Geflügelherde)
    - ○ Einhalterbetrieb (eine Geflügelherde auf dem Betrieb)
    - ○ Mehrhalterbetrieb (mehrere Geflügelherden in getrennten Abteilen)
- ○ Weiss nicht
- ○ Anders, bitte benennen:____

25. Führen Sie ein Stalljournal bzw. Register für Ihre Geflügelhaltung?

- ○ Ja
- ○ Nein
- ○ Weiss nicht

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VI. Ausstellungen

26. Wie oft waren Sie in den letzten zwölf Monaten auf Geflügelausstellungen bzw. Tiermärkten mit Geflügelsparte?

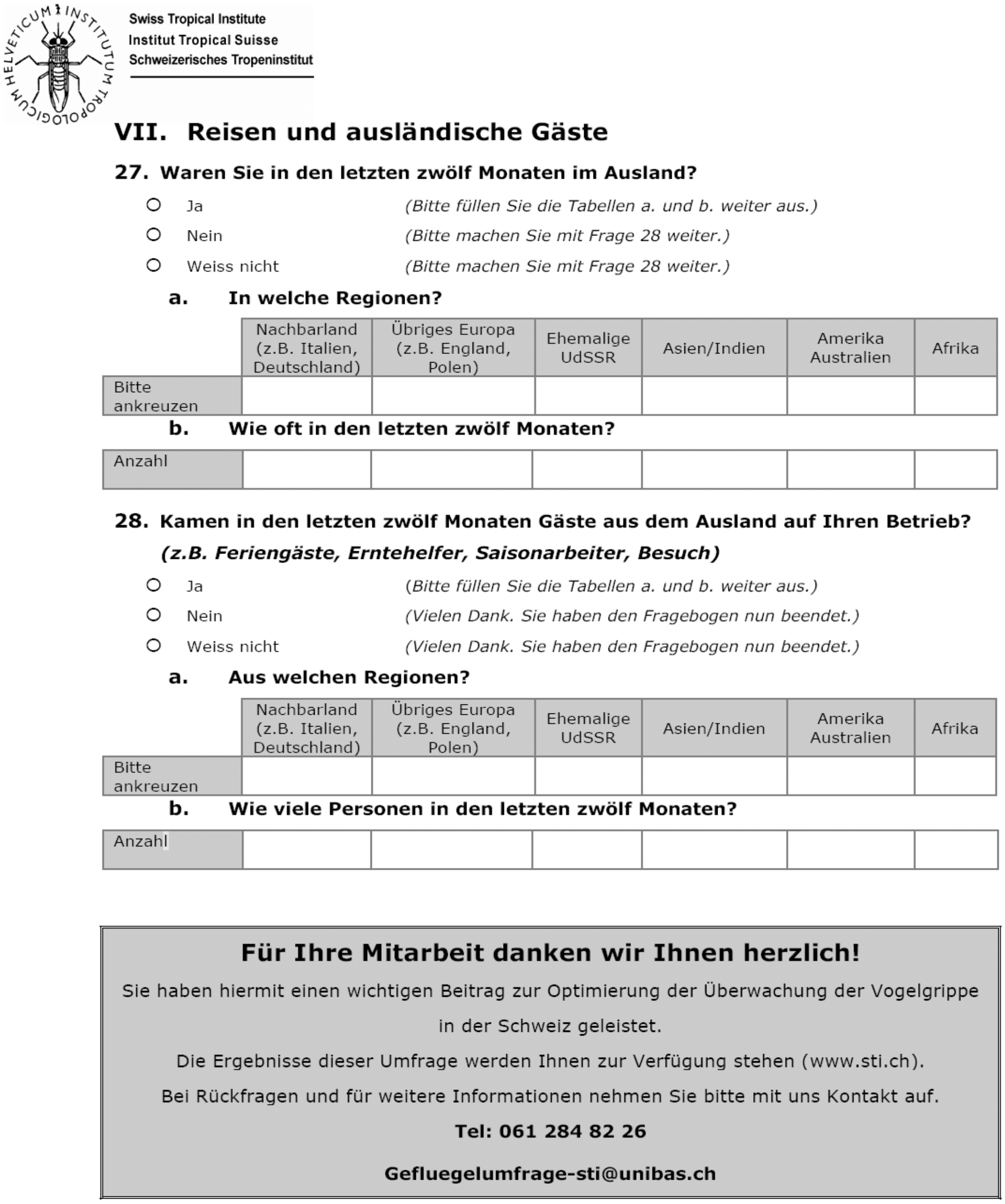
○ _____ Mal *(Bitte füllen Sie die Tabellen a. und b. weiter aus.)*
○ Nie *(Bitte machen Sie mit Frage 27 weiter.)*
○ Weiss nicht *(Bitte machen Sie mit Frage 27 weiter.)*

a. Angaben zur zuletzt besuchten Ausstellung

Name der Ausstellung	Datum Monat/ Jahr	Ort		Besuchszweck
		(PLZ/ Ortsname) ☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: _______________	○ als Besucher ○ als Aussteller ○ als Helfer/ Jurymitglied

b. Bitte geben Sie die weiteren Ausstellungen an, die Sie in den letzten zwölf Monaten besucht haben.

Name der Ausstellung	Datum Monat/ Jahr	Ort		Besuchszweck
		(PLZ/ Ortsname) ☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: _______________	○ als Besucher ○ als Aussteller ○ als Helfer/ Jurymitglied
		☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: _______________	○ als Besucher ○ als Aussteller ○ als Helfer/ Jurymitglied
		☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: _______________	○ als Besucher ○ als Aussteller ○ als Helfer/ Jurymitglied
		☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: _______________	○ als Besucher ○ als Aussteller ○ als Helfer/ Jurymitglied
		☐☐☐☐	○ Kanton: ☐☐ ○ Ausland: _______________	○ als Besucher ○ als Aussteller ○ als Helfer/ Jurymitglied



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VII. Reisen und ausländische Gäste

27. Waren Sie in den letzten zwölf Monaten im Ausland?

- ○ Ja *(Bitte füllen Sie die Tabellen a. und b. weiter aus.)*
- ○ Nein *(Bitte machen Sie mit Frage 28 weiter.)*
- ○ Weiss nicht *(Bitte machen Sie mit Frage 28 weiter.)*

a. In welche Regionen?

