Department Farm Animals and Veterinary Public Health
University of Veterinary Medicine Vienna
(Head: Univ.-Prof. Dr.med.vet. Martin Wagner, Dipl. ECVPH)

Institute Food Safety, Food Technology and Veterinary Public Health
Unit of Veterinary Public Health and Epidemiology
(Head: Univ.-Prof. Dr.med.vet. Annemarie Käsbohrer)

Zoonoses in Austria – a comprehensive assessment based on published literature

Diploma Thesis

University of Veterinary Medicine Vienna

submitted by
Anna E. Vogl

Supervisor:

Ass.-Prof. Amélie Desvars-Larrive, DMV, PhD.

Unit of Veterinary Public Health and Epidemiology

Institute of Food Safety, Food Technology and Veterinary Public Health

University of Veterinary Medicine Vienna

Reviewer:

Univ.-Prof. Dr.med.vet. Anja Joachim, Dipl. EVPC

Institute of Parasitology

University of Veterinary Medicine Vienna

Zusammenfassung

Zoonotische Krankheitserreger stellen ein erhebliches Risiko für die öffentliche Gesundheit sowie die Gesundheit von Tieren dar. Für das ordnungsgemäße Management und die Kontrolle zoonotischer Pathogene im Rahmen des „One Health“ Ansatzes ist die Verfügbarkeit umfassender und strukturierter Daten von entscheidender Bedeutung. Diese Datengrundlage ist in Österreich auf nationale Berichte, wissenschaftliche Studien sowie Diplom-, und Doktorarbeiten verteilt, was es schwierig macht das Risiko eines „spillovers“ aller in Österreich präsenten zoonotischen Krankheitserreger zu bewerten.

Ziel dieser Studie war es, durch eine systematische Literaturrecherche Daten zu den in Österreich zirkulierenden Pathogenen, den Wirten, Vektoren und deren Präsenz in Umwelt und Lebensmitteln zusammen zu fassen. Zwischen 1975 und 2022 wurden 228 zoonotische Krankheitserreger in Österreich untersucht, wobei zehn von ihnen in etwa 40 % der Publikationen behandelt wurden. Etwa 90 % der untersuchten Krankheitserreger wurden in 125 Wirtspezies (Menschen inkludiert), zwölf Vektorenspezies, 32 Lebensmittelkategorien und sechs Umweltmedien nachgewiesen. Am häufigsten untersucht wurden Wildtiere. Das Netzwerk, das die Beziehung zwischen Wirten und Krankheitserregern darstellte, ergab, dass Kühe, Hunde, Katzen, Rotfüchse und Schweine ein signifikantes zoonotisches Potential aufweisen. Die Analyse der Forschungstrends in Österreich zeigte ein größer werdendes Interesse an zoonotischen Krankheitserregern, während der Bereich Umweltmedien weitgehend vernachlässigt wurde.

Die in der Studie gesammelten Daten und ihre Analyse bieten eine Grundlage zur weiteren Forschung, und unterstreichen den erheblichen Arbeitsaufwand, der zur Harmonisierung der Daten und zur Weiterentwicklung des „One-Health“ Zugangs zu zoonotischen Krankheiten in Österreich erforderlich ist.

Abstract

Zoonotic pathogens represent a threat to animal and human health. For the proper management and control of zoonotic diseases under a One Health approach, the availability of extensive and structured data is key. Information regarding zoonotic diseases in Austria is spread across national reports, scientific papers, and student dissertations, making it challenging to evaluate spillover risks across zoonotic interfaces.

This study aimed to compile data on investigated zoonotic pathogens in Austria through a systematic literature search, providing an overview of circulating pathogens their hosts, vectors, and potential food and environmental source of infection. Between 1975 and 2022, 228 unique zoonotic pathogens were investigated in Austria, with ten of them accounting for around 40 % of the selected publications. Almost 90 % of investigated pathogens were evidenced across 125 different animal hosts (including human), twelve vector species, 32 categories of food, and six types of environmental media. Notably, wildlife species were the most investigated hosts. Furthermore, the network representation of the zoonotic pathogen-host relationship revealed that cattle, dog, domestic cat, red fox, and pig presented a significant zoonotic potential. Analysis of the research trend in Austria demonstrated an increased interest in zoonotic disease research in the country. It also evidenced that bacteria were the preferred investigated zoonotic agents while the environmental compartment has been largely neglected.

The data collected in this study and its analysis provides a base for future research. It highlights the substantial work required in harmonising data and advancing One Health approach to zoonotic diseases in Austria.

.

Contents

1 Introduction 1
2 Methods 4
2.1 Search strategy 4
2.2 Paper selection 4
2.3 Data extraction 5
2.4 Data validation, analysis, and visualisation 6
3 Results 8
3.1 Data records 8
3.2 Selected publications 11
3.3 Zoonotic pathogens and investigated compartments 14
3.4 Trends in scientific interest 30
4 Discussion 32
5 Conclusion 38
6 List of tables 39
7 Table of figures 40
8 Literature Cited 42

List of abbreviations

AGES	Österreichische Agentur für Gesundheit und Ernährungssicherheit [Austrian Agency for Health and Food Security]
DOI	Digital Object Identifier
ECDC	European Centre for Disease Prevention and Control
EFSA	European Food Safety Authority
EID	Emerging infectious disease
EU	European Union
HEV	Orthohepevirus A
IQR	Interquartile range
n	Number of publications
NCBI	National Center for Biotechnology Information
USUV	Usutu virus
WNV	West Nile virus

1 Introduction

Zoonoses are caused by pathogens naturally transmissible between humans and animals in either direction (1). Places where humans and animals or animal products interact create interfaces that facilitate zoonotic pathogen transmission (2, 3). Anthropogenic-driven changes such as habitat destruction, shifts in land use (4), agricultural intensification (5), animal domestication (6), the rising significance of companion animals and livestock, coupled with the resulting growing animal-human contacts, compounded by the increased interactions with wildlife due to hunting (7), the proliferation of exotic companion animals, or the increasing consumption and illegal trade of wild animals (8), collectively contribute to the expansion of human-animal interfaces. These interactions create new opportunities for pathogen transmission, potentially resulting in pathogen evolution and zoonotic disease emergence. Between 1940 and 2005, approximately 60 % of emerging infectious disease (EID) events (9), i. e., infections that have newly appeared in a population or have existed but are rapidly increasing in incidence or geographic range, were of zoonotic origin (10). The intertwined factors that contribute to the spread of pathogens between species (often referred to as “spillover”) and the emergence of novel zoonotic pathogens highlight the need for interdisciplinary and cross-sectoral collaborations, addressed under the concept of One Health (11, 12). The effective monitoring, prevention, and control of zoonotic diseases at human-animal-environment interfaces must rely on an integrated approach, involving a challenging collaboration between the human health, animal health, and environmental health sectors (13, 11, 14, 15).

Austria has a growing population of nine million people (in 2022) (16), residing in an area of 83,871 square kilometres, with a population density of 108 inhabitants per square kilometre (17). The fauna of Austria encompasses approximately 45,870 distinct species, with 626 of them categorised as vertebrates. Among the vertebrates, there are 110 mammalian species, 418 avian species, 16 reptilian species, 21 amphibian species, and 60 species of fish (18). Out of 3.9 million Austrian households 35 % own pets (in 2020). There are approximately 53,300 cows, one million of pigs, and five million of poultry spread across 154,953 agricultural operations, mainly smallholder family farms (in 2021). A total of 133,000 annual hunting permits were issued in 2022. Along with multiple slaughterhouses, food processing plants, and zoos (19–21), these numbers underline the importance of the human-animal interfaces at the national scale.

As a member of the European Union (EU), Austria has established active monitoring and surveillance programmes primarily targeting *Salmonella,* and other zoonotic agents, both in food stuffs of animal origin and livestock species (cattle, poultry, pigs), as required by EU Regulation 2160/2003 (22). Additionally, the Commission Implementing Decision (EU 2020/1729) (23) on the monitoring and reporting of antimicrobial resistance also applies in Austria. Furthermore, Austria complies with Directive 2003/99/EC, which mandates the monitoring of zoonoses, zoonotic agents, and related antimicrobial resistance (24). The Directive 2003/99/EC (22) in Austria is translated into the Federal Law on the Monitoring of Zoonoses and Zoonotic Pathogens (Zoonosis Act, “Zoonosengesetz”) (BGBl. I Nr. 128/2005) (25). Under this legislative framework, Austria, as required, reports data to the European Food Safety Authority (EFSA), which is then integrated into the annual EU One Health Zoonotic Report authored jointly by the EFSA and the European Centre for Disease Prevention and Control (ECDC). The Austrian Agency for Health and Food Safety (AGES) is mandated to compile these findings and the aggregated data is subsequently made publicly available (26).

Moreover, Austria operates within the legal frameworks of the Regulation (EU) 2016/429) on transmissible animal diseases (“Animal Health Law”) (27) and the Austrian Animal Epidemic Law (BGBl. Nr. 186/1950) (28), which govern the surveillance and control of animal diseases, including zoonoses. In this context, successful surveillance and control programmes implemented in Austria in the past 50 years have resulted in achieving an official "disease-free" status for several zoonotic diseases, such as canine rabies (since 2008) (29), bovine tuberculosis (since 1999) (30), bovine brucellosis (since 1999), or *Brucella melitensis* infections in small ruminants (since 2001) (31).

Some zoonotic diseases are notifiable, meaning that they are legally mandated to be reported to public health authorities. Notifiable zoonotic diseases include bacterial diseases such as plague, tularemia, leptospirosis (only in humans), psittacosis, and common food-borne diseases (e. g. infections caused by *Salmonella enterica*, *Campylobacter*, *Listeria*). It also includes viral diseases, such as rabies, hantaviruses, severe acute respiratory syndrome (SARS), infection by highly pathogenic avian influenza (HPAI) virus, or vector borne diseases (e. g. West Nile virus (WNV) disease, tick-borne encephalitis (TBE)), as well as some parasitic diseases (e. g. infestation by *Echinococcus granulosus* and *Echinococcus multilocularis*). The list of notifiable diseases is available from the Federal Ministry of Social Affairs, Health, Care and Consumer Protection (32).

A comprehensive understanding of circulating zoonotic diseases, their hosts, vectors, environmental reservoirs, and the key interfaces where spillover events may occur is essential for developing effective prevention and control measures of zoonoses (33). Information about zoonotic pathogens studied and evidenced in Austria is dispersed across scientific papers, reports from the AGES, and student dissertations (e. g. veterinary diploma theses, master theses).

The objective of this work is to compile data on zoonotic pathogens in Austria, along with information about their hosts, vectors, and environmental matrices. This effort seeks to characterise the various interfaces through which zoonotic transmission can occur. Additionally, this study aims to pinpoint research trends and research gaps on zoonotic pathogens in Austria.

2 Methods

2.1 Search strategy

Between 17 July and 23 August 2022, a systematic literature search was conducted using the query ("Zoono*" AND ("Austria" OR "Österreich")) in the following databases: PubMed® (National Center for Biotechnology Information (NCBI), United States), Scopus (Elsevier, Netherlands) and vetmed:seeker (University of Veterinary Medicine Vienna, Austria), including articles published between the inception of the databases and the date of the search.

Furthermore, the publication database of AGES (“https://www.ages.at/en/research/publication-database”) was also searched. The keyword "zoono*", Business area = "AGES TOTAL" was used, and the categories *Scientific publications – peer-reviewed*, *Popular science articles/articles in science journals* (editorials, overviews, reviews), *Scientific work* (post-doctorates, dissertations…), *Research reports*, as well as *AGES Folders and brochures*, *AGES statements*, and *AGES journals/reports* were selected.

Additional papers found in the reference section of reviews that provided relevant information were also included.

Publications found in the respective databases were compiled in the reference manager Citavi (Swiss Academic Software. 2023) where duplicate citations were identified and removed before the following selection processes.

2.2 Paper selection

Titles and abstracts were first screened for relevance using the following inclusion criteria: the publication presented data pertaining to at least one zoonotic disease or pathogen that was specifically investigated or documented in Austria and the pathogen was identified as zoonotic in the paper. Publications were excluded i) if they did not investigate or describe a zoonotic disease that was identified as such, ii) if research was not conducted in Austria, iii) if publications did not describe naturally occurring zoonotic infection, or iv) if publications described disease physiology or v) dealt with treatment or methods for pathogen detection.

Book chapters, posters, literature reviews, statistical forecasts, and conference proceedings were excluded. Regarding antimicrobial resistant bacteria, papers were included if they specifically explored the animal-human interface and/or the authors referred to zoonotic transmission. To prevent duplication of data, diploma-, master's-, and doctorate thesis were not included if a peer-reviewed research paper published the same data. If inclusion criteria could not be clearly evaluated from the title or abstract, the publication was proceeded to further selection steps.

In a second step, the full texts of the previously selected titles/abstracts were screened using the inclusion/exclusion criteria described above. Publications were excluded if they were not in German or English language or did not describe the situation in Austria. When a publication dealt with multiple countries, it was included if it provided specific information on zoonotic diseases in Austria. Citations of the selected articles were exported into Excel (Microsoft, 2023) where the information from the data extraction process was recorded.

2.3 Data extraction

The following data was extracted from the selected publications:

i) Publication: citation, year of publication, and type of publication (i. e., article, report, or thesis);

ii) Study design: type of study, i. e., case study or original research (based on definitions provided by "Springer Nature" (34) and national surveillance data;

iii) Investigated zoonotic pathogen:
- pathogen type (e. g., bacteria, virus, parasite, fungi, prion, or other),
- common and/or scientific names (when specified), as mentioned in the information source;

iv) Investigated host:
- type of host: human, companion animal (defined as domesticated animals possessed by a person for reasons other than food or resource production, e. g., cat, dog, horse, domesticated small rodents or exotic companion animals), livestock (defined as domesticated animal kept for resource and food production), wildlife (defined as free-ranging or captive wild animal species that are not domesticated);

- common and/or scientific names (when specified), as mentioned in the information source;
- if the pathogen was detected in the host, i. e., seropositive (confirmed by the presence of antibodies), positive (direct detection of the pathogen), or negative;

v) Investigated vector: common and scientific names (when specified) as mentioned in the information source; if the pathogen was detected in the vector (i. e., positive or negative);

vi) Investigated environmental matrix, as mentioned in the information source, and if the pathogen was detected in the matrix (i. e., positive or negative);

vii) Investigated food matrix: the specific type of food investigated; the origin of the food product (animal or plant); if the pathogen was detected in the food (i. e., positive or negative).

viii) Epidemiological context: the year the study was conducted; the location of the study (federal state(s) where samples were collected when this information was available), whether the case was imported (including most probable origin if provided); whether the pathogen was mentioned as emerging in Austria (i. e. “first description in Austria”, “first human case in Austria”, “first autochthonous case in Austria”); and whether specific professional activities are deemed to carry an elevated risk of exposure.

