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Transdisciplinary Epidemiology to Better Understand, Prevent and Control Emerging Transboundary Animal Diseases

Thibaud Porphyre

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Transdisciplinary Epidemiology to Better Understand, Prevent and Control Emerging Transboundary Animal Diseases

Habilitation à diriger des recherches

Mémoire présenté devant l'Université Claude Bernard – Lyon 1

École doctorale Évolution, Ecosystèmes, Microbiologie, Modélisation (E2M2)

Thibaud Porphyre

Chaire Industrielle de recherche et d'enseignement en Santé Publique Vétérinaire | VetAgro Sup

UMR CNRS 5558 – Laboratoire de Biométrie et Biologie Évolutive (LBBE)

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Composition du jury

Xavier BAILLY	Ingénieur de Recherche	INRAE	Rapporteur
Christine FOURICHON	Professeure des Écoles Nationales Vétérinaires	ONIRIS	Rapporteuse
Benjamin ROCHE	Directeur de Recherche	IRD	Rapporteur
Christelle LOPES	Maitre de Conférence	Univ. Lyon 1	Examinatrice
Florence AYRAL	Maitre de Conférence	VetAgro Sup	Examinatrice
Pascal HENDRIKX	Inspecteur Général de Santé Publique Vétérinaire	CGAAER	Examineur
Benoît DURAND	Directeur de Recherche	ANSES	Examineur

ACKNOWLEDGEMENTS

Many thanks to all the colleagues and collaborators (too many to be named) in either Scotland, France or in the rest of the world, whether they are scientist, policy makers or industry stakeholders, who gave me many opportunities to exchange, identify questions and learn new approach to get answers. My work would therefore not been this rich and diverse without them, I am more than grateful for that. In particular, this *Habilitation à Diriger des Recherches* would not have been possible without my colleagues and friends at the Centre of Expertise on Animal Disease Outbreaks (EPIC) and at the Laboratoire de Biométrie et Biologie Evolutive (LBBE). Special thanks to Mark Bronsvort, Estelle Loukiadis and Fabrice Vavre for their support and confidence in me through my time in the Edinburgh and Lyon.

I feel extremely fortunate to have worked, and still work, in close collaboration with Florence Ayrat and Sylvie Mialet in putting together the international Master 2 programme OHMHP. I have undoubtedly benefited from their support and expertise. I have learned a lot from them, and I couldn't be more grateful.

I would also like to thank the postdocs, PhD candidates and master students I have had the chance to co-supervise and mentor since 2010: Rémi Fay (Post Doc), Amandine Bibard (PhD), Tahreem Khalid (PhD), Lina Maria González Gordon (PhD), John Grewar (PhD), Isobel McLachlan (PhD), Jessica Flood (PhD), Kajetan Stański (mres), Eric Rucogoza (M2), Giorgio Mangiapia (M2), Beatriz Delgado Hernandez (M2), Sana Kalthoum (PhD), Michael Dunne (PhD), Paolo Motta (PhD), Cheryl Gibbons (PhD), Siwi Wijayanti (PhD), Raphaëlle Métras (PhD) Solenne Costard (PhD).

Finally, I would like to warmly thank the committee, Xavier Bailly, Christine Fourichon, Benjamin Roche, Christelle Lopes, Florence Ayrat, Pascal Hendrikx and Benoît Durand, for having accepted to assess this *Habilitation à Diriger des Recherches*, it is an honour for me.

The last words to my wife and kids: thanks for your unconditional support and love.

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CURRICULUM VITAE

Individual information

Full Name	Thibaud PORPHYRE
Date of birth	12/03/1979 at Sant Germain en Laye (78), France
Nationality	French
Grade	Ingénieur de Recherche, Chargé de Mission, Grade A
Research Unit	UMR CNRS 5558 - Laboratoire de Biométrie et Biologie Évolutive (DU Fabrice VAVRE)
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Education

2006 – 2008: PhD in Epidemiology

Thesis title: "Factors Associated with the Transmission Dynamics of Bovine Tuberculosis in New Zealand."
Massey University, Palmerston North, New Zealand.

Host institution: Epicentre, Institute of Veterinary, Animal and Biomedical Sciences (IVABS), New Zealand.

2004 – 2006: Post Graduate Diploma in "Preventive Veterinary Medicine" (Distinction)

Massey University, Palmerston North, New Zealand.

2001 – 2002: Diplôme d'Études Approfondies (DEA) "Modèles et Instruments en Médecine et Biologie"

Thesis title: "Abundance of arbovirus vectors in function of the flooding dynamics of a pond" (in French).
Joseph Fourier University, Grenoble, France.

Host institution: École National Vétérinaire de Lyon, Marcy l'Étoile, France.

2000 – 2001: Maitrise "Biologie des Populations et des Écosystèmes"

University of Lyon 1, Villeurbanne, France.

Work experience

Since 2020: VetAgro Sup, University of Lyon, France

Head of the IDEXLyon Industrial Chair in Veterinary Public Health

2016 - 2020: The Roslin Institute, The Royal (Dick) School of Veterinary Studies, Edinburgh, UK

Research Fellow in Epidemiological Modelling, funded by Scotland's Centre of Expertise on Animal Disease Outbreaks (EPIC, Programmes of Research 2016-2021).

2011 – 2016: School of Biological Sciences, University of Edinburgh, Edinburgh, UK

Senior Postdoctoral Researcher in Epidemiological Modelling, funded by Scotland's Centre of Expertise on Animal Disease Outbreaks (EPIC, Programmes of Research 2011-2016).

2010 – 2011: The Royal Veterinary College, London, UK

Research assistant funded by the FP7 project PILGRIM (FP7-HEALTH 223050) of the European Union.

Sep. – Oct. 2010: Agricultural Research for Development (CIRAD), French West Indies

Research assistant funded by the French National Institute for Agricultural Research (INRA).

2008 – 2010: Agricultural Research for Development (CIRAD), French West Indies

Postdoctoral Fellow financed by the French National Institute for Agricultural Research (INRA).

Teaching outputs and coordination

Coordination of teaching programmes

I have been involved in the development and coordination of multiple teaching and training programmes focusing on both risk assessment and implementing the One Health approach in supporting decision-making for managing complex health problems. Notably, I have been involved in the development of the training programme organized by the University of Edinburgh to fellows from public government institutions of Uganda as part of the Fleming Fund Fellowship programme funded by the UK Department of Health and Social Care (DHSC), and to year 4 veterinary students of the University of Lilongwe in Malawi as part of the Global Challenges Theme Development Fund programme funded by the Scottish Funding Council GCRF Strategy. Both programmes aimed to support the professional development of those directly that are (and will be) involved in national capacity to respond to public health threats like antimicrobial resistances (AMR) and African swine fever (ASF), we put in place training and research projects aiming to communication and integration of activities of between animal and public health.

Notably, the Fleming Fund Fellowship programme highlighted the institutional disconnections between institutions involved in veterinary public health and those involved in public health, and highlighted the gap in training health professionals to One Health approaches. In particular, it identified the needs to better consider the interconnections between people, animals, plants and their shared environment when designing and implementing measures to prevent and control hazards in crisis and non-crisis situations. In my current role as course co-coordinator of the international elective course (M2) “One Health – Managing Health of Populations” (OHMHP) of the MSc Public Health held at the University Claude Bernard Lyon 1, I used such observations when designing the curriculum of this master-level programme. In particular, the duality between “risk evaluation” and “risk management” was perceived very early on as a way to discuss and integrate all aspect of One Health. Indeed, it would cover needs that were critically missed when managing the COVID19 pandemic: the broader appreciation that each decision and action may have consequences on humans, animals and ecosystems. In addition, this aspect of improving the holistic understanding of critical health situations represented a good ground to introduce multiple discipline and highlight the importance of transdisciplinary approach in analysing and mitigating complex health issues.

To reach these goals, efforts were made to attract potential students of diverse discipline and experience, since it would promote dialogue and ensure that various points of view are covered when introducing our exemplars of complex health systems. We also ensured that dialogue and exchanges were occurring between participants of the different orientations, i.e. evaluators and managers, as it would open up students to the various challenges that each orientation is facing. Our objective is for evaluators to better understand what information managers requires to make their decision, and for managers to better communicate their needs to evaluators. To ensure this dialogue and increase the interdisciplinary nature of their training, most competencies are introduced in the core curriculum, notably in socio-economics, ecology, biostatistics, and legislation, and study group and common tasks are organised mixing students of all disciplines and backgrounds. We already went through two cohorts of students with positive feedback and the third cohort has started in September 2024.

However, introducing the concept of One Health in a way that students of varied disciplines and background was deemed challenging. After discussion and planning together with non-permanent staff of my team (Chloé-Louise Morbois) and colleagues in VetAgro Sup (Florence Ayrat, Amandine Gautier, Sylvie Mialet), we decided to develop a One Health Mural (“Fresque du One Health”). This mural was developed in partnership with the developers of the Biodiversity Mural (“Fresque de la Biodiversité”), who are also based in Lyon. Thanks to the hard work of a non-permanent staff of my team (Chloé-Louise Morbois), this mural is now available to a broader public and is being supported by the Geneva Health Forum and the One Sustainable Health Forum.

Teaching commitments

Since the start of my career in research, I have taught undergraduate students at the university of Edinburgh and French West Indies and was tutor for practical lectures for veterinary students at the National Veterinary School of Lyon (F), at Massey University (NZ) and University of Lilongwe (Malawi). On average, I gave an average of 3 hours of lectures and practicals each year, teaching students on modelling, data analysis and epidemiology. Since my recruitment at VetAgro Sup and my involvement in coordinating the international M2 OHMHP, I allocated more time in teaching. In particular, I am the coordinator of all UE (3) on risk evaluation. Not only I have the responsibility to put together an effective and interesting programme to teach student how to manage and analyse data as well as how to better understand sources

of complexity and uncertainty of disease data, I also give lectures on data management, spatial analysis, complexity and uncertainty. These activities required a lot of preparation time, notably for the first lectures, but there is a marked return on investment. It provides basis upon which I organised summer schools (particularly in Tunisia, in partnership with the CNVZ, WOAHA Collaboration centre for Continuing Education and Veterinary Capacity Building) can be organised. It also offered me opportunities to recruit students for MSc projects (4) and Veterinary final-year research project (4).

List of teaching coordination activities

- April 2024: Course coordinator of the Summer school “Analyse et cartographie des données épidémiologiques sur le logiciel R” organised by the Centre National de Veille Zoosanitaire (CNVZ), WOAHA Collaboration centre for Continuing Education and Veterinary Capacity Building, Tunis, Tunisia.
- 2021-onward: Co-coordinator of the international elective course (M2) “One Health – Managing Health of Populations” (OHMHP), MSc Public Health, Claude Bernard University Lyon 1
- Course Coordinator of the UE “Data management and analysis” of the M2 OHMHP, MSc Public Health, Claude Bernard University Lyon 1
- Course Coordinator of the UE “Risk evaluation” of the M2 OHMHP, MSc Public Health, Claude Bernard University Lyon 1
- Course Coordinator of the UE “Complex systems and uncertainty” of the M2 OHMHP, MSc Public Health, Claude Bernard University Lyon 1
- Course Co-coordinator of the UE “Atelier One Health” of the M1 Public Health, MSc Public Health, Claude Bernard University Lyon 1
- 2021: Member of the working group for the development of a One Health Mural (“Fresque du One Health”) <https://ensv-fvi.fr/fresque-one-health/>
- 2023: Member of the working group for the development of an online elective course “Epidémiologie et gestion de maladies animales et zoonotiques” (Master eEPI)
- 2022: Member of the working group for the development of the EUR EID@Lyon.
- February 2020: Course coordinator of the training programme “mitigating African Swine Fever in Malawi”.
- 2019-2020: Member of the course co-ordination team for the Fleming Fund Fellowship programme for Uganda.

List of teaching and training activities

- April 2024: 18h over 2.5 days training lectures and practicals, Summer school “Analyse et cartographie des données épidémiologiques sur le logiciel R” organised by the Centre National de Veille Zoosanitaire (CNVZ), WOAHA Collaboration centre for Continuing Education and Veterinary Capacity Building, Tunis, Tunisia.
- 2023 3h Lectures in the Option AEST (Agriculture, Environnement, Santé et Territoire), Agronomic engineering cursus (year 3), VetAgro Sup, agronomic campus, Lempdes
- 2023 27h lectures in the UE “Risk Assessment” of the M2 OHMHP, MSc Public Health, Claude Bernard University Lyon 1, Lyon
- 2023 6h Practical lectures in the optional UE “Atelier One Health”, M1 Public Health of the MSc Public Health, University Claude Bernard – Lyon 1, Lyon.
- 2023 3h Practical lectures, veterinary sciences cursus (year 3), VetAgro Sup, veterinary campus, Marcy l’Etoile
- 2023 1h Lecture in the UE “Epidémiologie”, veterinary sciences cursus (year 3), VetAgro Sup, veterinary campus, Marcy l’Etoile

- 2023 9h member of the evaluation committee for oral defenses of internship projects of the M2 OHMHP, MSc Public Health, Claude Bernard University Lyon 1, Lyon
- 2022 6h Practical lectures, veterinary sciences cursus (year 3), VetAgro Sup, veterinary campus, Marcy l'Etoile
- 2022 1h Lecture in the UE "Epidémiologie", veterinary sciences cursus (year 3), VetAgro Sup, veterinary campus, Marcy l'Etoile
- 2022 3h Practical lectures in the optional UE "Atelier One Health", M1 Public Health of the MSc Public Health, University Claude Bernard – Lyon 1, Lyon.
- 2022 3h lectures in the international M2 GLOQUAL (Global Quality in European Livestock Production), MSc STAAE (Sciences et technologies de l'Agriculture, de l'Alimentation et de l'Environnement), Université Clermont Auvergne, Clermont Ferrand
- 2022 17h lectures in the UE "Data Management and Analysis" of the M2 OHMHP, MSc Public Health, Claude Bernard University Lyon 1, Lyon
- 2022 3h Lectures in the Option AEST (Agriculture, Environnement, Santé et Territoire), Agronomic engineering cursus (year 3), VetAgro Sup, agronomic campus, Lempdes
- 2022 3h Member of the evaluation committee for oral defense of Agronomic engineering final-year dissertation project, VetAgro Sup, Lempdes.
- 2021 3h Practical lectures in the UE "Atelier One Health", Agronomic engineering cursus (year 3) Option AEST (Agriculture, Environnement, Santé et Territoire), VetAgro Sup, campus Agro, Lempdes
- 2020 1h recorded lecture on African Swine Fever, for BSc students to UNA Europa, GAAFS (Global Academy of Agriculture and Food Systems), University of Edinburgh, Edinburgh.
- 2020 1h lecture on epidemiology study design to year 4 veterinary students of University of Lilongwe (Malawi).
- 2019-2020: Design and delivery of the epidemiology and statistics courses as part of the Fleming Fund Fellowship programme. Total: 10h
- 2013: I was involved in the Honours Elective programme at the School of Biological Science, University of Edinburgh, participating in the delivery of lectures (2h) and evaluation of the students' research presentation (2h). Total: 4h
- 2009-2010: I taught epidemiology, statistics and GIS to veterinary officers as part of the Caribbean Veterinary Epidemiologist/Para-epidemiologist (VEP) programme. I was also guest lecturer (3h) to postgraduate students at the University of French West Indies (Guadeloupe).
- 2005: practical lectures (4h) on epidemiology for veterinary students at Massey University, Palmerston North, New Zealand.
- 2002-2003: practical lectures (6h) on data analysis for veterinary students at the National Veterinary School of Lyon, France.

Scientific outputs

Summary of scientific outputs

Since the beginning of my career, I have disseminated my research over a varied range of methods to maximise inputs to target audiences. Notably, I published 54 peer-reviewed articles (including 2 review and 1 editorial letter), 1 book chapter, 4 preprint articles, 4 peer-reviewed conference papers, 27 conference abstracts in proceedings and 12 posters. I presented my work and the work of my students mostly in international conferences. I have been invited as a keynote speaker to the OpenSession Meeting of euFMD in Marseille (in 2022) and in Alcalá de Henares (in 2024), and was invited to present in 17 seminars, including 4 to thematic symposiums with broad audience.

However, a large part of my research activities is to inform policy makers and industry stakeholders. As such, I focused on publishing research in media accessible to them, preferring publishing in open-access peer-reviewed journals over fee-access ones. In addition, I produced 3 peer-reviewed technical reports and 10 technical reports to animal health and welfare branch of 4 governments (Scotland, USA, Malawi, New Zealand) and to industry stakeholders (UK, South Africa, Uganda, New Zealand) and intensively contributed in 10 policy and research briefs to Scottish Governments. However, translational research is complicated to published as peer-reviewed articles. To this end, I have been involved as Guest Associate Editor and co-coordinated the Topic “Risk-Based Evidence for Animal Health Policy” for *Frontiers in Veterinary Science – Veterinary Epidemiology and Economics*. Although of low impact factor at the time of publication and requiring a large investment in time and efforts, this Topic offered a way for epidemiologist working in translational research to policy makers to showcase pieces of work that were difficult to publish otherwise (or hardly accessible to policymakers). In total, 7 of the 18 papers published in this Topic included at least 1 member of EPIC (incl. 2 papers in which I contributed). This Topic has been internationally successful, with published articles being viewed (total: 94k) and downloaded (total: 17k) multiple times.

Some of my research was used to produce communication material to general public and the farming communities as posters displayed in the Royal Highland Show, one of Europe's largest agribusiness shows, and in websites (see <https://www.veillecep.fr/2023/06/transport-danimaux-et-observance-des-consignes-sanitaires-le-role-des-chauffeurs/> for example). In particular, my research on the role of livestock haulage vehicles on the spread of diseases has demonstrated the importance of this route of transmission on the spread of disease and highlighted the need to improve cleaning & disinfection protocols in the UK. This work has led the Agriculture and Horticulture Development Board (AHDB) and the National Pig Association (NPA) to launch the #MuckfreeTruck national campaign to raise awareness and prevent economic losses in the event of future outbreaks (<https://www.nationalhogfarmer.com/biosecurity/scientists-predictions-lead-to-muckfreetruck-campaign>).

Activities in the national and international research landscape

Network

As a member of the Scottish Government's Centre of Expertise on Animal Disease Outbreaks (EPIC) since 2011, I am benefiting from the large network of scientist from 2 Scottish High Education Institutes (University of Edinburgh including the Roslin Institute and the Global Academy of Agriculture and Food Systems, University of Glasgow) and 4 Main Research Providers (the Moredun Research Institute [MRI], the James Hutton Institute [JHI], Biomathematics and Statistics Scotland [BioSS], and the Scottish Rural College [SRUC]). This opened up interesting opportunities for collaboration on modelling the spread of diseases. Notably, my work on COVID19 modelling was initiated due to EPIC being a core partner of The Scottish COVID-19 Response Consortium (SCRC) as part of the Rapid Assistance In Modelling The Pandemic (RAMP) strategic programme of the Royal Society. This consortium gathered more than 30 UK research organisation including collaborators from the University of St Andrews, University of Oxford and the University of Exeter with who I either published or involved in the MSc-level teaching programme (M2 OHMHP) that I am coordinating (see section “Teaching and supervision” of this Scientific Report for more details on this teaching programme). To continue with my work with EPIC and SCRC, I was Honorary fellow of the University of Edinburgh (2020-2023) and I am an associate member of BioSS since 2020.

Recently, I was also involved in the different working groups, particularly “Santé et Territoires”, “Maladies Infectieuses Emergentes” and “Données”, for the construction of the newly created Transdisciplinary Institute for Health, as part of the ShapeMed@Lyon programme funded by a PIA4 – France 2030 “Excellence dans toutes ses formes” (ExcellencES) grant. These working groups provided opportunity to network with different researchers from Lyon with keen interest in infectious diseases but from different disciplines. It is thanks to this network that I was involved as workpackage lead in the project EVASION newly funded by the ANR JCJC of Guillaume Minard (UMR 5557 Laboratoire d'Écologie Microbienne, LEM) and in the supervision teams of a new PhD project on the impact of nature-based solutions on the proliferation of tiger mosquitoes in urban areas in a multidisciplinary consortium led by the UMR LEM and involving the UMR GATE (economics) and UMR EVS (geography).

I am member of professional societies, especially the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), and lately the Réseau thématique de recherche pour la santé et le bien-être en Auvergne Rhône-Alpes (SAARA). These society and network enable an effective exchange of information within a dynamic and extensive professional network while provide opportunities to develop small project proposals. I encourage the non-permanent members of my team as well as PhD students to join the SVEPM and participate to the annual conference as it gives them opportunities to present their work in a benevolent environment and audience, and broaden their network by creating new contacts with colleagues from European research institutions and organisations. These are key when they are looking for postdoc position and a permanent job.

Conferences

I have presented in 48 international conferences (27) and seminars (21) to which I have been invited to speak. I also chaired multiple sessions and participated in panel discussions. These gave me visibility to my work and gave me some opportunities to strengthen my international network and initiate new collaborations. For example, I presented 2 papers at ISVEE14 in Mexico led to not only get involved in the PhD thesis of J. Grewar as co-supervisor with Peter Thompson (University of Pretoria) but also gave me the opportunity to initiate a new collaboration with the South African horse industry (SAEHP, see “Expertise and impact” section of the Scientific report) on assessing the role of zebra populations in the long-term circulation of African horse sickness in the Western Cape Province of South Africa.

Shortly after I was recruited as the Head of the IDEXLyon VPH Chair, I also contributed to the organization of the first international conference of the VPH Hub “One Health at the Confluence of human & veterinary public health” as the co-president of the scientific committee, together with Mark Bonneville (Fondation Merieux) and Emmanuelle Soubeyran (then Head of VetAgro Sup, currently Director General of the World Organisation for Animal Health, WOAH) and member of the organization committee. In this conference, I also chaired, together with X. Bailly (INRAE, UMR EPIA), the round table discussion of the Session “Surveillance and Control”.

I also organized round tables as part of the Journées Collaboratives of LyonBioPole on the topic of improving control and surveillance systems against emerging Infectious diseases. I also participated in several seminars and workshops, in particular PREZODE workshops Europe #2 and #3, chairing panel discussions and round discussions on this topic. These activities increased the visibility of my activities on surveillance and control of infectious diseases to a broad range of industry stakeholders and policymakers as well as to researchers from national and international organizations.

List of evaluation committee

- 2024: Member of the selection committee for INRAE research fellow [Chargé de Recherche de Classe Normale] in “Epidemiology, genetic et modelling for Health”.

Publication list

Book chapter

- G. Fournié, P. Walker, **T. Porphyre**, R. Métras, D. Pfeiffer (2011). Mathematical models of infectious diseases in livestock: concepts and application to the spread of highly pathogenic avian influenza viruses type H5N1. *In Human and Environmental Health and the Future of Animal Agriculture (Eds D. Zilberman, J. Otte, D. Roland-Holst, D. Pfeiffer)*. Springer, Berkeley, CA, USA, 250 p. ISBN-10: 1441970762.

Review papers – peer reviewed

- A. Renard, F. Pérez Lombardini, M. Pacheco Zapata, **T. Porphyre**, A. Bento, G. Suzan, D. Roiz, B. Roche, A. Arnal (2023) Interaction of human behavioral factors shapes the transmission of arboviruses by *Aedes* and *Culex* Mosquitoes. *Pathogens* 12(12), 1421. <https://doi.org/10.3390/pathogens12121421>
- L. Gonzalez Gordon, **T. Porphyre**, D. Muhanguzi, A. Muwonge, L. Boden, B.M.deC. Bronsvooort (2022) A scoping review of foot-and-mouth disease risk, based on spatial and spatio-temporal analysis of outbreaks in endemic settings. *Transboundary and Emerging Diseases* 69(6): 3198-3215

Editor letter – peer reviewed

- L.A. Boden, H.K. Auty, A. Delgado, J.D. Grewar, A. Hagerman, **T. Porphyre**, G. Russell (2020) Editorial: Risk-based evidence for animal health policy. *Frontiers in Veterinary Science*. <https://doi.org/10.3389/fvets.2020.00595>

Journal articles – peer reviewed

- R. Fay, M. Gamelon, E. Baubet, **T. Porphyre** (2024) The time of infection matters: seasonal interplay between host and pathogen drives epidemic dynamics. *Oikos* [Accepted] <https://doi.org/10.1111/oik.10750>
- R. Allen, L.A. Boden, I. Hutchinson, J. Stirling, **T. Porphyre** (2024) Cleaning practices of transport vehicles by commercial and non-commercial livestock markets users in Scotland. *Research in Veterinary Sciences*, 180: 105413. <https://doi.org/10.1016/j.rvsc.2024.105413>
- S. Kalthoum, S. Mzoughi, R. Gharbi, M. Lachtar, B. Bel Haj Mohamed, H. Hajlaoui, W. Khalfaoui, A. Dhaouadi, I. Ben Sliman, C. Ben Salah, H. Kessa, H. Benkirane, A.J. Fekih, K. Barrak, H. Sayari, C. Bahloul, **T. Porphyre** (2024) Factors associated with the spatiotemporal distribution of dog rabies in Tunisia. *PLoS Neglected Tropical Disease* 18(8): e0012296. <https://doi.org/10.1371/journal.pntd.0012296>
- A. Bibard, D. Martinetti, A. Giraud, A. Picado de Puig, K. Chalvet-Monfray, **T. Porphyre** (2024) Quantitative risk assessment for the introduction of Bluetongue virus into mainland Europe by long-distance wind dispersal of *Culicoides* spp.: a case study from Sardinia. *Risk Analysis*, 1-20. <https://doi.org/10.1111/risa.14345>

- A. Bibard, D. Martinetti, A. Picado, K. Monfray-Chalvet, **T. Porphyre** (2024) Assessing the risk of windborne dispersal of *Culicoides* midges in emerging epizootic hemorrhagic disease virus outbreaks in France. *Transboundary and Emerging Diseases*, 5571195. <https://doi.org/10.1155/2024/5571195>
- L. Gonzalez Gordon, **T. Porphyre**, A. Muwonge, D. Muhanguzi, N. Nantima, R.A. Ademun, F. Mwiine, L. Boden, B.M.deC. Bronsvoot (2023) Identifying target areas for risk-based surveillance and control of Transboundary Animal Diseases: A seasonal analysis of slaughter and live-trade cattle movements in Uganda. *Scientific Reports* 13:18619. <https://doi.org/10.1038/s41598-023-44518-4>
- C. Beslay, M. Bouix, H. Fauroux, A. Gautier, F. Luposella, J.-M. Pillon, **T. Porphyre**, M. Schell, N. Soleau (2023) « Un lavage, c'est un lavage ». Des chauffeurs bovins face aux consignes sanitaires [in French]. *Les mondes du Travail* 29 :147-163. <https://lesmondessdutavail.net/n-29-travail-et-ecologie-mars-2023/>
- E. Rydow, R. Borgo, H. Fang, T. Torsney-Weir, B. Swallow, **T. Porphyre**, C. Turkay, M. Chen (2023) Development and Evaluation of Two Approaches of Visual Sensitivity Analysis to Support Epidemiological Modeling. *IEEE Transactions on Visualization and Computer Graphics* 29(1), 1255-1265. <https://doi.org/10.1109/TVCG.2022.3209464>.
- A. Muwonge, C. Mpyangu, A. Nsangi, I. Mugerwa, B.M.deC. Bronsvoot, **T. Porphyre**, E.R. Ssebagala, A. Kiayias, E. Mwaka, M. Joloba (2022) A protocol for developing digital contact tracing tailored to haulage in East Africa to support COVID-19 surveillance. *BMJ Open* 12: e058457. <https://doi.org/10.1136/bmjopen-2021-058457>
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Journal articles – submitted

- I. McLachlan, G. Marion, I. J. McKendrick, B. M. Bronsvoort, **T. Porphyre** (submitted) Reviewing the performance of R_0 estimation methods using outbreak data: insights for foot and mouth disease vaccination programmes. *Preventive Veterinary Medicine*
- R. Fay, M. Gamelon, **T. Porphyre** (submitted) Climate warming drives pulsed-resources and disease outbreak risk. *Proceeding of the Royal Society B*
- S. Catterall, **T. Porphyre**, G. Marion (submitted) iPAR: A framework for modelling and inferring information about disease spread when the populations at risk are unknown. *PLoS Comput. Biol.*
- T. Khalid, **T. Porphyre**, M. Kimishima, E. Gilot-Fromont, H. Auty (submitted) Interactions between feral and domestic pigs on outdoor pig farms: a questionnaire survey of farmers' awareness and biosecurity practices in Scotland. *Research in Veterinary Sciences*

Journal articles – in preparation

- T. Khalid, E. Gilot-Fromont, **T. Porphyre** (in preparation) Assessing the risk of infection at the interface: quantitative assessment of African swine fever between wild boars and outdoor pigs in France.
- L. González-Gordon, D. Muhanguzi, A. Muwonge, N. Nantima, R. Ademun, S. Ochwo, N.F. Mwiine, L.A. Boden, B.M. de C. Bronsvoort, **T. Porphyre** (in preparation) Bayesian spatial analysis and risk factors of foot-and-mouth disease outbreaks in Uganda.
- G. Margiapia, C. Puppo, S. Gardon, **T. Porphyre** (in preparation) Surveillance of African swine fever in the Auvergne-Rhone-Alpes region, France: Understanding factors that may delay reporting suspected cases.
- **T. Porphyre**, A. Bibard, D. Martinetti, A. Picado, S. Zientara (in preparation) Modelling the spread of epizootic hemorrhagic disease virus serotype 8 in France.

Preprint

- T. Khalid, **T. Porphyre**, M. Kimishima, E. Gilot-Fromont, H. Auty (2024) Interactions between Feral and Domestic Pigs on Outdoor Pig Farms: A Questionnaire Survey of Farmers' Awareness and Biosecurity Practices in Scotland. *SSRN preprint*: <http://dx.doi.org/10.2139/ssrn.4983068>
- R. Allen, L. Boden, I. Hutchinson, J. Stirling, **T. Porphyre** (2024) Cleaning Practices of Transport Vehicles by Commercial and Non-Commercial Livestock Markets Users in Scotland. *SSRN preprint*: <http://dx.doi.org/10.2139/ssrn.4797905>

- S.N. Mitchell, A. Lahiff, N. Cummings, J. Hollocombe, B. Boskamp, D. Reddyhoff, R. Field, K. Zarebski, A. Wilson, M. Burke, B. Archibald, P. Bessell, R. Blackwell, L.A. Boden, A. Brett, S. Brett, R. Dundas, J. Enright, A.N. Gonzalez-Beltran, C. Harris, I. Hinder, C.D. Hughes, M. Knight, V. Mano, C. McMonagle, D. Mellor, S. Mohr, G. Marion, L. Matthews, I.J. McKendrick, C.M. Pooley, **T. Porphyre**, A. Reeves, E. Townsend, R. Turner, J. Walton, R. Reeve (2021) FAIR Data Pipeline: provenance-driven data management for traceable scientific workflows. *arXiv preprint* [arXiv:2110.07117](https://arxiv.org/abs/2110.07117)
- A. Muwonge, P.R. Bessell, **T. Porphyre**, P. Motta, G. Rydevik, G. Devailly, N.F. Egbe, R.F. Kelly, I.G. Handel, S. Mazeri, B.M.deC. Bronsvoort (2021) Inferring livestock movement networks from archived data to support infectious disease control in developing countries. *bioRxiv preprint* <https://doi.org/10.1101/2021.03.18.435930>

List of conference and seminar outputs

Conference – keynote presentation

- **T. Porphyre** (2022) Harnessing technology to collect and integrate data and convert to useful information for decision makers. EuFMD Open session (OS22), Marseille, France.
- **T. Porphyre** (2024) Complexity of modelling the spread and responses to TADs in a dynamic world. EuFMD Open session (OS24), Alcalà de Henares, Spain.