	Nachbarland (z.B. Italien, Deutschland)	Übriges Europa (z.B. England, Polen)	Ehemalige UdSSR	Asien/Indien	Amerika Australien	Afrika
Bitte ankreuzen						

b. Wie oft in den letzten zwölf Monaten?

Anzahl						

28. Kamen in den letzten zwölf Monaten Gäste aus dem Ausland auf Ihren Betrieb?

(z.B. Feriengäste, Erntehelfer, Saisonarbeiter, Besuch)

- ○ Ja *(Bitte füllen Sie die Tabellen a. und b. weiter aus.)*
- ○ Nein *(Vielen Dank. Sie haben den Fragebogen nun beendet.)*
- ○ Weiss nicht *(Vielen Dank. Sie haben den Fragebogen nun beendet.)*

a. Aus welchen Regionen?

	Nachbarland (z.B. Italien, Deutschland)	Übriges Europa (z.B. England, Polen)	Ehemalige UdSSR	Asien/Indien	Amerika Australien	Afrika
Bitte ankreuzen						

b. Wie viele Personen in den letzten zwölf Monaten?

Anzahl						

Für Ihre Mitarbeit danken wir Ihnen herzlich!

Sie haben hiermit einen wichtigen Beitrag zur Optimierung der Überwachung der Vogelgrippe in der Schweiz geleistet.

Die Ergebnisse dieser Umfrage werden Ihnen zur Verfügung stehen (www.sti.ch).

Bei Rückfragen und für weitere Informationen nehmen Sie bitte mit uns Kontakt auf.

Tel: 061 284 82 26

Gefluegelumfrage-sti@unibas.ch

APPENDIX 3: Interview guideline

FORSCHUNGSPROJEKT AM SCHWEIZERISCHEN TROPENINSTITUT
RISIKOBASIERTE ÜBERWACHUNG DER VOGELGRIPPE IN DER SCHWEIZ

Interview
Wissensstand über die Vogelgrippe
Kontakte zwischen Betrieben

Wir würden uns freuen, wenn Sie uns zu einem Interview zur Verfügung stehen würden.

Informationen zum Interview

- Dieses Interview dient einem besseren Verständnis und einer wirklichkeits-getreueren Interpretation von Ergebnissen aus der schriftlichen Befragung von 3'978 zufällig ausgewählten Geflügelhaltern (Rücklauf 39%) in der Schweiz im Jahre 2007.
- Das Interview umfasst drei Abschnitte
    1. Allgemeine Fragen zu den Geflügelbetrieben, die Ihrer Vermarktungs-organisation angeschlossen sind;
    2. Fragen zum Wissensstand der Geflügelhalter Ihrer Vermarktungs-organisation über die Vogelgrippe;
    3. Fragen zu charakteristischen Kontakten zwischen Geflügelbetrieben.
- Die Interviewfragen erhalten Sie auf den folgenden Seiten. Wir möchten Sie bitten, diese Fragen bereits vor unserem Interview zu lesen und den ersten Abschnitt auszufüllen. Hierzu können Sie sich gerne mit Kollegen besprechen.
- Das Interview wird etwa eineinhalb Stunden dauern. Der geplante Ablauf ist:
    1. Kurze Vorstellung unserer bisherigen Forschungsergebnisse;
    2. Interview zu Abschnitt zwei und Abschnitt drei;
    3. Zeit für Ihre Fragen an uns.
- Das Interview wird von Frau Fiebig geführt. Ein Protokollant wird ausserdem anwesend sein, um den Gesprächsverlauf schriftlich festzuhalten.
- Wir versichern Ihnen, dass alle Ihre Angaben vertraulich behandelt und ausgewertet werden.
- Die Ergebnisse unser Studie werden Ihnen zur Verfügung gestellt. Eine Veröffentlichung der Ergebnisse im *Schweizer Archiv für Tierheilkunde*, der *Schweizerischen Geflügelzeitung*, in der *Tierwelt* und in internationalen Fachzeitschriften ist vorgesehen.

Herzlichen Dank für Ihre Mitarbeit.

Lena Fiebig, Jennifer Saurina, Esther Schelling

Interviewleitfaden

Abschnitt I: Allgemeine Angaben zu den Geflügelbetrieben

In unserer Geflügelhalterumfrage wurden die Teilnehmer gebeten, Angaben zu ihrem Geflügelbetrieb zu machen. Wider Erwarten bezeichneten einige Teilnehmer mit geringen Geflügelzahlen (weniger als 100 Tiere) ihren Geflügelbetrieb als ‚professionell' und gaben an, an eine Vermarktungsorganisation angeschlossen zu sein.
Ihre Angaben in diesem Abschnitt dienen dazu, die Stimmigkeit der dieser erhobenen Daten zu überprüfen.

Hinweis zu Abschnitt I

- Wir möchten Sie bitten, die Fragen in diesem Abschnitt bereits soweit wie möglich vor dem Interviewtermin zu bearbeiten.
- Für „Ihrer Vermarktungsorganisation angeschlossene Geflügelhaltungen“ verwenden wir im Folgenden den kürzeren Ausdruck **„Ihre Betriebe“.**
- **Mehrfachnennungen** sind möglich, wenn für Sie mehrere Antworten zutreffen.
- Weitere Anmerkungen können Sie gerne zu den entsprechenden Fragen notieren.

1. Welche Geflügelarten werden auf Ihren Betrieben gehalten?

○ Hühner
○ Truten
○ Wachteln
○ Perlhühner
○ Enten
○ Rebhühner
○ Gänse
○ Straussen
○ Andere, bitte benennen: ____

2. Werden <u>alle</u> Geflügelarten, die auf Ihren Betriebe gehalten werden, erfasst?

○ Ja
○ Nein
○ Nur Geflügelarten, die zu gewerblichen Zwecken gehalten werden
○ Anderes, bitte benennen: ____

3. Gibt es eine vorgegebene Mindestanzahl von Geflügel bei Ihren Betrieben?

○ Ja, mindestens _________ Tiere
○ Ja, mindestens _________ Tierplätze
○ Nein
○ Anderes, bitte benennen: ____

4. Gibt es eine zulässige Höchstanzahl von Geflügel bei Ihren Betrieben?

○ Ja, höchstens _________ Tiere
○ Ja, höchstens _________ Tierplätze
○ Nein
○ Anderes, bitte benennen: ____

5. Liegt ein Teil Ihrer Betriebe im Ausland?

○ Ja, in ____

____*(Bitte Länder benennen)*

○ Nein
○ Anderes, bitte benennen: ____

6. In welchen Schweizer Kantonen liegen Ihre Betriebe?

○ In allen Schweizer Kantonen

○ In den folgenden Schweizer Kantonen:

7. In unserer Geflügelhalterumfrage gaben einige Teilnehmer an, mehreren Labeln und Vermarktungsorganisationen anzugehören. Bitte schätzen Sie ein: Kommen folgende Kombinationen häufig, selten oder gar nicht vor?