2.4 Data validation, analysis, and visualisation

Data validation, analysis, and visualisation were performed using the software R v. 4.3.0 (35).

2.4.1 Quality control & data cleaning

First, the data underwent quality control and cleaning procedures where the unique values of each field were checked to search for inaccurate (e. g., containing typographical errors or not belonging to a pre-defined list of values) or missing data in the dataset using the R base function *unique()*. Events containing detected errors were manually inspected against the original data source, and, when necessary, the erroneous values were modified, replaced, or removed.

2.4.2 Taxonomic validation

For each animal host, vector, and pathogen, common and scientific names as well as taxonomic classification were resolved against the NCBI Taxonomy database (36) using the R package taxize (37). For each animal host, vector, and pathogen species, validation of the scientific name, as provided in the information source, was performed using the function *gnr_resolve()*. When the scientific name of the host was not provided, it was retrieved (when possible) from the common name as mentioned in the information source, using the function *comm2sci()*. If a conflict occurred between scientific name and/or common name as provided in the information source and NCBI-resolved names, the information source was cross-referenced and searched for complementary information on the investigated species. Ultimately, the most up-to-date name (i. e., NCBI-resolved) was preferred. Finally, the taxonomic hierarchy for each animal host, vector, and pathogen was retrieved from the NCBI Taxonomy database (36) using the function *classification()*.

If the query to NCBI did not retrieve automatically animal species common and scientific names, those were searched manually into the NCBI database (https://www.ncbi.nlm.nih.gov/taxonomy). If not found, the search was further performed in Wikipedia and retrieved names were integrated manually to the final dataset. When the original source did not provide sufficient details for identification of scientific or common name, the most precise names available in the NCBI database were utilised as common and scientific names.

2.4.3 Data analysis and visualisation

Figures were produced using the R packages ggplot2, ggsankey (38), and igraph (39).

3 Results

3.1 Data records

The final dataset is a .csv. file that includes 2,128 rows and 48 data fields. Each row of the dataset represents one investigated pathogen that was mentioned in a publication along with the results of the investigation in the animal host(s), arthropod or gastropod vector(s), environment, or food matrix(-ices). Furthermore, the final dataset encompasses the NCBI-resolved name of each pathogen, animal host, and arthropod or gastropod vector species, as well as the taxonomic hierarchy of each of these entities, sourced from the NCBI database (Table 1).

Table 1: Field dictionary of the final dataset recording zoonotic pathogens investigated in Austria, 1975–2022. Fields whose names are followed by an asterisk were computed in R.

Field name	Description
ref_id	Unique identifier for each publication.
doi	Digital object identifier of the publication, if available.
permalink	Unique link used by vetmed:seeker for the publication.
ISSN	ISSN of the publication, if available.
pmid	PMID of the publication, if available.
reference	Title of the publication.
author	Authors of the publication.
type_publication	Type of publication: - **article** = article published in a journal; - **thesis** = publication written by students to finish their Magister or Doctorate degree. - **report** = document publishing official data from national surveillance and monitoring programmes.
year_published	Year of publication.
type_study	Type of study: - **original research** = *"publishes full reports of data from research"*; (34); - **case study** = *"reports specific instances of interesting phenomena"* (34); - **national surveillance data** = reports results of national surveillance.
location	Federal state or region where the study was conducted: - AUT = Austria (i. e. national study); - VIE = Vienna; - LA = Lower Austria; - UA = Upper Austria; - SA = Salzburg; - CA = Carinthia; - BU = Burgenland; - ST = Styria; - TY = Tyrol; - VO = Vorarlberg.
year_data_collect	Year(s) when the samples were collected.
type_pathog	Category of the pathogen investigated: - Bacteria; - Virus; - Parasite;

	- Fungi; - Prion; - Other.
pathogen_1	Name of the pathogen, as mentioned in the publication (i. e. not validated against the NCBI database). When several pathogens from the same genus were investigated, only the genus is mentioned.
pathogen_2	Name(s) of the pathogens to the species level, as mentioned in the publication, when several pathogens of the same genus were investigated in the same study and **pathogen_1** provides only genus (names are separated by a semi-colon). **pathogen_2** = **pathogen_1** otherwise.
type_vector	Vectors were categorised as follows: - Tick - Mosquito - Sand fly - Flea - Gastropod
sci_name_vector_1	Scientific name of the vector, as mentioned in the publication (i. e. not validated against the NCBI database). When several vectors from the same genus were investigated, only the genus was mentioned.
sci_name_vector_2	Scientific names of the vector to the (sub-)species level, as mentioned in the publication, when several vectors of the same genus were investigated in the same study and **sci_name_vector_1** provides only genus. **sci_name_vector_2** = **sci_name_vector_1** otherwise.
prev_vector	- positive = the pathogen was evidenced through direct or indirect testing methods; - negative = the pathogen was not evidenced through direct or indirect testing methods.
type_host	Category of host investigated: - human; - companion animal = domesticated animal possessed by a person for reasons other than food or resource production (cat, dog, horse), exotic companion animals, domesticated small rodents - livestock = domesticated animal kept for resource and food production - wildlife = defined as free-ranging or captive wild animal species that are not domesticated
name_host	Common name of host, as provided by the publication.
sci_name_anim_host	Scientific name of the host, as provided by the publication.
prev_anim_host	- positive = the pathogen was evidenced through direct testing method; - seropositive: the pathogen was evidenced through indirect testing method; - positive and seropositive = the pathogen was evidenced through indirect and direct testing methods; - negative = the pathogen was not evidenced through direct or indirect testing methods.
type_env	Environmental matrix investigated in the study.
prev_env	- positive = the pathogen was evidenced through direct or indirect testing methods; - negative = the pathogen was not Taxonomic through direct or indirect testing methods.
type_food_1	Source of the food product investigated (i. e. animal species or plant-based).
type_food_2	Specific description of the food product investigated.
prev_food	- positive = the pathogen was evidenced through direct or indirect testing methods; - negative = the pathogen was not evidenced through direct or indirect testing methods.
imported	When the article mentions the possibility that the pathogen has beeng imported into Austria: - no = the possibility is excluded by the authors; - yes = the authors evidenced that the pathogen was imported; - possible = the authors mention the possibility that the pathogen has been imported (but did not have evidence); - not sure = the authors are uncertain about whether the pathogen has been imported, although there is evidence supporting this hypothesis.
imported_country	The name of the country from which the pathogen was (potentially) introduced.
emerging	The authors mention the pathogen as emerging in Austria: - first discovered = the study reports the first description of the pathogen in Austria, or the first description of the pathogen in a specific Austrian animal species or vector. - first autochthonous = the study reports the first instance of a locally acquired infection with the pathogen in Austria. - first human case = the study reports the first human infection with the pathogen in Austria.

profession_risk	Profession(s) at higher risk of infection with the pathogen, as mentioned by the authors.
pathogen*	Name of the pathogen, as mentioned in the publication. Only one name per row.
ncbi_host_sci*	NCBI.resolved scientific name of the host, validated against the NBCI Taxonomy database.
ncbi_host_comm*	NCBI.resolved common name of the host, validated against the NCBI Taxonomy database.
class_host*	Class of the host, as retrieved from the NBCI Taxonomy database.
order_host*	Taxonomic order of the host, as retrieved from the NBCI Taxonomy database.
family_host*	Taxonomic family of the host, as retrieved from the NBCI Taxonomy database.
genus_host*	Genus of the host, as retrieved from the NBCI Taxonomy database.
ncbi_pathog*	NCBI-resolved names of the pathogen, validated against the NBCI Taxonomy database.
superkingdom_pathog*	Superkingdom of the pathogen, as retrieved from the NBCI Taxonomy database.
order_pathog*	Taxonomic order of the pathogen, as retrieved from the NBCI Taxonomy database.
family_pathog*	Taxonomic family of the pathogen, as retrieved from the NBCI Taxonomy database.
genus_pathog*	Genus of the pathogen, as retrieved from the NBCI Taxonomy database.
ncbi_vector*	NCBI-resolved scientific name of the vector, validated against the NBCI Taxonomy database.
order_vector*	Taxonomic order of the vector, as retrieved from the NBCI Taxonomy database.
family_vector*	Taxonomic family of the vector retrieved from the NBCI Taxonomy database.
genus_vector*	Genus of the vector retrieved from the NBCI Taxonomy database.

3.2 Selected publications

A total of 2,134 publications were identified through electronic database searches. In addition, 52 publications by AGES were included, as well as 17 publications found in excluded review articles. After removing duplicate entries, 1,661 publications titles, and abstracts were screened, of which 246 were ultimately included in this review (Figure 1), including 185 original research papers (74.6 %), 39 case studies (15.7 %), and 24 national surveillance reports (9.7 %). Of those 246 publications, 68.3 % (n = 168) were articles, 26.4 % (n = 65) thesis, and 5.3 % (n = 13) reports. Almost three-quarters (74.6 %) of the publications conducted active research.

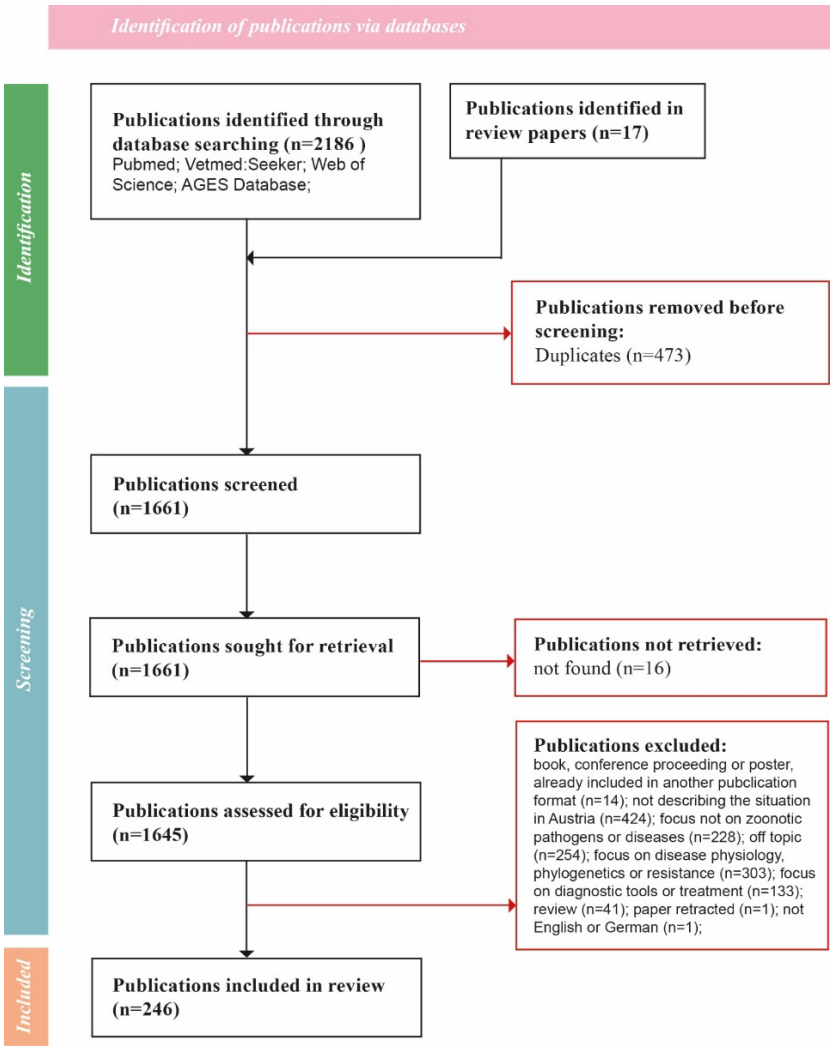


Figure 1: Workflow used in this study for literature search and paper selection (n = number of publications).

3.2.1 Timing of publications

All publications included were published between January 1975 and August 2022. There has been a more than 17-fold increase (17.8-fold) in the number of publications on zoonoses in Austria between the first (1975–1997) and the second half (1998–2022) of the study period, with 2017 exhibiting the highest number of articles being published (n = 20) (Figure 2). To provide context for the increase in publications it was compared with global data: a PubMed search using the terms (zoono* OR "zoono* disease*") from 1975 until 23 August 2022 (without restricting the search to Austria) generated a total of 64,282 results, revealed an increase of the same order (18-fold).

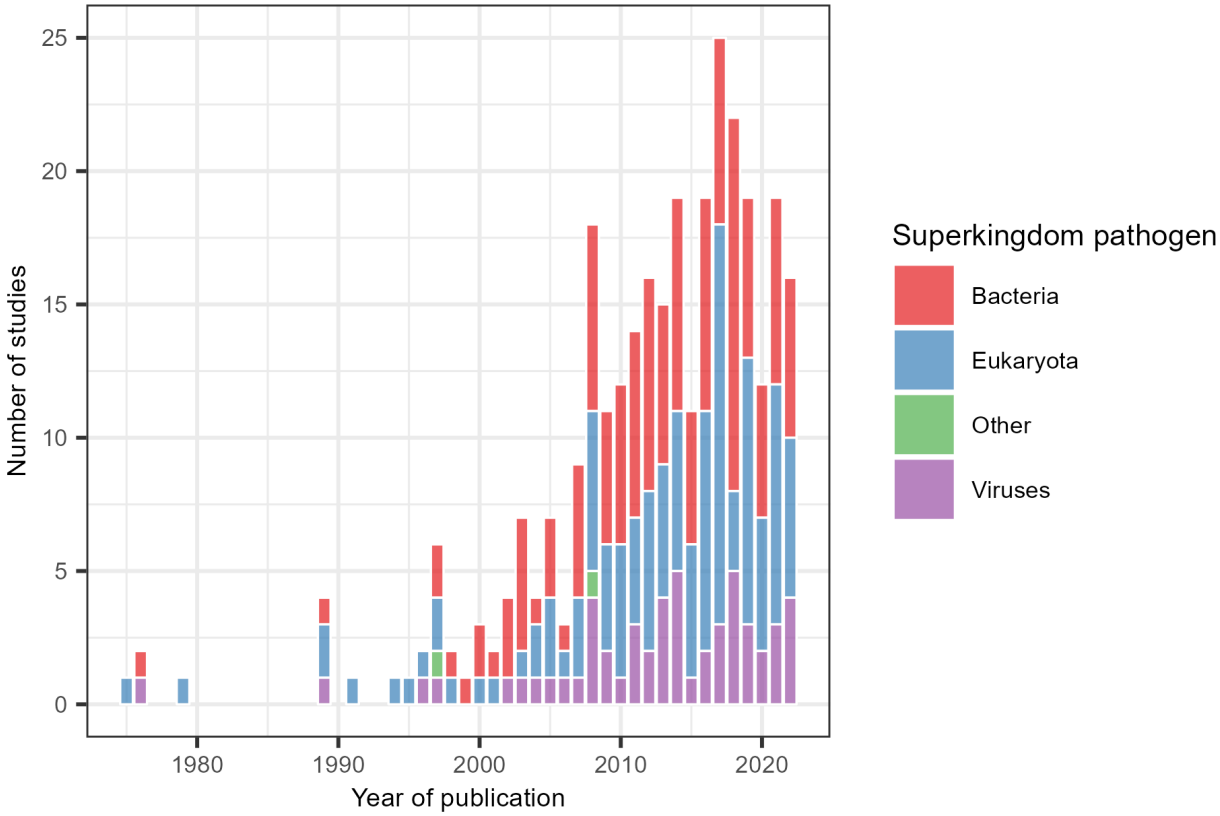


Figure 2 Stacked chart of the annual number of published studies that investigated zoonotic pathogens in Austria between January 1975 and August 2022 and types of pathogens.