Conference papers

- I. McLachlan, G. Marion, I. J. McKendrick, B. M. Bronsvoort, **T. Porphyre** (2023) Reviewing the performance of R_0 estimation methods using outbreak data: insights for foot and mouth disease vaccination programmes. Proceedings of the 2023 Annual Meeting of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), Toulouse, France.
- K. Stański, S. Lycett, **T. Porphyre**, M. Bronsvoort (2019) Data-driven modelling for improving herd-level bovine tuberculosis breakdown predictions in GB cattle. Proceedings of the 2019 Annual Meeting of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), Utrecht, the Netherlands.
- **T. Porphyre**, C. Correia-Gomes, G.J. Gunn (2017) Government preparedness for exotic incursions of swine fevers in Scotland: How can research help. Proceedings of the 2017 Annual Meeting of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), Inverness, Scotland, UK.
- K.D.C. Stärk & **T. Porphyre** (2011). How Modelling can Add Value to Infectious Disease Research: Illustrated Examples for LA-MRSA. 2nd ASM-ESCMID Conference on Methicillin-resistant Staphylococci in Animals: Veterinary and Public Health Implications. Washington DC, USA.

Conference – oral presentation

- **T. Porphyre** (2024). Why an international Master in One Health? 14th International Symposium for Higher Education (Universidad 2024), la Havana, Cuba.
- R. Fay, M. Gamelon, E. Baubet, **T. Porphyre** (2023). Modelling the interplay between demography and epidemiology dynamics: the case of African swine fever in wild boar 9th International Conference on Infectious Disease Dynamics (EPIDEMICS⁹), Bologna, Italy.
- I. McLachlan, G. Marion, I. J. McKendrick, B. M. Bronsvoort, **T. Porphyre** (2023) Reviewing the performance of R_0 estimation methods using outbreak data: insights for foot and mouth disease vaccination programmes. Proceedings of the 2023 Annual Meeting of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), Toulouse, France.

- **T. Porphyre**, K. Gamado, A. Delgado, M. Shoenbaum, M.K. Torchetti (2018) Inferring the spatial spread of highly pathogenic avian influenza H5N2 clade 2.3.4.4 during the 2015 epidemics in Iowa. 15th International Symposium for Veterinary Epidemiology and Economics (ISVEE XV), Chiang Mai, Thailand.
- **T. Porphyre** (2018) Multiplex network analysis unravels haulage vehicles as a hidden threat to the British swine industry. Infectious Disease Dynamics conference (IDDconf), Ambleside, UK.
- P. Motta, **T. Porphyre**, G. Rydevik, S. Hamman, V. Tanya, I.G. Handel, B.M. de C. Bronsvort (2017) Drivers of cattle market price formation in Cameroon. Inaugural Meeting of the International Society for Economics and Social Sciences of Animal Health (ISESSAH), Aviemore, Scotland, UK.
- **T. Porphyre**, K. Gamado, C. Correia-Gomes, A. Reeves, H.K. Auty, G.J. Gunn, G. Marion, M.E.J. Woolhouse (2015) How would classical swine fever spread in Great Britain? Data fit and predictions. 14th International Symposium for Veterinary Epidemiology and Economics (ISVEE XIV), Merida, Yucatan, Mexico.
- **T. Porphyre**, S.P.M. Wijayanti, M.E. Chase-Topping, A. Kohl (2015) Is weather really important for arbovirus infection? The case of dengue in Central Java. 14th International Symposium for Veterinary Epidemiology and Economics (ISVEE XIV), Merida, Yucatan, Mexico.
- **T. Porphyre**, C. Correia-Gomes, K. Gamado, I. Hutchinson, M.E. Chase-Topping, H.K. Auty, L.A. Boden, A. Reeves, G.J. Gunn, M.E.J. Woolhouse (2015) Vulnerability of the British swine industry to Classical Swine Fever. 11th International Conference on the Epidemiology and Control of Biological, Chemical and Physical Hazards in Pigs and Pork (SafePork), Porto, Portugal.
- **T. Porphyre**, E.S. Giotis, D.H. Lloyd, K.D. Stärk (2012) A metapopulation model to assess the capacity of spread of meticillin-Resistant *Staphylococcus aureus* ST398 in humans (2012). 13th International Symposium for Veterinary Epidemiology and Economics (ISVEE XIII), Maastricht, the Netherlands.
- **T. Porphyre**, A. Loeffler, D.H. Lloyd, E. Giotis, E. Broens, K.D.C. Stärk (2011). Modelling the spread of MRSA ST398 to communities: role of persistent carriage and pig exposure. 4th Symposium on Antimicrobial Resistance in Animals and the Environment (ARAE), Tours, France.
- **T. Porphyre**, J. McKenzie, J. Shepherd, A. Byrom, G. Nugent, I. Yockney. Spatial prediction of wildlife reservoir abundance: a basis to cost-effectively control bovine TB (2007). 3rd International Conference on the Applications of GIS and Spatial Analysis to Veterinary Science (GISVet), Copenhagen, Denmark.
- **T. Porphyre**, M. Stevenson, J. McKenzie. Analysis of cattle TB surveillance data to identify wildlife sources of infection (2006). 11th International Symposium for Veterinary Epidemiology and Economics (ISVEE XI), Cairns, Australia.
- **T. Porphyre**, M. Stevenson, J. McKenzie. Application of statistical and molecular tools in the epidemiology of TB (2006). 83rd New Zealand Veterinary Association Conference, Auckland, New Zealand.
- **T. Porphyre**, S. Titus, R. Jackson, M. Stevenson (2007). Heterogeneity of contacts between wild possums: How the tuberculosis R_0 can be affected? NZVA Veterinary Epidemiology Seminar, Massey University, Palmerston North, New Zealand.
- J. McKenzie & **T. Porphyre** (2005). Application of molecular epidemiology to wildlife-associated TB in NZ. 82nd New Zealand Veterinary Association Conference, Wellington, New Zealand.
- **T. Porphyre**, J. McKenzie, M. Stevenson (2005). Persistence of bovine TB in Featherston. National Possum Control Authorities National Technical Transfer Seminar, Wellington, New Zealand.

Conference – associated oral presentation (students, postdocs and collaborators)

- R. Fay, M. Gamelon, E. Baubet, **T. Porphyre** (2023) Bridging the gap between demography and epidemiology: the wild boar - African swine fever system as a case study. EvoDemoS2023: Evolutionary Demography Society 8th Annual Meeting, Paris, France.
- K. Stański, S. Lycett, **T. Porphyre**, M. Bronsvoort (2019) Machine learning for vector representation of GB farms within cattle movement network to predict future herd-level bTB and BVD breakdowns. 8th International Conference on Infectious Disease Dynamics (EPIDEMICS⁸), Charleston, SC, USA.
- **T. Porphyre**, J Grewar (2019) Establishing whether the population structure of zebra in the Western Cape African horse sickness control zones is competent to act as a reservoir host for AHSV. 17th Annual Congress of the South African Society of Veterinary Epidemiology & Preventive Medicine (SASVEPM), Umhlanga, South Africa.
- **T. Porphyre**, J Grewar (2019) Establishing whether the population structure of zebra in the Western Cape African horse sickness control zones is competent to act as a reservoir host for AHSV. Congress of the Wildlife group of the South African Veterinary Association (SAVA), Lanseria, South Africa.
- K. Stański, S. Lycett, **T. Porphyre**, M. Bronsvoort (2018) Improving herd-level bovine tuberculosis breakdown predictions in GB cattle by applying machine learning methods. 15th International Symposium for Veterinary Epidemiology and Economics (ISVEE XV), Chiang Mai, Thailand.
- S. Costard, F.J. Zagmutt, **T. Porphyre**, F. Roger, D.U. Pfeiffer (2011) African swine fever: Modelling the silent release from small scale farms and consequences for disease persistence in affected areas. 3rd International Conference on Infectious Disease Dynamics (EPIDEMICS³), Boston, MA, USA.
- E. S. Giotis, A.J. McCarthy, A. Loeffler, **T. Porphyre**, J.A. Lindsay, D.H. Lloyd (2011) Interactions of MRSA ST398 and inhibitor producing *S. aureus* strains *in vitro* and *in vivo*. 4th International Conference on Environmental, Industrial and Applied Microbiology (BioMicroWorld2011) Torremolinos, Spain.
- R. Jackson, **T. Porphyre**, C. Sauter-Louis, D. Ward, G. Baghyan, E. Stephanyan (2009). An epidemiological investigation of the occurrence of brucellosis in communities in Armenia during 2006 and 2007. 12th International Symposium for Veterinary Epidemiology and Economics (ISVEE XII), Durban, South Africa.
- R. Jackson, **T. Porphyre**, C. Sauter-Louis, D. Ward, G. Baghyan, G. Vardanyan, E. Stephanyan (2008) An epidemiological investigation of the occurrence of brucellosis in communities in Armenia during 2006 and 2007. The Brucellosis 2008 International Research Conference, Royal Holloway College, London, UK
- **T. Porphyre**, S. Naas, P. Sabatier, A. Leblond. Horse-baited Trapped Mosquitoes, Potential Vectors of West Nile Virus in Southern France (2003). 10th International Symposium for Veterinary Epidemiology and Economics (ISVEE X), Viña del Mar, Chile.
- D.J. Bicout, **T. Porphyre**, J-A. Ndione, P. Sabatier. Modelling Abundance of Aedes and Culex spp in Rain Fed Ponds in Barkedji, Senegal (2003). 10th International Symposium for Veterinary Epidemiology and Economics, Viña del Mar, Chile.

Conference – posters

- G. Margiapia, C. Puppo, S. Gardon, **T. Porphyre** (2024) Getting to the root of delays in reporting African swine fever suspected cases. Annual Meeting of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), Uppsala, Sweden.
- **T. Porphyre**, A. Delgado, M. Shoenbaum, M.K. Torchetti (2018) What can we say from the death of layer chickens? Estimating within-flock HPAI (H5N2) dynamics using an Approximate Bayesian

Computation framework. 15th International Symposium for Veterinary Epidemiology and Economics (ISVEE XV), Chiang Mai, Thailand.

- **T. Porphyre**, B.M.deC. Bronsvoort, G.J. Gunn, C. Correia-Gomes (2018) Assessing the impact of haulage companies on the pig trade network in Great Britain. Annual Meeting of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), Tallin, Estonia.
- **T. Porphyre**, B.M.deC. Bronsvoort, G.J. Gunn, C. Correia-Gomes (2017) Role of haulage companies in the connectivity of pig farms in Great Britain: a network analysis. 6th International Conference on Infectious Disease Dynamics (EPIDEMICS6), Sitges, Spain.
- **T. Porphyre**, A. Delgado, M. Schoenbaum, M.K. Torchetti (2017) What can we say from the death of layer chickens? Estimating within-flock HPAI (H5N2) dynamics using an Approximate Bayesian Computation framework. 6th International Conference on Infectious Disease Dynamics (EPIDEMICS6), Sitges, Spain.
- K. Gamado, G. Marion, **T. Porphyre** (2017) Risk assessment from small scale and early phase epidemics. 6th International Conference on Infectious Disease Dynamics (EPIDEMICS6), Sitges, Spain.
- **T. Porphyre**, C. Correia-Gomes, G.J. Gunn (2016) Research facilitation of pig sector and government preparedness for exotic incursions of swine fevers: the case of Scotland. 3rd Annual Global African Swine Fever Research Alliance (GARA) Scientific Workshop, Ploufragan, France.
- **T. Porphyre**, H. Auty, M.E.J. Woolhouse, G.J. Gunn, K.M. Rich (2015) The role of stocking constraints on the cost-effectiveness of vaccination against foot-and-mouth disease: the case of Scotland. 2016 Annual Meeting of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), Elsinore, Denmark. With Oral Presentation.
- **T. Porphyre**, H. Auty, M.E.J. Woolhouse, G.J. Gunn, K.M. Rich (2015) The role of stocking constraints on the cost-effectiveness of vaccination against foot-and-mouth disease: the case of Scotland. 14th International Symposium for Veterinary Epidemiology and Economics (ISVEE XIII), Merida, Yucatan, Mexico.
- **T. Porphyre**, C. Correia-Gomes, K. Gamado, I. Hutchinson, H.K. Auty, L.A. Boden, A. Reeves, G.J. Gunn, M.E.J. Woolhouse (2015) Silent spread of classical swine fever in the UK: where and when to worry? 2015 Annual Meeting of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), Ghent, Belgium. With Oral Presentation.
- **T. Porphyre**, H.K. Auty, M.J. Tildesley, G.J. Gunn, M.E.J. Woolhouse (2013) Vaccination against foot-and-mouth disease: do initial conditions affect its benefit? 4th International Conference on Infectious Disease Dynamics (EPIDEMICS⁴), Amsterdam, the Netherlands.
- **T. Porphyre**, E.S. Giotis, D.H. Lloyd, K.D. Stärk (2012) Assessing control measures against MRSA ST398 in farrow-to-finish pig farm: a modelling approach. 13th International Symposium for Veterinary Epidemiology and Economics (ISVEE XIII), Maastricht, the Netherlands.

Conference – associated posters (students, postdocs and collaborators)

- A. Bibard, D. Martinetti, A. Giraud, A. Picado de Puig, K. Chalvet-Monfray, **T. Porphyre** (2023) Risk assessment of BTV incursion in Europe from Sardinia by *Culicoides spp.* Wind dispersal. International Conference on Using Epidemiological Studies in Health Risk Assessments. Berlin, Germany.
- A. Bibard, D. Martinetti, A. Giraud, A. Picado de Puig, K. Chalvet-Monfray, **T. Porphyre** (2023) Risk assessment of BTV incursion in Europe from Sardinia by *Culicoides spp.* Wind dispersal. Annual Meeting of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), Toulouse, France.
- L. González, **T. Porphyre**, D. Muhanguzi, A. Muwonge, L. Boden, B. M. Bronsvoort (2023) Foot-and-mouth disease risk based on spatial and spatio-temporal analysis of outbreaks in endemic areas.

Annual Meeting of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), Toulouse, France.

- I. McLachlan, G. Marion, I. McKendrick, I. Handel, **T. Porphyre**, M. Bronsvort (2017) Modelling the role of carriers in endemic foot and mouth disease. 6th International Conference on Infectious Disease Dynamics (EPIDEMICS6), Sitges, Spain.
- J.S. Flood, **T. Porphyre**, M.J. Tildesley, M.E.J. Woolhouse (2013) Epidemics on realistic landscapes. 4th International Conference on Infectious Disease Dynamics (EPIDEMICS⁴), Amsterdam, the Netherlands.

Invited symposiums and panel discussions

- Apr. 2024: Invited speaker to the workshop “Fighting against infectious and tropical diseases: between historical legacy and global challenges”, organised by the Pasteur Network, the French Embassy in Panama, IRD and the City of Knowledge Foundation, held in Panama.
- Feb. 2024: Invited panel discussion speaker to the FSPI Cuba IES “Internationalisation of Cuban higher education” Workshop “Internationalisation of higher education in Cuba - A comparison with France”, title: “Double diploma: the ultimate tool for internationalisation? the example of the Master in One Health degree”. 14th International Symposium for Higher Education (Universidad 2024), la Havana, Cuba.
- Jun. 2023: Invited panel discussion speaker to IRD – ANRS|MIE Workshop "One Health Research in an international epidemic context", Montpellier, France
- Jan. 2023: Invited speaker to the seminar “Journée scientifique du réseau régional thématique de recherche pour la sante et le bien-etre animal en Auvergne Rhone-Alpes (SAARA)”, VetAgro Sup, Marcy l’Etoile, France. Title : "The Veterinary Public Health Hub".
- Mar. 2021: Closing remarks for the seminar “Restitutions des travaux collectifs en science politique – Master PAGERS” organised by SciencesPo Lyon - ENSV-FVI VetAgro Sup, held in Marcy l’Etoile, France.
- October 2019: Invited speaker to the workshop “Staying ahead of disease: A workshop for the Scottish pig industry” held in Oldmeldrum, UK. Title: “ASF spread and the role of livestock transport trucks: The science behind #muckfreetruck”.
- Oct. 2018: Invited speaker to the joint APHA-EPIC workshop “Use of pig movement data for modelling and demographics”, Animal and Plant Health Agency (APHA), Weybridge, UK. Title: “Impact of sharing haulage vehicles on the spread of pig diseases in GB” and “EPIC’s African swine fever risk model”.
- Feb. 2018: Invited speaker to the Moredun Research Institute’s Vaccine Efficacy Workshop 2018, Edinburgh, UK. Title: “Vaccinating against foot-and-mouth disease – constraints and requirements in European and African settings”
- Dec. 2017: Invited speaker to the Statistical and Mathematical Modeling in Biological Applications (SaMMBA) seminar, Institut Pasteur, Paris, France. Title: “Climbing the ladder to preparedness: modelling the spread of swine fevers in Great Britain”.

Chairing commitments

- Jun. 2023: Chaired the Session 4 of the IRD – ANRS|MIE workshop "One Health Research in an international epidemic context", Montpellier, France
- Dec 2021: Chaired the Break-out group “Surveillance systems” of the PREZODE EUROPE workshop #3 (online)

- Oct 2021: Chaired the Break-out group “Surveillance systems – capacity building” of the PREZODE EUROPE workshop #2 (online)
- Jan. 2022: Chaired the panel discussion “Surveillance and control” of the first conference “*One Health at the Confluence of human & veterinary public health*” (online).
- Oct 2018: Facilitated the joint APHA-EPIC workshop “Use of pig movement data for modelling and demographics” held in Weybridge, UK (Oct. 2018).

Invited seminars and workshops

- Apr. 2024: Invited speaker to the UNAM/IRD LMI ELDORADO internal seminar, Merida, Yucatan, Mexico. Title: “Modelling the risk of wind dispersion of EHDV in France”.
- Feb. 2024: Invited speaker to the UMR346 ‘Épidémiologie des maladies animales et zoonotiques (EPIA)’ internal seminar, Centre INRAE Clermont-Auvergne-Rhône-Alpes, Theix, France. Title: “Assessing ASF risks at the wild boar - domestic interface”.
- Mar. 2023: Invited speaker to the UMR754 ‘Infections Virales et Pathologie Comparée (IVPC)’ internal seminar, University Claude Bernard – Lyon 1, Lyon, France. Title: “Risk of emergence of bluetongue virus serotypes in Europe”.
- Sep. 2022 : Invited speaker to the Journée du pôle EVAAS (Expertise Vétérinaire et Agronomique Animaux Sauvages), VetAgro Sup, Marcy l’Etoile, France. Title: “La modélisation, un outil d'analyse de l'interface domestique-sauvage.”
- Apr. 2021: Invited speaker to the Boehringer Ingelheim VPH quarterly meeting, online. Title: “Disease modelling – tools for better preparedness”.
- May 2021 - Invited lecturer to the Matchmaking Event "Présentation des 3 stratégies d'accélération en santé" organised by LyonBiopole, online. Title: “Le concept One Health – Défis et opportunités”.
- Jun. 2020: Invited speaker to the UMR5558 ‘Laboratoire de Biométrie et Biologie Évolutive (LBBE)’ internal seminar, online.
- Mar. 2019: Invited speaker to the Agriculture and Horticulture Development Board (AHDB), Kenilworth, UK.
- Dec. 2017: Invited speaker to the Faculty of Veterinary Medicine of Université de Montréal, Canada. Title: “Climbing the ladder to preparedness: modelling the spread of swine fevers in Great Britain”.
- Feb. 2016: Invited speaker to US Department of Agriculture (USDA), Fort Collins, CO, USA. Title: “EPIC and its role to enhance veterinary response to disease incursions in Scotland”.
- Apr. 2014: Invited speaker to the French Agency for Food, Environmental and Occupational Health & Safety (ANSES), Maisons-Alfort, France. Title: “Amélioration des plans d'intervention contre les pestes porcine en Ecosse: Analyse de réseaux et modèles”.
- Nov. 2012: Invited speaker to the French Agency for Food, Environmental and Occupational Health & Safety (ANSES), Maisons-Alfort, France. Title: “Amélioration du contrôle de la fièvre aphteuse en Ecosse en utilisant une approche intégrée”.

List of outreach communication

Communication to the general public as well as farming and Animal Health communities through interviews, panel discussion and events organised at agricultural shows:

- Sep. 2022: Speaker at the panel discussion “Recherche en Santé humaine et animale: même combat!” as part of the “Santé humaine, santé animale, santé de l’environnement : l’équation de notre avenir” conference series organized by L’Obs and 1Health, Lyon, France.
- Nov 2021: Presentation at the BioTuesday meeting series of Lyon BioPole, Lyon, France
- Nov 2021: interview at the One Health webinar series of Boehringer Ingelheim.
- 2022: interview for Merieux group internal publication
- 2021: interview for Vetomecum
- May 2019: Communications and poster presentations at the Centre of Expertise on Animal Disease Outbreaks (EPIC) stand, Royal Highland Show, Edinburgh, UK.
- May 2018: Communications and poster presentations at the Centre of Expertise on Animal Disease Outbreaks (EPIC) stand, Royal Highland Show, Edinburgh, UK.
- May 2017: Communications and poster presentations at the Centre of Expertise on Animal Disease Outbreaks (EPIC) stand, Royal Highland Show, Edinburgh, UK.
- May 2016: Communications and poster presentations at the Centre of Expertise on Animal Disease Outbreaks (EPIC) stand, Royal Highland Show, Edinburgh, UK.

Some of my research was used to produce communication material in websites (see <https://www.veillecep.fr/2023/06/transport-danimaux-et-observance-des-consignes-sanitaires-le-role-des-chauffeurs/> for example). In particular, my research on the role of livestock haulage vehicles on the spread of diseases has demonstrated the importance of this route of transmission on the spread of disease and highlighted the need to improve cleaning & disinfection protocols in the UK. This work has led the Agriculture and Horticulture Development Board (AHDB) and the National Pig Association (NPA) to launch the #MuckfreeTruck national campaign to raise awareness and prevent economic losses in the event of future outbreaks (<https://www.nationalhogfarmer.com/biosecurity/scientists-predictions-lead-to-muckfreetruck-campaign>).

Expertise and impact

Summary of expertise activities

I have always been involved in project in strong interaction with policy makers and industry stakeholders. Early on, I was involved in consultancy project with Merial and funded most of my PhD project with successive expertise works to the FAO and to the Animal Health Board (New Zealand) that was, and still is, mandated by the NZ government to control bovine Tuberculosis in the country. As such, my research has a strong commitment to be applied on the field and translated to policy as well as industry guidelines and recommendations.

Since 2011, I am member of the Scottish Government's Centre of Expertise on Animal Disease Outbreaks (EPIC) for which I was co-principal investigator and co-leader of EPIC's Topic “Analyses of Potential Disease Control Options” between 2016 and 2020. In this role, I have closely worked with policy makers to review policy and provide suitable quantitative, risk-based evidences to support their activities and decisions within and outside outbreak situations. In particular, I have played a leading part in designing and carrying

out ambitious multidisciplinary research programmes aiming to better prepare Scotland and the UK for the incursion of African swine fever (ASF) and foot-and-mouth disease (FMD). In these programmes, I worked extensively with the British pig industry (QMS, AHDB), the Scottish Government, DEFRA and the Animal and Plant Health Agency (APHA) to integrate inferred epidemiological properties with both real-time movement and large industry-relevant datasets into a disease modelling framework and evaluate multiple risks of disease spread and quantify the epidemiological and economic impact of various mitigation strategies. These pieces of work have resulted in numerous publications in international journals as well as technical reports (4) and policy briefs (10) to the Scottish Government, which were used as the basis for the design of National Exercises on ASF preparedness (Exercise Holly, Exercise Ivy) and to support the joint University of Edinburgh-Scottish Rural College (SRUC) 4* impact case study to REF21 (i.e. the Research Excellence Framework used to evaluate the impact of research from British Higher Education Institutions). As part of the EPIC team, I had a significant role in regular national FMD exercises (such as Exercise Rohan in 2015 and Exercise Blackthorn in 2018) and ASF exercises (such as Exercise Walnut in 2012 and Exercise Waratah in January 2020, a joint pilot rapid risk assessment exercise between the UK and the New South Wales Department of Primary Industries, Australia).

In addition, my work in collaboration with Economist from SRUC contributed to estimate that future severe outbreaks in Scotland would result in GBP862,000,000 in direct costs (e.g. export, culling and movement ban) and GBP88,000,000 in indirect costs (e.g. impact on commodity markets). These represented benchmarks for cost-saving policy decisions from both government and industry stakeholders and we provided options for the Scottish Government's FMD preparedness and vaccination control policies to comply with European Union directive 2003/85/EC, which mandates countries to have an emergency vaccination strategy in place in case of an outbreak. Particularly, my research has been used to inform plans on vaccine stocks after Brexit in the event that the UK can no longer access the European vaccine bank. As well, my research identified the conditions when vaccination is most effective, and the optimal vaccine stocks required.

As Head of the IDEXLyon Chair in VPH, expertise work on vaccination against ASF and FMD is still ongoing and is further strengthened by the close relationship between the VPH Chair and Boehringer Ingelheim, developing bespoke research activities to support their activities, such as the new PhD project starting in September 2023 on ASF vaccination and co-funded by Boehringer Ingelheim.

Between 2016 and 2018, I led consultancy works with the United States Department of Agriculture (USDA) and South African Equine Health and Protocol (SAEHP). For the work for USDA, I developed and adapted Bayesian statistical methods, together with colleagues from Biomathematics and Statistics Scotland (BioSS), to infer within- and between-flock epidemiological properties from limited outbreak data and implemented these tools on the 205 outbreaks of highly pathogenic avian influenza (H5N2) that occurred in cage layers in Iowa. This work was used to evaluate the speed and efficacy of active surveillance activities that were implemented to mitigate the spread of H5N2. Consultancy with SAEHP aimed to assess the role of small population of zebra on the persistence of African horse sickness in the Western Cape Province of South Africa. In this work, I developed a simulated model, integrating the epidemiological dynamics of this arthropod-borne virus together with the population dynamic of zebra and variations of the environment (temperature, NDVI). This work was published and used to support SAEHP response to the European Union's audit to South Africa's export protocols for exporting horses directly into the European market (instead of moving horse after 3months stay in Mauritius).

I am currently member of the pole EVAAS (Expertise Vétérinaire et Agronomique Animaux Sauvages) as expert in epidemiology and modelling.

List of consulting experiences

Aug. 2018 – Nov. 2018: Consultant to South African Equine Health and Protocols NPC (SAEHP)

Modelling the spread of African horse sickness in the Western Cape Province's Zebra population to evaluate the potential of AHS to persist after introduction.

Sep. 2016 – Sep. 2017: Consultant to the US Department of Agriculture

Modelling the within-barn and between-farm spread of avian influenza H5N2 during the 2015 outbreak in Iowa for assessing the surveillance system implemented to control its spread.

Jan. – Jun. 2008: Consultant to the Food and Agriculture Organization of the United Nations

Modelling the spatial distribution of Brucellosis in Armenia to inform control policy (project GCP/ARM/001/ITA).

Jan. – Jun. 2003: Consultant to Merial

Modelling the population dynamics of Cat Fleas in the domestic environment to evaluate the efficacy of various control measures.

List of expertise outputs

Peer-reviewed technical reports

- **T. Porphyre**, A. Jennings, J. Stirling, S. Mohr, H. Auty (2021) Descriptive analysis of pig production pyramids in Great Britain, 2016 – 2018. A peer-reviewed technical report produced by EPIC Centre of Expertise on Animal Disease Outbreaks to the Animal Health and Welfare Division (AHWD) of the Scottish Government. <https://www.epicscotland.org/resources/reports-by-epic-members/>
- **T. Porphyre**, C. Correia-Gomes, H.K. Auty, A. Reeves, J. Stirling, M.E.J. Woolhouse, G.J. Gunn (2016) Descriptive analysis of breeding pig pyramids in Great Britain and impact assessment of the national movement ban policy proposed during Exercise Walnut. A peer-reviewed technical report produced by EPIC Centre of Expertise on Animal Disease Outbreaks to the Animal Health and Welfare Division (AHWD) of the Scottish Government.
- **T. Porphyre**, M.E.J. Woolhouse, H.K. Auty, M.J. Tildesley, G.J. Gunn (2013) Cost-efficiency of a ring vaccination strategy to control a foot-and-mouth disease epidemic within the Scottish cattle and sheep industry. A peer-reviewed technical report produced by EPIC Centre of Expertise on Animal Disease Outbreaks to the Animal Health and Welfare Division (AHWD) of the Scottish Government.

Expertise reports – policymakers

- C. Wood, B.O. Chikufenji, A. Jennings, **T. Porphyre** (2021) Analysing DAHLD's available livestock health data to inform infectious disease surveillance initiatives in Malawi. A technical report for the Malawi Department of Animal Health and Livestock Development (DAHLD).
- A. Jennings, K. Adams, **T. Porphyre** (2021) Pig keepers in Lilongwe, their biosecurity practices, and African swine fever. A technical report for the Malawi Department of Animal Health and Livestock Development (DAHLD).

- C. Kyle, L.-A. Sutherland, **T. Porphyre** (2021) Understanding attitudes to biosecurity in small scale pig keepers. A technical report produced by EPIC Centre of Expertise on Animal Disease Outbreaks to the Animal Health and Welfare Division (AHWD) of the Scottish Government. <https://www.epicscotland.org/resources/reports-by-epic-members/>
- **T. Porphyre**, K. Gamado (2018) Characterization of the within and between farm spread of H5N2 HPAI in Iowa. Report to the United State Department of Agriculture (USDA), Project No. 16-9200-0472-CA.
- R. Jackson & **T. Porphyre** (2008) Republic of Armenia Brucellosis Seroprevalence Report. Epicentre – Massey University report to FAO, Project No. GCP/ARM/001/ITA: Phase 1 – Pilot program for control of brucellosis in Armenia.
- J. Benschop, **T. Porphyre**, L. McIntyre, C. King, (2005). Project 7 – A profile of livestock movements in the upper North Island for May-June 2005. In G. MacKereth (2005) Operation Waiheke. Intelligence Report, Biosecurity, New Zealand.

Expertise reports – industry stakeholders

- **T. Porphyre**, John Grewar (2018) Modelling the natural circulation of African Horse sickness in Zebra in the Western Cape province. Report to the South African Equine Health and Protocol (SAEHP), Consultancy Agreement No: C14675.
- **T. Porphyre**, B.M.deC. Bronsvort, J. Muleme, R. Ayebale, C. Kyanka, A. Muwonge (2018) The state of peri-urban livestock production in Kampala, Uganda. Report to Edinburgh Global, University of Edinburgh, Edinburgh, UK.
- A. Byrom, G. Nugent, J. McKenzie, **T. Porphyre**, N. Poutu, J. Shepherd, J. Whitford, I. Yockney (2008). Cost effective control of TB in the Northern South Island High Country: Identifying the habitats and vector species requiring control. Landcare Research contractual report to the Animal Health Board, Project No. R-80629, New Zealand. <http://www.ahb.org.nz>
- **T. Porphyre**, J. McKenzie, M. Stevenson (2006). Identifying the cause of, and solutions to, vector-related TB persistence near Featherston. Massey University contractual report to the Animal Health Board, Project No.R-50634, New Zealand. <http://www.ahb.org.nz>

Policy and research briefs

- **T. Porphyre**, A. Jennings, H. Auty, L. Boden (2020) Identifying pig holdings at higher risk of contact with feral pigs in Scotland. EPIC policy brief (EPIC_202021_PB_004) to the Animal Health and Welfare Division (AHWD) of the Scottish Government.
- **T. Porphyre**, A. Jennings (2021) Descriptive analysis of pig production pyramids in Great Britain. EPIC policy brief (EPIC_202122_PB_003) to the Animal Health and Welfare Division (AHWD) of the Scottish Government.
- **T. Porphyre**, R. Allen, L. Boden (2021) Outcome of the questionnaire on cleaning practices of transport vehicles by Scottish cattle and sheep market users. EPIC policy brief (EPIC_202122_PB_001) to the Animal Health and Welfare Division (AHWD) of the Scottish Government.
- G. Innocent, **T. Porphyre**, I.J. McKendrick (2017) An analysis of bovine TB breakdowns in Scotland using statistical modelling to integrate bTB test results and animal movement data to identify geographical risk areas. EPIC policy brief (EPIC_201718_PB_001) to the Animal Health and Welfare Division (AHWD) of the Scottish Government.
- K. Stanski, S. Lycett, **T. Porphyre**, M. Fujiwara, H. Auty, L. Boden, M. Bronsvort (2020) Machine learning for herd-level bovine Tuberculosis breakdown prediction. EPIC research brief

(EPIC_202021_RB_001) to the Animal Health and Welfare Division (AHWD) of the Scottish Government.