Kombination	häufig	selten	gar nicht
IHRE ORGANISATION + Bio	○	○	○
IHRE ORGANISATION + Bts	○	○	○
IHRE ORGANISATION + Raus	○	○	○
IHRE ORGANISATION + COOP-Farm	○	○	○
IHRE ORGANISATION + COOP-Plan	○	○	○
IHRE ORGANISATION + Gallo suisse	○	○	○
IHRE ORGANISATION + M - Engagement	○	○	○
IHRE ORGANISATION + Proviande	○	○	○
IHRE ORGANISATION + Bell	○	○	○
IHRE ORGANISATION + Eico	○	○	○
IHRE ORGANISATION + Lüchinger & Schmid	○	○	○
IHRE ORGANISATION + Micarna	○	○	○
IHRE ORGANISATION + Kneuss	○	○	○
IHRE ORGANISATION + Frifag	○	○	○
IHRE ORGANISATION + Favorit	○	○	○
IHRE ORGANISATION + Hungerbühler	○	○	○
IHRE ORGANISATION + EiAG	○	○	○
IHRE ORGANISATION + Lehnherr	○	○	○
IHRE ORGANISATION + Fournier & Frères	○	○	○

Hinweis zum II. und III. Abschnitt

- An den folgenden Fragen werden wir uns im Interview orientieren.
- Wir möchten Sie bitten, diese Fragen bereits vor unserem Interviewtermin zu lesen.
- Sie können sich gerne bereits Notizen für das Interview machen.

II. Abschnitt: Wissensstand über die Vogelgrippe

Teilnehmer unserer Geflügelhalterumfrage, die die Frage „*Ist Ihr Betrieb einem Label bzw. einer Vermarktungsorganisation angeschlossen?“* bejahten, waren im Durchschnitt besser informiert über die Vogelgrippe als Geflügelhalter, die keine Vermarktungsorganisation angaben.
In diesem Abschnitt interessieren uns mögliche Gründe für diesen Unterschied.

1. Wie schätzen Sie den Informationsstand Ihrer Betriebe zur Vogelgrippe ein?

2. Welche Rolle nimmt Ihre Vermarktungsorganisation ein bei der Information Ihrer Betriebe über die Vogelgrippe?

○ **Welche Informationswege werden genutzt?**

○ **Welche Informationsquellen werden genutzt?**

○ **Über welche Themen (zur Vogelgrippe) wird informiert?**

○ **Wann und wie oft wird informiert?**

III. Kontakte zwischen Geflügelbetrieben

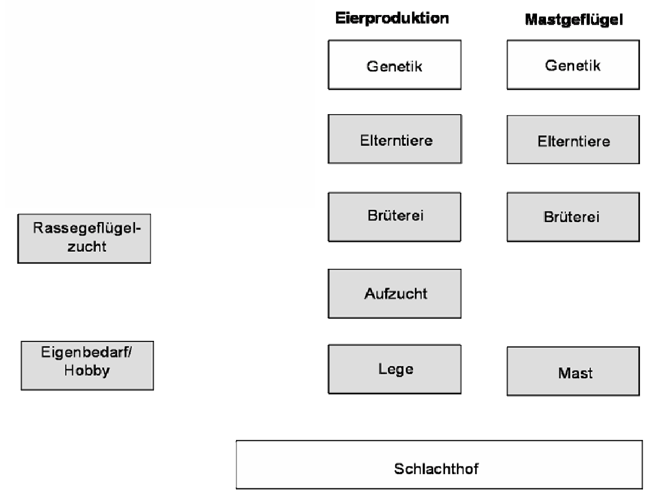
In der Tierseuchenüberwachung sind Ausbreitungsmodelle für Tierseuchen von immer grösserer Bedeutung, um Vorbeuge- und Kontrollmassnahmen gezielt einzusetzen. Wenn eine Tierseuche auftritt, ist die Wahrscheinlichkeit, dass ein Betrieb betroffen ist, von Haltung zu Haltung und je nach Region unterschiedlich. Diese Wahrscheinlichkeit hängt unter anderem ab von der Anzahl, der Entfernung und der Art direkter (z.B. Handel von Geflügel) und indirekter Kontakte (z.B. Gäste, die mehrere Betriebe besuchen). Insbesondere seit dem Ausbruch der Maul- und Klauenseuche in Grossbritannien im Jahre 2001 werden Methoden der sogenannten Kontaktnetzwerkanalyse angewandt, um Vorbeuge- und Kontrollmassnahmen zu planen.
In unserem Forschungsprojekt wird an einem Modell für den schweizerischen Geflügelsektor gearbeitet, mit dem Regionen und Betriebstypen, die für eine Vogelgrippeeinschleppung besonders gefährdet sind, bereits vor es zu einem Ausbruch kommt erkannt werden sollen. Zur Anpassung dieses Models dienen die Fragen in diesem Abschnitt.

1. Welche Typen von Geflügelbetrieben bzw. welche Produktionsstufen sind Ihrer Vermarktungsorgansiation als Mitglieder angeschlossen?

Bitte kreuzen Sie diese in der Abbildung an (s. unten). Sie können die Abbildung bei Bedarf ergänzen und anpassen.

2. Zwischen welchen Typen von Geflügelbetrieben bzw. welchen Produktionsstufen findet Geflügelverkehr statt INNERHALB Ihrer Vermarktungsorgansiation?

Bitte verbinden Sie in der Abbildung (s. unten) die entsprechenden Kästchen mit Pfeilen. Sie können die Abbildung bei Bedarf ergänzen und anpassen.