3.2.2 Location of the studies

Twenty-three publications (9.4 %) explored zoonotic diseases in multiple countries including Austria, often focusing on cross-border research within a European context.

Nationwide studies accounted for 11.4 % (n = 45) of the selected publications. The highest number of publications (n = 68, 17.3 %) were carried out in Lower Austria, and the lowest number in Carinthia (n = 12, 3 %) (Figure 3). Information about the exact location of the study was missing in 47 publications (coded as “NA” in the dataset). The data revealed fluctuating levels of interest in the types of investigated pathogens, depending on the federal state. The highest difference was observed with viral pathogens; specifically, Vorarlberg exhibited the lowest percentage of publications discussing viral pathogens with 3 % of the studies conducted in this federal state addressing viruses. In contrast, 33 % of studies conducted in Lower Austria discussed viral pathogens (Figure 3). Note that each publication may have investigated one or more than one pathogen in one or more than one federal state.

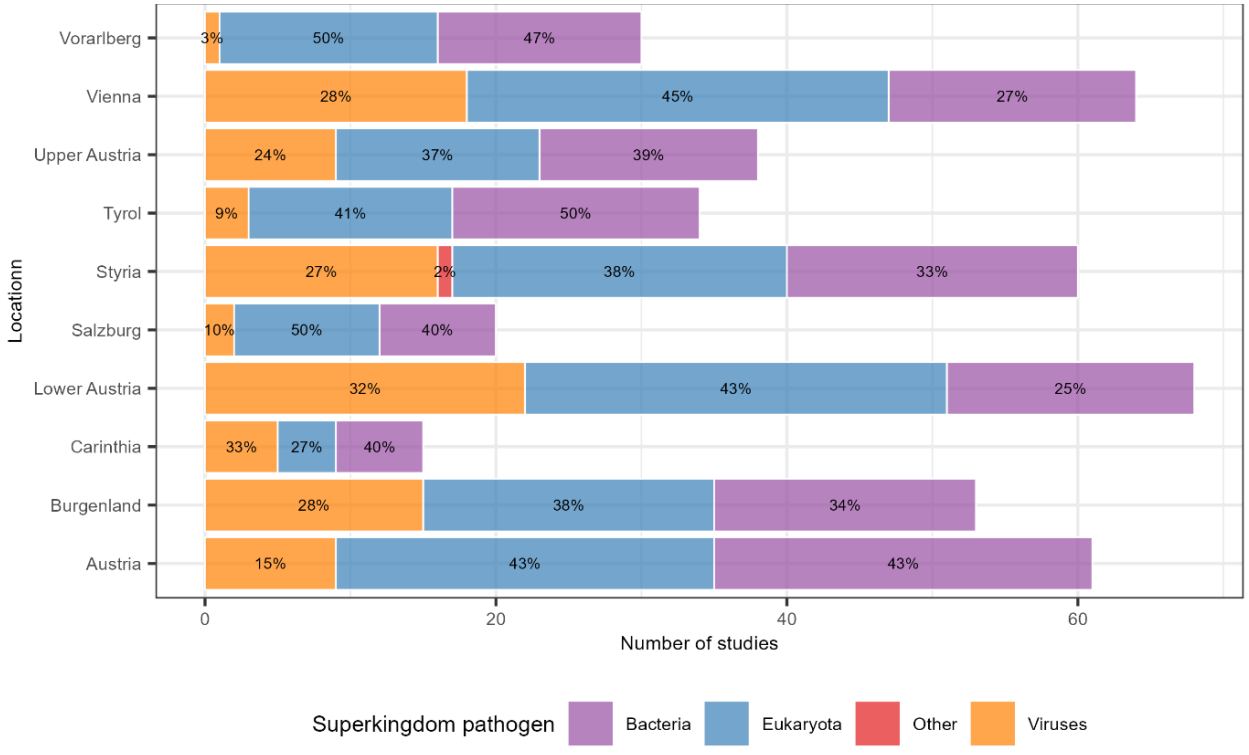


Figure 3: Number of publications on zoonotic diseases per Austrian federal state, Austria, 1975–2022. Studies conducted at a national scale are represented under “Austria”. The percentage of publications per type of pathogen within each federal state is indicated. Publications that did not specify the federal state (e. g. mentioning “eastern Austria”, “west Austria”, “south western Austria”, “south eastern Austria”, or “northern limestone alps”) are not represented. One publication may investigate one or more than one pathogen in one or more than one location.

3.3 Zoonotic pathogens and investigated compartments

3.3.1 Zoonotic Pathogens

Between 1975 and 2022, 228 unique zoonotic pathogens were investigated in Austria. Among them, the majority were bacteria (n = 115 investigated pathogens, 50.4 %), followed by Eukaryota (parasites and fungi) (n = 71, 31.1 %), viruses (n = 40, 17.5 %), and one article (0.4 %) mentioned dog hair as a zoonotic agent. No publications on zoonotic prions were retrieved. One study may investigate one or more than one type of pathogens.

In the second half of the study period, the proportions of the different types of pathogens remained relatively consistent over time (Table 2).

Table 2: Summary statistics of the relative annual proportion (percentage) of each pathogen type over the second half of the study period (1998–2022). Minimum, maximum, mean, median percentage, and interquartile range (IQR).

Superkingdom pathogen	Minimum	Maximum	Mean	Median	IQR
Bacteria	25	100	49.6	45.5	11.1
Eukaryota	0	60	35.4	37	14.1
Viruses	0	33.3	15.5	15.7	12.2
Other	0	5.6	0.4	0	0

A set of ten zoonotic pathogen genera collectively account for ~ 40 % of the selected literature: *Salmonella* (n = 37, 5.8 % of the selected articles), *Escherichia* (30, 4.7 %), *Listeria* (28, 4.4 %), *Echinococcus* (27, 4.2 %), *Orthoflavivirus* (26, 4.1 %), *Brucella* (25, 3.9 %), *Toxoplasma* (24, 3.8 %), *Campylobacter* (n = 23, 3.6 %), *Trichinella* (22, 3.4 %), and *Leptospira* (21, 3.3 %).

Out of 228 unique zoonotic pathogens investigated, 198 (86.8 %) were evidenced (Figure 4). Among them, 190 (96.0 %) were detected in 125 different animal hosts (including humans), 26 (13.1 %) pathogens were detected in 12 different invertebrate (vector) species, 21 (10.6 %) pathogens were detected in 32 categories of food, and twelve (6.1 %) pathogens were detected in six types of environmental media (some pathogens have been evidenced in more than one compartment).

Certain pathogens exhibited concentrated areas of research interest. West Nile virus garnered the most attention in Vienna (n = 14), Lower Austria (n = 10), Styria (n = 7), Burgenland (n = 6)

and Upper Austria (n = 4). Notably, there was only one study that encompassed the entirety of Austria, and no investigations specifically targeted WNV in Tyrol and Vorarlberg. Similarly, Usutu Virus (USUV) predominantly underwent investigations in the eastern part of Austria: Lower Austria (n = 12), Vienna (n = 12), Styria (n = 7), and Burgenland (n = 4). Conversely, *Mycobacterium tuberculosis* variant *caprae* was studied across Austria (n = 11 national studies) and there was a pronounced emphasis on research in Tyrol (n = 7) and Vorarlberg (n = 6).

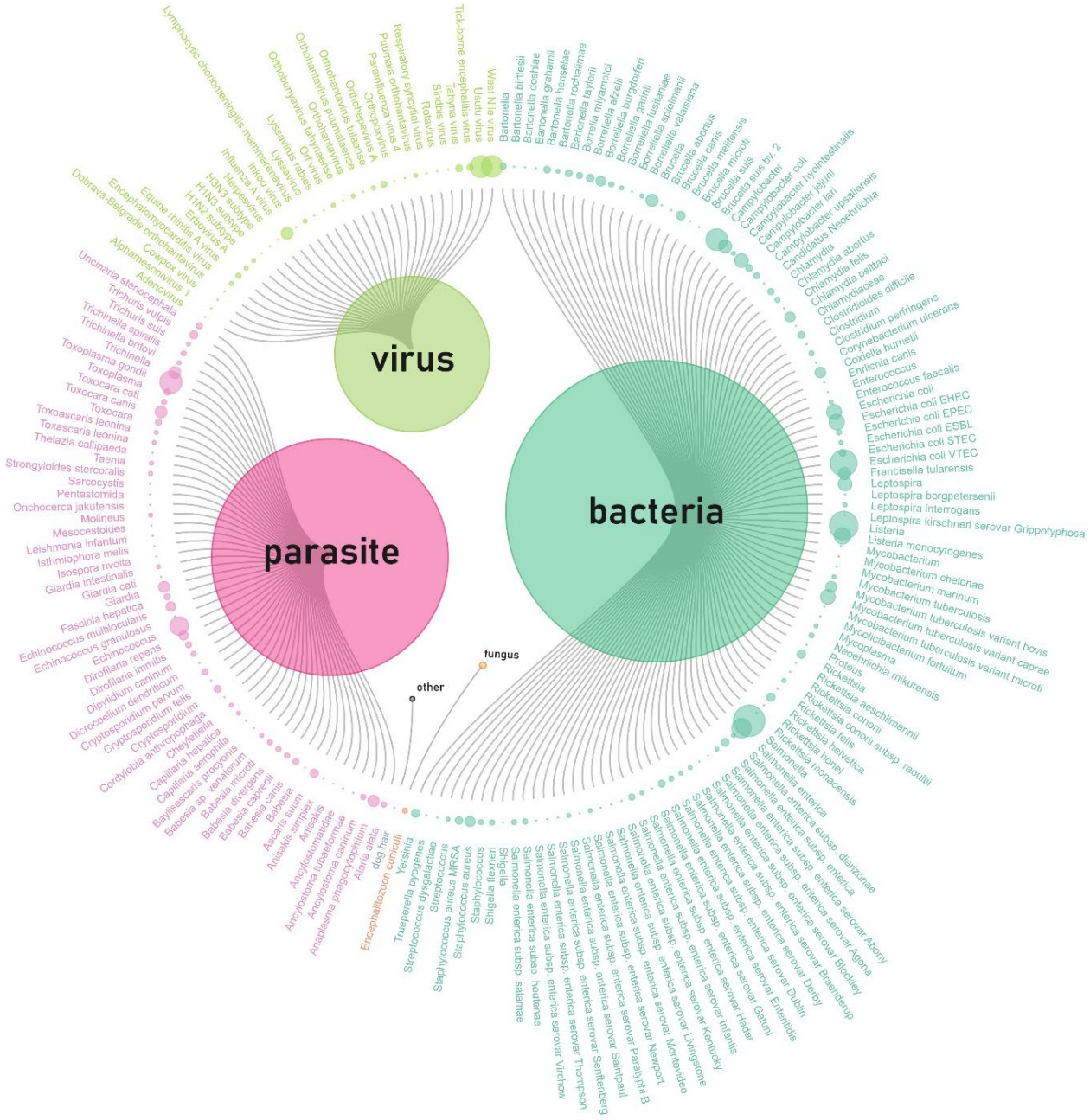


Figure 4: Evidenced zoonotic pathogens, Austria, 1975–2022. The colours correspond to the pathogen type (bacteria = turquoise, virus = green, parasite = pink, fungi = orange, other = blue); node size represents the number of times a pathogen was evidenced (and results published) between 1975 and 2022. All pathogen names are resolved against the NCBI Taxonomy database, when this was not possible the description of the pathogen as mentioned in the publication was used.

3.3.2 Animal hosts

Most zoonotic pathogens were investigated in wildlife hosts (n = 91 publications, 33.3 % of all selected publications), followed by humans (n = 71, 26 %), companion animals (n = 59, 21.6 %), and livestock (n = 52, 19 %). One publication may have investigated more than one type of host.

Wildlife hosts demonstrated the highest level of diversity, with 174 NCBI-resolved species investigated for zoonotic pathogens. Among all the wildlife species studied, birds constituted the majority at 77 % (134 species), spread across 20 publications, while mammals comprised 22.4 % (39 species) and were distributed across 73 publications. Additionally, fish accounted for a mere 0.6 % of the total. The primary species of interest within wildlife studies were the red fox (n = 17; 5 % of the 91 publications investigating wildlife), the red deer (n = 12, 3.5 %), and the wild boar (n = 12, 3.5 %).

Out of the 38 species examined as companion animals, the most frequently discussed ones were dogs (n = 28 publications, 29.2 % of the 59 publications related to companion animals), cats (n = 21 publications, 21.9 %), and horses (n = 8 publications, 8.3 %). The remaining species were mentioned only once or twice and encompass exotic pets such as different types of snakes, lizards, turtles, and rabbits.

A total of 13 species were examined within the category of livestock animals. The most extensively studied among these were cattle (n = 26, 21.5 % of the 52 publications investigating livestock), chickens (n = 19, 15.7 %), and pigs (n = 18, 14.9 %). Interestingly, there were cases where a single animal species could be considered as livestock in one study and classified as wildlife in another (for instance, *Anas platyrhynchos* was mentioned both as a wildlife and a livestock species). Furthermore, while lamas and alpacas were mentioned individually once, some publications discussed "new world camelids" collectively, treating them as a single, unspecified species.

Out of the 220 distinct NCBI-resolved animal host species (including human) that were investigated for zoonotic pathogens in Austria between 1975 and 2022, 125 of them were identified as having tested positive for either harbouring zoonotic pathogens or possessing antibodies against such pathogens (Table 3). Primates, Artiodactyla, and Carnivora exhibited the highest zoonotic potential, harbouring a wide range of zoonotic pathogens. Orthoflaviviruses were mostly found in birds and Perissodactyla (i. e. equids) (Figure 5). In

Figure 5, primates generally refer to humans. Most zoonotic pathogens are multi-host pathogens, affecting diverse animal species across taxonomic orders.



Figure 5: Bubble plot illustrating the distribution of the zoonotic pathogen genera across Austrian animal hosts, grouped by taxonomic order, 1975–2022. Only positive results are shown (seropositive or positive). Node size corresponds to the frequency with which a particular pathogen was detected within a specific taxonomic order during this timeframe. Colours correspond to pathogen type.