- S. Mohr, A. J. Nisbet, S. T. G. Burgess, **T. Porphyre**, M. Fujiwara, L. Matthews (2020) Evaluating the uptake of a new diagnostic test for sheep scab by livestock farmers using stochastic game theory. EPIC research brief (EPIC_201920_RB_002) to the Animal Health and Welfare Division (AHWD) of the Scottish Government.
- **T. Porphyre**, M. Fujiwara (2020) Predicting the spread of ASF following introduction in Great Britain and its implication for Scotland. EPIC research brief (EPIC_201920_RB_001) to the Animal Health and Welfare Division (AHWD) of the Scottish Government.
- **T. Porphyre**, M. Fujiwara, H. Auty, L. Boden (2019) Potential impact of using haulage companies on the network of pig movements. EPIC research brief (EPIC_RB_1819_003) to the Animal Health and Welfare Division (AHWD) of the Scottish Government.
- **T. Porphyre** (2018) Assessing the risk of CSF spread in Great Britain and its implication for Scotland. EPIC research brief (EPIC_RB_1819_002) to the Animal Health and Welfare Division (AHWD) of the Scottish Government.
- **T. Porphyre** (2018) Modelling the within-herd spread of ASF and implication for the British industry. EPIC research brief (EPIC_RB_1819_001) to the Animal Health and Welfare Division (AHWD) of the Scottish Government.

Expert committee presentation

- Nov. 2022: Invited speaker to DEFRA's Core Species Expert Group (PIGS), Online.
- Sep. 2020: Invited speaker to DEFRA's Core Species Expert Group (PIGS), Online.
- May 2019: Invited speaker to DEFRA's Animal Health and Welfare Sector Council Chairs meeting, Nobel House, London, UK. Title: "ASF spread and the role of livestock transport trucks".
- Mar. 2019: Invited speaker to DEFRA's Core Species Expert Group (PIGS), Nobel House, London, UK. Title: "ASF spread and the role of livestock transport trucks".

National Disease control exercises

- 2016-2020 Member of the EPIC response team to the UK- and Scotland-wide exercises testing governments' contingency plans against major exotic disease outbreaks (Exercise Blackthorn, Exercise Waratah, Exercise Holly, Exercise Ivy).
- 2011-2016 Member of the EPIC response team to the UK- and Scotland-wide exercises testing governments' contingency plans against major exotic disease outbreaks (Exercise Walnut, Exercise Rowan and Exercise Mercury).
- 2005 Member of the Epicentre response team to the hoax FMD incursion event in Waiheke Island, New Zealand (Operation Waiheke).

Supervision and Mentoring

Summary of supervision and mentoring activities

I am the main and co-director and supervisor on one (1) postdoc, ten (10) current and past PhD projects, seven (8) MSc projects and four (4) final year veterinary research projects.

Since 2008, most of my teaching experience has focused on supporting postgrad students and professionals in their research, not only advising them in better collection and analysis of their data but also how to better communicate their research findings. These mentoring activities, whether through mentor, technical advisor or co-supervisor positions, have resulted in numerous publications in international journals and initiated collaborations across various national and international organisations. I hope that my involvement in their project has contributed to their subsequent successes as most postgrad students found permanent position in their field after, or even during (!), their contract. For example, Cheryl Gibbons and Isobel McLachlan are now epidemiologist at Health Protection Scotland, and Cheryl has now been promoted as Lead Healthcare Scientist; Paolo Motta is now epidemiologist at the Food and Agriculture Organization of the United Nations; Kajetan Stanski is now a software development Engineer at Amazon; and Thareem Khalid is now in a position at the World Animal Health Information and Analysis Department (WAHIAD) of the World Organisation for Animal Health of the United Nations while still pursuing her PhD project.

Overall, I supervised students and contributed to their project from 11 different universities (7 international, 4 national).

List of post-doctorants

- **Rémi Fay** 2022-2024 Claude Bernard University – Lyon 1, France. “Modelling infectious diseases transmission in wild boar”.

List of supervised students

PhD students

- **Charlotte COLIN** 2024-2027 ‘Co-encadrant’ of PhD at the Université Savoie Mont Blanc, France. “Évaluation du rôle de réservoir pour les parasites gastro-intestinaux résistants aux antiparasitaires des populations d’animaux sauvages pour les animaux domestiques : exemple du bouquetin et du mouton dans les Alpes”. Director: Dr. Glenn Yannic (UMR LECA, Université Savoie Mont Blanc); co-director: Dr Gilles Bourgoïn (UMR LBBE, VetAgro Sup).
- **Agathe BEAUVOIS** 2024-2027 ‘Co-encadrant’ of PhD at the Université Claude Bernard – Lyon 1, France. “Impact des solutions fondées sur la nature sur la prolifération du moustique tigre en milieu urbain”. Director: Prof. Claire Valiente Moro (UMR LEM, Université Claude Bernard – Lyon1); co-director: Dr Marc Bourgeois (UMR EVS, Université Jean Moulin - Lyon 3), other co-encadrant: Dr. Nelly Exbrayat (UMR GATE, Université Lumière - Lyon 2).

- **Joyce VAN VELZEN** 2023-2026 Co-director of PhD student at VetAgro Sup, France. “Modelling vaccination strategies to control infectious diseases in wild boar populations”. Director: Dr. Marlène Gamelon (UMR LBBE, CNRS)
- **Amandine BIBARD** 2022-2024 Co-director of PhD student at the Université Clermont Auvergne, France. “Assessing the relative risk of introduction of Bluetongue Virus serotypes into new areas of Europe/US/Australia”. Director: Prof. Karine Chalvet-Monfray (UMR EPIA, VetAgro Sup).
- **Sacha KRAMER** 2021-2024 [student withdrawal for personal reasons] Co-director of PhD student at the Université Claude Bernard – Lyon 1, France. “Decision-making processes during disease outbreaks and its impact on the spread of infectious disease in livestock”. Director: Prof. Dominique Pontier (UMR LBBE, Université Claude Bernard – Lyon1); other co-director: Prof Benoit Tarroux (UMR GATE, Université Lumière - Lyon 2).
- **Tahreem KHALID** 2021-2024 Co-director of PhD student at the Université Claude Bernard – Lyon 1, France. “Assessing the risk of contact between domestic animals and wildlife in Europe”. Director: Prof. Emmanuelle Gilot-Fromont (UMR LBBE, VetAgro Sup).
- **Lina Maria GONZALEZ GORDON** 2020-2024 Co-supervisor of PhD student at the University of Edinburgh, UK. “Epidemiology of Foot-and-Mouth (FMD) disease in Eastern Africa”. Main supervisor: Prof. Barend Mark de Clare Bronsvoot (Roslin Institute, University of Edinburgh); other co-supervisors: Adrian Muwonge (Roslin Institute, University of Edinburgh), Lisa Boden (the Global Academy of Agriculture and Food Systems, University of Edinburgh).
- **John GREWAR** 2016-2020 Co-supervisor of PhD student at the University of Pretoria, South Africa. “Evaluation of African horse sickness surveillance in the controlled area of South Africa”. Main supervisor: Prof. Peter Thompson (University of Pretoria).
- **Isobel MCLACHLAN** 2016-2021 Co-supervisor of PhD student at the University of Edinburgh, UK. “Dynamic modelling to explore persistence of disease in endemic settings using foot and mouth disease as an exemplar”. Main supervisor: Prof. Barend Mark de Clare Bronsvoot (Roslin Institute, University of Edinburgh); other co-supervisors: Glenn Marion, Iain McKendriks (Biomathematics and Statistics Scotland).
- **Jessica FLOOD** 2011-2015 Co-supervisor of PhD student at the University of Edinburgh, UK. “Foot-and-mouth disease epidemiology in relation to the physical, social and demographic farming landscape”. Main supervisor: Prof. Mark Woolhouse (School of Biology, University of Edinburgh).

MSc students – MRes

- **Kajetan STANSKI** 2020-2023 “Machine learning for livestock surveillance”. MSc by Research (MRes) student, University of Edinburgh, UK. Main supervisor: Prof. Barend Mark de Clare Bronsvoot (Roslin Institute, University of Edinburgh); co-supervisor: Thibaud Porphyre, Samantha Lycett (Roslin Institute, University of Edinburgh).

MSc students – M2

- **Eric RUCOGOZA** 2024 “Analyse Spatio-Temporelle des Lymphomes Canins : corrélation avec l'exposition aux pesticides et recommandations pour la surveillance et la prévention”. Master 2

OHMHP, MSc *Public Health*, Université Claude Bernard – Lyon 1, France. Main supervisor: Prof. Thierry Marchal (UP ICE, VetAgro Sup), co-supervisor: Thibaud Porphyre.

- **Hajar BOUTAYEUR** 2024 “Eleveurs face à la Maladie Hémorragique Epizootique (Perception du coût et volonté de vaccination)”. Master 2 OHMHP, MSc *Public Health*, Université Claude Bernard – Lyon 1, France. Main supervisor: Dr. Guillaume Convert (Boehringer Ingelheim), co-supervisor: Thibaud Porphyre.
- **Giorgio MANGIAPIA** 2023 “A qualitative investigation of the African swine fever surveillance network in the Auvergne-Rhone-Alpes: what factors can delay a suspicion report?”. Master 2 OHMHP, MSc *Public Health*, Université Claude Bernard – Lyon 1, France.
- **Beatriz DELGADO HERNANDEZ** 2023 “Identification of TBD risk areas in Tanzania and potential risk factors between 2000 and 2010. Anaplasmosis and ECF cases”. Master 2 OHMHP, MSc *Public Health*, Université Claude Bernard – Lyon 1, France.
- **Amaël DAVAL** 2022 “Modélisation de la dynamique des agents pathogènes transmissibles par l’environnement à l’interface entre populations d’ongulés domestiques et sauvages”. Master 2 *Modélisation des Systèmes Ecologiques*, MSc BEE, Université Toulouse III - Paul Sabatier, France. Main supervisor: Dr Gilles Bourgoïn (UMR LBBE, VetAgro Sup), Co-supervisor: Thibaud Porphyre.

MSc students – M1

- **Romane DE ROZARIO** 2023 “Risque leptospirosique chez les petits mammifères sauvages en Europe de l’Ouest et en Europe Centrale”. Master 1 Public Health, MSc *Public Health*, Université Claude Bernard – Lyon 1, France. Main supervisor: Dr Florence Ayrat (UR RS2GP, VetAgro Sup), Co-supervisor: Thibaud Porphyre.
- **Émeline BESSE** 2021 “Réseau de communauté et risque leptospirosique”. Master 1 Public Health, MSc *Public Health*, Université Claude Bernard – Lyon 1, France. Main supervisor: Dr Florence Ayrat (UR RS2GP, VetAgro Sup), Co-supervisor: Thibaud Porphyre.

Veterinary research thesis

- **Amélie EXERTIER** 2026 “Pathogen transmission between wild and domestic ungulates: the example of resistant nematodes in transhumant sheep and wild ibex in the French Alps”. Thèse d'exercice vétérinaire, VetAgro Sup, France. Director: Thibaud Porphyre, 1er Assesseur: Gilles Bourgoïn (UMR LBBE, VetAgro Sup).
- **Sylvain BRENIERE** 2025 “Epidémiologie comparée de la MHE et FCO en France”. Thèse d'exercice vétérinaire, VetAgro Sup, France. Director: Thibaud Porphyre, 1er Assesseur: Emmanuelle Gilot-Fromont (UMR LBBE, VetAgro Sup).
- **Mathilde PICQ** 2023 “Epidémiologie rétrospective de la besnoitiose bovine dans les Alpes”. Thèse d'exercice vétérinaire, VetAgro Sup, France. Director : Thibaud Porphyre, 1er Assesseur: Lionnel Zenner (UMR LBBE, VetAgro Sup).
- **Rebecca ALLEN** 2021 “Cleaning practices and attitudes towards biosecurity at livestock markets by commercial and non-commercial market users”. Final year veterinary research project, University of

Edinburgh, UK. Main supervisor: Thibaud Porphyre, co-supervisor: Lisa Boden (the Global Academy of Agriculture and Food Systems, University of Edinburgh).

List of mentoring and technical support

Post graduate research students

- **Sana KALTHOUM** 2018-2023 PhD student: “Modélisation spatio-temporelle de la propagation de la rage canine en Tunisie”, Université de Tunis El Manar, Tunis, Tunisia.
- **Michael DUNNE** 2019-2024 PhD student: “Variance-based sensitivity analysis for History Matching”, University of Exeter, UK
- **Erik RYDOW** 2022-2025 PhD student: “Visualisation for Sensitivity Analysis”, University of Oxford, UK
- **Paolo MOTTA** 2013-2016 PhD student: “Characterisation and modeling of cattle movements in Cameroon”, University of Edinburgh, UK.
- **Claire GUINAT** 2013-2016 PhD student: “Integrated use of epidemiological tools to understand African swine fever transmission”, Royal Veterinary College, UK.
- **Cheryl GIBBONS** 2012-2015 PhD student: “The Epidemiology of MRSA in Scotland”, University of Edinburgh, UK.
- **Siwi WIJAYANTI** 2012-2015 PhD student: “Integrated Epidemiological Study of Dengue Virus Transmission in Java, Indonesia”, University of Glasgow, UK.
- **Raphaelle METRAS** 2009-2013 PhD student: “A spatial statistical approach towards understanding Rift Valley fever epidemics in South Africa”, Royal Veterinary College, UK.
- **Liam James HERBERT** 2012 MSc *Public Health* student: “An epidemiological analysis of *E. coli* O157 on Scottish cattle farms”, University of Edinburgh, UK.
- **Solenne COSTARD** 2007-2011 PhD student: “Epidemiological investigations of African swine fever in Madagascar”, Royal Veterinary College, UK.

Professional training programmes

- **Merab ACHAM** 2019-2020 Fleming Fund Fellowship programme, National Animal Disease Diagnostics and Epidemiology Centre (NADDEC), Uganda.
- **Patricia BARTLETTE** 2009-2010 Caribbean Veterinary Epidemiologist/Para-epidemiologist (VEP) programme, Chief Veterinary Officer of Nevis (USDA), Saint Kitts and Nevis.

Thesis examination and coordination

Examination committee membership

External commitment

- **Andrea RADICI** 2023 External examiner (rapporteur) for the PhD project: “Un cadre de modélisation pour le développement des stratégies éco-efficaces de lutte contre les agents pathogènes aériens des plantes : le cas de la rouille noire du blé et de la moniliose des pêchers.”. University of Avignon, Avignon.
- **Thanicha CHANCHAIDECHACHAI** 2023 External examiner for the PhD project: “An integrated epidemiological and economic analysis of foot and mouth disease (FMD) in Thailand”. Wageningen University, Wageningen, NL.
- **Justine LAGRANGE** 2021 External evaluation of the M1 internship report “Pilot study for the development of the European Antimicrobial Resistance Surveillance Network in Veterinary Medicine (EARS-Vet)”. Master 1 Public Health, *MSc Public Health*, Claude Bernard University – Lyon 1, Lyon.

Internal commitment

- **Soledad GIOVANNINI** 2023 Internal advisor for the agricultural engineering final-year dissertation: "Comment les approches basées sur le changement pour co-construire des initiatives en santé globale (One Health) sont-elles utilisées ?", VetAgro Sup, France.
- **Pauline BOUÉ** 2022 Internal advisor for the agricultural engineering final-year dissertation: "Etude de *S. calcitrans* et des taons en tant que vecteurs potentiels de la peste porcine africaine entre des populations de sangliers et de porcs domestiques en élevages porcins en France", VetAgro Sup, France.

Steering committee membership

- **Nicolas ROMAIN-SCELLE** 2023-2026 Steering committee (CSI) member for the PhD project: “Metropolitan Areas and Daily commute high Resolution modeling for Infectious Diseases control (MADRID)”. Université Claude Bernard – Lyon 1, France.
- **Lisa VORS** 2023-2026 Steering committee (CSI) member for the PhD project: “Evaluation éco-socio-environnementale du contrôle des maladies animales en élevage dans une perspective Une Seule Santé”. École Nationale Vétérinaire de Toulouse, France.
- **Nolwenn BLACHE** 2023-2025 Steering committee (CSI) member for the PhD project: “Analyse des liens entre processus infectieux et fonctionnalités des écosystèmes forestiers”. Université Clermont Auvergne, France.
- **Florian LECORVAISIER** 2021-2024 Steering committee (CSI) member for the PhD project: “Étude et modélisation de l'impact des vaccins et de la sélection génétique des variants sur le modèle coqueluche”. Université Claude Bernard – Lyon 1, France.
- **Fiona MCAULIFFE** 2019-2022 Steering committee member for the PhD project: “Investigating Causes of Lamb Loss on Highland Farms and Crofts”, University of Edinburgh, UK.

Research coordination and leadership

Summary of research coordination and leadership

Most of my research has been carried out in international research institutes and universities. Very early on in my career, I experienced coordination of research activities in epidemiology by taking the lead of all work packages and task related to data analysis. For example, I was involved in 3 projects funded by the Animal Health Board to analyse surveillance data on bovine tuberculosis and better understand the role of possums in bTB hotspots. These projects allowed me to understand the difficulties of collecting analysable and unbiased data for policy actions, particularly when this involves wildlife. I was also in charge of the data analysis for the FAO project (GCP/ARM/001/ITA) and worked in close relationship with Ron Jackson and Carole Sauter-Louis (currently Head of the Institute of Epidemiology of the federal research Institute for Animal Health, FLI) to best design the mitigation strategy carried out in Armenia against Brucellosis. These projects have also enabled me to create my network of scientific, institutional, professional and private partners that I am still rely on to this day.

Since 2010, I led multiple projects and work packages. I led the epidemiological modelling work package in the PILGRIM project (UE FP7) during which I had to integrate the data collected on the field and in the lab from my colleagues in the UK, the Netherlands and Denmark. We modelled the spread of MRSA and estimated the risk that a contaminated farm may pose to human communities. This project not only consolidated my network with scientist throughout Europe, but it also initiated interactions with colleagues at the University of Edinburgh (Mark Woolhouse) who were coordinating a similar EU FP7 project on MRSA. This interaction led to my involvement in the Centre of Expertise on Animal Disease Outbreaks (EPIC), under Mark Woolhouse (UoE), as lead modeller and in charge of the research programme on the evaluation of the benefits of vaccination against FMD for Scotland. From 2016, I took the lead of the EPIC programme for the Roslin institute and became co-principal investigator in this consortium of 7 institutes (University of Edinburgh including the Rolin Institute and the Global Academy of Agriculture and Food Systems; University of Glasgow; the Moredun Research Institute, MRI; the James Hutton Institute, JHI; Biomathematics and Statistics Scotland, BioSS; and the Scottish Rural College, SRUC). Involved in the development and coordination in all major stages of this project, I gained interesting experiences in the management of a large-scale collaborative project in the science-policy domain: mobilisation of the network to assemble the consortium, division of work and, accordingly, funding credits. In addition, in that time period, I coordinated with George Gunn (SRUC) the Topic “Analyses of Potential Disease Control Options” which involved scientists of various disciplines (epidemiologist, modellers, economist, social scientist) from different institutes and spread out on different sites across Scotland. This work package was the main provider of modelling outputs and advise to the Scottish Government and to industrial stakeholders but also allowed transdisciplinary research at the interface between statistics, epidemiology and economics. My work in this work package enabled me to develop my interest in transdisciplinary research and identify economist partners. This work let to exciting transdisciplinary collaboration with colleagues from SRUC and with Karl Rich (who is now Director of the Master of International Agriculture Program in the Ferguson College of Agriculture and a Professor of Agricultural Economics at Oklahoma State University) on the economic cost of FMD vaccination and optimization strategies when facing limitations in stock supply. In this work package, I also coordinated translational scientific projects to evaluate the risk and potential impact of an incursion of pig diseases (like ASF and CSF) in the British industry. This work consolidated interactions between the Roslin Institute and BioSS in order to study spatio-temporal dynamics of disease spread and inferring parameters in simulation models, and led to the

ambitious project (SCRC) funded by the Royal Society on COVID19 modelling response. This collaboration enabled me to lead one of the modelling team involved in the project (a team comprised of 1 modeller – me – 1 epidemiologist, and 6 research software engineers), developing modelling frameworks that were used to better understand COVID19 dynamics but also best prepared for next pandemics. My work on ASF and FMD preparedness allowed me to develop and pilot, alone or together with colleagues from the Roslin Institute, numerous small projects with international partners, particularly working on developing models to inform control and preventive activities against disease such as African Horse sickness in South Africa (funded by SAEHP) and highly pathogenic avian influenza in the USA (Funded by USDA) (see section “Expertise and impact” for details), or working with social scientist colleagues (Funded by SGCRF) and agribusiness consulting firms (PigBoost) to best manage pig production to improve Health in Uganda and Malawi.

Since November 2020, I am the Head of the industrial chair in Veterinary Public Health funded as part of the Programme d’investissement d’Avenir (PIA2) in the Axis “Biosanté et Société” of the IDEXLyon supported by Boehringer Ingelheim, CNRS, Claude Bernard University and VetAgro Sup. As part of this chair, I am coordinating the Veterinary Public Health group of the UMR CNRS 5558 LBBE and scientific advisor for the local consortium promoting VPH in Lyon (VPH Hub) involving both research institutions (University Claude Bernard - Lyon 1, VetAgro Sup, BioAster), industrial stakeholders (Boehringer Ingelheim, LyonBioPole, Fondation Mérieux), and local government bodies (Metropole de Lyon, the Region AURA), as well as INRAE and ANSES as associate partners. The research of my group is a direct continuation of the research I was (and still am) carrying out with EPIC on characterizing epidemiological processes driving emerging infectious diseases epidemics in livestock and modelling their spread to inform policy-makers and industrial stakeholders on best, most cost-efficient, mitigation strategies.

This transdisciplinary work combining modelling, epidemiology, ecology and socio-economics is centred around the work of 1 postdoc (R. Fay) and 3 PhD students. These activities enabled me also to identify a number of researchers that showed interest in animal epidemiology and disease spread modelling. This subsequently contributed to the development of a France Relance project (BTVRISK) as part of the action 2 PRRD call for which I am co-supervising a staff member of Boehringer Ingelheim (Amandine Bibard) in her PhD project together with Karine Chalvet-Monfray (VetAgro Sup, UMR EPIA). This project offered the opportunity to continue working on vector-borne diseases and at the interface with plant epidemiologist and modeller Davide Martinetti (INRAE, UR BioSP) on the evaluation of the risk of BTV caused by long-distance dispersal of the *Culicoides* vector due to wind movements in Europe. I am also coordinating the modelling work package in the project EVASION, funded by the ANR JCJC project of G. Minard (CNRS, UMR LEM), to evaluate the role of vector-microbiota diversity on the spread of viral pathogens (here Chikungunya) at population level.

In addition to remaining involved in EPIC, I am still working with my collaborators at the Roslin Institutes, developing projects to better understand the epidemiology of FMD in endemic settings. As such, I co-developed and co-coordinate the project (OpEnS-FMD) funded by a EuFMD-FAR grant. This project is aiming to evaluate how information resulting from network models and animal movement data bases could help support surveillance system in FMD endemic settings by providing targets for environmental sampling and nanopore sequencing. This work, centred on the research carried out by Lina Gonzalez in her PhD project, further extended the collaboration between The Roslin Institute, University of Makerere and VetAgro Sup and expanded it by involving Pirbright.

Evaluation committee membership

- 2024 : INRAE - Concours CRCN n°25 « Epidémiologie, génétique et modélisation pour la santé ».

Committee membership and leadership

- 2020 onward: Head of the IDEXLyon Industrial Chair in Veterinary Public Health.
- 2020 onward: Leading the Veterinary Public Health group, UMR CNRS 5558 LBBE (Laboratoire de Biométrie et Biologie Évolutive).
- 2020 onward: Member of the working group for the "One Health" Axis of the VetAgro Sup strategic plan.
- 2022 onward: Member of the Operational Committee of the VPH Hub initiative of Lyon.
- 2020 onward: Member of the Steering Committee of the VPH Hub initiative of Lyon.
- 2021: Member of the Strategic Review working groups "from Strategy to ARC" of Boehringer Ingelheim on Bluetongue (BTV) and transboundary Emerging Diseases (TED).
- 2019-2021 Member and lead modeller for The Scottish COVID-19 Response Consortium (SCRC) as part of the Rapid Assistance In Modelling The Pandemic (RAMP).
- Since Oct. 2017: Associate member of the Scottish Government Feral Pig Co-ordination Group.
- 2016-2020: Deputy representative for the Roslin Institute and member of the Core Governance Group and Science Leadership Committee of Scotland Centre of Expertise on Animal Disease Outbreaks (EPIC).
- 2016-2020: Co-lead of the EPIC Topic 4 "Analyses of Potential Disease Control Options".
- 2009 – 2010: Member of the expert group for modelling and data analysis of the Caribbean animal health network (CaribVet).

Research excellence framework

- Author and major contributor of the joint SRUC/UoE impact case study for the 2021 Research Excellence Framework (REF2021). Title: "Foot and mouth disease in Scotland: Improving preparedness and outbreak responses". Outcome 4*.
<https://results2021.ref.ac.uk/impact/85e7933f-0773-45da-8a03-ddd08a79beb7>

Conference and seminar organisation

- Oct 2022: Member of the organization committee for the round table "*One Health - Comment définir et répondre à l'émergence d'une zoonose X ?*" as part of the LyonBioPole journée collaborative, Grenoble, France.
- Oct 2021: Member of the organization committee for the round table "*Outils de surveillance précoce et de diffusion des épidémies*" as part of the LyonBioPole semaine collaborative, Lyon, France.

- Jan 2022: Co-lead of the scientific committee and member of the organisation committee of the first conference *“One Health at the Confluence of human & veterinary public health”* of the VPH Hub (online).
- Feb 2020: Developed & organised the workshop *“Mitigating African Swine Fever in Malawi”*, Lilongwe, Malawi.
- Oct 2018: Co-organised to the joint APHA-EPIC workshop *“Use of pig movement data for modelling and demographics”* held in Weybridge, UK.
- May 2018: Co-developed & organised the Interdisciplinary workshop *“Peri-Urban Livestock Production & Health”*, Kampala, Uganda.

Research network

- 2020 onward: Member of the Pôle d’Expertise Vétérinaire et Agronomique Animaux Sauvages (EVAAS) of VetAgro Sup.
- 2020 onward: Associate member of Biomathematics & Statistics Scotland (BioSS).
- 2020-2027: Honorary Fellow of the University of Edinburgh.

Academic society membership

- Since Sep. 2023: Member of the European wild boar collaborative project (Euroboar) as part of the Euromammals initiative (<https://euromammals.org>).
- Since Mar. 2018: Member of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM).

Grants and Awards

Coordination

- Jan. 2025 – Dec. 2026: Directrice générale de l’Alimentation (DGAL) du Ministère de l’Agriculture, de la Souveraineté alimentaire et de la Forêt *“Modélisation de la diffusion spatiale de la maladie hémorragique épizootique (MHE) et l’évaluation du rôle de ses routes de dispersion en France”* (PI) 67,000€
- 2024: Société Centrale Canine – Agria 2024 *“Etudier chez le chien l’exposome aux pesticides afin de déterminer son impact sur le développement des lymphomes”* (co-PI) 30,000€.
- 2022-2023: French embassy in Mexico - International Mobility Grant *“Supporting the development of a Dual MSc Degree program between France and Mexico”* (co-PI)
- Jan. 2022 - Dec. 2024: ANR – UE/France Relance (Préservation de l’emploi R&D – action 2) *“BTVRISK: Assessing the relative risk of emergence of novel bluetongue serotypes in the United States of America, Australia and Europe”* (PI) €156,000

- Aug. 2021 – Oct. 2022: Ninth Call EuFMD – Fund for Applied Research (EuFMD-FAR) “Optimization of an environmental sampling approach integrating network models and nanopore portable sequencing for FMD risk-based surveillance in endemic settings (OpEnS-FMD)” (co-A) £26,145.
- Aug. 2020 – Mar. 2021: DFID/GCRF Agri-tech Catalyst Seeding Award: “PorkMart: Data-driven market intelligence for a sustainable pork industry in Uganda” (co-I) £ 29,986
- Aug. 2020 – Feb. 2022: DHSC/UKRI Global Effort on COVID-19 (GECO): “Tracking Haulage in East Africa to support COVID-19 surveillance- THEA-C19” (Co-I) £504,514
- Apr. 2020 – Jul. 2020: Data-Driven Innovation Small Grants for COVID-19 Response & Accelerating Recovery: “Understanding the epidemiology of COVID-19 in Scotland to design and model lockdown exit strategies: A risk-based approach to policy prioritisation” (co-A), £18,895.
- Dec. 2019 – Jun. 2020: Global Challenges Theme Development Fund: “Equitable access to sustainable development - mitigating African Swine Fever in Malawi” (PI), £23,250.
- Nov. 2019 – Apr. 2021: Innovate UK Agri-Tech Round 8: “PigBoost: Sustainable data-driven pig production for Uganda” (co-I), £499,649.
- Mar. 2019 – Jun. 2021: UK Department of Health and Social Care through the “Fleming Fund Fellowship – Host institution: Uganda” grant (co-A), £520,000.
- Nov. 2018 – Feb. 2019: BBSRC Industrial Strategy Challenge Fund: Transforming Food Production Seeding Award: “Developing an online cost-estimator to support breeding and disease management decisions in the pig industry” (PI), £15,744.
- Feb. 2018: Edinburgh Global Research and Partnership Fund: “Interdisciplinary workshop on peri-urban livestock production” (co-Applicant), £13,060.
- Apr. 2016 – Mar. 2021: RESAS Scottish Programmes of Research: “Centre of expertise on Animal Disease Outbreaks” (co-I), £10 million.

Contribution

- 2023-2025 French embassy in Cuba. Contributor to the FSPI project “CUBA IES: Internationalisation de l'Enseignement Supérieur cubain” as representative of the French institution and work package lead.
- Apr. 2024 - Mar. 2028: ANR JCJC (Guillaume Minard, UMR LEM). Contributor to the project EVASION “Epidemiological consequences of invasion-induced simultaneous erosion of vector-microbiota diversity”. (293,570 €) as work package lead.
- Jun. 2023 - May. 2026: OFB - ECOPHYTO II. Contributor to the project PELYCANO “Pesticide Exposome, Lymphomagenesis, chemoresistance and Survival Outcomes” (499,482€) as lead epidemiologist for VetAgro Sup.
- Feb. 2023 - Jan. 2028: ANR – France 2030 (Compétence et métier d’avenir). Contributor to the EUR EID@Lyon “Transdisciplinary Graduate School In Emerging Infectious Diseases” (6M€) as head of stakeholder committee.
- Oct. 2020 – Sept 2025 : ANR - Programmes Investissements d’Avenir (PIA2). Contributor to the IDEXLyon (ANR-16-IDEX-0005) in the Axis “Health and Society” as Head of the Industrial Chair in Veterinary Public Health (1.2M€).

- Apr. 2022 – Mar. 2025: RESAS Scottish Programmes of Research. Contributor to the “Centre of expertise on Animal Disease Outbreaks” (£10 million) as subcontractor of the University of Edinburgh.
- Mar. 2019-Jul. 2020: UK Royal Society “Rapid Assistance In Modelling The Pandemic” (RAMP)” scheme. Contributor to the Scottish COVID-19 Response Consortium (SCRC) as Lead modeller.
- Apr. 2011 – Mar. 2016: RESAS Scottish Programmes of Research. Contributor to the “Centre of expertise on Animal Disease Outbreaks” (£10 million) as work package lead.
- Jan. 2009 – Dec. 2011: EU 7th Framework Programme – FP7. Contributor to the project PILGRIM “Preventing community and nosocomial spread and infection with MRSA ST 398 - instruments for accelerated control and integrated risk management of antimicrobial resistance” (€3 million) as modeller for the RVC and Task lead.

Consulting

- Aug. 2018 – Nov. 2018: Consultancy Agreement with South African Equine Health and Protocols NPC (SAEHP) “Assessing the potential of African horse sickness to persist in the Western Cape Province’s Zebra population” (PI), £20,000.
- Sep. 2016 – Sep. 2017: Cooperative Agreement with the US Department of Agriculture “Characterization of the within and between farm spread of H5N2 HPAI in Iowa” (PI), US\$50,000.
- Jan. 2003 – Jun. 2003: Merial: “Modelling the population dynamics of Cat Fleas in the domestic environment” (co-I) FF10,000.