3. Hat Ihre Vermarktungsorganisation Mitarbeiter, die Ihre Betriebe vor Ort besuchen?

4. Welche Kontakte gibt es zwischen Ihren Betrieben untereinander?

Unter Kontakten verstehen wir zum Beispiel, wenn Arbeitsgeräte geteilt werden, wenn dasselbe Personal auf mehreren Betrieben eingesetzt wird, oder wenn die Betriebe von die selben Lieferanten z.B. für Futtermittel haben.

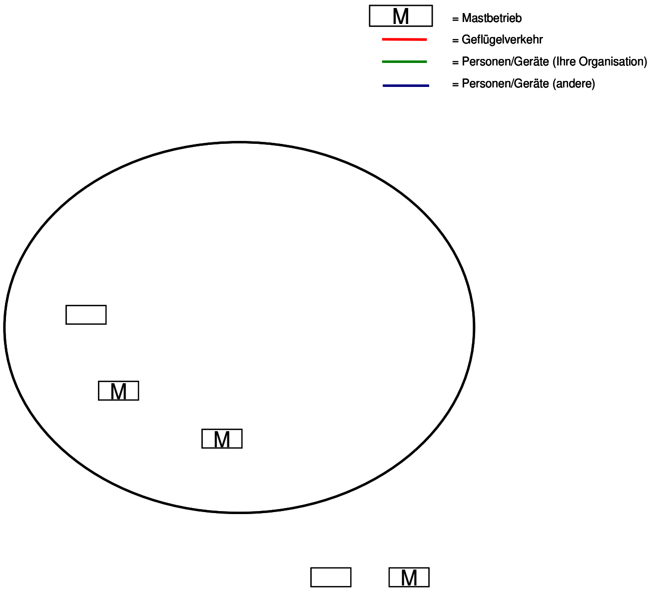
5. Wir freuen uns über Ihre Anmerkungen:

Für Ihre Mitarbeit danken wir Ihnen herzlich!

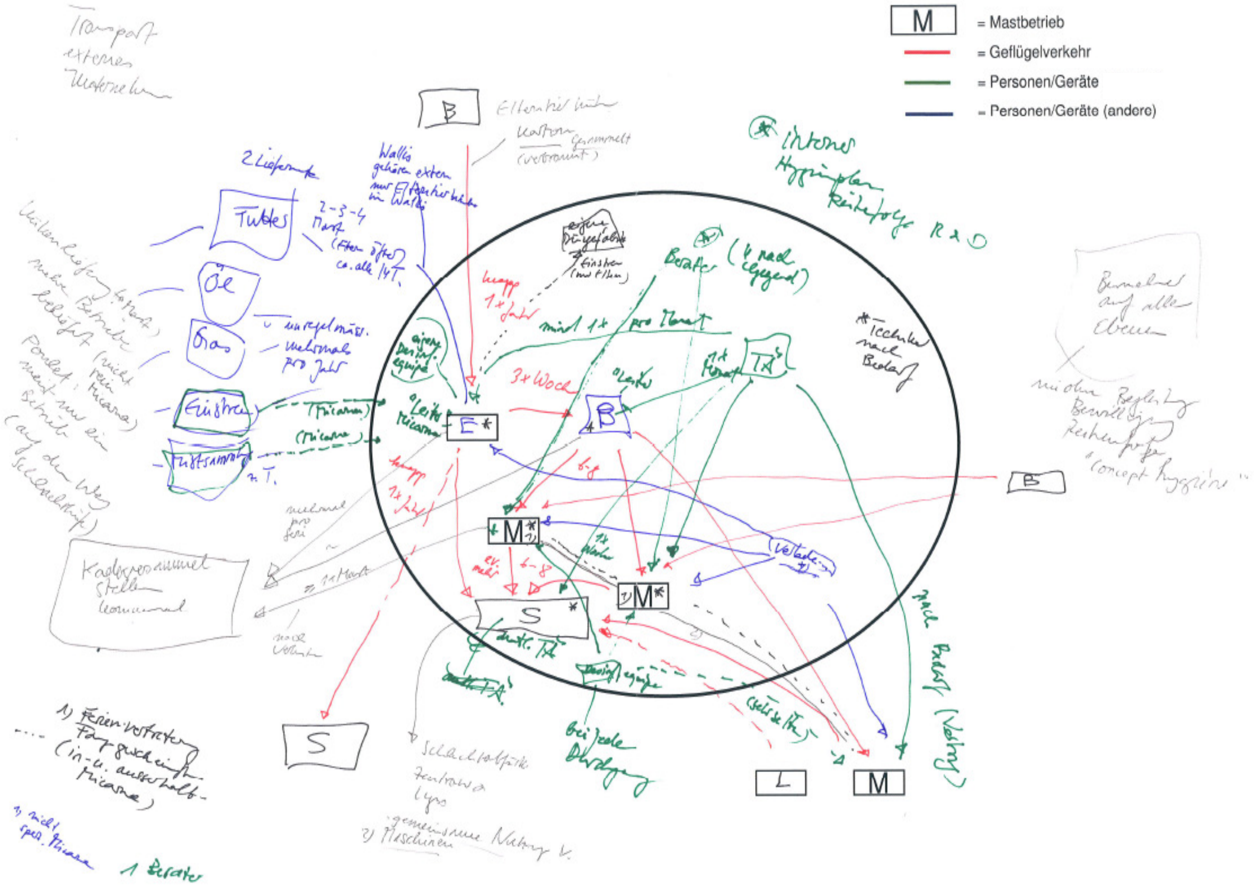
Sie haben hiermit einen wichtigen Beitrag zur Optimierung der Überwachung der Vogelgrippe in der Schweiz geleistet.

Bei Rückfragen und für weitere Informationen nehmen Sie bitte mit uns Kontakt auf.
Tel: 061 284 82 26

E-Mail: Lena.Fiebig@unibas.ch



Mapping tool



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APPENDIX 4: Results of the survey among poultry keepers in 2007

Forschungsprojekt zur Überwachung der Vogelgrippe in der Schweiz

Auswertung der Geflügelhalterumfrage 2007

Das Schweizerische Tropeninstitut in Basel hat von August bis Dezember 2007 im Rahmen des Forschungsprojektes „Constanze“ eine Umfrage unter Schweizer Geflügelhaltern durchgeführt mit dem Ziel, Daten zu erheben für eine bessere Planung der Früherkennung der Vogelgrippe beim Nutzgeflügel in der Schweiz. Die wichtigsten Umfrageergebnisse werden in diesem Artikel vorgestellt.