Table 3: List of animal hosts) that have been found (sero)positive for at least one zoonotic pathogen in Austria, 1975–2022.

Type of host	NCBI-resolved scientific name	NCBI-resolved common name
Companion animal	*Canis lupus familiaris*	dog
	Equus caballus	horse
	Felis catus	domestic cat
	Testudines	turtles
	Testudinidae	tortoises
	lizard (unspecified)	lizard (unspecified)
	Serpentes	snakes
	Oryctolagus cuniculus	rabbit
Human	*Homo sapiens*	human
Livestock	*new-world camelid (unspecified)*	new-world camelid (unspecified)
	Bos taurus	cattle
	Ovis aries	sheep
	Gallus gallus	chicken
	Capra hircus	goat
	Lama glama	llama
	Sus scrofa	pig
	Meleagris gallopavo	turkey
Wildlife	*Apodemus agrarius*	Eurasian field mouse
	Procyon lotor	raccoon
	Capreolus capreolus	western roe deer
	Cervus elaphus	red deer
	Ovis aries musimon	mouflon
	Salmo trutta fario	river trout
	Rattus norvegicus	Norway rat
	Turdus merula	blackbird
	Turdus philomelos	song thrush
	Passer domesticus	house sparrow
	Cyanistes caeruleus	blue tit
	Panurus biarmicus	bearded reedling
	Macaca fuscata	Japanese macaque
	Vulpes vulpes	red fox
	Accipiter gentilis	northern goshawk
	Falco	falcons
	Sus scrofa	pig
	Capra ibex	alpine ibex
	Nyctereutes procyonoides	raccoon dog
	Nestor notabilis	kea
	Columbiformes	pigeons and others
	Accipitriformes	hawks and eagles
	Falconiformes	falcons and others
	Passeriformes	song birds
	Anatidae	waterfowl
	Strigiformes	owls
	Charadriiformes	shorebirds and others
	Gruiformes	terrestrial and marshbirds
	Cuculiformes	cuckoos and others
	Piciformes	woodpeckers and others
	Cygnus olor	mute swan
	Falco tinnunculus	common kestrel
	Corvus corone	carrion crow
	Galliformes	landfowls
	Ciconiiformes	storks and others
	Apus apus	common swift
	Coraciiformes	kingfisher
	Corvus frugilegus	rook
	Marmota marmota	European marmot
	Rupicapra rupicapra	chamois
	Dama dama	fallow deer
	Castor fiber	Eurasian beaver
	Apodemus sylvaticus	European woodmouse
	Apodemus flavicollis	yellow-necked field mouse
	Myodes glareolus	Bank vole

	Microtus arvalis	common vole
	Gypaetus barbatus	lammergeier
	Bubo scandiacus	snowy owl
	Strix uralensis	Ural owl
	Ciconia ciconia	white stork
	Neophron percnopterus	Egyptian vulture
	Bubo bubo	Eurasian eagle-owl
	Falco rusticolus	gyrfalcon
	Gallus gallus	chicken
	Anser anser	domestic goose
	Buteo buteo	common buzzard
	Aquila chrysaetos	golden eagle
	Bos taurus	cattle
	Arvicola amphibius	Eurasian water vole
	Parus major	great Tit
	Sitta europaea	wood nuthatch
	Erithacus rubecula	European robin
	Macaca sylvanus	barbary ape
	Pongo pygmaeus	Bornean orangutan
	Lepus europaeus	European hare
	Vulpes	vulpes
	Erinaceus europaeus	western European hedgehog
	Cygnus	swans
	Anas platyrhynchos	mallard
	Anser sp.	goose
	Fulica	coots
	Ardeidae	herons
	Lepus timidus	mountain hare
	Aegypius monachus	cinereous vulture
	Aquila heliaca	eastern imperial eagle
	Accipiter nisus	Eurasian sparrowhawk
	Pernis apivorus	European honey-buzzard
	Aquila nipalensis	steppe eagle
	Circus aeruginosus	western marsh harrier
	Haliaeetus albicilla	white-tailed eagle
	Ciconia nigra	black stork
	Athene noctua	little owl
	Asio otus	long-eared owl
	Pica pica	Eurasian magpie
	Corvus cornix	hooded crow
	Coloeus monedula	jackdaw
	Mus musculus	house mouse
	Fulica atra	eurasian coot
	Anas	ducks
	Anserinae	goose
	Laridae	gulls
	Cervidae	deer
	Lepus	hares
	Phasianinae	phasianinae
	Sylvia atricapilla	blackcap
	Streptopelia decaocto	Eurasian collared-dove
	Dendrocopos major	great spotted woodpecker
	Strix aluco	tawny owl
	Garrulus glandarius	Eurasian jay
	Acrocephalus scirpaceus	Eurasian reed warbler
	Hirundo rustica	barn swallow
	Curruca curruca	lesser whitethroat
	Phasianus colchicus	ring-necked pheasant
	Emberiza schoeniclus	reed bunting
	Curruca communis	greater whitethroat
	Tyto alba	barn owl
	Phoenicurus ochruros	black redstart
	Sylvia borin	garden warbler
	Delichon urbicum	Northern house-martin
	Pavo cristatus	Indian peafowl
	Strix nebulosa	great grey owl

3.3.3 Food products

A total of 30 publications investigated food products. These products originated from 23 different sources, encompassing plant-based foods (n = 9, representing 5.6 % of all types of food investigated) and animal source foods (n = 21), such as livestock- and horse-derived food (65.6 % of the studies investigating food products), game-derived food products (13.8 %), and marine products (e. g. herring, mackerel, salmon, trout, 3.1 %). Only one publication investigated a bee product (i. e. honey) brought to Austria from Turkey and Egypt via Vienna international airport for *Listeria monocytogenes*, *Salmonella*, *Campylobacter,* and *Escherichia coli* but it was found negative.

In many publications, the animal origin of the investigated food was unspecified (n = 18, 11.2 %). The food derived from cattle sources was the most investigated (n = 15, 9.4 %), followed by food from swine origin (n = 14, 8.8 %). Overall, 32 different food products were investigated for zoonotic pathogens in Austria over the study period. For analytical purposes, categories of food products designating the same type of food were grouped. For example, “kebab”, “ground meat”, or “rillettes” were coded as “meat and meat product”; “milk” and “milk product” were coded as “dairy”; “egg” and “egg product” were coded as “egg”; “fish”, “fish filet”, or “rollmops” were coded as “marine product”; “salad”, “spices”, “fruit”, or “vegetable” were coded as “plant-based food”. A category for “cheese” (e. g., mozzarella, brie, Roquefort) and “sausage” (e. g., ham, salami, raw meat sausage) was also added for more accurate representation.

Zoonotic pathogens´ genera identified in food were mainly *Listeria* (33.7 % of evidenced pathogens in food), *Escherichia* (8.8 %), and *Salmonella* (22.9 %). Out of the 21 identified pathogens in food, all were bacteria except for three parasites (*Anisakis*, *Echinococcus*, and *Trichinella spiralis*). The categories of food that yielded most positive results were “meat and meat products” (45.9 %). While studies focusing on plant-based foods comprised only 6.9 % of the total food products found positive (Figure 6).

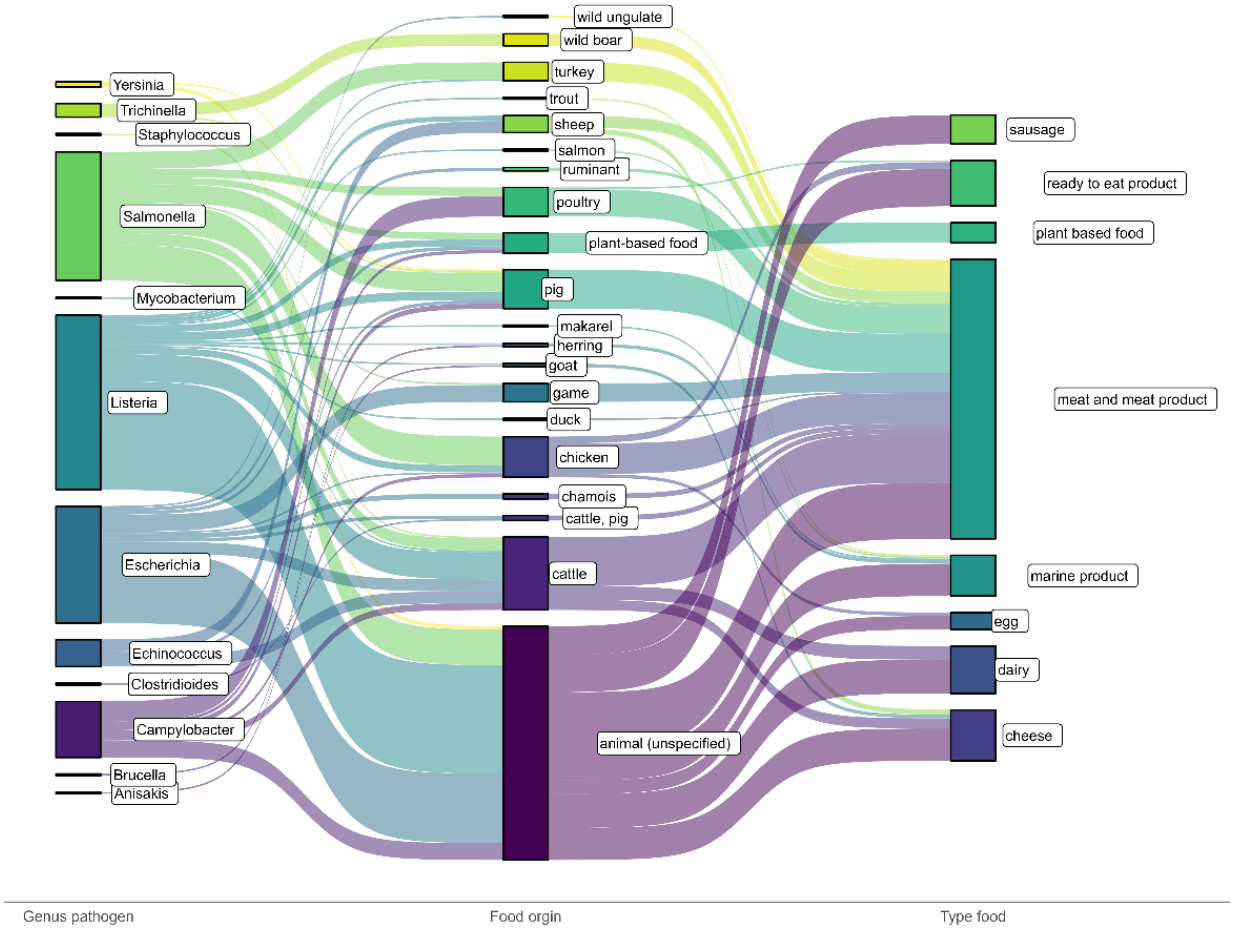


Figure 6:Sankey graph of the zoonotic pathogens found in Austria in food products, 1975–2022. The zoonotic pathogens´ NCBI-resolved genera are shown on the first axis, the food origin is displayed on the middle axis, and the food category is specified on the right axis. The height of each bar is proportional to the number of times a zoonotic pathogen was found.

3.3.4 Environment: invertebrates and environmental media

Across the selected publication, 21 invertebrate species were investigated as vectors of zoonotic pathogens. Vectors included mosquitos (n = 11 publications, 47.8 % of the studies investigating vectors), ticks (n = 9, 39.1 %), sand flies, gastropods, and fleas (n = 1, 4.3 %, each). Mosquitos showed the highest taxonomic diversity, dominated by the genera *Culex* (n = 10 studies), *Aedes* (n = 7), and *Anopheles* (n = 7).

Twenty-six unique zoonotic pathogens were investigated in vectors, among them, bacteria belonging to the genus *Rickettsia* were the most represented (n = 9 publications, 23 % of the publications investigating vectors), followed by viruses from the family Orthoflavivirus (n = 6, 15.4 %), and parasites belonging to the genus *Dirofilaria* (n = 4, 10.3 %). Twelve vectors were

found to be carriers of zoonotic pathogens (some names could not be resolved to species level due to lack of information in the source) (Table 4).

Table 4: Zoonotic pathogens evidenced in invertebrate vectors, Austria, 1975–2022.

Vector´s NCBI-resolved name	Zoonotic pathogen´s NCBI-resolved name
Aedes vexans	Orthobunyavirus tahynaense
Ctenocephalides felis	*Bartonella henselae; Rickettsia felis*
Culex	Orthobunyavirus tahynaense*; West Nile virus*
Culex pipiens	*Usutu virus; West Nile virus*
Dermacentor reticulatus	*Bartonella; Francisella tularensis; Rickettsia conorii* subsp. *raoultii; Rickettsia helvetica*
Haemaphysalis concinna	*Bartonella*
Haemaphysalis inermis	*Bartonella; Rickettsia helvetica*
Hyalomma	*Rickettsia*
Hyalomma marginatum	*Rickettsia aeschlimannii*
Ixodes sp.	*Rickettsia helvetica*
Ixodes ricinus	*Anaplasma phagocytophilum; Babesia divergens; Babesia microti; Babesia sp. venatorum; Bartonella; Borrelia miyamotoi; Borreliella afzelii; Borreliella burgdorferi; Borreliella garinii; Borreliella lusitaniae; Borreliella spielmanii; Borreliella valaisiana; Neoehrlichia mikurensis; Rickettsia; Rickettsia helvetica; Rickettsia monacensis*
Uranotaenia unguiculata	Alphamesonivirus 1

Eight distinct environmental matrices were investigated for the presence of zoonotic pathogens (representing nine of the selected publications). Six environmental matrices were found positive with foodborne pathogens (*Listeria monocytogenes*, *Salmonella*, *Escherichia coli*), parasites (*Cryptosporidium*; *Giardia*, *Toxocara*), and *Mycobacterium*. Investigated environmental media included public spaces, surfaces and tools in food processing environments, and natural matrices (Table 5).

Table 5: Zoonotic pathogens evidenced in environmental media, Austria, 1975–2022.

Type of environment	Zoonotic pathogen´s NCBI-resolved name
food processing plant	*Listeria monocytogenes*
meat processing plant	*Salmonella; Salmonella enterica* subsp. *enterica* serovar *Braenderup; Salmonella enterica subsp. enterica* serovar *Infantis; Salmonella enterica subsp. enterica serovar Livingstone*

public lavatory	*Listeria monocytogenes*
sandbox	*Toxocara*
slaughter knife	*Escherichia coli* EHEC*; Escherichia coli* EPEC*; Escherichia coli* VTEC
water	*Cryptosporidium; Giardia; Mycobacterium*

3.3.5 Describing the zoonotic interfaces in Austria

The various interfaces where zoonotic diseases could occur in Austria, as characterised between 1975 and 2022, can be represented using a network that illustrates the connections among zoonotic pathogens, hosts, vectors, food sources, and environmental matrices (Figure 7). The zoonotic risk was extensively studied for humans and food-borne pathogens, with most of the publications investigating food-borne pathogens focusing on *Salmonella, Campylobacter, Listeria,* and *Escherichia*. This demonstrates the scientific significance and the critical importance of understanding the spillover risk at the interfaces between humans and animal-derived food.