Editorship and reviewing activities

Reviewing articles, by ensuring that the quality of research is properly evaluated and examined, is a key activity in the scientific process. Personally, I have been involved in this process for many years and was at some point on the top 15% contributor for the University of Edinburgh. I was also involved as Member of the Study Design and Data Analysis (SDDA) Consultant Board of the *Equine Veterinary Journal* and associate editor for *Veterinary Record* and guest editor for *Frontiers in Veterinary Sciences*. However, since COVID, I had difficulties to cope with the frequent demands, which was affecting my research activities, my ability to effectively supervise my student and was placing additional burden on my peers due to delays in submitting my reviews. In fairness, I paused my reviewing and editorship activities but occasionally contribute to the evaluation of scientific articles that are close to my research activities.

List of editorship activities

- Guest Associate Editor for Frontiers in Veterinary Science – Veterinary Epidemiology and Economics Topic “Risk-Based Evidence for Animal Health Policy
- 2019 – 2020: Associate Editor for Veterinary Record.

List of reviewing activities

- 2017-2022: Member of the [Study Design and Data Analysis \(SDDA\)](#) Consultant Board of the *Equine Veterinary Journal*.

- Manuscript reviewer for 19 journals, including *Lancet*, *PLoS One*, *Biological Conservation*, *Preventive Veterinary Medicine*, *Epidemiology & Infection*, *Journal of the Royal Society Interface*, *Philosophical Transactions of the Royal Society B*, *Scientific Reports*, *Epidemics*, and *Transboundary and Emerging Diseases*. More details in publons.com/a/1363959/.
- I also reviewed for conference proceedings and BBSRC grants.

SCIENTIFIC REPORT

Research focus

Since 2003, my work focuses on risk evaluation and infectious diseases modelling to better understand the spatial and spatiotemporal dynamics of animal infectious disease infection to support decision-making for managing complex health problems in animal populations. Particularly, I focused my work on better understand the spatial and spatio-temporal dynamics of transboundary animal diseases, or TADs, in both endemic and disease-free settings. Recently, my work has moved to integrating these quantitative approaches into transdisciplinary frameworks as an implementation of the One Health approach.

General context

Transboundary animal diseases (TADs) are highly contagious, and transmissible infections linked to epidemics with the potential to spread rapidly into new areas, causing large-scale damage within and across countries (Clemmons et al., 2021). TADs are a major challenge for animal health and livestock industries across the world, despite remarkable progresses in treatment and prevention (Clemmons et al., 2021). These infectious diseases account for 20% of the global animal production losses and cost an estimated \$200 billion over 10 years in outbreak control (Narro et al., 2012). As they can easily spread to other countries and reach epidemic proportions, they pose a substantial public threat that need to be mitigated to protect animals, farmers, and society relying on agricultural products (Knight-Jones and Rushton, 2013), as well as a conservation threat for wildlife species sensitive to these pathogens (Anonymous, 2021; Gamarra-Toledo et al., 2023).

Foot-and-mouth disease (FMD), African (ASF) and Classical (CSF) swine fevers are examples of significant TADs (Otte, M.J. et al., 2004) listed by the World Organization of Animal Health (WOAH, previously named as OIE). Vector-borne diseases, such as Bluetongue (BTV), and African Horse sickness (AHS), and Epizootic haemorrhagic disease virus (EHDV), can also be defined as TADs.

In the last several decades, the intensification of food production and increases in local and international movements of both people and animals, together with a reduced biodiversity in a warmer, more crowded and socially diverse, environment, yield opportunities for infectious animal diseases, such as TADs, to emerge and spread (Morand, 2020). Mitigating the spread of infectious diseases is an evolving challenge, due to the numerous evolutionary opportunities for pathogen to mutate, infect and/or survive within and outside hosts. This situation is worsened by the constant reduction in the effectiveness of treatments due to the dramatic increase of resistances and the fast evolution of pathogens, while the rate of discovery of novel molecules and vaccine is slowing down, and the rise of public hesitancy, and its political consequences, for large culling campaign. Among such diseases, FMD and ASF are notably hazardous due to their quick and adaptable propagation (Dixon et al., 2020), their persistence in the environment and wildlife reservoir species, and their economic consequences (Knight-Jones and Rushton, 2013). Similarly to COVID-19, FMD and ASF have shown how animal infectious diseases can rapidly spread worldwide. However, they also highlighted how disease control programmes that were implemented in response to

their incursions can impede economic growth and set back by years all socio-economic gains in infected countries, hence radically changing risk perceptions on disease control activities in communities.

As mere spatial overlap between livestock populations and/or virus-shedding wild reservoir hosts is not sufficient for TADs to remain and spread, understanding the underlying processes contributing to disease incursion, transmission and maintenance is crucial for addressing all facets of the risk of TADs. Exposure of livestock to pathogens may vary with changes in the frequency and intensity of contact (direct or indirect) between and within host (in natural or domestic) populations, as well as with non-vertebrate vectors. Beyond the role of environmental conditions that influence population spatial occupancies and dynamics, human activities and behaviours play a key role in modulating the intensity of contacts and influencing efficacy and efficiency of disease control measures (**Figure 1**) – for example, pastoralism, land-use changes, implementation of biosecurity measures, livestock systems and marketing as well as budget restrictions. Such activities and behaviours create complex socio-eco-epidemiological situation influencing disease dynamics at the local level as well as hindering the robustness of disease surveillance, prevention and control strategies that are implemented at regional or national scales (Dlamini et al., 2020; Singer et al., 1998; Young et al., 2022). This is particularly important for TADs that are listed as notifiable terrestrial animal diseases by WOAHP and subject to stringent disease control procedures implemented at national level.

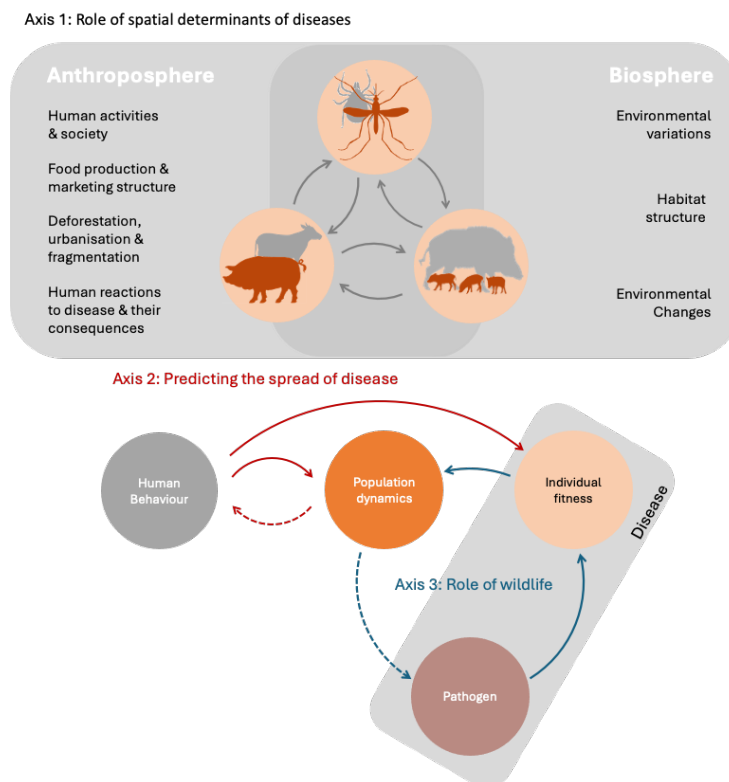


Figure 1. The complex socio-eco-epidemiological processes influencing disease dynamics and my research axis.

In this context, my research activity encompassed a broad range of scientific questions aiming to better understand the complex socio-eco-epidemiological processes influencing disease dynamics and identify key processes associated with disease outbreaks of TADs. In doing so, a broad range of modelling tools was developed, along a continuum going from the development of statistical models to dynamic theoretical models, upon which management actions to optimise prevention, surveillance and control strategies were

proposed, evaluated and compared. This general objective can be broken down into the following three inter-related axes (**Figure 1**):

- Axis 1: Identifying and evaluating the role of spatial determinants of diseases
- Axis 2: Predicting the spread of diseases for improving control and surveillance design
- Axis 3: Understanding the role of wildlife as a local driver of disease risk

It is therefore along these three axes, which have structured my research activities since the start of my professional career, that I have chosen to present an overview of my work since 2011. However, in recent years, I also complemented these quantitative approaches with qualitative research, looking at the impact of social and individual decision-making on infectious disease spread and control in order to better understand the role of local socio-epidemiological factors on disease transmission and provide novel transdisciplinary ways to address the complex issues raised by TADs.

Spatial determinants of diseases

Environmental, anthropogenic, epidemiological and economic factors can alter how TADs may spread over multiple geographical scales (local, national or international) and over multiple populations (González Gordon et al., 2022)(**Figure 2**), whether they are of the same species or not. In addition, changes in climate, environment, and trade patterns have impacted on the transmission dynamics at both local and global scale, thereby affecting our ability to respond to current and future epidemics. Improving our understanding of the socio-eco-epidemiological context and the geographical variability of disease risk is therefore critical.

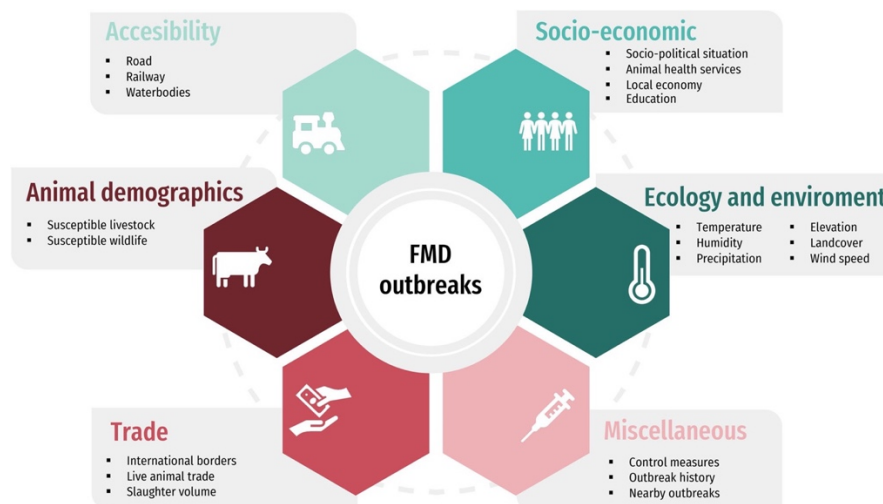


Figure 2. A few examples of the socio-eco-epidemiological factors identified as determinant of the spatial and spatio-temporal structure of foot-and-mouth disease outbreaks in endemic settings (González Gordon et al., 2022).

As a risk-based prioritization approach, a joint examination of the socio-eco-epidemiological context and the geographical variability of disease risk is key to design and deploy robust and cost-effective disease control measures that account for or tackle the underlying epidemiological factors associated with the risk

of outbreaks (Gunasekera et al., 2022; Hossain and Lawson, 2006; Lawson and Zhou, 2005). My first axis of research therefore focuses on understanding this heterogeneity and incorporating it into the statistical approaches used to identify risk factors associated with the spatial distribution of disease events (either number of cases, number of outbreaks, presence of infection, prevalence) and identify risk areas upon which further studies should be carried out.

To illustrate the research carried out in this axis by presenting the work on FMD in Uganda that was carried out during her PhD project (PhD thesis by L. Gonzalez, 2024) and is the subject of a paper in preparation to be submitted to a peer-review journal.

Ecological spatial factors and identification of risk factors: the case of FMD in Uganda

FMD is a highly contagious, transboundary viral disease circulating within wild and domestic cloven-hoofed animals (Knight-Jones et al., 2017; Knight-Jones and Rushton, 2013; Paton et al., 2018). It is considered endemic in Africa, Asia and the middle East with a few epidemic foci remaining in some parts of South America (WOAH, <https://wahis.woah.org>). Despite a low case fatality rate among adult animals, FMD is generally associated with high morbidity and among young animals it can progress to acute myocarditis, leading to sudden death (Kitching R.p, 2002; Kitching R.p and Hughes G.j, 2002). In susceptible livestock populations, widespread epidemics can be generated and significantly compromise animal welfare, reduce livestock productivity and decrease the profitability of the livestock sector, thereby threatening the livelihoods and food security of local communities (Baluka, 2016; Kerfua et al., 2023; Knight-Jones et al., 2017). As a result, FMD is one of the most important livestock diseases and is currently targeted for elimination in many endemic countries.

Since FMD continue to circulate, generating outbreaks in numerous parts of Uganda (Kerfua et al., 2023; Okello et al., 2022), practical approaches for geographic prioritization and targeting of disease control interventions are necessary to reduce the burden of the disease and optimize its control. In Uganda, FMD is considered a public good disease, therefore, outbreak data, routinely collected by the government, provides a unique opportunity to explore these spatial patterns.

To do this, we modelled the number of FMD outbreaks reported in the period between 2014-2019 and examined the possible association of socio-ecological factors with district-level disease risk. A Bayesian spatial modelling framework, based on integrated nested Laplace approximations (INLA) (Blangiardo et al., 2013; Rue et al., 2009), was used as we wanted to capture the uncertainty of estimates while accounting for the correlation due to the spatial interdependencies between districts. These spatial interdependencies were integrated in the modelling framework as random effects linking each observation to a district and thereby assessed the 'excess' risk within each district that cannot be explained by the associated socio-ecological factors.

In practice, spatial interdependencies can be either unstructured (that is uncorrelated noise at the district level) or structured due to being neighbours and sharing geographical borders (Bernardinelli et al., 1995; Lawson, 2021). Accounting for spatial structure while correcting for area-level noise in models was first introduced by Besag *et al.* (1991) and is known as the Besag-York-Mollie (BYM) convolution model (Besag et al., 1991), and is commonly used for disease mapping (Madden et al., 2021a; Schrödle et al., 2011; Wijayanti et al., 2016).

We first modelled the district-level number of outbreaks assuming a Poisson distribution but further explore if spatial distribution could be affected by overdispersion of outbreaks, arising from excess variation between district-level number of outbreaks or excess of zeros (Arab, 2015; Blasco-Moreno et al., 2019), by testing goodness of fit of alternative data count models (Lawson, 2021) such as negative binomial model and zero-inflated Poisson model and zero-inflated negative binomial. As accounting for these complexities in negative binomial and zero-inflated Poisson models did not improve further our model, the structure of the best spatial model was formulated such as:

$$\eta_i = \log(\rho_i) = \alpha + \sum_k^{\infty} \beta_k x_{ki} + \sigma_i$$

where the ratio ρ_i is the standard morbidity ratio (SMR, i.e. observed-to-expected number of outbreaks) for each district i during the entire study period. The expected number of outbreaks were assumed to be fixed over the period of study and represent the district-level expected number of outbreaks that would have arisen from the underlying population if it was distributed homogeneously (Elliott et al., 2000; Moraga, 2019). Here, α the intercept, quantifying the average the outbreak risk in the whole country; x_{ki} and β_k denote the value of and its coefficient for the k^{th} potential risk factor (or fixed effects) for each district, respectively. The component $\sigma_i = u_i + v_i$ is the random effects specific to each district i and is the sum of the structured v_i and unstructured u_i random effects.

Between 2014 and 2019, a total of 298 FMD outbreaks in cattle were reported across all districts in the country (median: 1, IQR: 3.5). All reports in the original database were successfully mapped to a district. Sixty districts (44.4%) did not report outbreaks during the study period. Baseline risk estimates showed that 64.4% of the districts (n =87) were below their calculated outbreak expectation (SMR<1); these districts extend across the north and southeast of the country. By comparison, 35.6% (n = 48) of the districts presented SMR>1, meaning a higher baseline outbreak risk (between 1.01 and 18.4) and these were predominantly distributed along the cattle corridor (**Figure 3**), a zone spanning from the southwest to the northeast of the country, characterized by pastoral rangelands and a diversity of livestock systems.

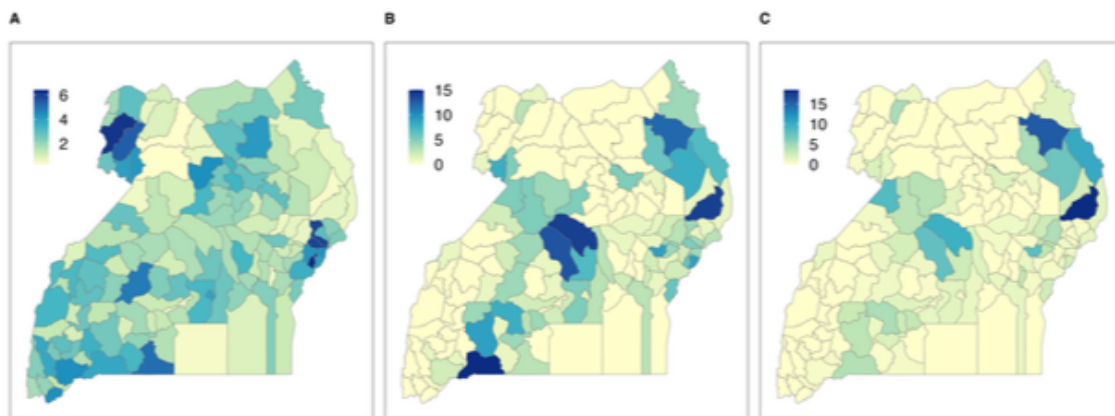


Figure 3. Observed, expected, and standardized baseline outbreak risk across Ugandan districts. (A) Expected outbreaks, (B) Reported outbreaks, (C) SMR.

The Poisson model including both structured and unstructured random effects at the district level was the best model, showing that the distribution of the outbreaks was not (or the least at a negligible level) affected by excess variation between district-level number of outbreaks or excess of zeros. Instead, the spatial distribution of FMD outbreaks in Uganda was associated with cattle and human density, deprivation scores and EVI. Each unit increases in cattle density was found increasing the risk of outbreaks in district by 4.95 (RR = 4.95; 95% CrI: 1.34-19.3). Likewise, districts with lower mean EVI during the second dry season were at increased risk (Q2, RR = 4.44; 95% CrI: 1.25-16.95 and Q1, RR = 5.53; 95% CrI: 1.26-26.84) of outbreaks. In contrast, districts with the lowest standard of living (Deprivation score Q1, RR = 0.2; 95% CrI: 0.05-0.76) and with lower human population density were less likely to report FMD outbreaks (RR = 0.14; 95% CrI: 0.04-0.5).

The district-specific residuals calculated from the spatial random effects offer information on the overall spatial excess risk when compared to the whole country (**Figure 4A**). Based on this, it was possible to highlight districts at higher risk of FMD outbreaks without considering the effect of the socio-ecological factors. Specifically, some districts located in the north, northwest, and southwest, where outbreaks reports were rare, exhibited a higher spatial risk.

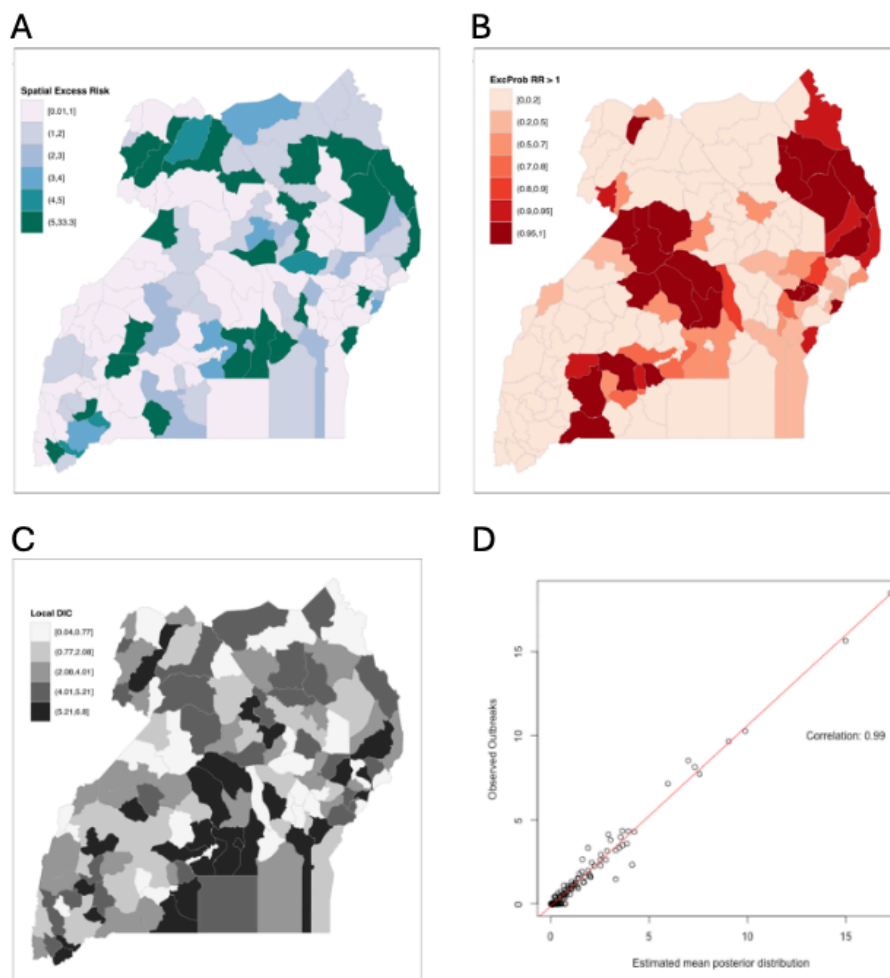


Figure 4. District-level FMD risk across the country using the best fitting model. (A) Spatial excess RR for the period 2014 to 2019, (B) Mapped exceedance probabilities (RR >1). (C) Local DIC maps and (D) scatterplot of posterior means predictive distributions against observed outbreaks (right) for the best fitting model.

The posterior exceedance probabilities were calculated for each district. Hotspot clustering was assumed with a RR threshold of 1. Based on this, high and low-risk clusters were identified (**Figure 4B**). Unusually high risk (Probability > 90%) was detected along the Karamoja, Bunyoro, Buganda and Ankole regions. Similarly, unusually low (Probability < 20%) clusters spanned most of the area of the West Nile, Acholi, Lango, Teso, Toro and Kigezi sub-regions. The model was scrutinized in terms of their plausibility and performance, showing optimal predictive distribution and fit (**Figures 4C and 4D**).

It is beyond the scope of this document to discuss these results, but it is essential to highlight how, based on routinely recorded outbreak data collected across a study area (whether it is a country or a region), the use of such Bayesian spatial models has improved our understanding on what eco-epidemiological factors were associated with the geographical distribution of FMD. Of greater interest, however, is that these ecological factors found associated in our model did not explain most of the spatial distribution of the risk. Instead, much of the variations was explain by the spatial random effects. This is not an unusual finding in small-area disease mapping models (Madden et al., 2021a, 2021b). However, these results suggest that accounting for large scale determinant may not fully drive the risk of outbreaks. Instead, these results confirm that disease outbreaks emerge from the complex and dynamic interplay between local social, economic and ecological factors and that these may be specific to each affected area. The complexity is further increased as we cannot disentangle with certainty the underlying epidemiological mechanisms related to increases in FMD events to those related to their reporting (Hierink et al., 2021).

Box 1. Other applications

The approach presented here to identify risk factors for spatial distribution FMD outbreaks in Uganda and identify risk areas has also been used to characterise the spatial and spatio-temporal structure of other disease events, such as dengue in Indonesia (Wijayanti et al., 2016), tick-borne diseases of animals in Tanzania (M2 thesis of B. Hernandez, 2023), Besnoitiosis in France (DVM thesis of M. Picq, 2023) and rabies in Tunisia (Kalthoum et al., 2024). These works have been extended from early work on disease distribution (Porphyre et al., 2007; Porphyre et al., 2008; Porphyre et al., 2010; Métras et al., 2012; Porphyre et al., 2013; Herbert et al., 2014; Metras et al., 2015) and species distribution (Porphyre et al., 2013) to identify target areas for disease control, albeit 1080 poison aerial dropping and vaccination campaign respectively.

Conclusion

Using routinely recorded outbreak data collected at national or regional levels, disease mapping is a valuable epidemiological tool for deciphering the mechanisms driving spatial patterns of disease events distributions and clarifying how disease risk may vary over space and time. It has the advantage to exploit large quantity of data that have been routinely collected but little (or poorly) analysed. However, benefit of such an approach to support policy-making is inherently complex as it is demanding not only a broad understanding of the socio-eco-epidemiological factors that may influence disease risk at the local level but also an understanding of what epidemiological processes is being analysed. Indeed, covariates (or spatial determinants) employed in analysing spatial and spatio-temporal patterns of disease events may be associated to various epidemiological process, notably the risk of becoming infected, the risk of propagating disease, the risk of maintaining disease and the risk of being control, detected as infected and reported. Although the statistical framework that we used is not optimum for disentangling these complex mechanisms affecting occurrence of disease events over space, it has the advantage to represent a robust

framework to generate hypotheses on what may drive the risk of disease events to increase (or decrease) locally and depart from the overall mechanisms of disease spread. In particular, this framework can identify areas where localized disease behaviour is unexplained and upon which further investigations could be implemented (Lawson, 2021, 2018).

Beside the fact that it depends on large scale (and possibly of good quality) disease monitoring data recorded homogeneously over national or regional scale, such a framework is based on assumptions that limit its ability to predict how disease may spread and assess the effectiveness of mitigation protocols for future emergencies. In the next section, we present how we used and analysed networks to predict the spatial spread of diseases in order to contribute to defining optimal strategies for surveillance of infectious animal diseases.

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Predicting the spread of diseases for improving control and surveillance design

To control efficiently infectious diseases requires the implementation of effective mitigation protocols (in term of surveillance and control), capable to modulate resources as a function of where is most needed. This is of paramount importance when the diseases of interest are regulated diseases with major consequences for the economy of the sectors affected such as TADs. This represents an overarching theme in my research, particularly focusing on (i) exploring how populations are structured to identify areas of greater risk of disease spread, and (ii) evaluating how such heterogeneities would affect disease transmission within and between populations, and impact efficiency of mitigation strategies. While the former principally uses descriptive methods and simple risk assessment modelling framework based on available livestock and traceability data, the latter consists in developing complex simulation models to integrate infectious processes occurring at multiple geographical scales.

Network analysis to assess spatio-temporal risk

Networks and network-based approaches, which were once confined to physics and social science problems (Newman, 2003), have proliferated in the field of human (Balcan et al., 2009; Eames and Keeling, 2002) and animal (Bajardi et al., 2012, 2011; Ciccolini et al., 2012; Green et al., 2006) health and are increasingly used to inform disease control strategies as part of national contingency plans. When applied to animal diseases, these networks typically consider farms as nodes but, depending on geographical scale of interest or question in hand, they can also be aggregated to lower resolution units, such as livestock markets (Motta et al., 2017), administrative areas (González-Gordon et al., 2023) or grid cells (Bibard et al., 2024a, 2024b). Irrespective of the unit of interest, however, nodes are linked by the transfer or movement of animals which are recognized as an important route of direct and indirect transmission of diseases in livestock (Fèvre et al., 2006; Ortiz-Pelaez et al., 2006; Porphyre et al., 2016, 2014).

As the movement of animals, either host or vectors, carries the risk of transmitting infectious diseases across substantial geographical distances, understanding the complexity of the animal movement networks is critical to predict the spread of infectious diseases in population (Green et al., 2006), identify regional and local movement patterns (Bajardi et al., 2012; Green et al., 2006), and provide guidance for the design of efficient control and surveillance strategies (Bajardi et al., 2012; Ciccolini et al., 2012). This is not new as a wealth of research has been carried out to describe networks formed by the movement of livestock in developed countries due to presence of large traceability data sets (Bajardi et al., 2011; Relun et al., 2016). However, relatively little has been done to explore how livestock mobility network are structured in limited resources settings (such as Sub-Saharan Africa) or how the mobility of insect vectors may inform on the risks of vector-borne diseases.

In this section, I will illustrate the first theme by presenting a network analysis of animal mobility data in Uganda (González-Gordon et al., 2023) and a risk assessment modelling framework using wind-dispersion networks to evaluate the risk of *culicoides*-borne virus (here bluetongue) incursions (Bibard et al., 2024a), both used to guide novel strategy for TADs surveillance.

The role of animal movements on disease spread and mitigation strategies

The role of cattle movements on TADs spread has been widely studied. In Africa, recent research highlights unique features and drivers of livestock mobility within constantly developing and diverse livestock systems (Ekwem et al., 2021; Motta et al., 2017; VanderWaal et al., 2017). Grazing mobility (e.g., pastoralism or nomadism) and trade-related mobility (e.g., farm-to-farm, farm-to-market, market-to-market, market-to-slaughterhouse, farm-to-slaughterhouse) are the two components of the livestock movement network in Uganda. While grazing mobility is a huge component of the cattle movement network, studying it requires the use of participatory approaches (e.g., surveys, focus groups) or cattle tracking (Turner and Schlecht, 2019). In contrast, country-wide analyses of trade-related mobility can rely on the information extracted from official movement permits for a general overview of the system. The latter has become a popular approach to study animal networks that coincides with improved identification and traceability systems for livestock implemented in some African countries (Miguel et al., 2013; Valerio, 2020).

In Africa, there is evidence showing that cultural practices, husbandry systems, herd size, distribution of food and water resources, cattle prices, and market activity influence the timing and volume of live cattle trade and grazing movements, and with it the risk of disease spread (Motta et al., 2018; VanderWaal et al., 2017). In contrast, because slaughterhouses often constitute sinks in cattle networks, little attention has been paid to slaughter movements, its seasonal calendar, and the possible role of key slaughter zones as active risk pathways for TADs transmission. A few studies document possible risk pathways for TADs in slaughter livestock, discussing the role of subadjacent slaughter networks and their unique features linked to alternative livestock production systems in East Africa (Adamchick et al., 2021a, 2021b). Thus, unravelling the architecture, cohesiveness, and district centrality network based on country-wide cattle movement traffic offers an opportunity for intelligent monitoring of TADs and can contribute to an integral outbreak response (Gerken et al., 2022; Gunasekara et al., 2021). It not only provides the foundation on which tools such as pathogen genomic epidemiology and serologic landscaping of infectious diseases can be anchored, but it is also a framework for risk-based surveillance and data-driven decision making for managing outbreaks of TADs across the country. This is of great interest for smart allocation of resources towards a feasible, sustainable, and cost-effective disease prevention and control.

In this study, we used network analysis to describe cattle mobility networks in Uganda based on official data collected in 2019. These mobility data include information of all livestock moving across national administrative (sub-counties or districts) or international borders that were authorised and received a short-term Animal Movement Permit (AMP). AMPs are implemented in Uganda, and most of Sub-Saharan Africa, to improve the traceability of animal transactions, support disease control programmes, and, above all, reduce livestock theft. Although current regulations do not include husbandry-linked movements for local livestock grazing or watering purposes (therefore not recording pastoral movements), this data still provides the opportunity for a better understanding of cattle mobility in Uganda. It allows to explore the relationship with naturally occurring livestock production zones and possible risk pathways for the spread of TADs, taking into account seasonal variations and complex market dynamics.

In 2019, 5114 and 16,910 between-district batch movements were officially registered for live trade and slaughter (**Figure 5**). These movements involved a total of 234,229 animals moved mainly for slaughter purposes (87.65%). While trucks were the predominant vehicle used to transport cattle to livestock markets, from farm- to-farm and to slaughterhouses (79.93%), it is noteworthy that a small proportion of

cattle were moved on boats (0.25%) and smaller vehicles (19.82%) (e.g., cars, motorcycles, and bicycles). Movements edges indicated that cattle mobility in Uganda was highly asymmetrical; most cattle transactions tended to remain local with a clear geographical pattern showing that the movements frequently occurred within the sub-regions. Kampala, the capital city of Uganda, was the largest sink for slaughtered animals most of which originated from the central (Buganda), southwest (Ankole), and northern (Lango) parts of Uganda.