Hintergrund und Ablauf der Studie

Die Schweiz ist amtlich anerkannt frei von Vogelgrippe beim Nutzgeflügel, die korrekterweise als „klassische Geflügelpest“ bezeichnet wird. Grippeepidemien mit neuen Virustypen, wie H5N1, können jedoch jederzeit und überall (wieder) auftreten. Daher ist eine ständige Überwachung notwendig, die eine frühere Erkennung von Fällen und schnelle Massnahmen möglich macht. Die Vogelgrippe wird „passiv“ überwacht, indem alle gemeldeten Verdachtsfälle abgeklärt werden, und „aktiv“, indem auch gesunde Bestände stichprobenweise beprobt werden. Überwachung, insbesondere die aktive, sollte risikobasiert sein. Das heisst, am intensivsten sollte dann und dort überwacht werden, wo die Einschleppungsgefahr am grössten ist und das Schadensausmass am höchsten wäre, wenn ein Ausbruch verspätet erkannt würde.

Um neue Daten über den Schweizer Nutzgeflügelbestand und die Verteilung von Risikofaktoren für eine mögliche Einschleppung zu gewinnen, wurden:

- eine Gesamtliste aller in der Schweiz registrierten Geflügelhaltungen erstellt;
- ein Fragebogen an eine Zufallsstichprobe von 3'978 Geflügelhaltungen geschickt (August 2007);
- Interviews mit 28 Geflügelhaltern von kleinbäuerlichen Freilandhaltungen im Bodenseeraum geführt (Oktober und November 2007);
- Interviews mit fünf Fachpersonenen von Vermarktungsorganisationen für Mastgeflügel und Eier geführt (März und April 2009);
- und die erhobenen Daten statistisch ausgewertet.

Durch die Zusammenstellung aller registrierten Geflügelhaltungen ergab sich eine Gesamtliste von 49'437 Geflügelhaltungen und ein Gesamtbestand an Nutzgeflügel von 9'959'367 am Stichtag. Die Zahlen des Bundesamtes für Statistik aus demselben Erhebungszeitraum (2007) fallen mit 15'500 Geflügelhaltungen und einem Bestand von 8'101'800 Tieren deutlich geringer aus. Grund dafür ist, dass in unserer Studie erstmals die seit Oktober 2005 von den Gemeinden neu registrierten Geflügelhaltungen berücksichtigt wurden. Es ist jedoch anzunehmen, dass diese Zahlen zu hoch sind, da einige der seit 2005 und 2006 registrierten Haltungen in 2007 nicht mehr bestanden, und einige Geflügelhaltungen vermutlich mehrfach erfasst wurden. Die neue Gesamtliste dient als grober Überblick über die Standorte und Bestandsgrössen der Geflügelhaltungen. Sie wurde verwendet für eine neue Dichtekarte der Geflügelhaltungen in der Schweiz (siehe Abbildung 1) und zum Ziehen der Stichprobe für die Geflügelhalterumfrage.

Geflügelbestand der Schweiz

Durch die Zusammenstellung aller registrierten Geflügelhaltungen ergab sich eine Gesamtliste von 49'437 Geflügelhaltungen und ein Gesamtbestand an Nutzgeflügel von 9'959'367 am Stichtag. Die Zahlen des Bundesamtes für Statistik aus demselben Erhebungszeitraum (2007) fallen mit 15'500 Geflügelhaltungen und einem Bestand von 8'101'800 Tieren deutlich geringer aus. Grund dafür ist, dass in unserer Studie erstmals die seit Oktober 2005 von den Gemeinden neu registrierten Geflügelhaltungen berücksichtigt wurden. Es ist jedoch anzunehmen, dass diese Zahlen zu hoch sind, da einige der seit 2005 und 2006 registrierten Haltungen in 2007 nicht mehr bestanden, und einige Geflügelhaltungen vermutlich mehrfach erfasst wurden. Die neue Gesamtliste dient als grober Überblick über die Standorte und Bestandsgrössen der Geflügelhaltungen. Sie wurde verwendet für eine neue Dichtekarte der Geflügelhaltungen in der Schweiz (siehe Abbildung 1) und zum Ziehen der Stichprobe für die Geflügelhalterumfrage.

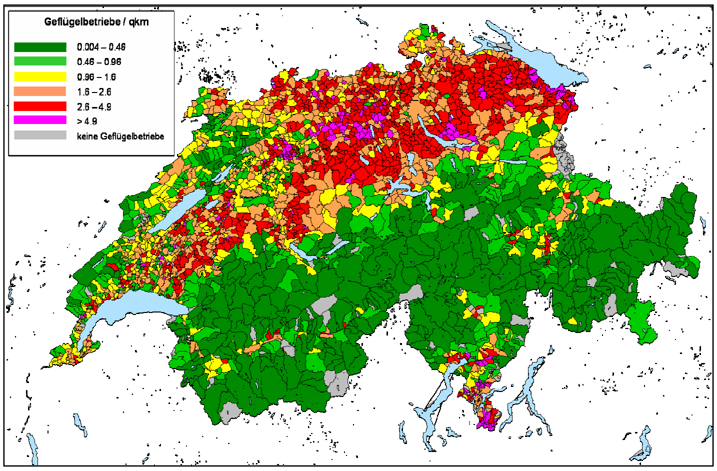


Abbildung 1 Dichte an Geflügelhaltungen (Kartengrundlage © swisstopo 2008, bearbeitet von H. Schwermer, M. Binggeli (BVET), Georeferenzierung durch K.W. Axhausen (ETHZ))

Umfrageergebnisse

Erfreulicherweise nahmen mehr als der Hälfte der angeschriebenen Geflügelhaltenden an der Umfrage teil und insgesamt 39% der Fragebögen waren vollständig ausgefüllt. Alle Kantone und verschiedene Typen von Geflügelhaltungen sind vertreten. Die Einteilung in Betriebstypen beruht auf den Angaben, welche die Teilnehmenden im Fragebogen machten. Für vergleichende Analysen erfolgte zudem eine Einteilung in zwei Gruppen (siehe Tabelle 1): „Grossbetriebe“ (gewerbliche Zwecke) und „Kleinhaltungen“ (Geflügelhandel zum Eigenbedarf, zum kleinem Nebenerwerb, zur Rassegeflügelzucht und als Hobby).