The network analysis reveals that the node *human* is relatively central in the network, exhibiting extensive connections to various zoonotic pathogens. Likewise, *cattle, dog, domestic cat, red fox,* and *pig* are influential nodes within the network, suggesting significant zoonotic potential.

Furthermore, nodes representing zoonotic pathogens such as *Salmonella, Escherichia, Listeria*, and, to a lesser extent, *Chlamydia, Bartonella*, and *Staphylococcus*, exhibit numerous hosts, which underscores the broad host range of these pathogens. Furthermore, the interface Orthoflaviviruses-bird hosts was intensively investigated, with WNV and USUV evidenced in numerous bird hosts. The two subsets of nodes representing WNV and USUV and their respective avian hosts provide an example of pathogen-wildlife host interfaces which is only connected to the node *human* by the node representing the vector *Culex*, illustrating the central role of the animal host-mosquito-human interface in the epidemiology of these zoonotic viruses. Similarly, the node representing the tick *Ixodes* plays a central role in the connection of *Rickettsia* species to their hosts.

Figure 8 displays a subgraph of the network presented in Figure 7, specifically highlighting the interfaces of zoonotic pathogens-hosts. The strong connections of domestic and livestock species to zoonotic pathogens in the network indicate a heightened risk to humans when compared to wildlife species.

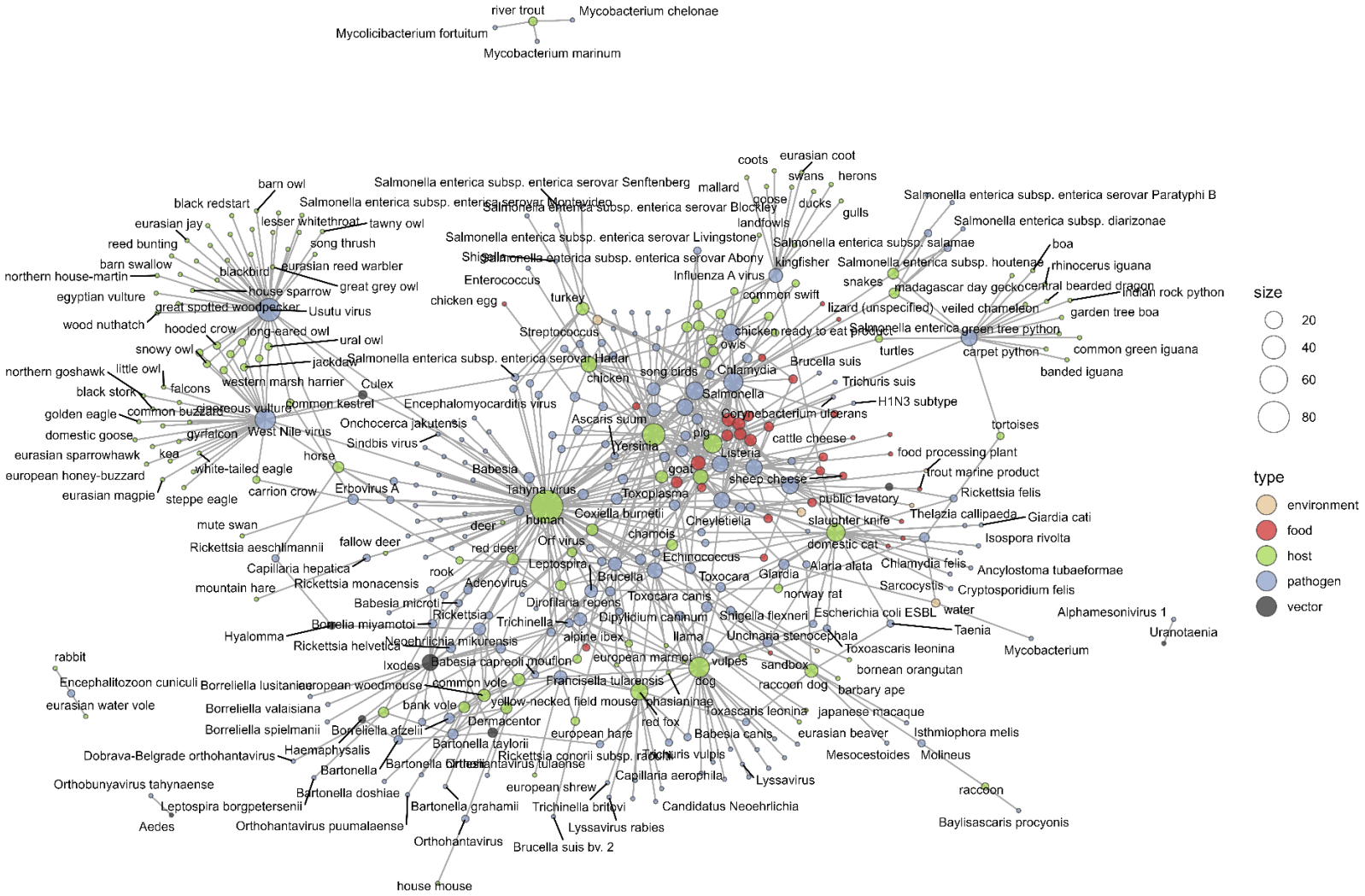


Figure 7: Network of the zoonotic interfaces in Austria, 1975–2022. The network depicts the connections between zoonotic pathogens and their corresponding animal hosts, food, and environmental matrices (including vectors). Size of the node represents the number of study that reported the node as present (for the pathogens) or positive (hosts, vectors, environmental or food matrices).

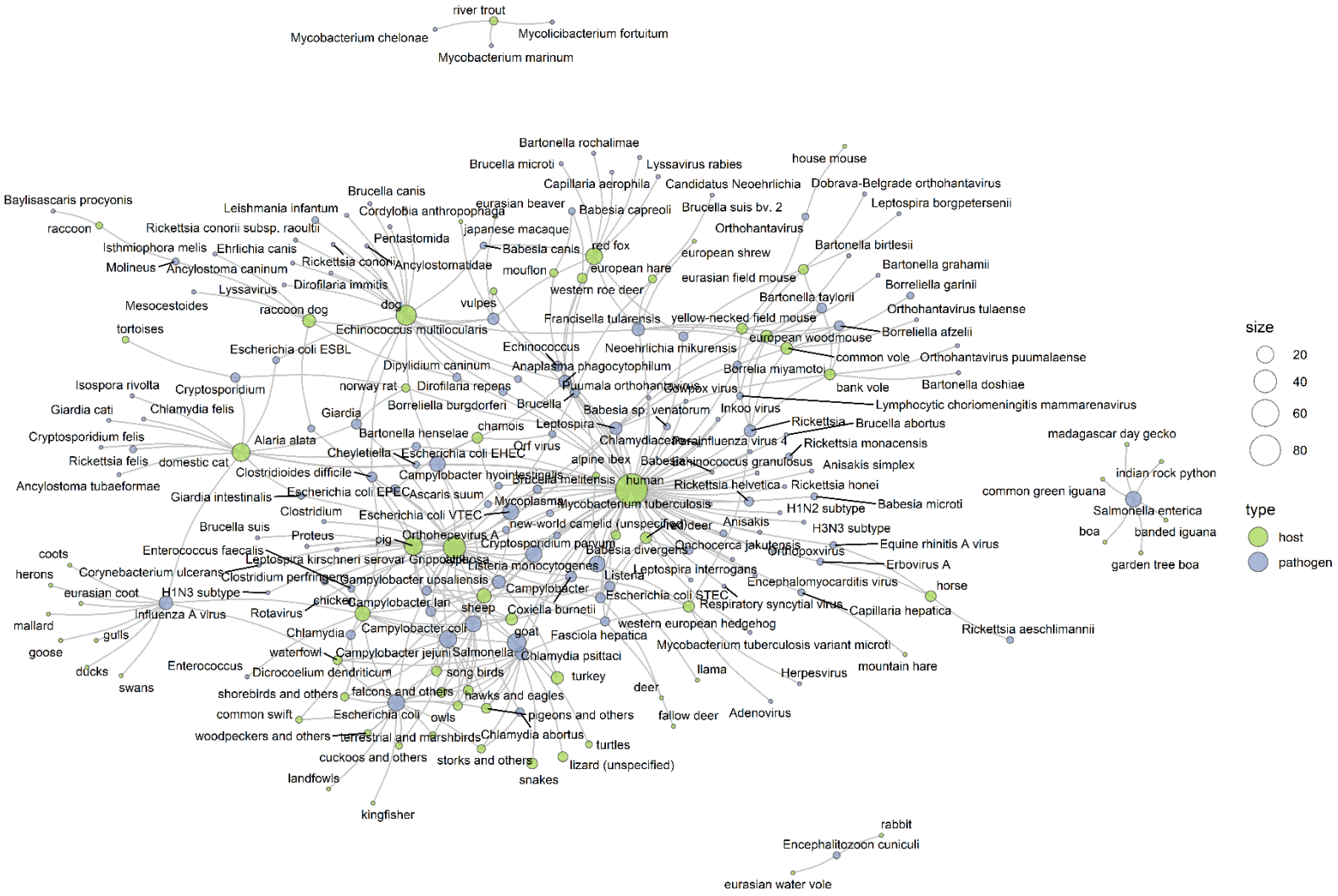


Figure 8: Subgraph of the host-pathogen network in Austria, 1975–2022. The network depicts the direct interactions between zoonotic pathogens and their corresponding animal hosts. Size of the node represents the number of publications that reported the node as present (for the pathogens) or positive (hosts).

3.3.6 Imported zoonotic diseases and pathogens

The publications underwent screening to identify any references to the potential acquisition of pathogens from sources outside of Austria. Among the selected publications, eleven (4.5 %) clearly affirmed that the pathogens were not imported, whereas 14 (5.6 %) either expressed uncertainty about importation or acknowledged the possibility. The presence of zoonotic pathogens that were definitively imported was confirmed in 21 (8.5 %) publications (Table 6).

These imported pathogens were documented as entering through diverse channels, mainly food, but also infected dogs or humans, and in one case, a tick. Notably, a study conducted at the Vienna international airport investigated the prevalence of major foodborne pathogens found in confiscated food and found pathogens in 5 % of samples taken, mainly *Listeria monocytogenes*, *Escherichia Coli* VTEC and *Salmonella*.

Table 6: Zoonotic pathogens with clear evidence of introduction into Austria, 1975–2022.

Zoonotic pathogen´s NCBI-resolved name	**Country of origin**	**Number of times importation was evidenced**
Anisakis simplex	Alaska	1
Babesia microti	USA	1
Brucella	NA	8
Brucella melitensis	NA	2
Cordylobia anthropophaga	Gambia	1
Dirofilaria immitis	USA, Spain, Hungary, Greece	1
Dirofilaria repens	USA, Spain, Hungary, Greece	1
Echinococcus	NA	7
Ehrlichia canis	Greece, Hungary, Spain, Italy, Portugal, France, USA, Asia, Argentina	1
Escherichia coli	Ethiopia, Nigeria, South Africa	1
Escherichia coli	Turkey, Egypt, China, United Arab Emirates, Russia, other	2
***Escherichia coli* VTEC**	Turkey, Egypt, China, United Arab Emirates, Russia, other	2
Leishmania infantum	Greece, Hungary, Spain, Italy, Portugal, Croatia, Africa, Asia	1
Leptospira	South-East Asia, Africa, South America, Central Europe	1

Listeria monocytogenes	Mozambique, China, Turkey, United Arab Emirates, Albania,	1
Listeria monocytogenes	Turkey, Egypt, China, United Arab Emirates, Russia, other	2
Lyssavirus	Serbia	1
Pentastomida	USA	1
Rickettsia aeschlimannii	NA	1
Rickettsia conorii	Greece, Spain, Italy, Africa	1
Salmonella	Ethiopia, Nigeria, South Africa	1
Salmonella	Turkey, Egypt, China, United Arab Emirates, Russia, other	2
Trichinella	Bosnia Herzegovina	1
Trichinella	NA	5
Trichinella spiralis	Bosnia	1
Trichinella spiralis	Poland	1

3.3.7 Emerging pathogens

Nine zoonotic pathogens were described as emerging in Austria (as mentioned in the respective papers) over the period 1975–2022, this includes pathogens first discovered in Austria in certain species, as well as pathogen discoveries described as first autochthonous cases (Table 7).

Table 7: Emerging zoonotic pathogens in Austria, 1975–2022.

Type of emergence	NCBI-resolved pathogen scientific name	Year of publication	Number of times emergence was evidenced
First autochthonous	*Anisakis*	2009	1
First autochthonous	*Thelazia callipaeda*	2019	1
First discovered	*Baylisascaris procyonis*	2021	1
First discovered	*Brucella canis*	2012	1
First discovered	*Rickettsia conorii subsp. raoultii*	2016	1
First discovered	*Rickettsia helvetica*	2008	1
First discovered	West Nile virus	2020	1
First discovery outside of Africa	Usutu virus	2002	3
First human case	*Babesia*	2003	1

3.3.8 Professions at risk

Twenty-five publications specifically mentioned professions that were at a higher risk of contracting zoonotic diseases in Austria over the study period. This included professions that work in close contact with animals (e. g., veterinarians, farmers, hunters, pet shop employees, dog handlers, zoo employees) or animal products, such as workers in food production (e. g., butchers, slaughterhouse workers). Moreover, people working in environments where wildlife is abundant, thus increasing the risk of direct contact with wildlife pathogens or indirect contacts through contaminated environment (e. g., forestry worker, farmers, gardeners, agricultural workers) as well as other professions such as sewer maintenance workers and miners, faced an elevated risk of acquiring zoonotic diseases. Additionally, military personnel stationed overseas were found to have an increased risk of contracting Orthohepevirus A (HEV).

3.4 Trends in scientific interest

Although limited data is available for the period preceding 2000, there has been a noticeable upward trend in the scientific interest in Austria for the three types of zoonotic pathogens, Bacteria, Viruses, and Eukaryota (Figure 9). Notably, bacteria garnered the most attention, exhibiting a marked surge in the quantity of studies conducted throughout the study period.

Similarly, we observed an upward trend across all compartments, as recognised by the traditional One Health triad, i. e., animal, human, and environment (40), since 2000, followed by a subsequent decrease. The environmental aspect was not considered in studies on zoonotic diseases in Austria until 1997. Subsequently, it demonstrated the most gradual increase in scientific interest. Unlike the other compartments, the environmental factor did not display a decline towards the end of the search period (Figure 10).