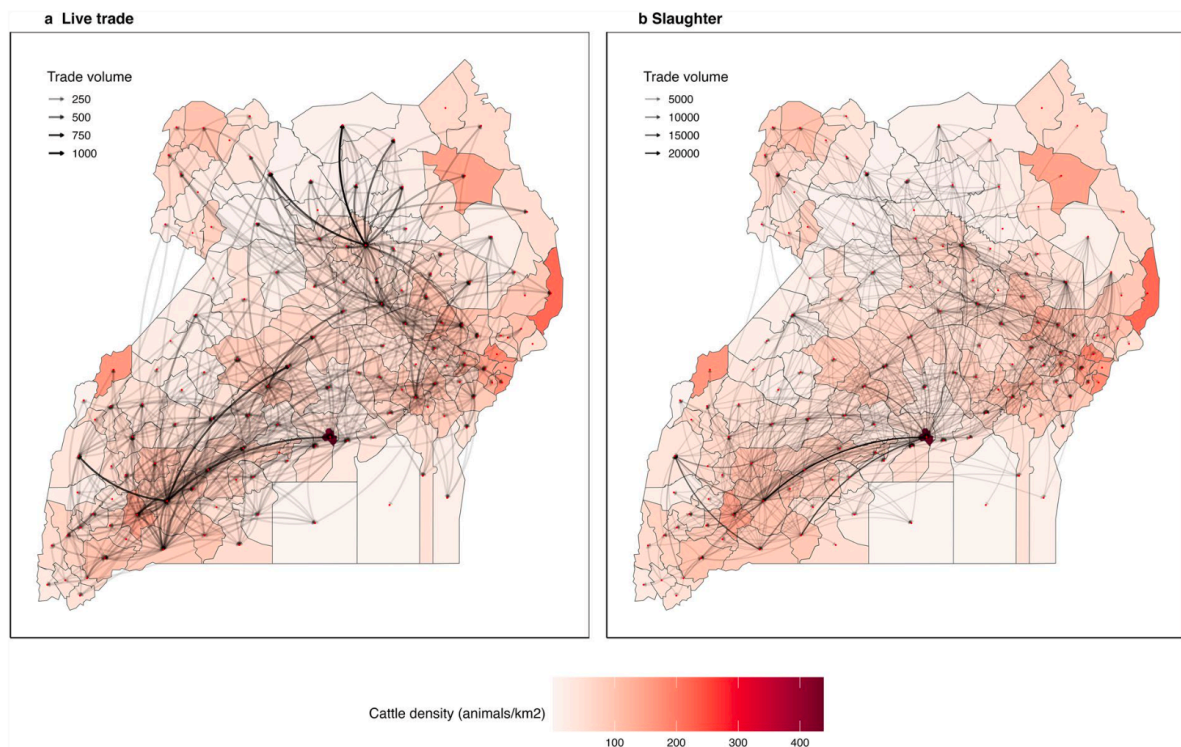


Figure 5. Cattle movement networks in Uganda, 2019. Between-district movements are weighted based on trade volume. (a) Live trade and (b) Slaughter.

We hypothesised that the season (wet or dry) and reasons for moving animals (slaughter or live trade) impact the network structure and cohesiveness, and thus, the possibility of disease transmission and the effectiveness of outbreak prevention and response measures. We then constructed seasonal networks, related to the two dry and two wet seasons (each lasting three months) that are occurring in Uganda. Our results showed that the cattle movement network in Uganda was characterised by a high level of seasonal variability, with seasonal networks being much smaller, less connected, and characterised by lower topographic metrics than those of the annual network. In addition, the comparison of the trade events occurring between seasonal and annual networks showed poor loyalty (<10%) for all seasons suggested that the annual network is not a reliable representation of the seasonal system.

The results here suggested that the collective movement of cattle was marked by a temporal component, indicating that the static annual network was not a good proxy of the dynamic, seasonally aggregated network for the same year. Upon comparing these findings with the mapping output (such as network communities, **Figure 6**), it became evident that both live trade and slaughter movement networks seem

to be influenced by a complex supply-demand ecosystem that varies across livestock systems and sub-regions, with an emphasis on seasonal movements.

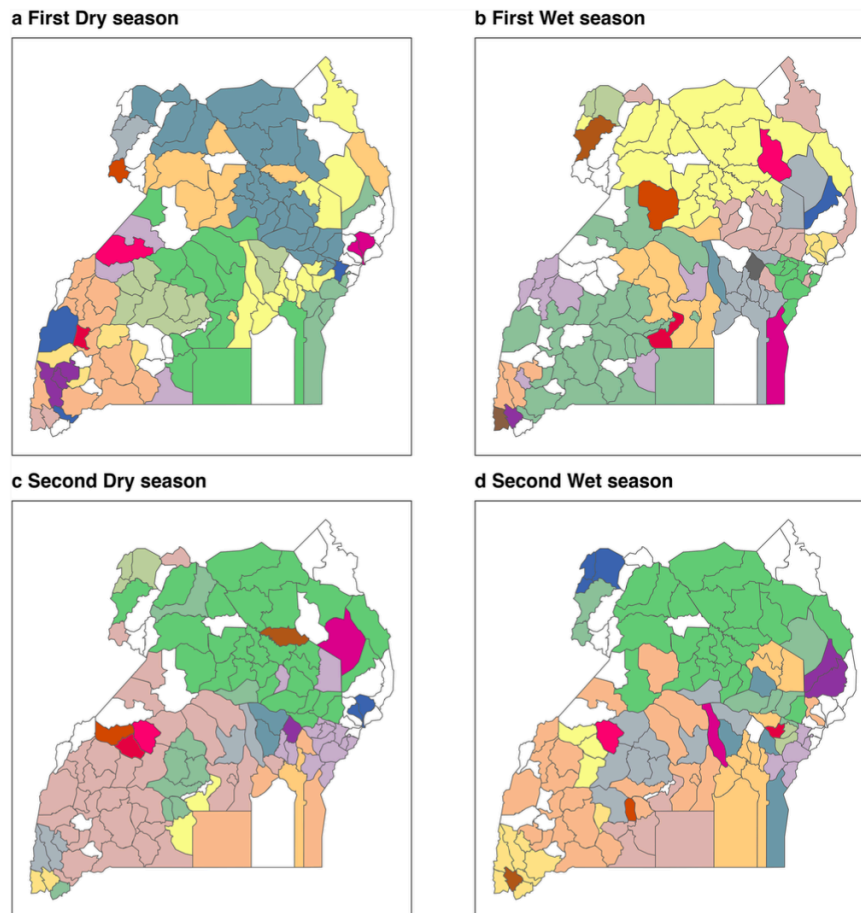


Figure 6. Live-trade network communities and its spatial distribution across the seasons. Districts in white were not active in the network for the assessed period. Each community is depicted by a unique colour.

If between-district trade events are to be related to the spread of TADs, our analysis of the cattle mobility data indicated that TADs could spread widely across a temporally heterogeneous movement network and that the first dry and wet seasons were likely to be associated with larger epidemics in Uganda. It also suggested that local and long-haul disease spread are likely to occur via live cattle trade, with up to 20% of the districts potentially becoming infected after an outbreak and infection occurring over large vast geographical distances in potentially three sequential between-district trade events.

The analysis of the network distribution showed that all networks (annual and seasonal) exhibited scale-free properties (Power-law distribution), with most districts showing very few connections and few districts acting as network hubs characterised by a larger number of links. Node centrality measures for each district of the cattle mobility seasonal networks were then computed and a percolation analysis (**Figure 7**) was performed upon them to identify the best centrality-targeting strategy to preferentially allocate disease resources (e.g., personnel, vaccines, etc.) for prevention and control interventions (Bajardi et al., 2011). The outputs of the analysis offered multiple options to enhance the identification of influential districts

and leverage the value of the cattle network, highlighting the potential utility of these approaches for disease control. These included single-measure and composite classifications based on district centrality.

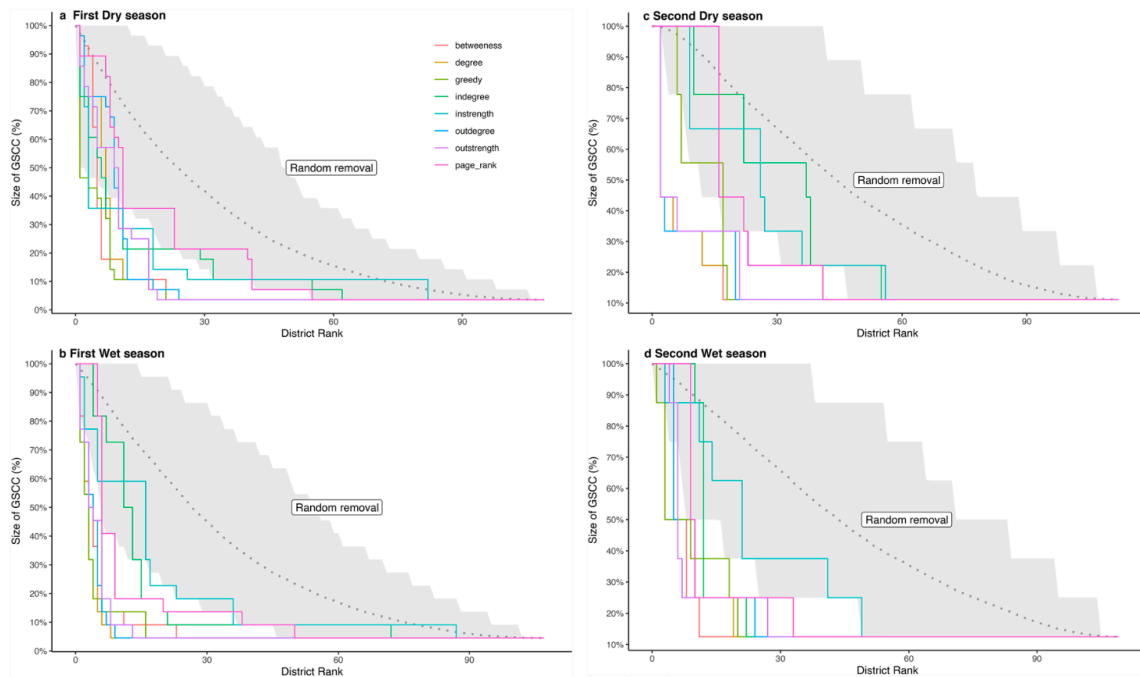


Figure 7. Plot of centrality-based percolation per season—Live trade. Performance measured through the proportional size of the giant strongly connected component (GSCC) after the removal of ranked districts.

Because these networks describe the spatio-temporal structures of the key pathways for the propagation of diseases at a higher spatial level, the analysis presented here revealed preliminary patterns that can inform decision-making. While the best targets may vary across seasons, having a guiding framework for network-based prioritization can be transformative for managing TADs, particularly FMD, in Uganda. Although efficient theoretically, such an approach has been rarely tested on the field.

As part of a research project funded by the European Commission for the Control of Foot-and-Mouth Disease (EuFMD), we carried out a pilot study (PhD Thesis of L. Gonzalez, 2024) to evaluate the performance of network-based approach to identify the best sentinel sites for environmental sampling (using ONT MinION™ for fast and cost-effective diagnostic approach) and optimise surveillance strategy to detect FMD circulation within and between districts.

This field-trial was organised in a group of districts heavily involved in livestock trading, located in south-eastern Uganda. A total of 17 livestock markets within 11 districts were surveyed. Samples were collected from cattle, the market environment, and from vehicles. Evidence of the virus was detected in five out of 11 surveyed districts (45.5%) and six out of 17 markets (35.3%). Positive markets were typically medium or large-sized, well-connected, enclosed livestock markets that traded higher numbers of cattle per day of operation (>300 animals).

This pilot study demonstrated the potential of network-based targeting as a tool for identifying optimal monitoring sites for the detection of FMD in eastern Uganda. By optimizing sampling locations and employing flexible, low-resource, non-invasive, and field-deployable methods for sample collection, storage, transport, and processing, it was possible to detect evidence of FMD virus genomes in outbreak and non-outbreak areas, after integrating multiple environmental and animal sample types. Healthy-looking cattle infected with FMD and evidence of viral contamination were documented in various static (e.g., crushes, ramps, fences) and mobile (e.g., sticks) elements within the market environment, as well as in lorries used for mixed-species livestock transportation.

In the following section, we present another application of network-based approach to identify optimal surveillance sites for detecting vector-borne TADs combining both dispersion pathways and ecological characteristics of environment occurring at both departures and destinations.

Box 2. Other applications

Animal movement is an important factor for disseminating in many livestock industries and provide information upon which spatial distribution of risk can be inferred from trade behaviour (Motta et al., 2017; Porphyre et al., 2020; Muwonge et al., 2021; Gonzalez Gondon et al., 2023), husbandry practices (Motta et al., 2018; DVM thesis of M. Picq, 2023), industry structure (Porphyre et al., 2014) or landscape features (PhD thesis of R. Flood, 2015). Social network analysis methodology was used to describe livestock structure (Motta et al, 2017; Technical report of T. Porphyre, 2020) and explore the impact of other mechanisms related to animal movements on their resilience to disease control activities (Porphyre et al., 2020). Lately, these works have been extended to analysed how animal species may be in contacts and facilitate the spread of leptospirosis (M1 report Ameline Besse, 2022).

Risk of vector-borne disease introduction from wind dispersal

Bluetongue disease is recognized as a global veterinary concern due to its economical and animal health impact. It affects both domestic and wild ruminants and it is mostly transmitted by small flying diptera (midges) of the genus *Culicoides*. In Europe, since the Bluetongue virus (BTV) serotype 10 (BTV-10) first emerged in Portugal and Spain in 1956-1960, 12 additional viral serotypes among the 36 identified nowadays have been reported in the continent (BTV-1,-2,-3,-4,-6,-8,-9,-11,-14,-16,-25,-27) (Saminathan et al., 2020). BTV-3 first emerged in Sicily (2017), then in Sardinia (2018), and very recently in September 2023, in the Netherlands (Holwerda et al., 2023). No new cases have been reported in Sicily since 2017 (WAHIS, www.woah.org) while the virus has been reported circulating in Sardinia every year until now but the infected area has not so far exceeded the official endemic zone in the southern part of the island.

Several routes of BTV introduction have been imputed solely or in combination: import of live animals through legal or illegal trade, import of germplasm (semen and/or embryos), movement of wild animals, airborne dispersion of vectors, import of adult vectors by aircraft or use of poorly attenuated modified live vaccines (Hoar et al., 2004; Mintiens et al., 2008; Napp et al., 2013; Simons et al., 2019). While the route of introduction into the Netherlands in 2023 is still under investigation, the suspected route of BTV-3 introduction into Sicily and Sardinia was the Long-Distance Wind Dispersal (LDWD) of infected vectors from Tunisia (Aguilar-Vega et al., 2019; Cappai et al., 2019). The BTV-3 circulation in Sardinia, on the doorstep of mainland Europe poses a real threat to surrounding free countries in Europe. In this study, we investigated which European countries could be at risk of BTV-3 introductions from Sardinia as a direct consequence of LDWD of infected vectors.

In this study, we have developed a generic Quantitative Risk Assessment to estimate the risk of BTV incursion from LDWD of infected vectors. This model framework considers the impact of having two susceptible host species h (cattle and small ruminants) and two competent vector species v (*C. imicola* and the *Obsoletus* complex, comprising *C. obsoletus* and *C. scoticus* species) on the risk. In this way, this QRA framework considers the complex vector-host-environment interactions of BTV that occurs at the source i and destination j , but also inside the airmass carrying BTV vectors.

To illustrate this framework, we estimated the risk of BTV-3 incursion into mainland Europe via LDWD from the southwestern parts of Sardinia and identified key epidemiological and ecological drivers to this risk. As such, the source area i was defined as the southwestern part of Sardinia where BTV-3 outbreaks have been reported, whereas j are all 0.5° cells that cover the areas of Europe and Northern Africa, and in which at least 1 cattle or small ruminant was reported in international livestock databases (Gilbert et al., 2018).

The QRA was developed based on three evaluation steps (**Figure 8**):

1. $Inf_{v,i}$: the level of infection in each vector species v at the source i , *i.e.* the number of vectors of species v that are infected (and therefore infectious) within the infection source area i ;
2. $P_{v,ij}$: the probability of long-distance wind dispersal of alive vectors of species v from source i to any destination j in Europe;
3. R_{0j} : the potential of onward virus transmission at destination j , *i.e.*, the geometric average rate of secondary infections generated by one primary vector infection at destination j .

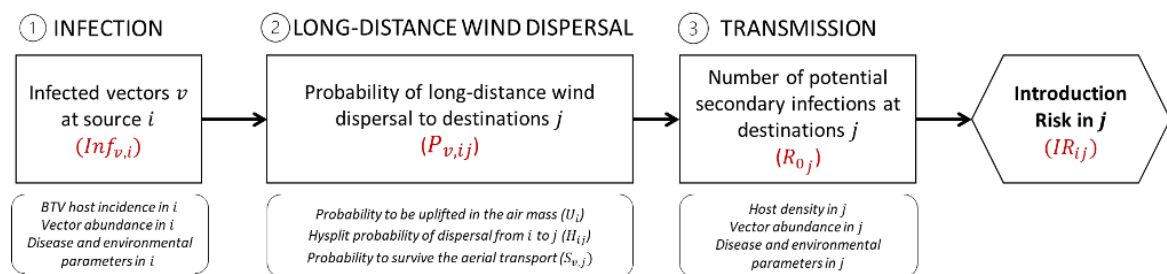


Figure 8. Risk Assessment (RA) framework. The risk assessment framework quantifies the risk of Bluetongue virus introduction (IR_{ij}) from a source area i to a destination area by Long-Distance Wind Dispersal (LDWD) of an infected culicoides vector of species v as a function of 3 steps, including Introduction risk calculation at destination j is a combination of 3 steps.

For each week of the study period, the risk of a new BTV introduction into any destination j (IR_{ij}) in Europe from source i was computed by combining the three evaluation steps, as follows:

$$IR_{ij} = \sum_{v=\{1,2\}} (Inf_{v,i} \times P_{v,ij}) \times R_{0j}$$

Here, the value IR_{ij} should be interpreted as a daily rate of new infections generated by both vector species v at destination j , and considering the total number of infectious vectors of each species v that could be dispersed by the wind from i to j . As such, $IR_{ij} > 1$ indicates that a potential introduction of the virus at destination j may originate from source i and may be established in the local population, whereas $IR_{ij} < 1$ indicates that no introduction of the virus into destination j may occur. The number of weeks with

a risk greater than 1 ($W_{IR>1}$) and the mean of IR over the entire study period (\overline{IR}) were also calculated for each destination j and mapped to evidence high-risk regions.

While the number of infected vectors (i.e., the sum of latent and infectious vectors) of species v in i ($Inf_{v,i}$) was evaluated as a function of the size of both vector and host populations as well as the BTV-3 prevalence reported in the literature, the probability of LDWD from source to destination ($P_{v,ij}$) was computed from a constructed time-variant wind-connectivity network for which nodes represent all 0.5° cells considered in our study area (**Figure 9**). Notably, edges connecting all nodes resulted from the application of an atmospheric dispersion model, the HYSPLIT (HYbrid Single-Particle Lagrangian Integrated Trajectory) model (Stein et al., 2015). Using the HYSPLIT model, air-mass trajectories were simulated over 24 hours while accounting for the impact of meteorological, atmospheric and biophysical variables on air flow as well as vectors' flight activities and survival in the air-mass (e.g. air mass temperature, thickness of the Planetary Boundary Layer, initial starting time). As a result, a series of connectivity matrices was generated informing on the expected probability of LDWD (P_{ij}) from i to j for each of the 36 weeks of the study period.

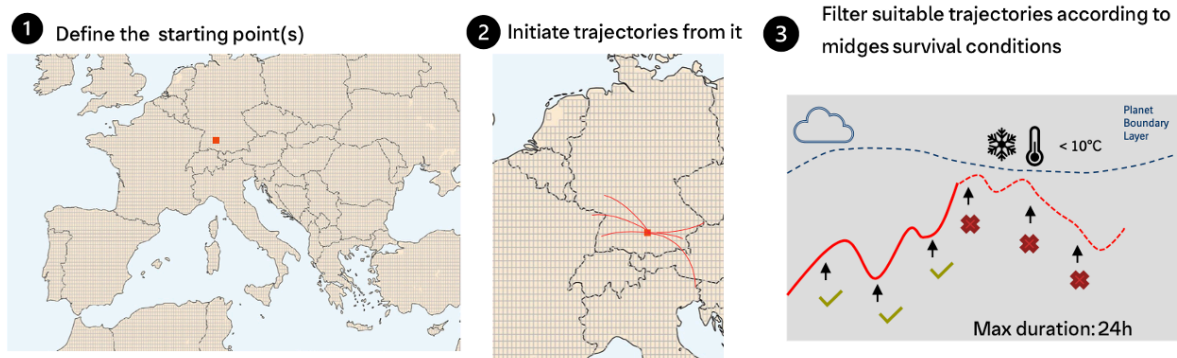


Figure 9. The three steps used to construct the wind-dispersion network using HYSPLIT.

Finally, disease transmissibility in each destination cell j was estimated through the R_{0j} (basic reproduction number), usually defined as “the expected number of secondary cases produced, in a completely susceptible population, by a typical infectious individual” (Anderson and May, 1992). The R_{0j} is equivalent to the average number (geometric mean) of secondary infections at destination produced by one single infection. As such, an estimate of $R_{0j} < 1$ implies that disease transmission would not be sufficient for BTV to sustain in these conditions, whereas BTV would spread where $R_{0j} > 1$. We used the R_0 formula defined for BTV by Turner et al. (Turner et al., 2013) considering two-host and two-vector populations. It combines four R_{xy} components, with x defining the vector species at destination j that get infected due to one primary infectious vector of species y incoming from source i , such as:

$$R_{0j} = \sqrt{\frac{1}{2} \left[(R_{11} + R_{22}) + \sqrt{(R_{11} + R_{22})^2 - 4(R_{11}R_{22} - R_{12}R_{21})} \right]}$$

where R_{11} is the average number of infectious *C. imicola* produced at destination by one infectious *C. imicola* incoming from source; R_{22} the average number of infectious Obsoletus complex midges produced at destination by one infectious Obsoletus complex midge incoming from source; R_{12} is the average number of infectious *C. imicola* produced at destination by one infectious Obsoletus complex incoming

from source; and R_{21} is the average number of infectious *Obsoletus* complex produced at destination by one infectious *C. imicola* incoming from source.

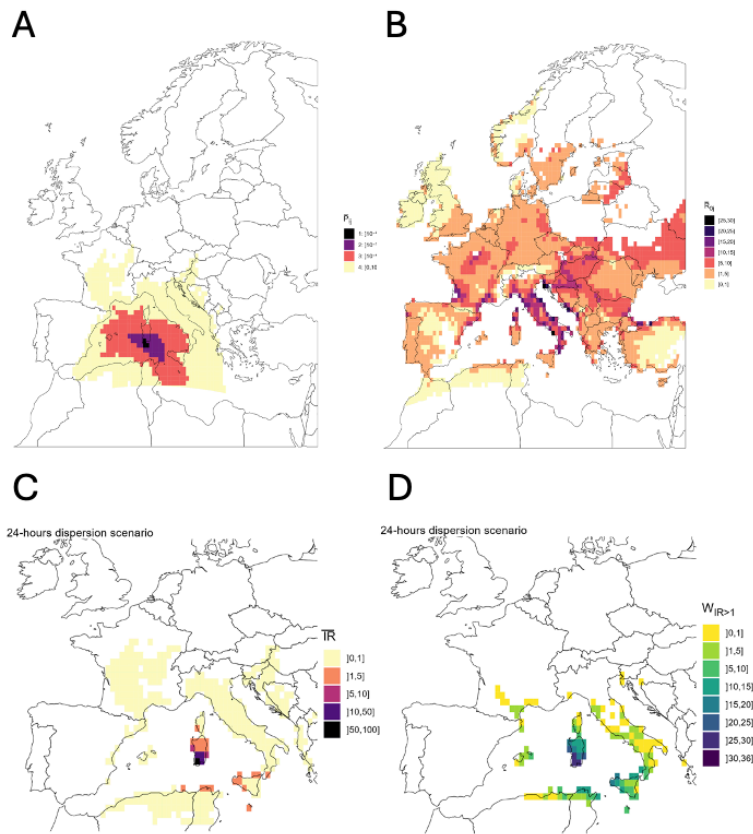


Figure 10. Spatial distribution of the risk. (A) Spatial distribution of the overall mean probability of long-distance wind dispersal from southwestern Sardinia to any destination in Europe considering 24-h maximal flight duration. Here, overall mean probability \overline{P}_{ij} is computed over the 36 weeks of the study period. (B) Spatial distribution of the overall transmissibility \overline{R}_{0j} of BTV in Europe considering 2 host types (cattle and small ruminants) and 2 vector populations (*C. imicola* and *Obsoletus* complex). (C-D) Spatial distribution of the overall risk of introduction from southwestern Sardinia to any destination in Europe, considering a 24-h maximum flight duration of vectors. Here, the risk of introduction was expressed as (C) the overall risk of introduction (\overline{IR}) in Europe and (D) the number of weeks in which the mean risk of introduction IR is greater than 1 ($W_{IR>1}$).

One of the greatest strengths in this framework is the inclusion of atmospheric simulations to assess vector dispersion from wind while accounting for its variations at a relatively fine spatial and temporal scales. This enables us to identify wind pathways that would be overlooked at lower resolution or timescales. For example, HYSPLIT simulations predicted some sporadic wind incursions to the northwest direction towards continental France in June and October, despite a global wind pattern pointing in the southwestern direction (**Figure 10A**).

From our results, high-risk areas and high-risk periods of BTV-3 introduction into European free areas were identified (**Figures 10C & D**). The at-risk destinations identified by the model applied for BTV-3, are consistent with historical data for other serotypes and provided valuable information that may facilitate preparedness and target surveillance.

In this work, we have shown that spatial distribution of the risk of BTV incursion from a given source will vary with time as wind conditions supporting long distance transportation of living vectors may arrive in different location depending on the week of the year. This study results further showed the importance

of accounting for multiplicity of vector species and host species when assessing the risk of incursion; taken them separately would result in a marked underestimation.

Box 3. Other applications

The wind dispersion matrix presented here has also been applied to assess the risk of wind-borne dispersion for other *culicoides*-borne diseases such as EHDV from the first reported cases in France (Bibard et al., 2024b) or accounting for the secondary infections by integrating it into a simulation model (Porphyre et al, in preparation). Although assessing the potential of vector spread due to wind is critical, such information is difficult to be manipulated by policy makers. The development of a web application tool to efficiently and easily exploit such data is currently on-going (PhD thesis A. Bibard).

Use of simulation models for policy guidance

As described above, animal movement is recognized as an important route of transmission of diseases in livestock (Fèvre et al., 2006; Ortiz-Pelaez et al., 2006). However, although understanding the complexity of the live animal trade network is critical, it is not sufficient to predict the spread of infectious diseases in structured populations.

Other mechanisms and relationships may indirectly connect farms to each other and represent additional routes of infection. Not accounting for these indirect contacts (such as spatial proximity, veterinarian routes, sharing livestock transport vehicles, or movements of other commodities) will lead us to underestimate the role of individual farms and limit the benefit of targeted strategies to control and prevent infectious diseases (Bernini et al., 2019; Porphyre et al., 2020; Rossi et al., 2015).

This is further complicated by the facts that networks are, by definition, “static” (i.e. with contacts between individuals that are fixed within the time period within which the network is built). Although this may not pose a problem in most situations, analysing structures of static networks typically lacks the ability to account for the epidemiological dynamics of the infection in nodes (that is their potential to infect others depending on when they have been infected and for how long they remain infectious) (Nickbakhsh et al., 2013), and therefore the changes in their infectious contacts over time, have the potential to overestimate the central role of nodes and mislead targeted disease control strategies.

In this section we present simulation models developed as part of the Centre of Expertise on Animal Disease Outbreaks (EPIC) to respond to queries from the Division of Animal Health and Welfare of the Scottish Government for the development of their protocols on swine fever surveillance (Porphyre et al., 2017) and on vaccination against FMD (Porphyre et al., 2013). These models either integrated the dynamic nature of the different transmission pathways occurring over different scales (within farm, between farm) or accounted for the complexity (in time and space) of disease control activities during outbreaks.

Areas of onward transmission and actors of spread

Classical swine fever (CSF) is a notifiable, highly contagious viral disease of swine, both domestic and wild, which results in severe animal welfare and economic consequences in affected countries (Moennig et al., 2003). Because of the potential for severe socio-economical costs associated with CSF (Meuwissen et al., 1999), efforts have been carried out to control and eradicate CSF in the European Union (EU) with a

common strategy implemented by EU legislation (Council Directive 2001/89/ EC). Although there are regulations in place to reduce the risk of CSF spread within Europe (for example regarding the import of live animals and the feeding of food waste), the risk of CSF incursions still remains. In Great Britain (GB), the last outbreak of CSF that occurred in GB in 2000 was found caused by legal and illegal imports of contaminated pork products.

Once the detection of CSF virus in a farm occurs, strict measures are implemented to control disease spread, including depopulating infected premises (IPs), tracing high risk premises, and strict movement restrictions for farms in the vicinity of IPs, in line with domestic and international legislation. Depopulation of IPs is aimed at limiting disease spread by removing sources of infection, whilst movement restrictions are designed to prevent the transmission of CSF virus to naive animals through direct contact with infected animals or via contaminated fomites. The impact of various factors on the effectiveness of these mitigation strategies in controlling disease have been described for CSF in other countries, or for other notifiable disease that spread in similar ways. In particular: (i) the location and timing of the incursion, which relate to farm density and the frequency of animal movements to or from the; (ii) the strain of the virus (Porphyre et al., 2013); (iii) the efficacy of surveillance systems for rapid detection of incursions (Tildesley et al., 2006); and (iv) human behaviour and the degree of compliance with control measures such as movement restrictions (Brosig et al., 2014; Thulke et al., 2011) have all been found to affect the effectiveness of control. However, little information exists on the impact these factors may have on the risk of CSF spread in the British swine industry. Such information is critical to optimise surveillance and control strategies and ensure that CSF epidemics are detected and eradicated quickly and cost-effectively.

In this study, the spread of CSF within the British swine industry was modelled using a hybrid stochastic-deterministic, spatially explicit, premises-based, discrete-time model where within-farm prevalence is modelled explicitly. Using this model, we evaluated how CSF may spread from single incursion events in the British pig industry. Specifically, we investigated (1) how the risk of CSF spread and the size of generated epidemics vary with the time taken to detect an incursion as well as the geographical location and the producer type of the primary case, and (2) explore which other factors involved in the transmission and control of CSF would influence the risk of spread and the size of generated epidemics.

Here, the model comprises modules which account for (1) the transmission of the disease between premises, (2) the influence of the within-farm prevalence on disease transmission between premises, and (3) mitigation and surveillance activities carried out to control epidemics. The model assumes that each j^{th} susceptible premises would be infected by an infectious premises j with a daily probability P_j depending on (1) the number of animals that have been received from premises j , (2) the animal-level disease prevalence $w_{j,t}$ that occurs in premises j at the time t movement is carried out, and (3) its spatial location, relative to that of infected premises j . However, because the order in which different transmission processes occur may have some impact on the rate of disease spread, we assumed that movements to gathering places would be carried out first at the start of every simulation day, followed by movements to other premises, followed finally by transmission through local spread at the end of the simulation day. As such, we separated the daily probability of premises to be infected due to local spread $L_{ji,t}$ to that due to the movements of pigs $M_{ji,t}$ such as:

$$L_{ji,t} = 1 - \exp(-K(d_{ij}) \cdot \Delta t)$$

and

$$M_{ji,t} = 1 - (1 - w_{j,t})^{b_{ij,t}}$$

where $b_{ij,t}$ is the number of pigs that have been received by the premises i from any infected premises j at time t . Values of $b_{ij,t}$ were extracted from historical records of pig movements that occurred in Great Britain from January 1st 2012 to May 31th 2013. The component $K(d_{ij})$ denotes the “between-farm transmission kernel function” and determines the rate at which an infected premises may infect susceptible ones as a function of inter-farm Euclidean distance d_{ij} . In other words, $K(d_{ij})$ describes the spread that results from local transmission dynamics that are independent from the movements of animals. This encompasses several routes of infection, including travel of farm workers, sharing farm materials or other locally driven processes linking premises, which are likely to occur more often between spatially-close farms than between farms separated by longer distances. We used data collected during the last epidemic of CSF in GB to inform a spatially explicit, premises-based model to infer parameters value (Gamado et al., 2017).