	„Grossbetriebe“					**„Kleinhaltungen“**	
Betriebstyp	**Mast**	**Lege**	**Aufzucht**	**Elterntier**	**Sonstige***	**Bäuerliche Kleinhaltung**	**Rasse-geflügelzucht**
Anzahl Teilnehmer	**334**	**208**	**31**	**9**	**44**	**695**	**161**
Anzahl Geflügel pro Haltung (Zentralwert)	**5400**	**1387**	**4500**	**2750**	**7740**	**15**	**17**
Freilandhaltungen (in %)	**49**	**86**	**26**	**22**	**59**	**92**	**96**
Betriebe mit Enten oder Gänsen und gleichzeitig anderem Geflügel (in %)	**3**	**9**	**-**	**13**	**16**	**16**	**29**

Tabelle 1 In der Umfrage vertretene Geflügelhaltungen und ausgewählte Eigenschaften; *Teilnehmende, die zwei oder mehr der (gewerblichen) Betriebstypen angaben.

Mögliche Einschleppung von Vogelgrippe durch wilde Wasservögel

Wildvögel, insbesondere Wasservögel wie Enten, Schwäne, Gänse, Bless- und Teichhühner, können Vogelgrippeviren verbreiten, ohne selbst zu erkranken. Um Kontakte zwischen Wildvögeln und Nutzgeflügel in Freilandhaltung möglichst zu vermeiden, galt im Winter

2005/2006 schweizweit, und im Wintern 2006/2007 in Risikogebieten ein Freilandhaltungsverbot (Stallpflicht). Im Winter 2007/2008 galten in Risikogebieten in der Nähe grosser Gewässer verschärfte Massnahmen.

13% der Befragten, die eine Freilandhaltung haben, gaben an, bereits wilde Wasservögel im Geflügelauslauf beobachtet zu haben. Die Wahrscheinlichkeit, wilde Wasservögel im Auslauf zu beobachten, war höher, wenn ein Teich oder Bach im Freilandbereich lag. Die Jahreszeit (Sommer oder Winter) und ob die Geflügelhaltung in einem sogenannten Risikogebiet liegt, hatte keinen Einfluss darauf, wie häufig wilde Wasservögel beobachtet wurden. In Interviews mit Umfrageteilnehmern aus dem Bodenseeraum, stellte sich heraus, dass als „beobachtete Wasservögel“ oft auch jene mitgezählt wurden, die ausserhalb des Geheges oder in der Luft gesehen wurden. Ein direkter Kontakt zwischen wilden Wasservögeln und Nutzgeflügel in Freilandhaltung ist als seltener einzustufen als zuvor angenommen. Diese Ergebnisse waren eine Grundlage für die Entscheidung des Bundesamtes für Veterinärwesen (BVET), im Winter 2008/2009 auf die Festlegung von Risikogebieten und auf eine Stallpflicht zu verzichten.

Mögliche Einschleppung von Vogelgrippe durch Menschen

Vogelgrippe kann auch über Menschen in Tierbestände eingeschleppt werden, wenn Personen mit infizierten Tieren in Kontakt waren (zum Beispiel Wildvögeln oder Geflügel im Ausland) und dann mit kontaminierter Kleidung oder Geräten Geflügelbestände betreten. Ein weiteres Risiko stellen (illegal) importierte Vögel oder Geflügelprodukte dar.

Dieses Risiko ist schwer bezifferbar. In der Umfrage wurden nur Angaben zum Personenverkehr und zu Auslandsreisen erhoben. Es zeigte sich, dass sich auf Gross- und Kleinbetrieben zumeist insgesamt zwei Personen täglich auf dem Betrieb aufhalten, aber auf einzelnen Betrieben auch 120 Personen. Bei Grossbetrieben sind diese zumeist Mitarbeiter und Lieferanten, auf Kleinbetrieben vor allem Familienmitglieder und Feriengäste. 51% der Teilnehmenden waren im Vorjahr der Umfrage einmal oder mehrfach auf einer Auslandsreise, 31% der Teilnehmenden hatten Gäste aus dem Ausland. 2% der Auslandnennungen betrafen Asien, von wo immer wieder Vogelgrippefälle gemeldet werden.

Wachsamkeit ist überall wichtig. Personen, die mit Geflügel arbeiten, müssen Hygienemassnahmen befolgen und Hygieneschleusen nutzen. Betriebsfremde Personen sollten möglichst keinen Zugang zum Geflügelbestand haben und informiert werden über Einfuhrbestimmungen und generelle Betriebshygiene. Wer von anderen Betrieben oder Auslandsreisen zurückkehrt, sollte vor Betreten des eigenen Stalls unbedingt die Kleidung wechseln. Im Ausland sollte enger Kontakt mit Geflügel und Ziervögeln vermieden werden.

Verbreitung der Vogelgrippe über Geflügelhandel und Ausstellungen

In der gewerblichen Geflügelproduktion geht es nicht ohne regelmässigen Zukauf und Abgabe von Geflügel oder Bruteiern. Auch bei Kleinhaltungen wird Geflügel zugekauft und abgegeben. Zukäufe aus dem EU Raum wurden in 2% aller Zukäufe angegeben. Innerhalb der Schweiz überschreitet der Geflügelhandel Kantonsgrenzen. Mehr als ein Viertel der angegeben Zulieferer- und Abnehmerbetriebe lagen in einer Entfernung von 50km oder mehr, sowohl bei Klein- als auch bei Grossbetrieben. Das heisst, im Tierseuchenfall wären nicht nur direkt benachbarte Geflügelbetriebe gefährdet, sondern auch Handelspartner in der ganzen Schweiz. Was Geflügelhalter tun können für sicheren Geflügelhandel, ist Geflügel nur aus zuverlässiger Quelle zu kaufen (Zulieferbetrieb mit gutem hygienischen Standard) und ein Stallregister zu führen. Darin werden alle Zukauf- und Abgabedaten und -orte aufgeschrieben. Fast alle Grossbetriebe führen ein solches Register, aber weniger als 10% der Teilnehmenden von Kleinhaltungen, und dort fast nur in der Rassegeflügelzucht.