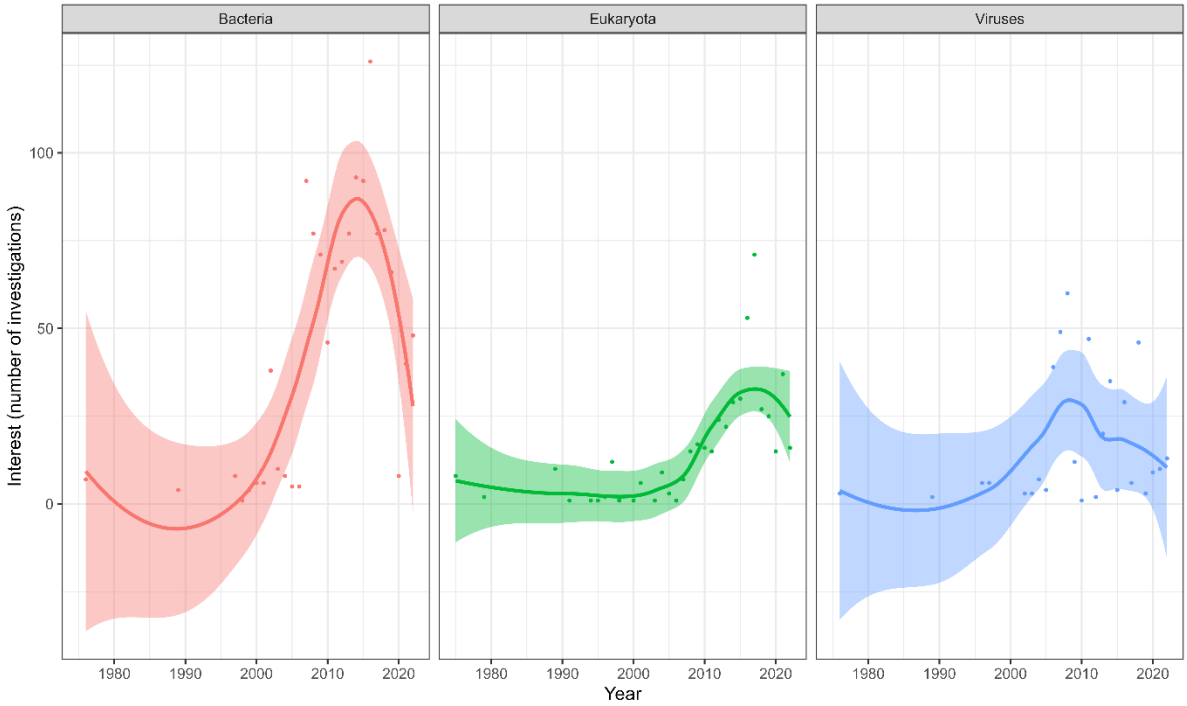


Figure 9: Trend in research interest, as measured by the number of studies involving each type of pathogen (note that a single publication might encompass multiple pathogen types).

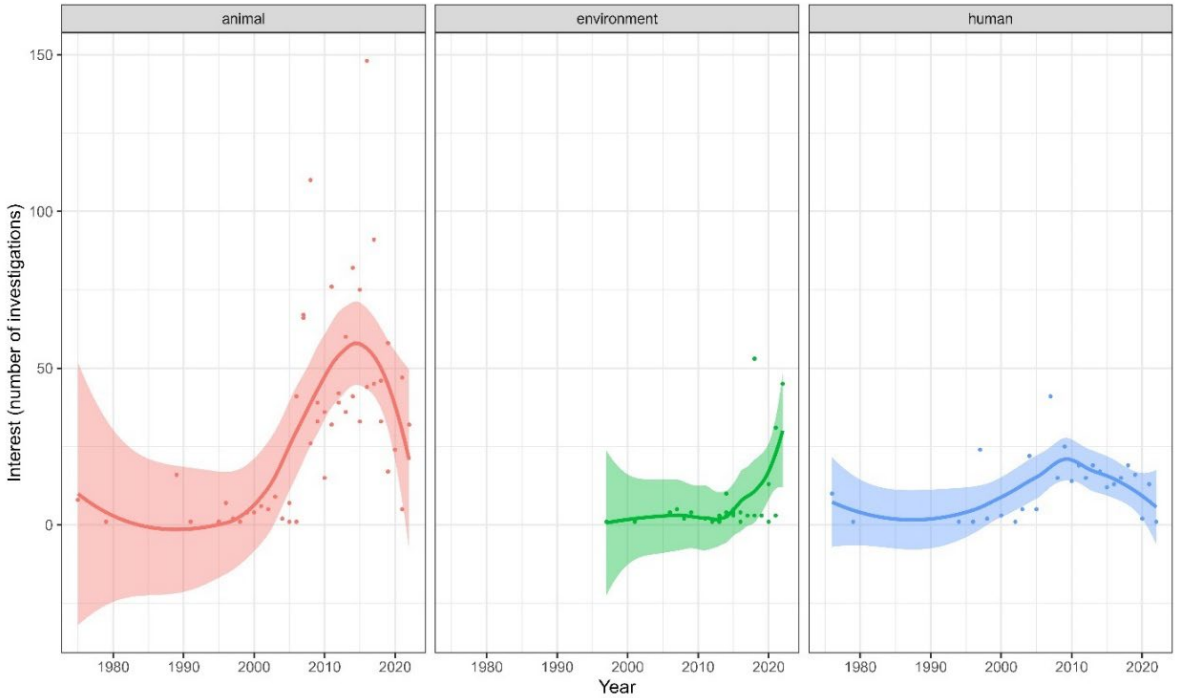


Figure 10: Trend in research interest, as measured by the number of studies involving each compartment, as recognised in the traditional One Health view (note that a single publication might encompass multiple compartment-host associations).

4 Discussion

In this review, 246 publications were identified that investigated zoonotic pathogens in Austria from 1975 to 2022. In this timeframe, the number of publications investigating zoonoses exhibited a substantial 17-fold increase, indicating both the growing scientific curiosity within the Austrian research community regarding this topic and echoing the worldwide trend of heightened research interest in zoonotic pathogens.

The ten most investigated pathogens in Austria between 1975 and 2022 counted for 40 % of the studied zoonotic pathogens and included *Salmonella*, *Escherichia*, *Listeria*, *Echinococcus*, Orthoflavivirus, *Brucella*, *Toxoplasma*, *Campylobacter*, *Trichinella* and *Leptospira.* With the exception of *Toxoplasma,* these pathogens cause notifiable diseases (32), and, according to the Federal Law on the Monitoring of Zoonoses and Zoonotic Pathogens (BGBl. I Nr. 128/2005), seven of them are explicitly subjected to compulsory surveillance and reporting in humans and/or animals (*Toxoplasma,* Orthoflavivirus and *Echinococcus* are subjected to mandatory surveillance based on the epidemiological situation) (25). Of these ten most investigated pathogens, all except for Orthoflaviviruses were featured in the yearly AGES´s zoonoses report, constituting a significant portion of the dataset. Another reason for the considerable scientific interest in these pathogens could be related to the high annual human case numbers. For instance, in 2021, *Campylobacter* was responsible for the most illnesses in Austria, causing 6,019 human cases and it is the most frequently reported foodborne illness in the EU (127,840 cases in 2021). Following closely, *Salmonella* accounted for 1,048 human cases in Austria and 60,050 in the EU (second most common zoonotic disease in the EU) (41). Such significant public health threats often garner funding and research attention.

Interestingly, despite SARS-CoV-2 being a notifiable disease for both humans and animals (28, 42), and notwithstanding the extensive research prompted by the pandemic, none of the COVID-19-related publications concerning human cases refer to it as a zoonotic disease. Likewise, the sole publication investigating SARS-CoV-2 in animals in Austria fails to mention its zoonotic potential (43), and there are no publications reporting SARS-CoV-2 infections in animals within the country.

The federal states in the east of Austria showed a higher number of publications dedicated to viral pathogens compared to western states. This discrepancy can be attributed to the geographical proximity of the Eastern states to Vienna and Mödling, where the University of

Veterinary Medicine and AGES have established their laboratory facilities, respectively. This pattern may also be due to the restricted geographical distribution of WNV and USUV (which account for a substantial portion of the publications included in this review) in this part of the country (44–46). Furthermore, most farms in Austria are located in Lower Austria (24 %), Styria (22 %), and Upper Austria (19 %) (47), which may partly explain the variation in the geographic distribution of included studies.

Findings of this study showed the complexity of the zoonotic pathogen-host-environment-food interfaces in Austria. Notably, it demonstrated that a large amount of zoonotic agents are multi-host pathogens, capable of infecting humans, wildlife, and livestock, with livestock being bridge hosts between wildlife and humans (5, 48). This interface encompasses the shared environments, especially “ecotones” (i. e., edges between human and natural landscapes) (49), common grazing pastures, and water points (50). In Austria, a significant example of a spillover event from wildlife to livestock that has the potential to pose a risk to human health is the case involving red deer, cattle, and *Mycobacterium tuberculosis* variant *caprae* in the Tyrol and Vorarlberg regions (51). The control programme to reduce the risk of human infection involves hunting of red deer and subsequent examination for tuberculosis-typical changes as well as regular tuberculin-tests in cattle (30).

Major changes in land-use globally have resulted in the dramatic expansion of the human-wildlife interfaces, with humans encroaching on the habitats of wild animals (52), further increasing the risk of wildlife-to-human (and reciprocally) spillover events (53, 9). Awareness of these risks is reflected in Austria through the emphasis placed on research related to zoonotic diseases in wildlife hosts. Indeed, wildlife was identified as the most extensively studied group, comprising 33.3 % of the investigations, including a broad range of species (174 species) across 31 taxonomic orders over the study period, with zoonotic pathogens evidenced among 26 orders. The publications focused mainly on the red fox, wild boar, and red deer. Red foxes are an important bridge in the wildlife-human and wildlife-companion animal interfaces, they are a widely distributed species that thrive in rural as well as urban environments, such as Vienna, and can carry many relevant zoonotic pathogens (54, 55). Red deer and wild boars are part of the most hunted and consumed furred game species (56), additionally, more than 2,000 agricultural operations keep red deer as farm game (47). Therefore, interfaces involving red fox, wild boar, and red deer in Austria potentially represent an important risk for zoonotic disease transmission to humans. Notably, in Austria, wild boars are included in a surveillance

programme for *Trichinella*, integrated into official meat inspection procedures, which also includes pigs and horses (57).

While companion animals comprise 38 investigated species, dogs, cats, and horses are the most investigated ones, probably due to the range of zoonotic pathogens they can carry,their popularity in the population (58), and their close contact with humans. Companion animals may act as a reservoir of zoonotic pathogens (e. g., dog and *Dirofilaria repens* and *Dirofilaria immitis)* (61). They may also act as a bridge between wildlife hosts and humans, e. g. in the system horses/wild birds/humans and the vector-borne diseases WNV and USUV (62). All exotic pet species investigated in the selected publications (e. g., *Testudo hermanni*, *Boa constrictor*, *Morelia viridis*) were investigated for *Salmonella.* This pathogen constituted the main zoonotic risk associated with exotic pets (63). Domestic animal-to-human spillover events may occur through direct contact with the animals, for example via aerosols (e. g., equine rhinitis A/B virus), bites (e. g., rabies), and scratches (e. g., *Bartonella henselae,* the pathogen causing cat scratch disease). Indirect transmission of pathogens from companion animals to humans also occurs. For example, due to inadequate hygiene practices, there is a risk of accidentally ingesting fleas contaminated with cysticercoids of *Dipylidium caninum* or the larval stage of *E. multilocularis* excreted in the faeces of infected dog (59, 60).

Furthermore, the zoonotic risk at the companion animal-human interface is evolving. For example, feeding pets with raw meat-based diets, which has been gaining popularity, has been identified as a source of potential infection with Enterobacteriaceae (64). Additionally, pet travel and transport pose significant risks for disease introduction (65). The most popular European travel destinations for Austrians include Italy, Germany, Croatia, Spain, and Greece (66), where autochthonous cases of *Leishmania infantum* have been recorded (67). This raises concerns about the potential introduction of the disease into Austria, as global warming might create optimal conditions for the establishment of *Leishmania* in Austria (68).

The analysis evidenced the importance of the livestock-human interfaces in the zoonotic disease risk in Austria. Indeed, livestock species live in close proximity to humans while sharing a wide range of pathogens with them, such as *Coxiella burnetii*, *Mycobacterium tuberculosis* variant *caprae*, *Ascaris suum*, and Orthohepevirus A. Veterinarians, farmers, and slaughterhouse workers interact directly and daily with ruminants, pigs, and poultry and therefore present a higher risk for zoonotic infection. Several zoonotic pathogens can be transmitted at human-livestock interfaces through infected abortion materials, such as

Borreliella burgdorferi (the agent of Q-fever), *Chlamydia abortus*, *Brucella melitensis*, *Listeria monocytogenes* and *Salmonella* (69). Other examples of direct transmission of zoonotic pathogens of livestock include e. g., methicillin-resistant *Staphylococcus aureus* (MRSA) in pigs (70, 71) and highly pathogenic avian influenza (72). Pathogens at the human-livestock interface may also infect humans indirectly, e. g., through contact with water contaminated with manure (e. g., *Leptospira, Giardia*) used to fertilise fields (60, 73), or through the ingestion of contaminated food stuff like unpasteurized dairy products (e. g., *L. monocytogenes*) (74, 75).

With an average consumption of 88.5 kg of meat, 115.2 kg of milk and dairy products, 14.5 kg of eggs, and 8 kg per capita in 2021 (76), food plays a crucial role in the human-livestock and human-game species interfaces in Austria. Food products, mainly meat and meat products, dairy, and eggs are being actively investigated in research and following surveillance programmes based on the Directive 2003/99/EC (24). Within this framework, *Listeria* (33.7 %), *Salmonella* (22.9 %), and *Escherichia* (8.8 %) were the most evidenced pathogens in food products across the included publications.

Austria has accumulated substantial data on WNV, USUV, and several other Orthoflaviviruses. This extensive data collection stems from the regular mosquito surveillance efforts in the country. All seven genera of mosquitos investigated in the included publications are being actively monitored in Austria in 37 selected areas as well as the international airport of Vienna. Collected mosquitos are screened for WNV, USUV, Sindbis virus, and Orthobunyavirus tahynaense, and there is monitoring for alien mosquito species in place (77). This research has highlighted the crucial role of arthropod vectors, such as *Culex*, in the risk of zoonotic viral disease transmission to humans. As a result of climate change and globalisation, there is a growing likelihood of new arthropod species populations becoming established in Austria (78). Therefore, integrated surveillance of humans, animals, and vectors is key for tracking the emergence and spread of pathogens, facilitating the establishment of early warning systems (79–81).