Using the model, we first looked at how the duration of the “high risk period” (HRP) (that is the length of time between introduction and detection of a disease, during which no control measures have yet been implemented and disease continues to spread) would affect the size of the outbreaks generated by a single incursion. Over 240,000 simulations carried out per HRP scenario, we showed that incursions would be restricted to the primary case in 91.3%, 84.9%, 82.5%, 81.3% of the time for a HRP of 2, 4, 6 and 8 weeks, respectively (**Figure 11A**). Although all incursions would be detected if the HRP lasted no more than 2 weeks, only 15%, 8.5%, 8.0% of the epidemics would last long enough to be detected when the duration of the HRP is 4, 6 and 8 weeks, respectively. When detected, the median duration of the epidemic (defined as the length of time between detection of the disease to the depopulation of the last IP) was 1 day (95% range 1–30 days), 15 days (95% range 2–88 days), 20 days (95% range 1–105 days) and 21 days (95% range 1–109 days) when the HRP lasts 2, 4, 6 and 8 weeks, respectively. In these situations, the median number of infected farms would be 1 (95% range 1–3), 2 (95% range 1–25), 3 (95% range 1–25) and 3 (95% range 1–30) farms, respectively. However, substantial disease spread may still occur regardless of the HRP duration. For a HRP of 2, 4, 6 and 8 weeks, as many as 102, 100, 113 and 107 farms were infected during at least one of the simulation runs, respectively.

To investigate the likelihood that an epidemic may be generated from a single incursion event in GB, we assessed the probability of epidemic take-off (defined as the probability that a primary case generates epidemics which involves at least two other farms) for the entire set of simulated incursions. The probability of epidemic take-off for a single incursion event in GB was 0.028, 0.053, 0.067 and 0.078 for a HRP of 2, 4, 6 and 8 weeks, respectively. Furthermore, there was little monthly variation in the probability of epidemic take-off (**Figure 11B**).

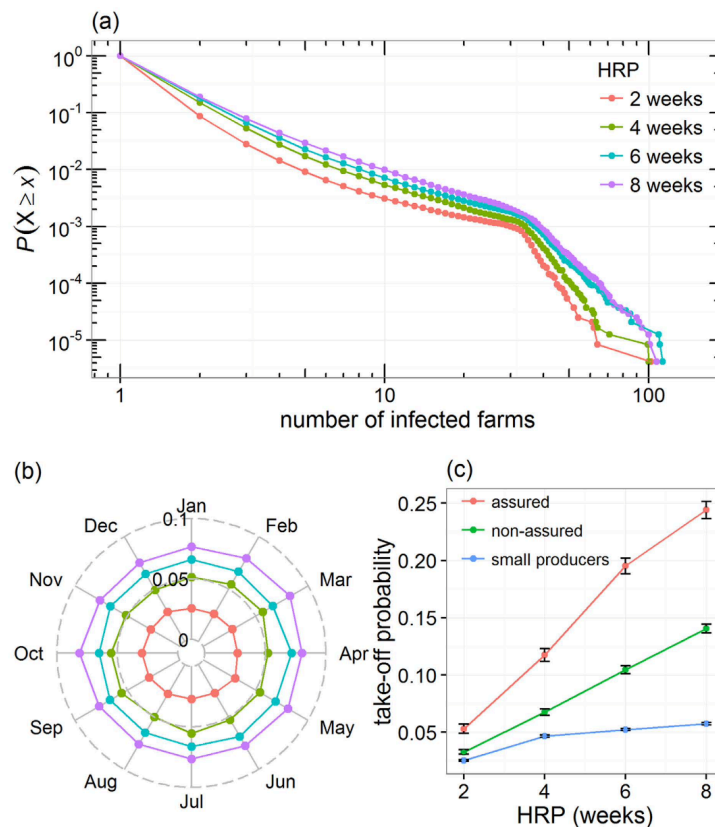


Figure 11. Temporal variation in the risk of CSF spread in Great Britain. (a) Decreasing cumulative probability function of the total number of infected farms involved in epidemics generated from a single incursion for various duration of the high-risk period (HRP). (b,c) Changes in the overall probability of epidemic take-off generated from a single incursion as a function of (b) the month of the incursion and HRP duration or (c) the producer type of the farm in which incursion occurred. The HRP is defined as the length of time between the incursion and the date of the first detected infected premises. The probability of epidemic take-off is defined as the probability that a primary case generates epidemics which involves at least two other farms. Note that both axes in panel (a) are \log_{10} -scaled.

Under the extreme (but not unlikely) scenario that eight weeks passes before an incursion is detected, we produced a smoothed map of the farm-level probability of epidemic take-off. In doing so, we showed that there was a clear spatial structure in the risk of disease spread in GB. Indeed, **Figure 12A** showed distinct areas where the overall CSF risk is greater than the rest of the country and defined areas where the risk of epidemic take-off is low, medium and high. Most high-risk areas are concordant with locations with a high density of pigs, indicative of the location of industry hotspots. We then compared how the distributions of the probability of epidemic take-off for all primarily infected farms (**Figure 12B**), and the resulting epidemic size (**Figure 12C**) for incursions occurring either in high or in low-risk areas. By doing so, we showed that although incursions in low-risk areas have a much lower chance to generate epidemics, widespread epidemics still occurred from incursions in low-risk areas, potentially generating epidemics of more than 100 farms. In addition, some high-risk areas were located in areas where the density of pigs was low but the density of pig farms was high, highlighting that, despite small producers having low number of animals, when gathered in sufficient density, they may also generate large epidemics.

There was little research on the role of small producers, which in GB predominantly includes backyard holdings and traditional small-scale farms, in the spread of notifiable disease in Europe. Small producers are usually regarded as having little impact on the risk of CSF spread, only participating in the persistence

of diseases in the industry (Alexandrov et al., 2011; Martínez-López et al., 2013). Our results suggest, however, that the risk of CSF spread in GB when incursion occurs in small producers is potentially not negligible, and that incursions could generate widespread epidemics, particularly when those incursions occurred in high-risk areas.

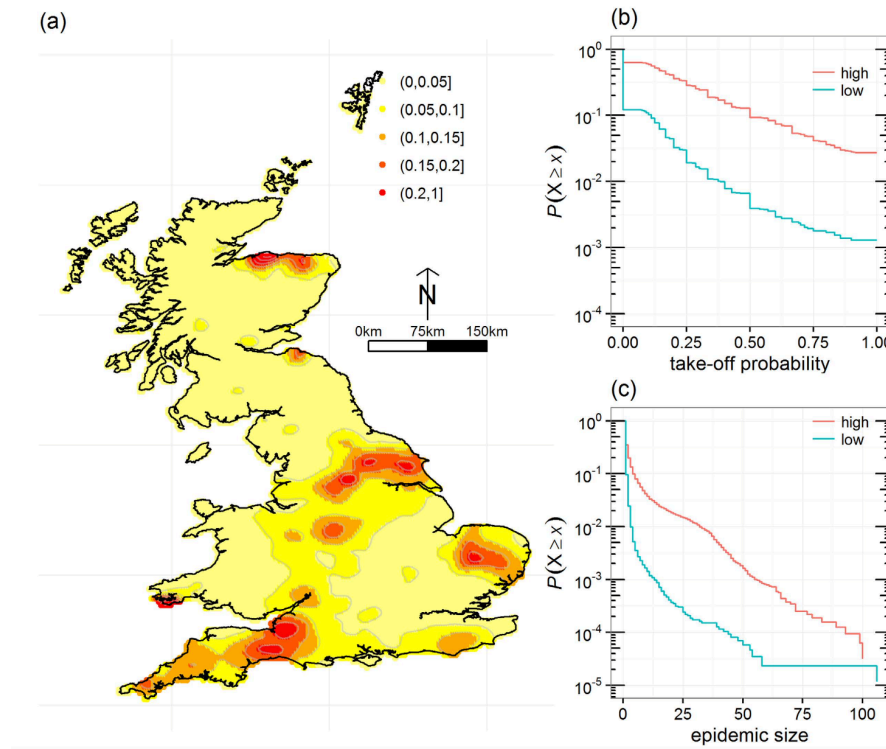


Figure 12. Spatial variation in the risk of CSF spread in Great Britain. (a) Smoothed spatial distribution of the probability of epidemic take-off generated from a single incursion. (b,c) Decreasing cumulative probability function of (b) the probability of epidemic take-off for individual primary cases and (c) the epidemic size for incursions occurring in either low or high risk areas. Low and high-risk areas are defined as areas in panel (a) where the smoothed probability of epidemic take-off is ≤ 0.05 and > 0.15 , respectively. The probability of epidemic take-off in panels (a,b) is defined as the probability that a primary case generates epidemics which involves at least two other farms. Epidemic size in panel (c) was characterized by the total number of infected farms (excluding primary cases) involved in epidemic generated by individual primary cases. All simulations in these figures considered an eight-week high risk period (HRP). Note that the y-axis in panels (b,c) are \log_{10} -scaled.

Carrying out a global sensitivity analysis over all the parameters of the model enabled us to identify which aspects of the model most affect the spread of CSF in GB and how they may vary between risk areas. Beside local spread parameters which have the greatest impact on the model in all situations, parameters affecting the duration that CSF may remain within farms showed a greater influence on the median size of epidemics when incursions occurred in a low-risk area than when they occurred in a high-risk area (Figure 13). Global sensitivity analysis further showed that varying compliance to post-detection movement restrictions of small pig producers did not significantly influence the risk of CSF spread in GB.

This was a surprising result since movement restrictions are a key component of outbreak control strategy and was shown to drastically affect the spread of disease (Brosig et al., 2014; Thulke et al., 2011). We assumed that it was either because movements from/to small producers are infrequent and involve small number of pigs per batch (Porphyre et al., 2014) or because many of the moves involving small pig keepers also involve assured producers, and hence would be stopped anyway, is unclear. However, these findings

indicated that rather than enforcing 100% compliance to movement restrictions on all producers across GB, it would be more cost-efficient to advise movement restrictions to all producers but ensure 100% compliance on all assured producers.

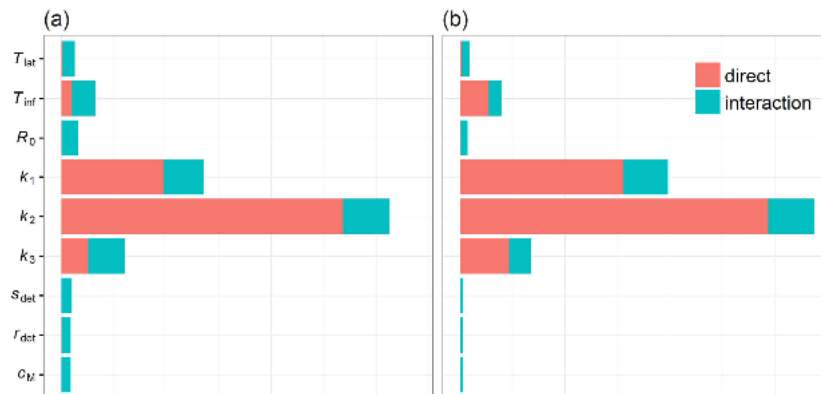


Figure 13. Influence of the model's parameters on the risk of CSF spread. Results of the global sensitivity analysis on the probability of epidemic take-off for single incursion events occurring in either (a) high and (b) low risk areas. Influence of the model's parameters was measured by the total sensitivity index (DT_k), which captures the overall effect of parameter variations, including direct effects and interactions between model parameters.

This study provided insight on how notifiable diseases such as CSF could spread within the British swine industry. We found that large outbreaks of CSF would be rare and generated from a limited number of areas in GB. Although our results confirm that the British swine industry has a low vulnerability to large CSF outbreaks, we identified concerns with respect to the role played by the non-commercial sector of the industry. This study has highlighted several areas where efforts could be made to improve preparedness for CSF incursions in the British swine industry. Particularly, further work was deemed required to better understand the role of small pig producers in GB in the spread of notifiable diseases and how local spread would be affected by their behaviours.

Box 4. The swine fevers preparedness research programme

This study represents a key output in an extensive programme of research initiated by Scottish Government, through its Centre of Expertise on Animal Disease Outbreak (EPIC), to improve evidence used for prevention and control decisions against swine fever outbreaks in GB. Over the course of the programme, studies integrating pig movement databases with industry-relevant information were carried out to describe the structure of the British swine industry and unravel trading behaviours between different sectors of the industry (Porphyre et al., 2014; Porphyre et al., 2020; technical reports of T. Porphyre et al., 2016, 2021). These descriptive studies were further completed with non-structured interviews of small pig keepers (technical reports of C. Kyle et al., 2021) and surveys (Allen et al, 2024) to better grasp how current biosecurity guidelines are perceived and put into practices in the different sectors of the industry.

Inference models were developed to better analysis outbreak data in order to better characterise the dynamics of disease spread within (Guinat et al., 2018; Ewing et al., 2022) and between herds (Gamado et al., 2017). These were integrated into mathematical models that simulate the course of epidemics, allowing us to assess the potential outcomes of incursions in GB and assess the impact of various uncertainties when responding to these emergencies (Porphyre et al., 2016). This programme has generated invaluable knowledge for developing more robust biosecurity and surveillance plans for emerging swine diseases. This is now extended to better understand role of wildlife (Fay et al., 2024) and reporting (M2 report of G. Margiapia, 2023).

Spatial variations of disease control action

For various TADs, vaccination is an important weapon to prevent and/or limit their spread in animal populations. While social and behavioural constraints limit its implementation in humans (Brewer et al., 2007; Galvani et al., 2007), use of vaccination in livestock populations is predominantly driven by economic considerations. This is particularly true when disease is highly transmissible and can have major economic impact, such as FMD, CSF or highly pathogenic avian influenza. In countries where these diseases are absent, epidemics are subject to strict control measures, dictated by both regional and national level policies. In this situation, the decision of whether to implement vaccination as part of control measures when facing incursion of such diseases is left at the national level. To make this decision, governments must consider whether the benefits of vaccination are sufficient to outweigh potential additional costs, including further trade restrictions that may be imposed due to the implementation of vaccination.

For FMD, prophylactic vaccination outside of an epidemic is not permitted within the EU, but reactive ring vaccination may be used alongside animal movement restrictions and “stamping out” measures (culling of infected premises (IPs) and farms that had epidemiological contact during the silent period and are potentially infected, known as dangerous contacts (DCs), which is required under EU legislation (Commission Regulation No. 2003/85/EC). When facing a FMD epidemic, vaccination may be implemented following two different strategies: firstly, as a measure to restrict disease spread as quickly as possible, followed by culling of all vaccinated animals.

Despite the obvious logistical and social advantages vaccination may conceive by reducing the number of animals culled due to disease control purposes, there are inherent factors which may offset the likely effectiveness of a vaccination strategy. For example, the vaccine requires 4-5 days for immunity to develop and the vaccine efficacy is related to the antigenic match between the vaccine strain and the circulating strain (Barnett and Carabin, 2002). These limitations render the effectiveness of vaccination policies very sensitive to the initial conditions of an epidemic. In addition, models have suggested that the benefit of vaccination varies with the specific conditions of the outbreak (Backer et al., 2012; Traulsen et al., 2011). The reasons for this variation have not been fully characterised and it remains unclear whether real benefit can be obtained when applying vaccination in different incursion scenarios. This makes it difficult for policy-makers to make definitive decisions regarding whether vaccination should be implemented (Parent et al., 2011) and may cause delays in decision-making, which could, in itself, potentially affect the efficiency of the strategy. Starting from this observation, we explored the influence of different putative drivers on the effectiveness of a vaccination strategy for FMD. In particular, we tested whether changes in the delay of implementation and the location of the incursion would affect the epidemiological benefit of a vaccination policy against an infectious disease such as FMD.

In this work, we adapted a fully stochastic, spatial, premises-based model that was developed and used during the FMD epidemic in 2001 in Great Britain (Keeling et al., 2001; Tildesley et al., 2006) to assess how robust the benefits of vaccination are to specific outbreak conditions in the situation where FMD was detected in Scotland. In this model, premises pass through four epidemiological states; they are either: susceptible; infected but not infectious; infectious; or reported infected and thereby culled. The model assumes that each i^{th} premise would be infected with a daily probability depending on its own susceptibility S_i and on the transmissibility T_j of the surrounding j premises. For the n premises involved in the study population, each i^{th} premise has a daily probability M_i to be infected such as

$$M_i = 1 - \exp\left(-S_i \sum_{j \neq i}^n T_j K(d_{ij})\right)$$

where S_j and T_j depends on the species structure (type and herd size of cattle and sheep) present on premise. Similar to the model above, the component $K(d_{ij})$ denotes the “between-farm transmission kernel function” and is a function of the inter-farm distance d_{ij} .

Using this model and over all tested initial incursion events ($n=310,000$) involving a rapid detection of infection, FMD incursion would rarely spread in Scotland. When looking at epidemics arising from an initial case in each county of Scotland, on average, an epidemic would last for approximately 11 days with less than 3 infected premises (2.87) and less than 1500 animals culled (1168), including about 310 cattle, for disease control purposes. However, there are very large variations in the size and duration, with the most severe epidemics reaching a maximum of 1109 infected premises or lasting for more than 630 days. Although epidemics of more than 1000 IPs were extremely rare (less than once in 3000 incursions), the consequences would be disastrous for the Scottish livestock industry, with between 1.9 and 2.5 million animals culled for disease control purposes, representing 24% to 31% of the Scottish national herd. Overall, 8.8% and 11.3% of the generated outbreaks would result in epidemics of more than 100 infected premises or lasting more than 60 days, respectively.

Vaccination was then implemented in the model considering restriction related to the number of vaccination teams being mobilised and the time it would time for them to be actively vaccinating cattle. We also considered physical limits of vaccination team, each of which can vaccinate up to 250 animals per day. To test the cost-efficiency of various scenario of incursion, vaccination benefit (VB) of each scenario k was computed in relative terms by comparing the epidemic impact when vaccination is implemented in complement to routine mitigation procedures (i.e. NMB + IP/DC culling), c_v , with the epidemic impact when it is not, c_0 , such as:

$$VB_k = 1 - \frac{\hat{c}_{v,k}}{\hat{c}_{0,k}}$$

where the value of VB can be interpreted as the proportion of the epidemic impact that was saved due to the implementation of a vaccination policy.

When considering the location of the incursion, Scotland was found divided into two areas that exhibit relatively distinct patterns in vaccination benefit (**Figure 14**): (i) the area comprising the 14 counties in the south of Scotland (now referred to as “Southern counties”); and (ii) the rest of the country (17 counties, now referred to as “Northern counties”). Vaccination was indeed more effective in preventing FMD spread in the situation where incursion occurred in the Southern counties of Scotland than if it occurred elsewhere. Vaccination shows a marked impact on the number of animals that are required to be culled to control a FMD epidemic. When incursion occurs in the Southern counties of Scotland, the implementation of a reactive vaccination strategy would, on average, reduce the number of animals culled for disease control purposes by nearly 1600 animals (32%), including 544 cattle (42%). In contrast, little benefit was recorded if incursions occurred in the Northern counties of Scotland, with about 10 animals (3%) saved.

Looking at the benefit of vaccination in more detail, vaccination is however of most value in reducing the extent of severe epidemics regardless of where incursions occurred (Figure 15).

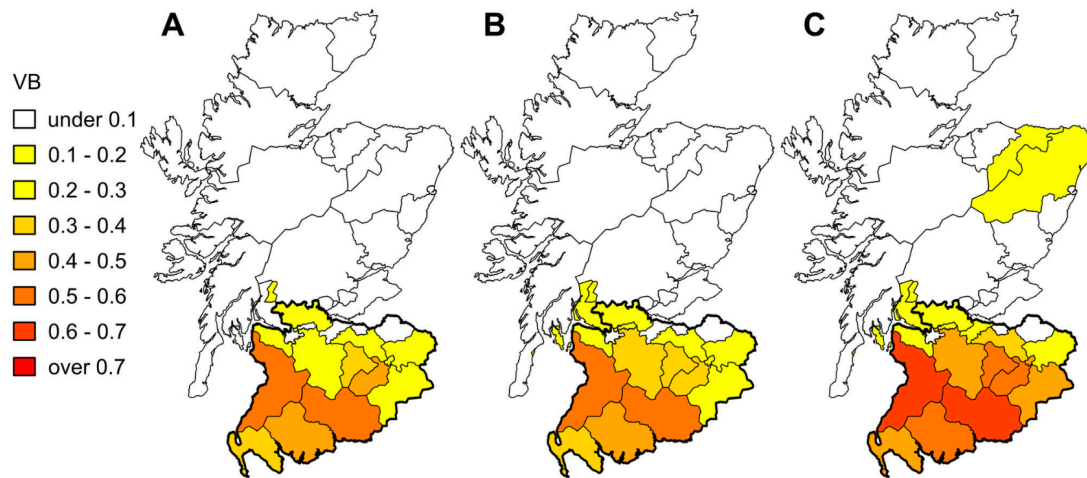


Figure 14. Spatial pattern in the benefit of the vaccination (VB) policy. Proportions of infected premises (A), animals culled (B) and cattle culled (C) that would be saved by implementing the vaccination policy in the field at 7 days in comparison with a strategy involving the culling of IP/DC premises alone. The darker the colour, the more vaccination is beneficial. Thick contour indicates counties defined as “southern counties”, which showed high epidemic impact.

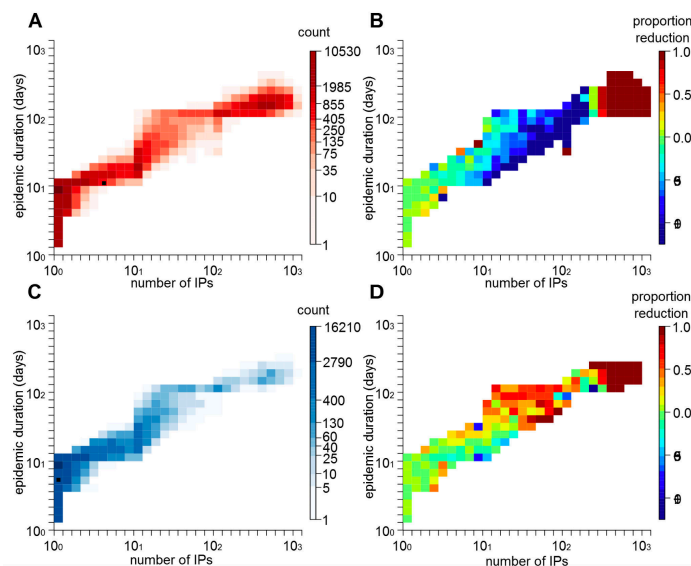


Figure 15. Epidemiologic impacts of a single FMD incursion when routine control measures are implemented alone or together with vaccination. A and C show the number of premises infected (IP) in a given epidemic generated from a single incursion in Southern (A) and Northern (B) counties, versus the number of days that epidemic would last. B and D show the proportion reduction in the number of epidemics when vaccination is implemented in the field at day 7 and for incursions in Southern (B) and Northern (D) counties. Black rectangle in A and C marks the geometric mean of the number of IPs and epidemic duration for all epidemics generated from incursions in the Southern or Northern counties, respectively. Negative values in B and C indicate an increase in the number of epidemics compared to when no vaccination is implemented, while positive values indicate a decrease in the number of epidemics.

When investigating the effect of delaying the field implementation of vaccination on its benefit, we restricted our analyses to incursions occurring either in Ayrshire or in Aberdeenshire. These counties were

chosen since they are both areas with a high density of premises and animals and represent good examples of the different patterns seen in the southern and northern counties of Scotland (**Figure 16A**). For both counties, highest VB values were obtained when no delay in implementing the policy occurs (**Figure 16B**). Obviously, this has marked implications when incursions occur in Aberdeenshire, where implementing vaccination shows inherently little benefit. Indeed, waiting 10 days to implement the policy would produce little additional epidemiological benefit for Aberdeenshire incursions, as most epidemics would be finished (**Figure 16B**). Again, vaccination is of most value in reducing the extent of severe epidemics (**Figure 15**). This means that vaccination was still beneficial for Ayrshire incursions (where the risk of severe epidemics is higher) even if there was a large delay in implementation (**Figure 16B**).

Looking at the effect of late detection, increasing the number of IPs at first report would increase VB (**Figure 16C**). When five premises are infected at first report, applying vaccination would be about 3.5 and 1.4 times more beneficial than when a single premise is infected in Aberdeenshire and Ayrshire, respectively. However, VB showed a greater sensitivity to delays in the implementation of policy in the field. When the number of IPs prior first to report increases, VB would not only reduce faster for each day increase in delay (**Figure 16D**) but also would markedly increase the number of cattle which must be vaccinated. Note however that this latter finding was dependent on the location of the incursion. In the situation where FMD is introduced in Aberdeenshire and vaccination is implemented, a stable number of vaccinated animals was generated, on average, that is unaffected by the delay in implementation.

In this work, we found that the celerity at which vaccination is implemented in the field is critical for the effectiveness of the policy. For instance, every day increase in delaying its implementation would linearly reduce its effectiveness, not only increasing the number of IPs, the duration of epidemics and the number of animals culled for disease control purposes, but also the number of vaccinated animals. The likelihood of severe epidemics (here, defined as epidemics with >100 IPs and lasting for >60 days) would also be reduced if the policy is implemented rapidly. While these findings are consistent with other simulation outputs carried out in a German context (Traulsen et al., 2011), we further show that the rate at which benefit is lost strongly depends on the location of the incursion as well as the efficacy of the vaccination available and extent of the silent spread (in terms of number of premises infected prior to first detection).

Beyond the effect of delays in its implementation, the epidemiological advantage of a reactive vaccination strategy in Scotland was found sensitive to the conditions of the incursion at hand, especially the geographical location of the incursion. For Scotland, deploying a reactive vaccination strategy at the end of the first week would save the slaughter of nearly a third of the animals if incursion occurs in the southern counties, when comparing with a no vaccination strategy. In contrast, not much difference was observed if incursion occurs in the rest of the country. Applying vaccination when incursion events occur strictly in these high-risk (Southern) counties would, then, avoid unnecessary cost.

Livestock density is widely believed to be the main driver for such spatial pattern (Backer et al., 2012; Bessell et al., 2010a, 2010b; Parent et al., 2011; Tomassen et al., 2002; Traulsen et al., 2011) and, indeed, the density of susceptible animals happens to markedly differ between these high-risk counties and the rest of the country. In particular, there are nearly 4 times more cattle and sheep in the Southern counties than for the rest of the country (Table 1). However, livestock density alone does not predict the susceptibility of premises to be infected nor their infectiousness (Bessell et al., 2010a, 2010b), and thereby transmission. Our results were consistent with this, and suggested that the spatial variation in VB is

inherently related to the spatial variation in the farm-level reproduction value, R_i , rather than simply being due to livestock density.

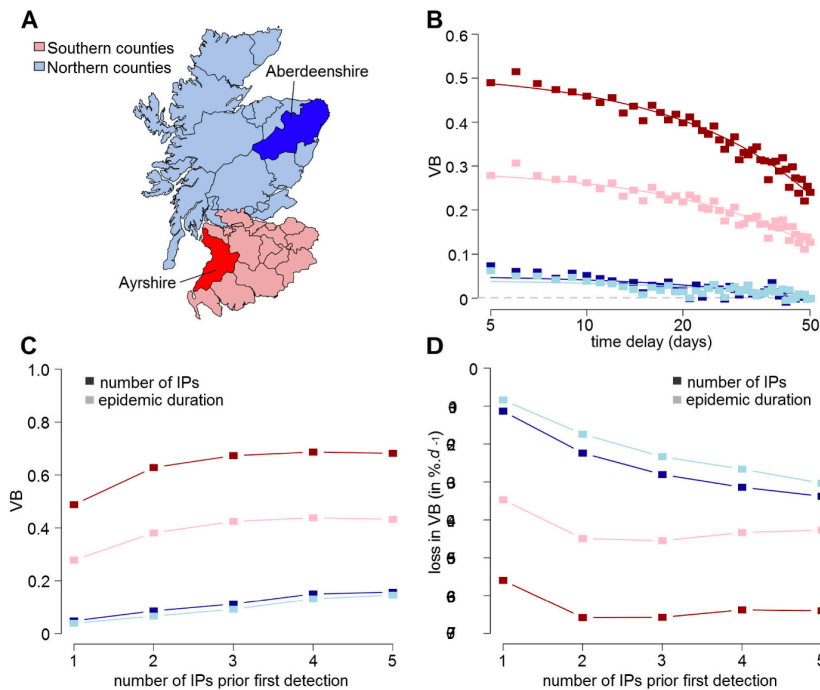


Figure 16. Resilience of vaccination benefit to delays in field implementation. (A) Map showing the location of Aberdeenshire and Ayrshire as examples for the different dynamics identified in Scotland. (B) Effect of delaying the implementation of vaccination in the field on its benefit (VB) for epidemics generated from a single premise in Ayrshire (red) and Aberdeenshire (blue). (C) Risk ratio in VB for each infected premise (IP) increase prior to first detection. (D) Variations in the rate of VB loss for each day increase in delaying its implementation in the field. Values of VB in B, C and D were computed over the number of IP (dark symbols) and the duration (light symbols) of generated epidemics. The probability of severe epidemics was defined as the probability of epidemics either showing >100 IPs (dark symbols) or lasting >60 days (light symbols). Grey dashed line in B indicates the null benefit.

In conclusion, we explored the effect of several factors that influence the benefits of implementing a reactive vaccination policy when facing epidemics of infectious disease such as FMD in Scotland. We have shown that the decision to vaccinate, or not, is not straightforward and strongly depends on the spatial variation in the farm-level basic reproductive ratio values R_i , illustrated here by the differences between the southern and northern counties of Scotland. However, if a decision to vaccinate is made, we have shown that delaying its implementation in the field may markedly reduce its benefit.

Box 5. follow-up story

In this paper, we defined the benefit of a vaccination strategy based on the number of animals, premises, and days saved by the implementation of vaccination. However, the benefit associated with vaccination in term of animals saved needs to be counterbalanced against the extra costs related to its implementation in the field. Notably, costs directly related to the control activities should be balanced with those associated with export restrictions, variations in market prices and diminished future production. Given the temporal variations in the effect(s) of these latter factors, vaccination would not always be economically beneficial, even when it appears to be epidemiologically beneficial. As such, considering the economic impact of epidemics, along with its epidemiology, may affect the time-window within which the policy is cost- efficient. In particular, short and small epidemics may be most penalised economically from the additional trade restrictions induced by vaccination. Consequently, we developed two economic model to assess both the impact of FMD control on direct (Porphyre et al., 2018) and indirect (Barratt et al., 2019) cost. Particularly, we looked at the impact of restrictions on bank supplies and time required to resupply FMD vaccines.

Conclusion

Effective management of infectious diseases requires the most accurate possible understanding of transmission processes and the relative contribution of transmission routes. In this section, we described several studies using various quantitative epidemiological tools to achieve this. We focused on how spatial distribution of risks can be direct and indirectly inferred to identify high-risk areas to strategically allocate resources for disease control and surveillance, enabling disease outbreaks to be proactively, efficiently and promptly mitigated and limit their impact.

However, such strategies ought to consider the characteristics of the local environment and the unique challenges of the local communities, dynamic livestock markets and the typical operation of the livestock systems to maximize its utility for disease control. This could significantly mitigate the epidemiological cascade that follows outbreaks and thus, can aid in reducing the overall burden of the disease and the unintended socio-economic consequences for the whole livestock sector.

One of these local characteristics that may impact how TADs may remain circulating in the environment is the presence of wild host population that may act as reservoir host and maintain disease circulating over time (Gortázar et al., 2016; Miller et al., 2013a; Wiethoelter et al., 2015). In the following section, we will show how we sought to study how wild host populations may maintain TADs and influence their epidemic success in a given local environment, representing local characteristics to be considered when designing disease mitigation strategies.