Auch Geflügelausstellungen können die Ausbreitung von Vogelgrippeviren und anderen Krankheitserregern begünstigen, da sie Geflügelhaltende und Tiere aus dem In- und Ausland auf engem Raum zusammenbringen. In der Umfrage gaben 37% der Rassegeflügelzüchter an, im Vorjahr ein bis drei, in Ausnahmen bis zu 30 Ausstellungen besucht zu haben, im Durchschnitt jedes zweite Mal als Aussteller. Bei Legebetrieben (12%) und Mast- und anderen Grossbetrieben (6%)) waren Ausstellungsbesuche seltener (einmal im Jahr) und zumeist als Besucher. Um von Ausstellungen keine Krankheitserreger in den eigenen Bestand mitzubringen, müssen Quarantänevorschriften (wenn eigene Tiere ausgestellt werden) und Hygienemassnahmen strikt eingehalten werden, insbesondere bevor wieder der eigene Geflügelstall betreten wird.

Mögliche Verbreitung von Vogelgrippeviren über Kadaver und Wildtiere

Korrekt ist es, totes Geflügel in Kadaverbehältern oder in einer Tiefkühltruhe zu sammeln und zu den örtlichen Tierkörpersammelstellen zu bringen und 63% der Umfrageteilnehmer gehen auch nur so vor. Totes Geflügel sollte nicht für Wildtiere in den Wald gelegt werden (von 23% genannt) und das Verfüttern an Haustiere ist strikt verboten (von weniger als 1% genannt). Haustiere, Wildtiere und Schadnager können sich nämlich auch mit Vogelgrippeviren infizieren und die Erreger verbreiten.

Als Vorsichtsmassnahme empfiehlt eine Vermarktungsorganisation ihren Produzenten, Einweg-Plastiksäcke zu verwenden anstatt Tonnen, die zu den Kadaversammelstellen und wieder zurück auf den Betrieb transportiert werden, und dabei möglicherweise kontaminiert werden. Nach dem Besuch von Tierkörpersammelstellen sind Hygienemassnahmen und Kleiderwechsel wichtig, bevor der eigene Geflügelstall betreten wird.

Wie gut wissen Geflügelhalter über die Vogelgrippe bescheid?

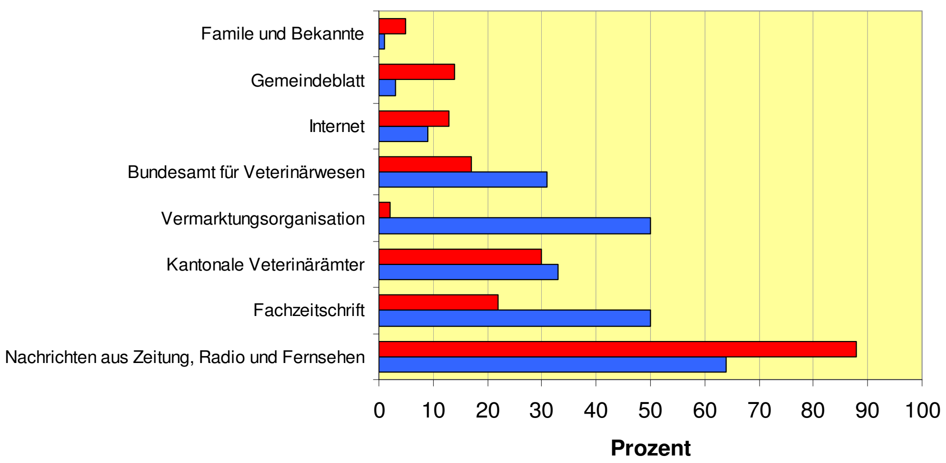
Eine passive Überwachung von Vogelgrippe ist nur wirksam, wenn Tierhalter Verdachtsfälle bei ihrem Geflügel erkennen und sofort einem Tierarzt melden. Wie gut das passive Überwachungssystem im Ernstfall funktionieren würde, ist schwer vorherzusagen. Für eine Einschätzung wurden daher Fragen zum Kenntnisstand und zu Ansichten der Geflügelhaltenden gestellt.

Die Vogelgrippe führt bei den meisten Nutzgeflügelarten zu einer hohen Sterblichkeit beziehungsweise Leistungsrückgang und vielfältigen Krankheitsanzeichen (siehe Box für weiterführende Informationen). Enten und Gänse können aber Vogelgrippeviren verbreiten, ohne selbst deutlich krank zu werden. Dies haben lediglich 2% der Befragten gewusst. Eine gleichzeitige Haltung von Enten oder Gänsen mit anderem Geflügel, was von 13% der Befragten praktiziert wird (siehe Tabelle 1), gilt als risikoreich, da die unscheinbare Verlaufsform der Vogelgrippe bei Enten und Gänsen die frühe Erkennung der Verbreitung der Krankheit im Betrieb verhindern kann.

Es wurde auch gefragt, woher die Geflügelhalter Informationen zur Vogelgrippe bekommen. Insgesamt wurden Nachrichten bei Grossbetrieben (zu 68%) und bei Kleinhaltungen (zu 88%) am häufigsten als Informationsquelle benannt. Während bei Grossbetrieben meist zwei bis drei Quellen angeführt wurden, waren bei 45% der Kleinhaltungen Nachrichten die einzige Quelle (siehe Abbildung 2).

Die Umfrage zeigte, dass nur 12% der Teilnehmenden wussten, dass die „Vogelgrippe“ und die „Klassische Geflügelpest“ dieselbe Krankheit mit denselben Anzeichen ist. Die Verwendung verschiedener Begriffe für eine Tierseuche kann also irreführend sein. Gemäss der Umfrage sind insbesondere jene Geflügelhalter gut informiert, die einer Vermarktungsorganisation angeschlossen sind und die mehrere Informationsquellen nutzen, darunter die Informationen der Veterinärbehörden (BVET, kantonale Veterinärämter) und aus Fachzeitschriften, wie der SGZ.