Impacts of climate change are already observable in Austria. Notably, a rise of 1.0 °C to 1.5 °C in the average temperatures was observed at a national level during the past 30 years, heightening the risk of extreme weather events, such as drought and heavy rainfalls (82), thereby increasing the risk of infectious disease outbreaks (83). For example, a study investigating the spread of tularemia has linked the emergence of this pathogen in western Austria to global warming and its effects on local temperatures and precipitations (84).

Additionally, *D. repens*, evidenced in mosquitoes in Burgenland, may be able to successfully establish and spread in Austria as a result of climate change (85). During the period 1975–2022, nine pathogens emerged in Austria, corresponding to a frequency of one EID every five years. This statistic holds particular significance since models suggest that the occurrence rate of EIDs is projected to rise in the future (9, 86), underscoring the critical importance of preparedness for (novel) infectious disease outbreaks (87). Furthermore, land-use changes, driven by socio-economic factors including a growing human population, significantly and adversely affect the country´s ecosystem services. The Austrian urban area has almost doubled in the last 50 years, leading to a substantial increase in land consumption compared to other European countries. Moreover, only 0.8 % of the Austrian forests are dedicated to the conservation of biodiversity and maintenance of natural forest dynamics, while the majority are managed primarily for economic purposes (88). These factors decrease the ecosystem's resilience to stress and therefore threaten the tight link between environment, animal, and human health (89).

The research trend is showing a growing interest in the investigation of zoonotic pathogens in the three compartments. Despite the growing interest in the subject, very few publications address zoonotic diseases within the environmental context. This gap in research is consistent on a global scale, despite the undeniable link between environmental, animal, and human health (89). Research focused on the human compartment has not experienced the same rapid surge in interest as research involving animals. This discrepancy could be attributed to the challenges associated with obtaining ethical approval for studies involving humans.

This study presents limitations. First, information about zoonotic pathogens in Austria is very scattered, and the process of manually collecting/selecting publications which results were not overlapping was fastidious. Moreover, if AGES compiles and provides information about foodborne and some other pathogens, their hosts, and circulation, information about the status of lesser-known pathogens in Austria is very dispersed. Additionally, the compiled list of zoonotic pathogens circulating in Austria between 1975 and 2022 might suffer from incompleteness. This is because our selection criteria included the identification of the pathogen as zoonotic by the authors. Although this criterion eased the publication selection process, it excluded *de facto* all publications investigating zoonotic agents without mentioning “zoonotic” or “zoonoses” in the text or tags. Furthermore, if the authors mistakenly identified a non-zoonotic pathogen as zoonotic, this pathogen was included in the dataset. Some errors have been found and corrected already, e. g., mention of bovine viral diarrhoea in (90). Another

example to illustrate this point is that while *Giardia* has been considered a potential zoonotic pathogen, a study has reported that cases of human giardiasis have not been linked to the same subtype of *Giardi*a frequently observed in animals (91).

Many papers did not reference animal species, vectors, and pathogen names according to current NBCI taxonomy. The taxonomic validation of all species names was time-consuming. Nevertheless, it was done programmatically for the major part, offering the possibility to update all names relatively quickly and in a systematic way when required (e. g., if the dataset is used in a few years or if the dataset is further expanded). Finally, the prevailing practice of not publishing negative results poses a challenge in confirming whether certain pathogens were investigated but not detected. This data gap hinders the accurate spatiotemporal characterisation of potential emerging pathogens within Austria.

Although the primary objective was to characterise the interfaces for zoonotic transmission in Austria, it proved challenging to identify these interfaces based on the information sources. Interfaces are not solely defined by transmissible pathogens but depend on multiple factors. Rarely does a study explicitly acknowledge the interfaces relevant to the publication's topic, making it impossible to extract objective data that could quantify and describe the studied interfaces. The challenge becomes particularly pronounced when dealing with indirectly transmitted zoonotic pathogens. For instance, when authors examine the presence of a pathogen in the faeces of an animal host, is the study investigating the animal host-human interface? The environment (faeces)-human interface? Or the animal host-environment interface? One Health places significant emphasis on understanding these “interfaces”, and the findings of this study underscore the need for clearer definitions of this term within studies to enhance our theoretical understanding of the dynamics of zoonotic disease transmission.

5 Conclusion

Zoonotic diseases pose an ever-increasing risk to human and animal health. Many drivers of zoonotic disease emergence are present in Austria, underscoring the importance of data-driven preparedness. This data is crucial for the prevention and timely management of both existing and emerging zoonotic diseases. Currently, information on zoonotic pathogens in Austria is dispersed and heterogeneous, making it difficult to obtain a clear overview of existing data or identify data gaps. The lack of a readily accessible and structured comprehensive dataset on zoonotic pathogens investigated and circulating in Austria poses significant challenges in identifying spillover risk. This challenge is compounded by the uneven distribution of data among the three compartments of the interfaces (animal, human, environment) and the intricate interplay of numerous interconnected factors, that make the mathematical modelling of cross-species transmission events extremely challenging (92, 93).

It is vital to have a broader perspective of zoonotic pathogens, the interfaces where transmission occurs, and the factors that influence them. To advance research in this field, an interdisciplinary and systemic strategy is needed. The international call towards a One Health approach to managing zoonotic disease (14) is not noticeable in Austria in most approaches to zoonotic diseases. This review has taken the first step to gather the available data about zoonotic pathogens in Austria, their hosts, vectors, and food and environmental sources, thus providing a basis for further research.

6 List of tables

Table 1: Field dictionary of the final dataset recording zoonotic pathogens investigated in Austria, 1975–2022. Fields whose names are followed by an asterisk were computed in R... 8
Table 2: Summary statistics of the relative annual proportion (percentage) of each pathogen type over the second half of the study period (1998–2022). Minimum, maximum, mean, median percentage, and interquartile range (IQR). 14
Table 3: List of animal hosts) that have been found (sero)positive for at least one zoonotic pathogen in Austria, 1975–2022. 20
Table 4: Zoonotic pathogens evidenced in invertebrate vectors, Austria, 1975–2022. 24
Table 5: Zoonotic pathogens evidenced in environmental media, Austria, 1975–2022..... 24
Table 6: Zoonotic pathogens with clear evidence of introduction into Austria, 1975–2022. .. 28
Table 7: Emerging zoonotic pathogens in Austria, 1975–2022..... 29

7 Table of figures

Figure 1: Workflow used in this study for literature search and paper selection (n = number of publications). 11

Figure 2 Stacked chart of the annual number of published studies that investigated zoonotic pathogens in Austria between January 1975 and August 2022 and types of pathogens. 12

Figure 3: Number of publications on zoonotic diseases per Austrian federal state, Austria, 1975–2022. Studies conducted at national scale are represented under “Austria”. The percentage of publications per type of pathogen within each federal state is indicated. Studies which did not specify the federal state (e. g. mentioning “eastern Austria”, “west Austria”, “south western Austria”, “south eastern Austria”, or “northern limestone alps”) are not represented. One publication may investigate one or more than one pathogen in one or more than one location. 13

Figure 4: Evidenced zoonotic pathogens, Austria, 1975–2022. The colours correspond to the pathogen type (bacteria = turquoise, virus = green, parasite = pink, fungi = orange, other = blue); node size represents the number of times a pathogen was evidenced (and results published) between 1975 and 2022. All pathogen names are resolved against the NCBI Taxonomy database, when this was not possible the description of the pathogen as mentioned in the publication was used. 16

Figure 5: Bubble plot illustrating the distribution of the zoonotic pathogen genera across Austrian animal hosts, grouped by taxonomic order, 1975–2022. Only positive results are shown (seropositive or positive). Node size corresponds to the frequency with which a particular pathogen was detected within a specific taxonomic order during this timeframe. Colours correspond to pathogen type. 19

Figure 6:Sankey graph of the zoonotic pathogens found in Austria in food products, 1975–2022. The zoonotic pathogens´ NCBI-resolved genera is shown on the first axis, the food origin is displayed on the middle axis, and the food category is specified on the right axis. The height of each bar is proportional to the number of times a zoonotic pathogen was found. 23

Figure 7: Network of the zoonotic interfaces in Austria, 1975–2022. The network depicts the connections between zoonotic pathogens and their corresponding animal hosts, food, and environmental matrices (including vectors). Size of the node represents the number of study that reported the node as present (for the pathogens) or positive (hosts, vectors, environmental or food matrices). 26

Figure 8: Subgraph of the host-pathogen network in Austria, 1975–2022. The network depicts the direct interactions between zoonotic pathogens and their corresponding animal hosts. Size of the node represents the number of study that reported the node as present (for the pathogens) or positive (hosts). 27

Figure 9: Trend in research interest, as measured by the number of studies involving each type of pathogen (note that a single publication might encompass multiple pathogen type)..... 31

Figure 10: Trend in research interest, as measured by the number of studies involving each compartment, as recognised in the traditional One Health view (note that a single publication might encompass multiple compartment-host associations)..... 31

8 Literature Cited

1. Bauerfeind R, Krauss H, editors. Zoonoses: Infectious diseases transmissible between animals and humans. Fourth edition. Washington, D.C.: ASM Press; 2016. Available from: URL: https://permalink.obvsg.at/.
2. Heymann DL, Dixon M. Infections at the animal/human interface: shifting the paradigm from emergency response to prevention at source. Curr Top Microbiol Immunol 2013; 366:207–15.
3. Reperant LA, Osterhaus AD. The human-animal interface. Microbiol Spectr 2013; 1(1).
4. Plowright RK, Reaser JK, Locke H, Woodley SJ, Patz JA, Becker DJ et al. Land use-induced spillover: a call to action to safeguard environmental, animal, and human health. Lancet Planet Health 2021; 5(4):e237-e245.
5. Jones BA, Grace D, Kock R, Alonso S, Rushton J, Said MY et al. Zoonosis emergence linked to agricultural intensification and environmental change. Proc Natl Acad Sci U S A 2013; 110(21):8399–404.
6. Fournié G, Pfeiffer DU, Bendrey R. Early animal farming and zoonotic disease dynamics: modelling brucellosis transmission in Neolithic goat populations. R Soc Open Sci 2017; 4(2):160943.
7. Abrantes AC, Vieira-Pinto M. 15 years overview of European zoonotic surveys in wild boar and red deer: A systematic review. One Health 2023; 16:100519. Available from: URL: https://www.sciencedirect.com/science/article/pii/S2352771423000393.
8. Milbank C, Vira B. Wildmeat consumption and zoonotic spillover: contextualising disease emergence and policy responses. Lancet Planet Health 2022; 6(5):e439-e448.
9. Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL et al. Global trends in emerging infectious diseases. Nature 2008; 451(7181):990–3.
10. Morse SS. Factors in the emergence of infectious diseases. Emerg Infect Dis 1995; 1(1):7–15.
11. Adisasmito WB, Almuhairi S, Behravesh CB, Bilivogui P, Bukachi SA, Casas N et al. One Health: A new definition for a sustainable and healthy future. PLoS Pathog 2022; 18(6):e1010537.
12. Gruetzmacher K, Karesh WB, Amuasi JH, Arshad A, Farlow A, Gabrysch S et al. The Berlin principles on one health - Bridging global health and conservation. Sci Total Environ 2021; 764:142919. Available from: URL: https://www.sciencedirect.com/science/article/pii/S0048969720364494.
13. Neff EP. Keeping an eye on the human-animal interface. Lab Anim 2021; 50(3):55–8. Available from: URL: https://www.nature.com/articles/s41684-021-00725-y.
14. Lefrançois T, Malvy D, Atlani-Duault L, Benamouzig D, Druais P-L, Yazdanpanah Y et al. After 2 years of the COVID-19 pandemic, translating One Health into action is urgent. Lancet 2023; 401(10378):789–94.
15. Ghai RR, Wallace RM, Kile JC, Shoemaker TR, Vieira AR, Negron ME et al. A generalizable one health framework for the control of zoonotic diseases. Sci Rep 2022; 12(1):8588. Available from: URL: https://www.nature.com/articles/s41598-022-12619-1.

16. Annual average population; 2023 [cited 2023 Mar 3]. Available from: URL: https://www.statistik.at/en/statistics/population-and-society/population/population-stock/annual-average-population.

17. Wikipedia. Österreich; 2023 [cited 2023 Jan 5]. Available from: URL: https://de.wikipedia.org/wiki/%C3%96sterreich#Geographie.

18. Elisabeth Geiser. Wie viele Tierarten leben in Österreich? Erfassung, Hochrechnung und Abschätzung. Verhandlungen der Zoologisch-Botanischen Gesellschaft in Österreich 1998; (135:81-93). Available from: URL: https://www.zobodat.at/pdf/VZBG_135_0081-0093.pdf.

19. Statistik Austria, editor. Haustiere in Österreich [Konsumerhebung 2019/20]; 2020. Available from: URL: https://www.statistik.at/fileadmin/pages/339/Themenblatt_Haustiere_2019-20.pdf [cited 2023 Feb 3].

20. Statistik Austria, editor. Jagdstatistik: Jagdjahr 2020/2021; 2021 [cited 2023 Feb 3].

21. Statistik Austria, editor. Statistik der Landwirtschaft; 2021 2021 [cited 2023 Feb 3].

22. Regulation (EC) No 2160/2003 of the European Parliament and of the Council of 17 November 2003 on the control of salmonella and other specified food-borne zoonotic agents: Regulation (EC) No 2160/2003; 2003. Available from: URL: https://eur-lex.europa.eu/legal-content/DE/ALL/?uri=CELEX%3A32003R2160.

23. Commission implementing decision (EU) 2020/1729 of 17 November 2020 on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria and repealing implementing decision 2013/652/EU (notified under document C(2020) 7894): Comission Implementing Decision (EU) 2020/1729; 2020.

24. Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC; 2003 [cited 2023 Mar 5]. Available from: URL: https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=celex%3A32003L0099.

25. Bundesgesetz zur Überwachung von Zoonosen und Zoonoseerregern (Zoonosengesetz): BGBl. I Nr. 128/2005; 2005. Available from: URL: https://www.ris.bka.gv.at/eli/bgbl/I/2005/128.

26. AGES - Pathogens from A to Z; 2023 [cited 2023 Jul 22]. Available from: URL: https://www.ages.at/en/human/disease/pathogens-from-a-to-z.

27. Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016 on transmissible animal diseases and amending and repealing certain acts in the area of animal health (Animal Health Law): Regulation (EU) 2016/429; 2016. Available from: URL: https://eur-lex.europa.eu/eli/reg/2016/429/2021-04-21.

28. Epidemiegesetz 1950: BGBl. Nr. 186/1950; 2020.

29. Tollwut; 2023 [cited 2023 Feb 8]. Available from: URL: https://www.ages.at/mensch/krankheit/krankheitserreger-von-a-bis-z/tollwut.

30. Tuberculosis; 2023 [cited 2023 Jan 24]. Available from: URL: https://www.ages.at/mensch/krankheit/krankheitserreger-von-a-bis-z/tuberkulose.

31. AGES. Brucellosis; 2023 [cited 22.01.23]. Available from: URL: https://www.ages.at/en/mensch/krankheit/krankheitserreger-von-a-bis-z/brucellosis.