Publications related to this section

A. Bibard, D. Martinetti, A. Giraud, A. Picado de Puig, K. Chalvet-Monfray, **T. Porphyre** (2024a) Quantitative risk assessment for the introduction of bluetongue virus into mainland Europe by long-distance wind dispersal of *Culicoides* spp.: A case study from Sardinia. *Risk Analysis*. <https://doi.org/10.1111/risa.14345>

A. Bibard, D. Martinetti, A. Giraud, A. Picado de Puig, K. Chalvet-Monfray, **T. Porphyre** (2024b). Assessing the Risk of Windborne Dispersal of *Culicoides* Midges in Emerging Epizootic Hemorrhagic Disease Virus Outbreaks in France. *Transboundary and Emerging Diseases*, 5571195. <https://doi.org/10.1155/2024/5571195>

A. Bibard, D. Martinetti, A. Giraud, A. Picado de Puig, K. Chalvet-Monfray, **T. Porphyre** (2024, *in press*) Quantitative risk assessment for the introduction of Bluetongue virus into mainland Europe by long-distance wind dispersal of *Culicoides* spp.: a case study from Sardinia. *Risk Analysis*

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The role of wildlife as a local driver of disease risk

Although sharing many pathogens, the epidemiology of TADs in domestic livestock and wildlife can differ vastly and create complex systems where pathogens may be exchanged (in both ways) between these two populations. Wild host populations can play a significant role in maintaining TADs in an environment and provide a persistent risk of infection for domestic animals (OIE, 2018; Siembieda et al., 2011), affecting the cost-effectiveness of livestock-focused mitigation strategies.

Even though wildlife-domestic animal interface is now a focus of growing interest (Karmacharya et al., 2024), the complex host-pathogen dynamics in wild populations remain poorly understood. This is mainly due to the complex ecological relationships between hosts and pathogens (Lisovski et al., 2017; Sweeny et al., 2021) resulting from the interplay among pathogens, hosts and their environment (Altizer et al., 2006; Begon et al., 2009; Martinez-Bakker and Helm, 2015), with pathogens affecting host vital rates (e.g. survival), and host ecology modulating pathogen spread, while environmental conditions influence both (Altizer et al., 2006). In particular, the seasonal variation in environmental conditions often shapes within-year variations in host population size and structure and in pathogen survival, which play critical roles on host-pathogen dynamics (Altizer et al., 2006; Sweeny et al., 2021; Wilber et al., 2022) and would affect our ability to efficiently manage disease spread. It is therefore necessary to try to better understand the epidemiology of TADs in relation to the seasonal and ecological-bond dynamics of natural populations.

In this section, I will present work aiming to clarify (1) how local demographic variations and population dynamics (age structure and population size) may influence persistent circulation of disease in the environment (Porphyre & Grewar, 2019) and (2) how they may influence the epidemic success and importance of transmission routes (Fay et al., 2024).

Potential of a natural population to maintain disease circulation in environment: the case of African horse sickness in plains zebra

African horse sickness (AHS) is a viral disease of equids caused by the African horse sickness virus (AHSV), a RNA virus from the genus *Orbivirus*. The virus is principally transmitted by *Culicoides* spp. midges (similar to BTV) and is affecting domestic horses, donkeys and wild equids, such as zebra. Although horses and donkeys have a high mortality rate (up to 95% in horses), zebras remain unaffected by the disease and represent a natural reservoir of the disease (Zientara et al., 2015). AHS is endemic in South Africa except

for a controlled area in the Western Cape Province (WCP) where sporadic outbreaks have occurred in the past 2 decades, mostly linked to the re-assortment and/or reversion to virulence of the live attenuated AHS vaccine in use in the country (Weyer et al., 2016).

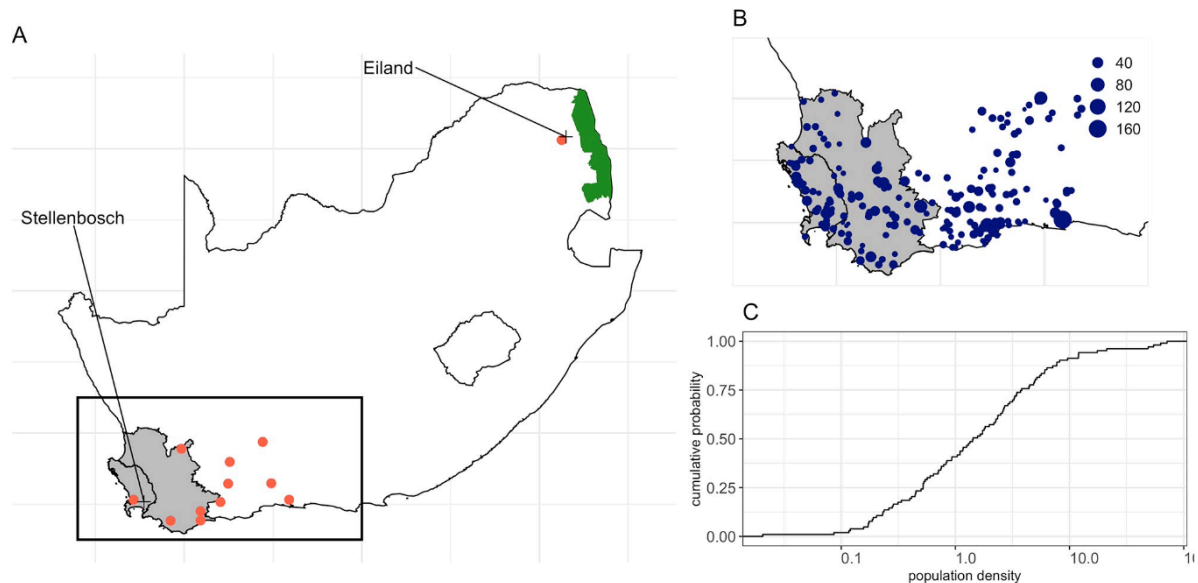


Figure 17. Study area and holdings with a reported population of plains zebra. (A) Location of the 12 sites in which climate data were extracted from. Red solid dots indicate sites at which climate information were downloaded, whereas crosses indicate the location for which midge abundance data were reported. Rectangle represents the extent of the study area. (B) Location of the 212 holdings with at least 1 reported plains zebra that were considered in this study. Size of each dots are indicative of the size of the zebra population. (C) Distribution of the population density of the 102 holdings with at least 1 reported plains zebra and a known surface area. Grey shaded areas in A and B represent the AHS controlled area of the Western Cape Province, while the green shaded area in A is the Kruger National Park (KNP).

This controlled area, located at the very south-western tip of South Africa (**Figure 17A**), was established in the WCP principally on the basis that the distance to the Kruger National Park (KNP), located in the north-eastern extremity of the country, would be large enough to effectively isolate the local horse industry from the large zebra population present in KNP and in which AHSV circulates persistently (Barnard, 1993), thereby lowering the risk of AHS introduction through seasonal spread. However, as AHS results in a non-tariff barrier to the trade of live equids from affected countries, questions were raised regarding the role of zebra populations to maintain AHS circulating in the situation where vaccine-related AHSV were to emerge in the WCP.

As part of a project on African horse sickness (AHS) funded by the South African equine industry (SAEHP), we attempt to clarify the impact of demography dynamics of zebra on the long-period persistence of AHS in local populations of the WCP. In this work, we focused our analyses to plains zebra (*Equus quagga*, formerly *E. burchellii*), the most abundant wild equid in South Africa and in which AHS is endemic in KNP (Barnard, 1993). We developed a hybrid deterministic-stochastic, age- and sex-structured host-vector compartmental model, where the spread of AHSV in the host (i.e. plains zebra) population is stochastically modelled whereas the spread of AHSV in vectors is assumed deterministic. We used available zebra population dataset within the WCP (**Figure 17B**), along with published parameters relating to the populations and dynamics of AHS transmission, to inform the model and evaluate the likelihood that introduction events in the WCP would result in persistent AHSV circulation within a zebra population, similar to what is observed in KNP.

In this model, the transmission process of AHSV in plains zebra was considered only driven by *Culicoides imicola* and that only adult females were involved in AHS transmission dynamics. We therefore discarded the fine population dynamics of vectors and the impact of environmental factors on eggs, larvae and nymphs, and assumed vectors would be subject to a constant hazard of dying depending on temperature. We further considered that transmission between vector and host populations would be temperature-dependent. **Figure 18** illustrates how both vector and host populations are structured and describes each population in regard to the spread of AHSV in the population.

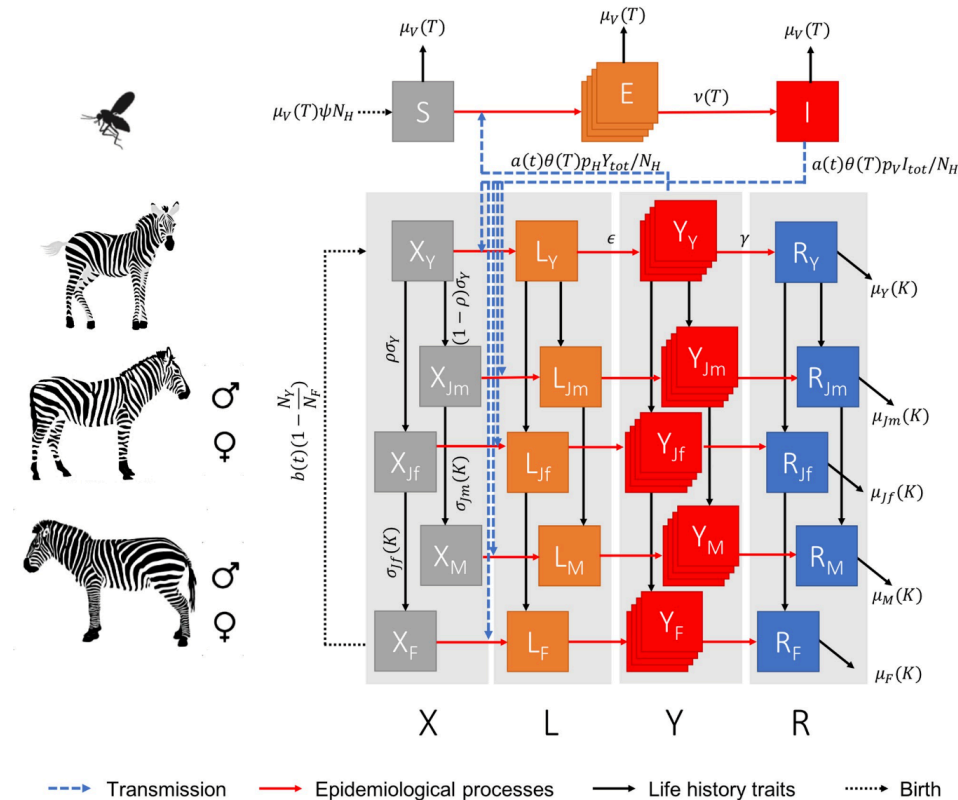


Figure 18. Schematic representation of the vector-host model. An individual Zebra is either in a susceptible (X), latently infected (L), infectious (Y) or recovered (R) state, with subscripts Y , Jf , Jm , F or M indicating the age class of the animal, being foal, female juvenile, male juvenile, adult female and adult male, respectively. Vectors are either in a susceptible (S), latently infected (E) or infectious (I) state. The stacked squares denote that this compartment is divided into multiple stages. Some rates depend on environmental conditions, denoted in brackets, with conditions being the daily mean temperature (T) recorded at sunset (i.e. between 18:00 and 21:00), the yearly carrying capacity (K) or the calendar month of the year (t). For clarity, rates were given only once per epidemic state or age class. Note also that the rate of mortality for each zebra age class would be constant for all epidemic states.

To account for the demographic dynamics of plain zebras, we adapted our model on the age- and sex-structured population dynamic model of a plains zebra population in Laikipia District, Kenya, developed by Georgiadis et al. (Georgiadis et al., 2003). Briefly, the model adjusts vital rates and age at first reproduction through a rainfall-mediated density-dependent (RMDD) mechanism. This RMDD modulates vital rates by a factor that depends on the ratio of carrying capacity K_y to population size N_H . Here, the carrying capacity is defined as the maximum number of individuals that could be supported in a given year, at maximum reproductive output and was estimated as a function of the total rainfall (R_y , in mm) recorded in the location of interest over an entire year y such as $K_y = hR_y^i$, where h and i are constant variables. All vital

rates and parameters used to model the zebra population dynamics were fitted from empirical observations and related to changes in annual records of rainfall in Laikipia District (Georgiadis et al., 2003). Although ecological conditions in the Laikipia District and our study sites are markedly different, we capitalised on the relationship between rainfalls and vital rates found in Georgiadis et al. (Georgiadis et al., 2003) to characterise the population dynamics of plains zebra in both WCP or KNP study sites.

We further adapted this modelling framework to account for the temporal variations of births within each given year. While foal numbers for each given year were calculated as equal to the number of adult females surviving from the previous year and that did not give birth in the previous year, the number of foals born in each given month varies as a function of the monthly density of foals $b(t)$. The birth function $b(t)$ was derived from empirical observations in the proportion of <1-month-old foals for two populations of plains zebra in the KNP between August 1969 and March 1973 (Smuts, 1976).

The comparison of demographic dynamics between the plains zebra populations in KNP and in the WCP showed that these two populations behave differently. The population in KNP showed little stochastic variations in abundance, with an initial increase in population with an annual rate of population growth of 4.2% (95% CI 4.1%–12.5%), reaching a maximum of 36,672 individuals. From January 2015, however, the population of KNP declined progressively due to poor availability of forage from successive years of low precipitations similar to what has been observed on the field. In contrast, the population in the WCP showed high variability in predicted abundance, with high chances for significant reduction due to unsustainable population densities. Such a marked variability is partly due to the fact that the surface area of this population was unknown and therefore imputed from known population densities in the WCP. However, in simulations with population density of <3.77 individuals per km^2 , the population will increase with a mean annual rate of 4.8% (IQR: 2.9%–6.6%), reaching a max of 235 animals.

In KNP, introducing an infected AHS adult female in the zebra population at the start of the study period resulted in AHS becoming endemic in 100% of the 40 simulations tested but at a low level of prevalence. One year post introduction, i.e. when an endemic equilibrium is reached, 0.99% (95% CI 0.62%–1.36%) of zebras would be infected either at the exposed (L) or infectious (Y) stages, whereas 98.9% (95% CI 98.6%–99.4%) of zebra would be immune to AHS (i.e. in R state). These results were concordant with field observations showing that almost 100% of the free-living zebra foals born in the KNP were sero-positive for at least one serotype of AHSV once reaching adulthood (Barnard, 1993) and that a continuous transmission cycle of virus between *Culicoides* midges and zebras occurred in the KNP (Barnard, 1998). In contrast, the introduction of an infected AHS adult female in the largest population of plains zebra in the WCP never resulted in an endemic situation. Instead, AHS persisted in the population for a median period of 155 days (95% CI 147–161) and never circulated for more than 1 year.

When looking for the spatial variations in the risk of AHS persistence in the WCP, an AHS incursion in any of the possible sites of the WCP would generate outbreaks lasting for a median of 135 days (IQR 123–161), with AHS circulating for less than 300 days in 94% of simulations (**Figure 19A**). Although AHS was never found persisting for more than 4 years in the WCP, 78, 5 and 1 holdings were able to generate outbreaks lasting >1 year, >2 years and >3 years, respectively. Among the 78 holdings that were able to keep AHS circulating for >1 year (denoted as high risk in **Figure 19B**), 13% and 26% generated outbreaks lasting for >1 years in only 1 or 2 simulations over the 40 considered.

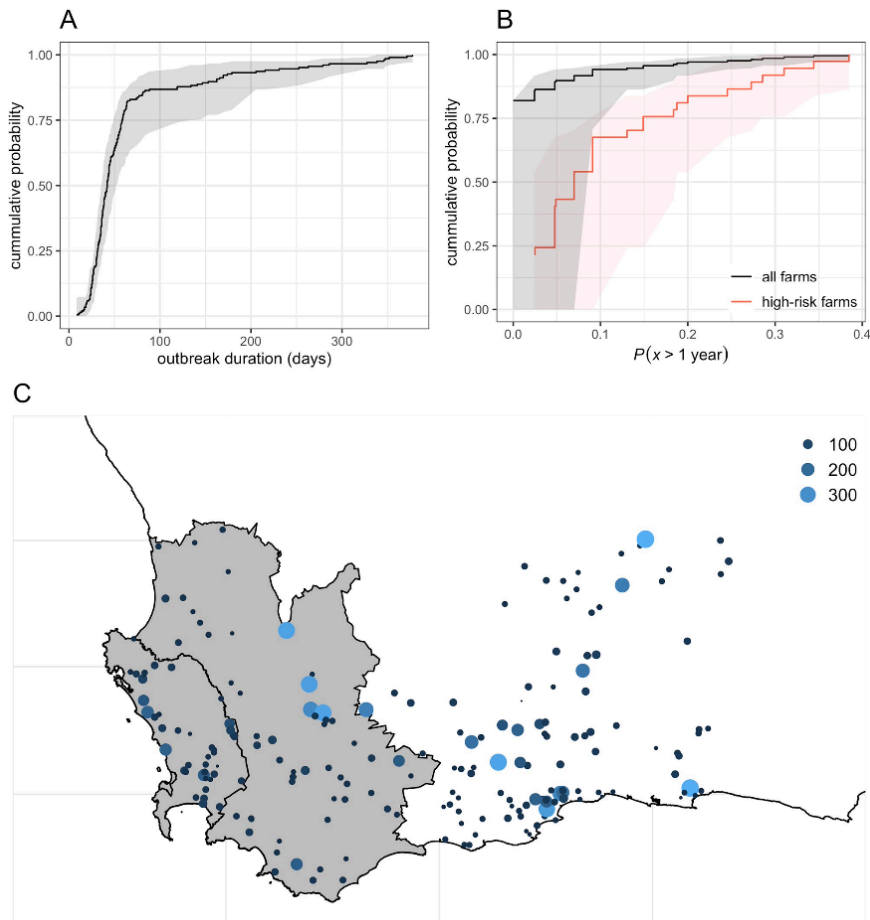


Figure 19. Distribution of the risk of AHS persistence among all individual holdings with plains zebra in the WCP. Cumulative probability distributions of (A) the median and IQR outbreak durations and (B) the probability that AHS outbreaks would persist for >1 year computed over 40 independent AHS introductions in all individual holdings. (C) Spatial distribution of the risk of AHS persistence as measured by the median outbreak duration (in days) among holdings with plains zebra in the WCP. Here AHS was consistently introduced in April 2012.

To explore what conditions would allow long-lasting circulation of AHS in the WCP, we plotted the distribution of the median outbreak duration as a function of the size of the zebra population at the start of the simulation (**Figure 20A**). Two distinct groups of population may be observed with population denoted “A” showing orders of magnitude shorter median outbreak duration than those denoted “B”. These two groups are spatially defined (**Figure 20B**), with group A involving populations along the coast of the WCP, whereas group B includes populations located inland, on the plateau. Differences in the dynamics of the temperature used to drive AHS epidemiology for each population affected the risk of AHS persisting in the WCP, with sunset temperatures in populations of group B warmer in summer (more often between 25°C and 30°C) and colder in winter (more often between 5°C and 10°C) than those in group A. Our model indicates that these temperatures enable *C. imicola* to survive and allow AHS to persist in the environment for 2 to 3 seasons after the initial outbreak period.

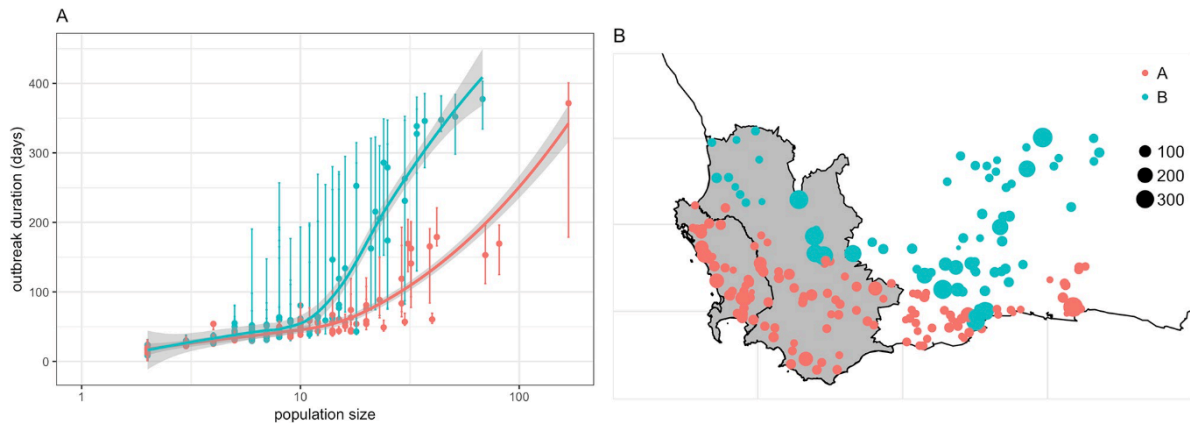


Figure 20. Distribution of the risk of AHS persistence as a function of the size of the plains zebra population in all individual holdings in the WCP. (A) Median, and IQR, duration of AHS outbreaks in all holdings considered in the WCP. This distribution shows two groups (groups “A” and “B”) of holdings differing from outcomes of AHS incursion events. (B) Spatial distribution of the risk of AHS persistence stratified by their group. Note that the large error bars in (A) highlight the large uncertainty for holdings that has no record of surface areas. Curves in (A) are the smoothed conditional means of the median outbreak duration. Size of dots in (B) represent the median outbreak duration (in days).

Sensitivity analysis further showed that populations of plains zebra present in the WCP are not sufficiently large for AHS introduction events to become endemic and that coastal populations need to be >2500 individuals for AHS to persist >2 years, even if zebras are infectious for more than 50 days. Should AHSV be introduced in the coastal population of the WCP, AHS cannot become endemic unless the population involves at least 50,000 individuals. In contrast, inland populations of zebra in the WCP may represent a risk for AHS to persist if populations grow beyond 500 individuals.

Beyond the benefit of improved knowledge regarding the epidemiology of AHS in zebra in the WCP, our model provided a basis to review and justify the current regulations from both South African Veterinary Services and international trade stakeholders to prevent introduction of AHSV in the wild and domestic equine populations of the WCP and, should an introduction occur, ensure the disease-free status is regained quickly. In our study, we found that the highest risk of prolonged circulation of AHS in zebra populations is likely to occur if AHSV is introduced in April, when sunset temperatures range from 13°C to 27°C and midges biting activity is high. In contrast, lowest risk period was between June and September, where introduction events would rarely generate outbreaks lasting for more than a month. These findings consolidate animal movement regulations currently enforced for the AHS controlled area which only allow the import of zebra between June and August. In addition, they further support the recent amendment in the vaccination protocols that strictly restricts the use of vaccination to the period between June and October to avoid AHSV outbreaks due to re-assortment and/or reversions to virulence of live attenuated vaccines (Weyer et al., 2016). Both of these measures are likely to mitigate the risk of introducing AHSV in zebra populations and ensure the virus would not remain circulating for extended periods within the controlled area.

Because zebras are not affected by the disease, it is unlikely that epidemics of AHS would affect the seasonal dynamics of population. This is unlikely to be the case for other TADs, as shown in the following example.

Modelling the interplay between demography and epidemiology dynamics: The case of African swine fever in wild boar

As seen above, epidemic dynamics are shaped by demographic dynamics of natural populations, as their size, spatial distribution of individuals and their structure (e.g. age) are all demographic parameters that can influence the transmission of infectious diseases between individuals. In turn, the dynamics of populations, i.e. changes in population size, distribution and structure, are shaped by, among other things, the dynamics of infectious diseases. For example, infectious diseases can increase mortality in infected hosts, decrease population size and change population structure if certain age groups are more susceptible than others. Understanding these interactions between epidemic dynamics and demographic processes is fundamental to improve our understanding on how disease may invade and remain circulating in a population as well as better control epidemics and limit their deleterious effects on the affected populations (e.g. reduced survival, reproduction, numbers).

In Europe, the demography of many natural populations is seasonal with births occurring over a period of a few weeks and mortality rising during less favourable seasons. Such demographic seasonality results in strong variation in host population density and structure within a year, which impact both the number of susceptible individuals and the rate of pathogen transmission. Here, we investigate the influence of wild boar *Sus scrofa* demographic seasonality on the dynamics of ASF.

ASF is one of the highest-consequence diseases of domestic pigs (Food and Agriculture Organization of the United Nations and the World Organization for Animal Health, 2020). Caused by the African swine fever virus (ASFV), this viral hemorrhagic fever has near 100% mortality and is economically devastating to both affected farms and countries (Food and Agriculture Organization of the United Nations, 2009). Following its anthropogenic escape from sub-Saharan Africa and entry onto the Eurasian mainland in 2007, ASFV has since spread across the Eurasian continent, with multiple EU nations (Bulgaria, Germany, Italy, Latvia, Lithuania, Poland, Romania and Slovakia) still affected today.

Transmission pathways of ASFV vary between affected areas, with some countries experiencing outbreaks only among wild boar and others seeing cases among both wild boar and low-biosecurity domestic pig herds. Although the wild boar plays a key role in the spread and persistence of ASF (Palencia et al., 2023), the understanding of how its population dynamics may influence ASFV dynamics remains a challenge for the development of cost-effective mitigation strategies. Particularly, little is known how seasonality in both host and pathogen dynamics drive epidemic success, and how the timing of pathogen introduction influences its spread within the host population.

Taking advantage of a unique long-term (40 years) individual monitoring of the hunted wild boar population of Châteauvillain-Arc-en-Barrois (48°02N, 4°56E) in the north-eastern France, a stochastic individual based model (IBM) was developed combining the demographic structure (in age and sex) of wild boar with the transmission dynamics of ASF. Briefly, the model is composed of two major components, representing (1) the demographic dynamics of the host population, and (2) the transmission dynamics of the virus within the population. Our model assumed a closed wild boar population, corresponding to situations where a population has been isolated following disease detection, as has been done in Europe (Sauter-Louis et al., 2021). Hosts were modelled individually and characterized by sex, age and health status. Each day, individuals may successively survive or die, breed or not, and change health status (**Figure 21A**). The infection dynamics in the population was modelled considering an SEIR epidemiological process,

in which individuals are either susceptible (S), exposed but not infectious (E), infectious (I) or recover (R). We further considered that individuals that died overtime, either from natural causes or from the disease, remain as carcasses in the environment for a time that depends on temperature (**Figure 21C**). As such, susceptible individuals can be infected through direct contacts with infectious individuals or with infected carcasses that remain in the environment. All animals killed during the hunting season were removed from the population and thus do not participate in the disease transmission dynamics.

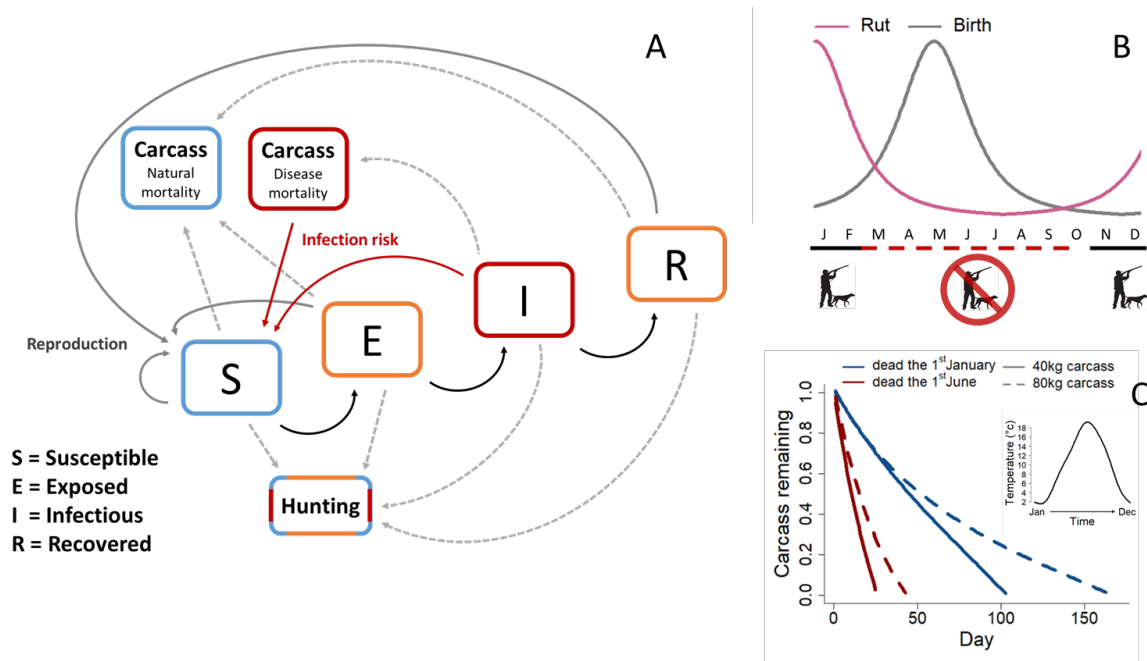


Figure 21. Schematic overview of the Individual-Based Model. (A) Demographic processes and infection dynamics. Gray arrows figure host demographic processes (solid = reproduction, dashed = mortality), black arrows figure disease course and red arrows figure infection risk. The colour of frames indicates the sanitary state: blue = no virus, naïve individuals, orange = virus present currently or formerly but individuals not contagious, red: virus present, contagious individuals. (B) Seasonality in demographic processes. (C) Example of temperatures- and mass-dependent carcass degradation as a driver of seasonality in virus persistence.

Seasonality of age- and sex-specific demographic rates was accounted for by estimating daily-breeding probability, which shows a clear peak during the spring, and by distinguishing mortality rate during the hunting season to that during the non-hunting season. Age-specific litter size were estimated based on the analysis of reproductive tracts of pregnant females shot, whereas all other demographic parameters were obtained from previous studies conducted in the studied population (Gamelon et al., 2012; Veylit et al., 2021).

Transmission of ASF was considered occurring through direct contact with infected individuals (direct contact, DC) and through contact with infected carcasses (indirect contact, IC), for which decaying rate depends on their size and temperatures.

The daily number of direct contacts was considered both age- and sex-dependent to mimic the social structure of the wild boar that is based around matriarchal groups composed of a few subadult and adult females and their offspring (Kaminski et al., 2005). The number of contacts of solitary adult males with conspecifics varied seasonally and peaked during the mating season (Maselli et al., 2014). Furthermore,

because contact rate increases typically nonlinearly with population density (Hopkins et al., 2020), we simulated the density-dependent direct contact numbers DC_0 using a generalized logistic model, such as:

$$DC_0 = A + \frac{K - A}{(1 + e^{-rN})^{1/v}}$$

where N is the total population size, A and K are the lower and higher asymptotes respectively, r is a growth rate, and v influences the population size near which asymptote maximum growth occurs. We then corrected this daily number of contacts for each individual by modulating DC_0 as a function of age and sex as well as time to account for the seasonal change in contacts of sexually mature males during rut (Maselli et al., 2014) such as:

$$DC_{i,t} = \frac{DC_0}{\gamma_{age_i} + \gamma_{sex_i}} \times f_{t,sex_i}$$

where i and t are indices for individuals and days respectively, γ_{age} have three levels corresponding to juvenile individuals (< 6 months), sub-adults (6 months to 2 years) and adults (> 2 years), and γ_{sex} has two levels, one per sex. We assumed no differences between males and females when individuals were < 6 month-old since both sexes live together within social groups at this early age (Maselli et al., 2014). $f_{t,sex}$ is a function which modulates the number of contacts according to the day t of the year, and applies for old males only (> 2 years). This function, with the same shape than the birth distribution (appendix S2), allows modelling males behaviour change during the rut from a solitary to a harem mode of life (Maselli et al., 2014).

In contrast, we assumed that the number of contacts with carcasses was frequency dependent. The daily number of contacts with carcasses per individual IC was modelled using the following linear model:

$$IC = C \times \delta$$

where C is the total number of wild boar carcasses remaining in the environment, and δ the rate of increase of indirect contact per unit of carcasses available in the environment. Here, we used $\delta=0.01$ to ensure IC remains low, hence reflecting the limited attractivity of carcasses as food resources observed in natural populations (Cukor et al., 2020; Probst et al., 2017). Obviously, carcasses (including those that are infected) will not persist indefinitely in the environment, but will progressively be degraded. The rate at which individual carcasses are decaying was considered varying as a function of their size and the air temperature (**Figure 21C**).