A. Woher erhalten Sie hauptsächlich Informationen über die Vogelgrippe?



B. Anzahl verschiedener genutzter Informationsquellen und -kanäle

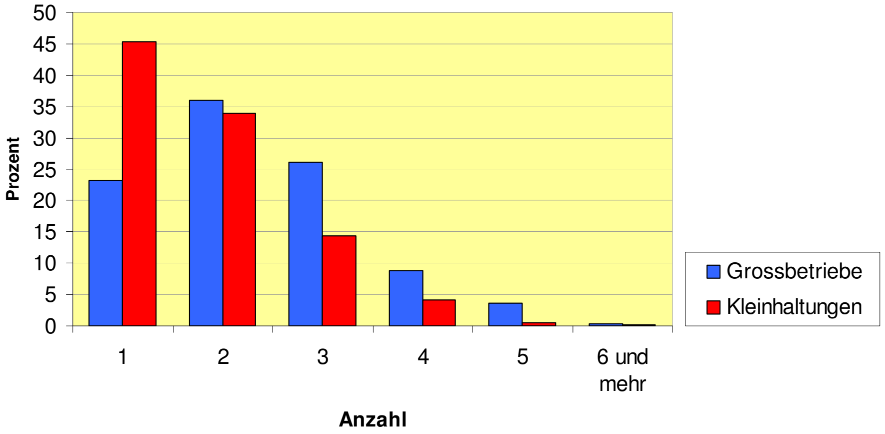


Abbildung 2 Von den Befragten genutzte Informationsquellen zum Thema Vogelgrippe

Interviews mit Fachpersonen von fünf bedeutenden Schweizer Geflügelvermarktungsorganisationen zeigten, dass diese mehrere Wege (Briefsendungen, persönliche Beratung, telefonische Auskunft, Produzententagungen und weitere) nutzen, um sicherzustellen, dass die Produzenten über wichtige Themen der Vogelgrippe und Tiergesundheit informiert sind. Die Fachpersonen selbst informieren sich vor allem über Kontakte zu nationalen und internationalen Behörden, zu Fachkollegen und zu wissenschaftlichen Einrichtungen, um qualitativ hochwertige und aktuelle Informationen zusammenzustellen. Haltungen, die keiner Vermarktungsorganisationen angeschlossen sind, haben schwerer Zugang zu einheitlicher und regelmässiger Information.

Das Internet bietet zahlreiche Informationsmöglichkeiten, und mit dem Internetauftritt des BVETs und der Fachverbände stehen der Öffentlichkeit regelmässig aktualisierte und hochwertige Information zur Verfügung. E-Mails sind ein schneller und preiswerter Weg, um viele Personen zu erreichen. Allerdings zeigt diese Studie, dass Internet und E-Mail-Verkehr derzeit nicht der Hauptweg für die Verbreitung Informationen sind. Die E-Mail-Adressen der Geflügelhalter sind bislang nicht systematisch in Geflügelregistern erfasst. Die befragten Fachpersonen der Vermarktungsorganisationen schätzten, dass sie nur 50-75% ihrer Produzenten über E-mail erreichen können. In der Umfrage gaben nur 11% der Geflügelhaltenden „Internet“ als Informationskanal an.

Schlussfolgerung und Ausblick

In dieser Studie wurden erstmals an einem breiten Querschnitt von Geflügelhaltungen Einfluss- und Risikofaktoren für eine mögliche Einschleppung von Vogelgrippe untersucht. Eindeutige „Risikobetriebe“, „Risikojahreszeiten“ oder „Risikogebiete“ lassen sich anhand der Ergebnisse nicht festlegen. Das Risiko steigt, je mehr Faktoren gleichzeitig wirken, beispielsweise bei einem Betrieb, bei dem sich zahlreiche Wasservögel im Freilandbereich aufhalten UND Enten mit Hühnern gemeinsam gehalten werden UND Ausstellungen besucht werden UND die Betriebshygiene zu wünschen lässt UND bei erhöhter Sterblichkeit tagelang zugewartet wird.

Die Studie zeigt, dass der Austausch von Informationen zwischen Geflügelhaltungen, insbesondere den Kleinhaltungen, und Veterinärbehörden noch verbessert werden kann. Geflügelhaltende sollten aktiv und regelmässig Informationen zur Vogelgrippe und zu aktuellen Tierseuchen aus verlässlichen Quellen suchen (von Veterinärämtern, Vermarktungsorganisationenen, Aviforum) und den Empfehlungen folgen. Die Behörden könnten in ihrer Informationspolitik jene Geflügelhaltende noch besser berücksichtigen, die bislang nicht systematisch erreicht werden, da sie erst seit 2005 registriert sind, die an keine Vermarktungsorganisation angeschlossen sind und die keinen Internetzugang haben bzw. nutzen. Aus diesem Grund versandte das BVET Anfang Februar 2009 die DVD „Vogelgrippe – jetzt vorbeugen!“ an rund 15'000 Geflügelhaltende in der Schweiz.

Eine sinnvolle Investition wäre es, ein aktualisierbares zentrales Geflügelregister für die Schweiz zu führen, in der die Anschrift, Betriebsnummer und der Geflügelbestand einheitlich dargestellt, und neue Informationen wie bevorzugte Kommunikationssprache, Mitgliedschaft bei Vermarktungsorganisationen und Betriebstyp systematisch miterfasst würden.

In der Schweiz gibt es weit mehr laufende Forschungs- und Überwachungsprogramme als in diesem Artikel erwähnt. Weitere Informationen sind beim BVET erhältlich (siehe Box).

Insgesamt wurde festgestellt, dass Geflügelhalter, Vermarktungsorganisationen und die Veterinärbehörden in der Schweiz viel tun, um den Schweizer Nutzgeflügelbestand vor der Vogelgrippe zu schützen.

Allen Teilnehmenden an der Geflügelhalterumfrage, allen Fachpersonen und allen Projektpartnern sei herzlich gedankt. Finanziert wurde diese Studie durch das Bundesamt für Veterinärwesen (BVET) und über Projektmittel aus dem trinationalen Forschungsprojekt „Constanze“.

Mehr Informationen zur Vogelgrippe (klassische Geflügelpest), zu Massnahmen und Reglementen erhalten Sie beim Bundesamt für Veterinärwesen. Kostenlos können Sie hier ausserdem die Informations-DVD „Vogelgrippe - jetzt vorbeugen!“ bestellen.

- Internet: www.bvet.admin.ch, Themen, Kapitel Tiergesundheit, Vogelgrippe
- Per E-Mail: info@bvet.admin.ch
- Postanschrift:
  Bundesamt für Veterinärwesen
  Schwarzenburgstrasse 155
  3003 Bern
- Telefonische Auskunft: 031 323 30 33

Box Weitere Informationen

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