32. Bundesministerium für Soziales, Gesundheit, Pflege und Konsumentenschutz, editor. Jahresbericht meldepflichtige Erkrankungen 2022; 2023 2023 May 26.

33. World Health Organization. Taking a multisectoral, One Health approach: A tripartite guide to addressing zoonotic diseases in countries. Geneva, Rome, Paris: World Health Organization; The Food and Agriculture Organization of the United Nations; World Organisation for Animal Health; 2019.

34. Types of journal articles; 2022 [cited 13.10.22]. Available from: URL: https://www.springer.com/gp/authors-editors/authorandreviewertutorials/writing-a-journal-manuscript/types-of-journal-articles/10285504.

35. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing; 2023. Available from: URL: https://www.R-project.org/.

36. Schoch CL, Ciufo S, Domrachev M, Hotton CL, Kannan S, Khovanskaya R et al. NCBI Taxonomy: a comprehensive update on curation, resources and tools. Database (Oxford) 2020; 2020.

37. Chamberlain SA, Szöcs E. taxize: taxonomic search and retrieval in R. F1000Res 2013; 2:191.

38. Sjoberg D. ggsankey: Make sankey, alluvial and sankey bump plots in ggplot: R package version 0.0.99999; 2021 [cited 2023 Jul 22]. Available from: URL: https://github.com/davidsjoberg/ggsankey.

39. Csardi G, Nepusz T. The igraph software package for complex network research. InterJournal 2005; Complex Systems:1695.

40. Destoumieux-Garzón D, Mavingui P, Boetsch G, Boissier J, Darriet F, Duboz P et al. The One Health concept: 10 years old and a long road ahead. Front Vet Sci 2018; 5:14.

41. European Union. The European Union One Health 2021 zoonoses report. EFSA journal; 2022. (vol 20).

42. World Organization for Animal Health, editor. Terrestrial animal health code. 28th edition; 2019. Available from: URL: https://www.woah.org/en/what-we-do/standards/codes-and-manuals/terrestrial-code-online-access/.

43. Moreira-Soto A, Walzer C, Czirják GÁ, Richter MH, Marino SF, Posautz A et al. Serological evidence that SARS-CoV-2 has not emerged in deer in Germany or Austria during the COVID-19 pandemic. Microorganisms 2022; 10(4).

44. West Nil Virus; 2023 [cited 2023 Jul 28]. Available from: URL: https://www.ages.at/mensch/krankheit/krankheitserreger-von-a-bis-z/west-nil-virus?sword_list%5B0%5D=west&sword_list%5B1%5D=nile&sword_list%5B2%5D=virus&no_cache=1.

45. Usutu-Virus; 2023 [cited 2023 Jul 28]. Available from: URL: https://www.ages.at/en/human/disease/pathogens-from-a-to-z/usutu-virus.

46. Aberle SW, Kolodziejek J, Jungbauer C, Stiasny K, Aberle JH, Zoufaly A et al. Increase in human West Nile and Usutu virus infections, Austria, 2018. Euro Surveill 2018; 23(43).

47. Bundesminister für Land- und Forstwirtschaft, editor. Grüner Bericht 2022: Die Situation der österreichischen Land- und Forstwirtschaft; 2022. Available from: URL: www.gruenerbericht.at.

48. Cleaveland S, Laurenson MK, Taylor LH. Diseases of humans and their domestic mammals: pathogen characteristics, host range and the risk of emergence. Philos Trans R Soc Lond B Biol Sci 2001; 356(1411):991–9.

49. Hassell JM, Begon M, Ward MJ, Fèvre EM. Urbanization and disease emergence: Dynamics at the wildlife-livestock-human interface. Trends in Ecology & Evolution 2017; 32(1):55–67. Available from: URL: https://www.sciencedirect.com/science/article/pii/S0169534716301847.

50. Caron A, Miguel E, Gomo C, Makaya P, Pfukenyi DM, Foggin C et al. Relationship between burden of infection in ungulate populations and wildlife/livestock interfaces. Epidemiol Infect 2013; 141(7):1522–35.

51. Fink M, Schleicher C, Gonano M, Prodinger WM, Pacciarini M, Glawischnig W et al. Red deer as maintenance host for bovine tuberculosis, alpine region. Emerg Infect Dis 2015; 21(PMID: 25695273):467.

52. Daszak P, Cunningham AA, Hyatt AD. Emerging infectious diseases of wildlife--threats to biodiversity and human health. Science 2000; 287(5452):443–9.

53. Taylor LH, Latham SM, Woolhouse ME. Risk factors for human disease emergence. Philos Trans R Soc Lond B Biol Sci 2001; 356(1411):983–9.

54. Duscher GG, Leschnik M, Fuehrer H-P, Joachim A. Wildlife reservoirs for vector-borne canine, feline and zoonotic infections in Austria. Int J Parasitol Parasites Wildl 2015; 4(1):88–96.

55. Walter T, Zink R, Laaha G, Zaller JG, Heigl F. Fox sightings in a city are related to certain land use classes and sociodemographics: results from a citizen science project. BMC Ecol 2018; 18(1):50. Available from: URL: https://bmcecol.biomedcentral.com/articles/10.1186/s12898-018-0207-7.

56. Statistik Austria. More game shot and game losses in the 2021/2022 hunting season; 10.12.22 [cited 2023 Jul 4]. Available from: URL: https://www.statistik.at/fileadmin/announcement/2022/10/20221012Jagd20212022EN.pdf.

57. Much P, Arrouas M, Herzog U. Zoonoses and zoonotic agents in Austria report 2018; 2019. Available from: URL: https://www.ages.at/download/sdl-eyJ0eXAiOiJKV1QiLCJhbGciOiJIUzI1NiJ9.eyJpYXQiOjE2MDk0NTkyMDAsImV4cCI6NDA3MDkwODgwMCwidXNlciI6MCwiZ3JvdXBzIjpbMCwtMV0sImZpbGUiOiJmaWxlYWRtaW5cL0FHRVNfMjAyMlwvMl9NRU5TQ0hcL0tyYW5raGVpdFwvXHUwMGQ2ZmZlbnRsaWNoZV9HZXN1bmRoZWl0X1NlcnZpY2VzXC9CZXJpY2h0ZV9Gb2xkZXJcL1pvb25vc2VuYmVyaWNodF8yMDE4LnBkZiIsInBhZ2UiOjIxNDZ9.V6PtDr9W3n5DA3JOmIJBCw_j5Xhp4owKwr5hPeKGsgQ/Zoonosenbericht_2018.pdf.

58. Stull JW, Brophy J, Weese JS. Reducing the risk of pet-associated zoonotic infections. CMAJ 2015; 187(10):736–43.

59. Dhaliwal BBS. Parasitic zoonoses. 1st ed. New Delhi: Springer (India) Private Limited; 2013. Available from: URL: https://ebookcentral.proquest.com/lib/kxp/detail.action?docID=1399013.

60. Alber G, Amtsberg G, Bauer J, Bauerfeind R, Beer M, Ewers C et al. Tiermedizinische Mikrobiologie, Infektions- und Seuchenlehre. 10., aktualisierte Auflage. Stuttgart: Georg Thieme Verlag; 2015.

61. Riebenbauer K, Weber PB, Walochnik J, Karlhofer F, Winkler S, Dorfer S et al. Human dirofilariosis in Austria: the past, the present, the future. Parasit Vectors 2021; 14(1):227. Available from: URL: https://parasitesandvectors.biomedcentral.com/articles/10.1186/s13071-021-04696-4.

62. Heus P de, Kolodziejek J, Camp JV, Dimmel K, Bagó Z, Hubálek Z et al. Emergence of West Nile virus lineage 2 in Europe: Characteristics of the first seven cases of West Nile neuroinvasive disease in horses in Austria. Transbound Emerg Dis 2020; 67(3):1189–97.

63. Varela K, Brown JA, Lipton B, Dunn J, Stanek D, Behravesh CB et al. A review of zoonotic disease threats to pet owners: A compendium of measures to prevent zoonotic diseases associated with non-traditional pets: Rodents and other small mammals, reptiles, amphibians, backyard poultry, and other selected animals. Vector Borne Zoonotic Dis 2022; 22(6):303–60.

64. Nüesch-Inderbinen M, Treier A, Zurfluh K, Stephan R. Raw meat-based diets for companion animals: a potential source of transmission of pathogenic and antimicrobial-resistant Enterobacteriaceae. R Soc Open Sci 2019; 6(10):191170.

65. Trotz-Williams LA, Trees AJ. Systematic review of the distribution of the major vector-borne parasitic infections in dogs and cats in Europe. Vet Rec 2003; 152(4):97–105.

66. Daul R. Urlaubs- und Geschäftsreisen - Jahresergebnisse 2022; 2023 2023. Available from: URL: https://www.statistik.at/fileadmin/user_upload/SB_3-4_Urlaubs-und-Geschaeftsreisen-2022.pdf [cited 2023 Aug 3].

67. Maia C, Conceição C, Pereira A, Rocha R, Ortuño M, Muñoz C et al. The estimated distribution of autochthonous leishmaniasis by Leishmania infantum in Europe in 2005–2020. PLoS Negl Trop Dis 2023; 17(7):e0011497.

68. Kniha E, Aspöck H, Auer H, Walochnik J. Leishmania infections and Leishmania species in central Europe. Wiener Tierärztliche Monatsschrift 2023; (110).

69. Barkallah M, Gharbi Y, Hassena AB, Slima AB, Mallek Z, Gautier M et al. Survey of infectious etiologies of bovine abortion during mid- to late gestation in dairy herds. PLoS One 2014; 9(3):e91549.

70. Taus K, Schmoll F, El-Khatib Z, Auer H, Holzmann H, Aberle S et al. Occupational swine exposure and Hepatitis E virus, Leptospira, Ascaris suum seropositivity and MRSA colonization in Austrian veterinarians, 2017-2018-A cross-sectional study. Zoonoses Public Health 2019; 66(7):842–51.

71. Lewis HC, Mølbak K, Reese C, Aarestrup FM, Selchau M, Sørum M et al. Pigs as source of methicillin-resistant Staphylococcus aureus CC398 infections in humans, Denmark. Emerg Infect Dis 2008; 14(9):1383–9.

72. Jong JC de, Claas EC, Osterhaus AD, Webster RG, Lim WL. A pandemic warning? Nature 1997; 389(6651):554.

73. Vicente J. Diseases at the wildlife-livestock interface: Research and perspectives in a changing world. Cham: Springer International Publishing AG; 2021. (Wildlife Research Monographsv.3). Available from: URL: https://ebookcentral.proquest.com/lib/kxp/detail.action?docID=6578697.

74. AGES. Listeria; 2023 [cited 2023 Sep 13]. Available from: URL: https://www.ages.at/en/human/disease/pathogens-from-a-to-z/listeria.

75. Wagner M, Auer B, Trittremmel C, Hein I, Schoder D. Survey on the Listeria contamination of ready-to-eat food products and household environments in Vienna, Austria. Zoonoses Public Health 2007; 54(1):16–22.

76. Infos zu Gelsen & Stechmücken; 2023 [cited 2023 Aug 1]. Available from: URL: https://www.ages.at/mensch/krankheit/infos-zu-gelsen-krankheiten?tx_abagelsendb_pi1_jahr=2022&tx_abagelsendb_pi1_virus=West+Nile+Virus&tx_abagelsendb_pi1_land=#c3824.

77. Fuehrer H-P, Schoener E, Weiler S, Barogh BS, Zittra C, Walder G. Monitoring of alien mosquitoes in western Austria (Tyrol, Austria, 2018). PLoS Negl Trop Dis 2020; 14(6):e0008433.

78. Petrić D, Bellini R, Scholte E-J, Rakotoarivony LM, Schaffner F. Monitoring population and environmental parameters of invasive mosquito species in Europe. Parasit Vectors 2014; 7:187. Available from: URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4005621/#B3.

79. Vidanović D, Barbić L, Jeličić P, Lazić S, Radmanić L, Lupulović D et al. Importance of multidisciplinary and regional collaboration in integrated West Nile virus surveillance - the „One Health" concept. Infektol. Glas. (Online) 2020; 39(2):40–7.

80. V. Savić, L. Barbić, T. V. Čavlek, M. Balenović, V. Stevanović, G. Savini. Chickens and horses as sentinels for early warning system in prevention of human west nile virus infections in Croatia. Slovenian Veterinary Research 2017.

81. Klimafakten Österreich kompakt; 2021 [cited 2023 Sep 3]. Available from: URL: https://www.zamg.ac.at/cms/de/klima/news/klimafakten-oesterreich-kompakt.

82. McMichael AJ. Extreme weather events and infectious disease outbreaks. Virulence 2015; 6(6):543–7.

83. Deutz A, Guggenberger T, Gasteiner J, Steineck T, Bago Z, Hofer E et al. Investigation of the prevalence of tularaemia under the aspect of climate change. Wiener Tierärztliche Monatsschrift 2009; 96:107–13.

84. Fuehrer H-P, Auer H, Leschnik M, Silbermayr K, Duscher G, Joachim A. Dirofilaria in humans, dogs, and vectors in Austria (1978–2014)-from imported pathogens to the endemicity of Dirofilaria repens. PLoS Negl Trop Dis 2016; 10(5):e0004547.

85. Marani M, Katul GG, Pan WK, Parolari AJ. Intensity and frequency of extreme novel epidemics. Proc Natl Acad Sci U S A 2021; 118(35).

86. Lee VJ, Aguilera X, Heymann D, Wilder-Smith A. Preparedness for emerging epidemic threats: A lancet infectious diseases commission. Lancet Infect Dis 2020; 20(1):17–9.

87. Schirpke U, Tasser E, Borsky S, Braun M, Eitzinger J, Gaube V et al. Past and future impacts of land-use changes on ecosystem services in Austria. J Environ Manage 2023; 345:118728.

88. Essack SY. Environment: the neglected component of the One Health triad. Lancet Planet Health 2018; 2(6):e238-e239.

89. Nowotny N, Deutz A, Fuchs K, Schuller W, Hinterdorfer F, Auer H et al. Prevalence of swine influenza and other viral, bacterial, and parasitic zoonoses in veterinarians. J Infect Dis 1997; 176(5):1414–5.

90. Haas E. Genotypisierung von Giardia aus österreichischen Feldproben. Universität für Veterinärmedizin Wien; 2015.

91. Cross PC, Prosser DJ, Ramey AM, Hanks EM, Pepin KM. Confronting models with data: the challenges of estimating disease spillover. Philos Trans R Soc Lond B Biol Sci 2019; 374(1782):20180435.

92. Viana M, Mancy R, Biek R, Cleaveland S, Cross PC, Lloyd-Smith JO et al. Assembling evidence for identifying reservoirs of infection. Trends in Ecology & Evolution 2014; 29(5):270–9.