Using this model, we showed that epidemic dynamics varied strongly according to seasonality (**Figure 22**). The probability that the virus invaded the population successfully was the lowest when it was introduced in winter (February-March, ~60%), and the highest when it was introduced in late spring or early autumn (May or September, ~80%) (**Figure 22B**). The basic reproduction number (R_0) varies overtime with a clear seasonal effect, being twice higher in case of virus appearance during the autumn than then the virus is introduced in the winter (**Figure 22B**), as contact with carcasses is critical when disease is introduced in winter. In case of successful invasion, the outbreak generated by virus spreading into the population was also influenced by the timing of the virus introduction. Maximum daily incidence rate was 56% larger and was reached three time faster for outbreaks generated by virus incursions in summer compared to those generated by virus incursions in winter (**Figures 22C & 22D**). Finally, outbreaks lasted for longer duration when the virus was introduced at the end of the summer (July-August), about 375 days, compared to when

it is introduced in spring (April-May), about 280 days. The epidemic duration distribution was strongly bimodal, with most of virus extinction occurring during the summer, either from the first or the second year of epidemic.

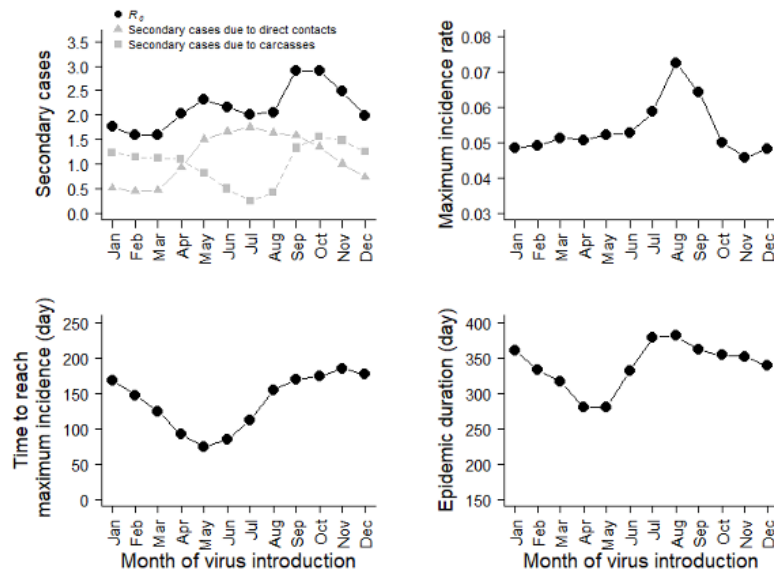


Figure 22. Epidemic dynamics as a function of time of virus introduction in the population.

The sensitivity analysis showed that most patterns described above were robust to parameter uncertainty regarding wild boar contact rates (**Figure 23**). One exception was the R_0 , and the closely related introduction success probability, for which seasonality varies according to the contact rate with carcasses. When the contact rate with carcasses was low ($\delta < 0.015$ daily contact per carcass), R_0 and the introduction success were both higher in case of summer virus appearance (**Figure 23**). In contrast, when $\delta > 0.015$ daily contact per carcass, a greater R_0 value was observed when ASF was introduced during the winter, whereas the risk of onward transmission remained constant across seasons.

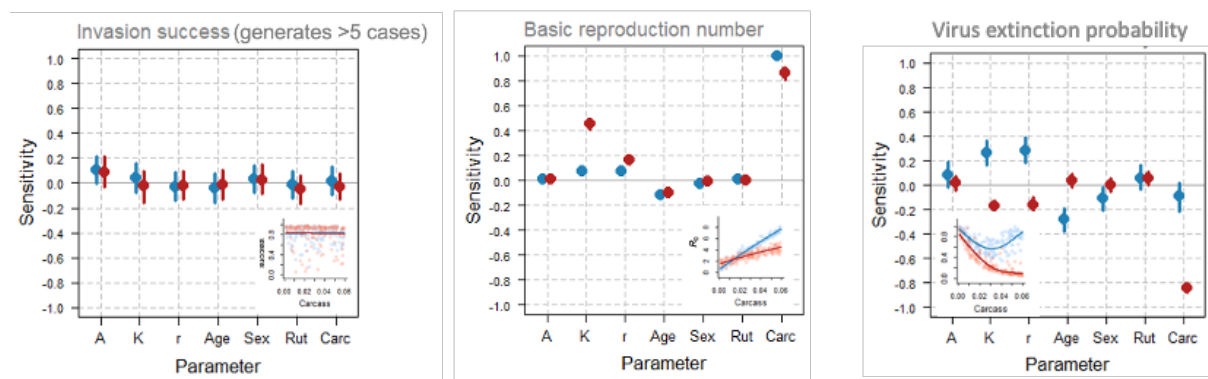


Figure 23. Sensitivity of the epidemic dynamic to parameters determining host contact rates with relative and carcasses, according to two dates of virus introduction: 1st January (blue) and 1st June (red). Epidemic metrics include the introduction success, defined as the probability that the first infected individual generates at least one secondary case, the invasion success, defined as the probability that at least five individuals were infected, and the basic reproduction number R_0 , that is the number of secondary infections generated by the first infected individual. Parameter A , K , r , Age , Sex and Rut modulate wild boar daily contact rate with relative, and $Carc$ modulate the daily contact rate with carcasses.

Concomitantly, the wild boar population response to virus introduction strongly varied according to the timing of virus appearance (**Figure 24**). Two timescales could be distinguished for population size response: the short-term (within four months) and the long-term (> six months). Over the short-term, in case of summer virus introduction, the host population size strongly decreased, on average by 60%, compared to the reference situation (scenario without virus introduction). In contrast, in case of winter or early spring virus introduction, population size was similar to the reference situation. Over the long-term, host-population size fluctuated at a low level, 40 to 20% of the reference population size, regardless of the date of virus introduction. The outbreak also impacted the population age structure which became biased towards older age classes. The proportion of juveniles was up to two time lower compared to the age structure observed for the same month when no virus was introduced.

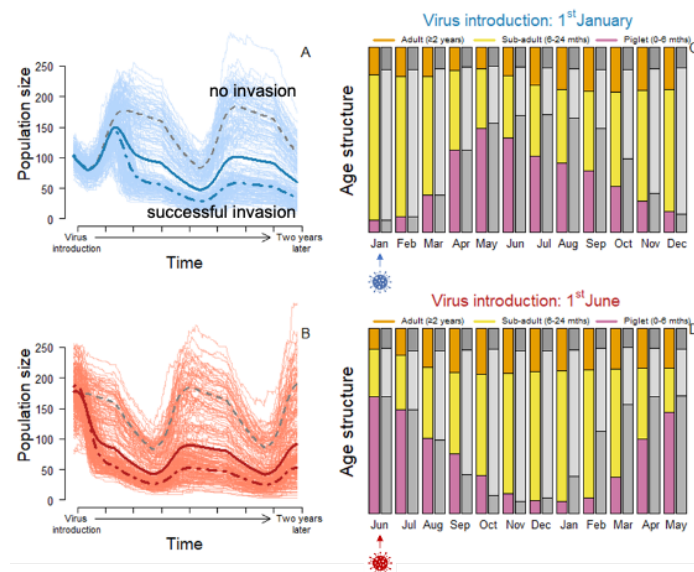


Figure 24. Wild boar population response to virus introduction according to virus introduced in January 1st and in June 1st. Panels A and B show the population size response to virus introduction: the bold coloured lines show the mean population trajectory, the thin light-coloured lines show the individual simulations, the bold coloured dotted-dashed lines show the average population trajectory for simulations with successful virus invasion (at least five secondary cases), and the dashed grey lines show the average population trajectory in the absence of virus for comparison. Panel C and D show the population age structure change on a monthly basis following virus introduction (dark coloured bars). Gray coloured bars show, for each corresponding month, the age structure observed in the absence of virus for comparison.

While many epidemiological studies accounted for pathogen or host seasonal variation, few have investigated both simultaneously (Kronfeld-Schor et al., 2021). Because seasonality in host and pathogen are dependent, considering only one component would inevitably lead to bias epidemic projections (Altizer et al., 2006; Paull and Johnson, 2014). For instance, in the wild boar – ASF system, considering only the seasonality of pathogen persistence in the environment would wrongly lead to the conclusion that R_0 is the highest during winter months, overestimating the importance of the indirect pathway through carcasses. Indeed, ASF epidemic outbreaks emerge from the trade-off between higher pathogen persistence in carcasses during the cold season and higher pathogen spread among individuals during the warm season, when both population size and the proportion of young individuals peak. Concordant to our findings on AHS in zebra (see above), higher population density led to higher contact rates among individuals, resulting in greater transmission of pathogens, while younger population could be more susceptible to pathogens due to the immaturity and naïve state of the immune system of young individuals. These findings suggest

that the implementation of realistic host demographic dynamics component in epidemiological models is critical for our understanding of disease ecology.

In a seasonal system, the timing of virus introduction is critical for the subsequent epidemic dynamics, an aspect which has been overlooked in previous studies that often consider a virus introduction at a fixed date (Hayes et al., 2021). In accordance with previous studies showing that the timing of pathogen introduction influences post-epidemic fade-outs probability (Peel et al., 2014), we found that the timing of virus introduction strongly influences R_0 and the invasion success probability. The importance of timing of introduction has previously been emphasized in the theory on invasive species, where the fluctuating resource hypothesis suggests that fluctuations in resources availability modulate competition intensity, promoting invasion success probability of non-native species when resources are plentiful (Davis et al., 2000). In such systems, the success of the invader is thus closely link to the timing of propagule introduction relatively to the availability of the fluctuating resources (Li and Stevens, 2012), analogously to our epidemiological context, where available resources are the number of susceptible individuals.

Box 6. Wildlife ecology and its interface with domestic populations

I have been involved in several pieces of work to better understand the ecology (Porphyre et al., 2013; Jackson et al., 2019) and social organization of natural populations (Porphyre et al., 2008), explore how natural populations may interact in their local ecosystem (M1 projects of R. Rozario and E. Besse), and explore how these affect disease transmission (Porphyre et al., 2011; Walker et al., 2016; Porphyre & Grewar, 2019; Fay et al, 2024). Notably, the work carried out in my PhD project on brushtail possums, the wildlife reservoir hosts of bovine TB in New Zealand, have been precursor to numerous studies looking at the spread of diseases in natural animal populations and confirmed theoretical research on the association of centrality measures with the probability of infection was valid. However, due to limitations in the data collection it was impossible at the time to explore how demography could impact on disease spread.

Conclusion

The risk for a pathogen to circulate between wild and domestic animal populations depends on the rate contacts between the species (Miller et al., 2013b). As such, quantifying interactions between wildlife and livestock is an important aspect of understanding disease spread and how mitigation strategies may be affected at the wildlife-livestock interface. Again, the events associated to pathogen transmission between wild and domestic hosts (and potentially humans) are poorly understood (Miguel et al., 2013). The absence of data like host characteristics, ecological characteristics, movement pattern and varied human practices are the main challenges to quantify the contact rates at wildlife-domestic animals interface (Huyvaert et al., 2018; Miguel et al., 2013). Models can therefore be used to explore characteristics of the interplay between host ecology and epidemiology. Unfortunately, disease models looking at transmission dynamics of infectious diseases in wild populations typically focus on temporal dynamics of infection but often neglect the ecology of host species as well as the impact disease may have on their population dynamics. In this section, we have shown how we are using mathematical models to reach a mechanical understanding of the interplay between pathogens and host population, accounting for their demography in relation with environment. In particular, we have highlighted how seasonal variations in environmental conditions and demography of wild host populations can shapes within-year variations in disease dynamics and, in some situation, maintain disease circulation in the environment.

The role of these seasonal variations on the efficiency of mitigation protocols remains to be understood. As such, the model on ASF developed in Fay et al. (2024) is currently being extended (PhD thesis of J. Van Velzen, 2026) to explore how the efficacy of vaccines, that would be available in the future, could be optimised to control ASF in wild boar populations and its robustness to variations in ecological contexts.

Publications related to this section

R. Fay, M. Gamelon, E. Baubet, **T. Porphyre** (2024) The time of infection matters: seasonal interplay between host and pathogen drives epidemic dynamics. *Oikos*. accepted

R. Fay, M. Gamelon, **T. Porphyre** (submitted) Climate warming drives pulsed-resources and disease outbreak risk. *Proceedings of the Royal Society B*

Romane DE ROZARIO 2023 Master 1 Public Health report : “Risque leptospirosique chez les petits mammifères sauvages en Europe de l’Ouest et en Europe Centrale”. MSc *Public Health*, Université Claude Bernard – Lyon 1, France.

Amaël DAVAL 2022 Master 2 *Modélisation des Systèmes Ecologiques* report: “Modélisation de la dynamique des agents pathogènes transmissibles par l’environnement à l’interface entre populations d’ongulés domestiques et sauvages”. MSc BEE, Université Toulouse III - Paul Sabatier, France.

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J.D. Grewar, **T. Porphyre**, E. Sergeant, C.T. Weyer, P. Thompson (2020) Post-outbreak African horse sickness surveillance: A scenario tree evaluation in South Africa’s controlled area. *Transboundary and Emerging Diseases* 67(5): 2146-2162

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T. Porphyre, J. McKenzie, M. Stevenson (2011). Contact patterns as a risk factor for bovine tuberculosis infection in a free-living adult brushtail possum *Trichosurus vulpecula* population. *Preventive Veterinary Medicine* 100: 221– 230.

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A. Byrom, G. Nugent, J. McKenzie, **T. Porphyre**, N. Poutu, J. Shepherd, J. Whitford, I. Yockney (2008). Cost effective control of TB in the Northern South Island High Country: Identifying the habitats and vector species requiring control. Landcare Research contractual report to the Animal Health Board, Project No. R-80629, New Zealand. <http://www.ahb.org.nz>

T. Porphyre, J. McKenzie, M. Stevenson (2006). Identifying the cause of, and solutions to, vector-related TB persistence near Featherston. Massey University contractual report to the Animal Health Board, Project No.R-50634, New Zealand.

Complexity of modelling the spread and responses to TADs

Adapting to policymaking needs and uncertainties

In essence, my work can be described as translational epidemiology as it focuses on questions related to the feasibility, accessibility, appropriateness, cost, among other practical aspects relevant to making sustainable changes in real-world scenarios and inform policy (Neta et al., 2018). The interplay between decision-makers and epidemiologists (the evidence-providers), when effective, is challenging and is driven by the need to reconcile the specific topic of concern to decision-makers, most often expressed as “raw” and relatively unformulated policy questions, with a wide variety of constraints and limitations – for example, the identification of the relevant modelling framework, the presence of epidemiological and biological expertise, the availability and quality of data, or having sufficient computing facilities and time to deliver valid information. As well, policy and decision-making is not based on scientific evidence alone, but also influenced by political will, existing governance structures, public opinion, and other exogenous factors (Boden et al., 2020). Engaging with all of these facets of decision-making and understanding such constraints would therefore ensure intake of the produced modelling outputs. Best managed via a dialogue with decision-makers, the outcome of this conversation is a consensus on what is to be achieved from the modelling exercise, which is progressively refined to provide an agreed understanding of the expected information as well as the utility (in term of temporal or spatial scale) of the modelling outputs for policy development, while limiting the complexity of the design of the chosen modelling framework (Knight et al., 2016).

Again, for models to be “useful” to decision-makers, they must be both relevant and methodologically sound to the formulated policy question (Knight et al., 2016). However, these represent the bare minimum to inform policy. Outputs need to be produced on a time schedule consistent with the needs of decision-makers, who also need to have confidence in the credibility of the evidence delivered. In this context, such a “credibility” captures aspects of the validity of the methodology, and the reliability and ethical value of the outcome.

Complexities arise as models most often are based on assumptions made to overcome unknown features of the dynamics, and associated parameters, of the considered epidemiological system. As well, the outcome of any model can only be as accurate as their supporting data. On the one hand, both aspects in the development of models create uncertainties that are often not well-understood by public health stakeholders (who often do not have formal statistical training), and as a result, model outputs may be seen as difficult to interpret and untrustworthy (Knight et al., 2016). On the other hand, when properly explained and communicated, the width of confidence intervals for modelling results, which reflect data and parameter uncertainties, is often valuable to decision-makers, as it shows the current state of knowledge (Manski, 2013) and avoids the false sense of certainty that a single-value result can provide (and on which they can be attacked in public debates and reviews).

Such contrasted perception of modelling outcomes requires evidence-providers to find a fine balance between aiming for simplicity and informativeness, while ensuring the robustness of the considered modelling framework and the sensitivity of its outcomes to variation in the used parameters. Efforts in carrying out uncertainty and sensitivity analyses around the main components of the model are therefore critical. Here, uncertainty analysis consists in assessing the impact of uncertainties in model ‘inputs’, such as the local density of wild boar population, into uncertainty in model ‘outputs’, such as the risk of ASF

infection of outdoor pig farms. Sensitivity analyses aim to attribute portions of this uncertainty to specific parameters (Saltelli et al., 2008).

In that context, a large portion of my work focused in better characterizing epidemiological processes and their uncertainty (1) by estimating the range of values of model parameters that may best recapture observations in disease processes using inference approaches, such as MCMC or ABC (Guinat et al, 2018; Ewing et al, 2022; Gamado et al, 2017; Porphyre et al, 2018 technical report), and (2) by carrying out sensitivity analyses to evaluate the impact (directly as well as in interaction) of uncertainty in model parameters on their outputs (Porphyre et al, 2012; Porphyre et al, 2013; Porphyre et al, 2017; Porphyre et al, 2020; Bibard et al, 2024a; Fay et al, 2024; PhD thesis of T. Khalid, 2024; and M2 internship project of A. Daval). This further led to collaboration, as part of my implication in the Scottish COVID-19 Response Consortium (SCRC), with B. Swallow (University of St Andrews) and P. Challenor (University of Exeter), both Professors of mathematics and expert in 'uncertainty quantification' (UQ), a field of statistics that aims to measure, account and visualise uncertainties inherent in the modelling process of real-world complex systems. This collaboration not only resulted in several papers (Dunne et al., 2022; Rydow et al., 2023) but also highlighted to me the difficulties for common inference frameworks (such as MCMC or ABC) to account for uncertainties in presence of higher order interactions between parameters, which are common in complex infection disease transmission models.

Building bridges between actors of Health

The foundations of evidence-based decision-making begin with robust data collection, access and sharing (Boden et al., 2020). Nowadays, there is a wealth of data generated from different organizations (business, regulatory bodies and academic organisations) and for diverse purposes, making them difficult to integrate together (due to data architecture and structure) and ensure similar level of data accuracy and reliability (Houe et al., 2019). Data entry errors, missing information or lack of completeness may lead to inaccurate, non-representative outcomes, which could yield negative implications to all or, even worst, a specific subset of the population considered in the disease mitigation protocols. For TADs, the need to prevent, detect and respond to shifting disease threats in ever more complicated contexts led to develop data-driven tools that can be used upon integrated data sets, involving open access georeferenced data, and official epidemiological information collected by animal health authorities. However, despite their increasing versatility and quality, the use of these tools is not without pitfalls, and the dangers of "garbage in, garbage out" are increasingly present.

Beyond the issues of (oh-so time consuming) cleaning data sets from data entry errors and missing information, questions remain on how to ensure the unbiased collection, analysis and use of data to produce unbiased modelling outputs during a disease outbreak and beyond. As trust in modelling outcome may depend on when and how "up-to-date" (that is, most often, the latest version available or collected, which can be many years prior our period of interest) data are collected and managed, enhancing the transparency of the provenance and adequacy of the data used in the modelling process is critical. This is an important component of the Findable, Accessible, Interoperable and Reusable (FAIR) data principles (Wilkinson et al., 2016), that proposed guidelines for both researchers and machines to efficiently and transparently find, access and (re)use data (Mitchell et al., 2022). The principles have been widely adopted to enable interoperability with other systems and support integrating and exchanging well-documented data in a straightforward way, and upon which data pipeline, such as the one we developed as part of our activities in the SCRC (Mitchell et al., 2022), have been developed to provide open, traceable and reproducible mechanism to process data and integrate them in modelling tools.

Such an open-source FAIR pipeline requires a data registry and metadata that is aligned to existing formats and vocabularies. The information contained in the metadata of these “up-to-date” data captures details of the purpose of their primary use and the methodology that is resulting. Such details are however poorly reported, often affecting our ability to infer from them. One way to overcome such potential problem is to seek the implication of the different stakeholders (of the Health sectors – human and animal – as well as those involved in agriculture, the environment, urban planning, etc.) who designed and collected data to clarify data collection procedures. In doing so, this would not only improve our understanding of the data used in generating our modelling outputs, particularly their associated limitation(s), but also ensure stakeholders’ involvement in improving and refining models, ensure current and future needs and goals of all stakeholders are met, and increase confidence in modelling outcomes, leading to robust policy making in line with holistic needs.

Clearly, working in isolation and focusing solely on specific issues will limit our ability to develop novel strategies, restricting our understanding to a small part of the disease systems which may lead to unwanted, potentially expensive, consequences. However, this demands an interdisciplinary dialogue – in particular, with social sciences – to deliver appropriate and effective policy, whether to detect, control or prevent incursion or spread of TADs, which reflect the economic, social, and cultural values of their communities, and anchor them in the society. This is non-trivial as it translates into a decompartmentalization of disciplines and interests. To do so, there is a need for a new generation of scientists capable of talking to specialists and build a common language with which better designing strategies in line with holistic needs.

Being able to participate in multidisciplinary, multi-actor and multi-sectorial conversations is however challenging for anybody. Most often, despite our willingness and openness to other disciplines, we may (most often unconsciously) use our own language and drive conversation to our own interests, instead of other’s. If we want to have specialists of the interface between science and policy, able to converse with experts of multiple disciplines to ensure robust and integrative policy to improve our prevention, surveillance and control protocols against complex health issues, such as TADs, integrative and transdisciplinary training programmes are needed (**Figure 25**).



Figure 25. Toward an integrative and interdisciplinary training programme as a mean to ensure efficient dialogue between actors of health and improve response to complex health issues.

This is to partly answer these needs, F. Ayral (VetAgro Sup), S. Mialet (ENSV-FVI) and I developed the curriculum of the international elective course (M2) “One Health – Managing Health of Populations” (OHMHP) around the concept of “One Health” (OHHLEP et al., 2022). Based upon three pillars articulating “risk evaluation” and “risk management” around practical disease issues (**Figure 26**), this master-level programme aims to train scientist, from all sectors of health, to be able to work in interdisciplinary collaboration and navigate cross-sector space. Indeed, the development of global strategies against TADs, as for emerging infectious diseases, requires to better account for the interconnections between people, animals, plants and their shared environment. It also requires a holistic understanding of critical health situations, built upon a broad appreciation of the consequences that each decision and action may have on humans, animals and ecosystems. As such, it would cover needs that are most often missed when managing the infectious disease outbreaks: the broader appreciation that each decision and action may have consequences on humans, animals and ecosystems. In addition, the duality between “risk evaluation” and “risk management” was perceived very early on as a way to discuss and integrate all aspect of the “One Health” approach, making it more tangible and practical for responding to complex health issues, such as TADs.



Figure 26. The three pillars of the international M2 “One Health – Managing Health of Populations” teaching program

Future-proofing mitigation protocols

Integrating our epidemiological understanding of TADS in the broader landscape of disease control has the potential to prevent implementation failures of control measures and avoid resource wastage (Card et al., 2018; Tsagkarliotis and Rachaniotis, 2023; Xia et al., 2017). However, considering that mitigation strategies designed upon our current understanding would be resilient enough to challenges ahead is questionable. Indeed, the landscape of disease control is not static and may change over time. For example, policy and industry regulation may change depending on the interest and political agenda of governments and stakeholders, whereas the underlying processes contributing to disease transmission and maintenance

may vary, in the short-term as well as the long-term, in response to external factors, such as climate, market pricing and cultural changes.

To characterise how TADs may spread in the future to inform resilient and sustainable mitigation protocols, numerous probabilistic forecasting models and risk assessments have been developed (Endo and Amarasekare, 2022; Roberts et al., 2011), integrating state-of-the-art scientific knowledge to different scenarios of the future, most often limited to their question at hand without looking at the problem holistically. For example, models assessing the impact of global warming of vector borne diseases will only look at the impact of temperature changes on transmission and survival, but would assume that distribution of hosts and livestock husbandry practices would remain the same (Endo and Amarasekare, 2022). As such, although these modelling frameworks may be able to quantify uncertainty around the probability that risks will occur, their usefulness is contingent on knowing and identifying these risks in advance as well as the assumption that the situations (i.e. the abundance, structure and dynamics of the host(s) population), as well as the parameters, of the future can be directly related to that of the present or recent past.

Beyond the impact of the long-term changes in the structure of the agricultural sectors – for example, due to changes in industry demographics, in the role of government support and regulation, and in technological advancements (Boden et al., 2015), data-driven tools and models are limited to account for the uncertainties inherent in the diverse range of factors (such as climate change, consumer preferences and market pricing, regulation perception, beliefs and politics) which interact at the interface between anthroposphere and biosphere (**Figure 1**) to compound risks of TADs. To future-proof our mitigation protocols (that is, our ability to adapt and respond swiftly to challenges ahead), we therefore need to explicitly address how concurrent changes may affect the risk of disease incursion and alter the spread and persistence at a local or national scale (Baker et al., 2022).

In particular, as shifting patterns of climatic and demographic factors are expected to modify how diseases may persist and spread in the future (Baker et al., 2022; Cohen et al., 2020; Ostfeld and Keesing, 2000; Thomas and Blanford, 2003), it is yet to be clear how such shifts would increase (or decrease) these risks and impact mitigation protocols of TADs. Temperature not only influences the demographic rates of hosts and pathogens, i.e. their survival, reproduction, infectiousness (Johnson et al., 2007; Marcus et al., 2023; Paniw et al., 2022), but also can indirectly influence the hosts-pathogens dynamics, through changes mediated by food resources. Changes in food availability can impact host demographic rates (Becker et al., 2015; Johnson et al., 2007), its movements and aggregation (Merkle et al., 2018), and its immune defences by strengthening or weakening allocation trade-off among competing physiological functions (Martin et al., 2008).

In a first attempt to clarify how climate warming directly and indirectly influences host-pathogen dynamics in the case of TADs, we are currently exploring how temperature-driven changes on nature wild boar population dynamics would affect the epidemiological dynamics of ASF. Capitalizing on the model framework presented above and published in Fay et al (2024, in press), we are currently projecting host-pathogen dynamics under the RCP 8.5 climate warming scenario to anticipate potential epidemic changes in the coming decades. This represents a direct continuity of the work initiated in Axis 3 and represent an opportunity to further work with biodemography and evolutionary biologists (such as M. Gamelon, CNRS) and expand my research questions at the interface between disease ecology and veterinary public health.

Similarly, epidemics of infectious diseases, such as TADs, are increasingly recognised as complex spatio-temporal bio-social events that not only have clinical, ecological causes and consequences, but also social, economic, and geopolitical ones. It is now recognised that effectively responding to these ever-changing,

complex and uncertain contexts urgently requires a broader range of expertise beyond the biomedical, infectiology, ecology and epidemiological disciplines. In particular, there is an urgent need to integrate social sciences in epidemics preparedness and response, in order to mitigate the impact of short- and long-term socio-economic burdens associated with surveillance and emergency responses, and future-proof our mitigation protocols to the challenges ahead. This is perhaps highlighted most clearly in the world's efforts to address COVID-19, ASF and highly pathogenic avian influenza (HPAI). Again, this offers an opportunity to expand our Axis 2 work and represents great perspectives in transdisciplinary research.

Perspectives in transdisciplinary research

To develop trusted, robust and sustainable modelling framework to shape and inform policy and industry decision, modellers are facing many challenges around data collection and integration into modelling framework to provide realistic projection of risk. One of these challenges is to properly address the role of individual behaviours into the different processes that drives disease transmission dynamics within and between populations, during outbreak situations as well as before their incursion (Bedson et al., 2021).

As individuals act upon their interpretation and trust of policy recommendations as well as based on their beliefs, perception of disease threats and socio-economic constraints, social and behavioural factors are critical to the emergence, spread and containment of infectious diseases and key determinants of the course, duration and outcomes of outbreaks, irrespective to those occurring in either human or animals (Bedson et al., 2021; Funk et al., 2010; Verelst et al., 2016). As such, better incorporating social and behavioural factors into disease models will probably improve their predictive accuracy and thereby inform more effective response measures and policies (Manfredi and D'Onofrio, 2013).

Nevertheless, although offering opportunities to build on methodologies and insights, the existing modelling approaches that attempted to integrate human behaviour are limited in their understanding of the interplay between social and behavioural factors on disease transmitting activities (Bedson et al., 2021). This is further pronounced in the context of livestock diseases and veterinary public health, with relatively little work has been done. A quick search of the modelling literature that sought to incorporate behaviour factors in PubMed¹ showed that among the 11,578 articles with full text available and in English that were published between 2016 and 2023, only 1591 articles were related to animal health, most of those being on studies modelling the public health impact of either zoonosis or vector-borne diseases. Although this is a crude screening of the literature and most of these papers may not be relevant, the scale of the difference clearly highlights the need of better understand what factors drive the behaviour of farmers and incorporate these short-term decision-making processes in animal health models.

In this context, **I aim to extent my current** research activity (Axes 1 and 2) to **build an innovative transdisciplinary research programme to clarify the impact of individual decision-making processes of**

¹ The search query used in PubMed (access on 20 May 2024) is an extension of the query used by Verelst et al (2016) in his review: "(behavio* OR decision*) AND (change* OR influence* OR dynamic* OR adapta* OR adapt OR adaptive OR strategic*) AND (infect* OR epidemic OR epidemics OR epidemiology OR epidemiological OR epidemiologic OR pandem* OR outbreak*) AND (disease* OR vaccin*) AND (model OR models OR modelling OR modeling OR simulat* OR transmission*) NOT (review) NOT (meta*)"

livestock owners (or farmers) on the spread of TADs in livestock to meet the challenges of global animal health and specificities of veterinary public health. By doing so, we would develop novel modelling framework that integrate perspectives of multiple disciplines in order to optimise the epidemiological and economic efficiency of disease mitigation strategies. This approach would complement our previous research activities by improving how we consider process feedback and uncertainties. In particular, this work would promote a transdisciplinary dynamic based on the "One Health" approach to veterinary public health. In particular, research projects developed in this project are at the interface between epidemiology and socio-economics.

This research project is organised around two interconnected activities:

- Perspective 1: Understand social drivers of disease distribution
- Perspective 2: Role of individual decision-making processes on disease spread

Understand social drivers of disease distribution

Farmer's compliance and individual choices are critical factors that affects the success of control measures (Dürr et al., 2014; Jemberu et al., 2015). However, this has mostly been ignored in most predictive epidemiological models of livestock diseases, or, when considered, assumed in the context of economic rationality (farmers will behave to optimise their net gain, as in our work on sheep scab (Mohr et al., 2020)). Although farmers' decisions and compliance to regulations (either on livestock trading, biosecurity, reporting and/or disease control) may well vary with changes in commodity prices and their own expectations on revenue forgone, they also markedly depend on cultural aspect and can be disrupted by various triggers such as disease outbreaks, introductions of animals with undesired characteristics, and farm relocation (Hidano et al., 2019).

Here, we will focus on better understand how farmers perceive regulations with regards to biosecurity, reporting and disease control measures and act upon such perceptions. These were selected as they have the potential to either increase or reduce the apparent incidence and local distribution of diseases. This work is a direct extension of the various work initiated in collaboration with social scientists, looking at social constraints on biosecurity (technical report of C. Kyle et al., 2021; technical report of Jennings et al., 2021; Beslay et al., 2023; Allen et al, 2024) and disease reporting (M2 internship project of G. Margiapi, 2023). These studies were great opportunities to generate hypothesis upon which models can be developed or support our assumptions during modelling development.

Publications related to this section

R. Allen, L.A. Boden, I. Hutchinson, J. Stirling, **T. Porphyre** (2024) Cleaning practices of transport vehicles by commercial and non-commercial livestock markets users in Scotland. *Journal of Veterinary Sciences*, 180: 105413. <https://doi.org/10.1016/j.rvsc.2024.105413>

Giorgio MANGIAPIA 2023 "A qualitative investigation of the African swine fever surveillance network in the Auvergne-Rhone-Alpes: what factors can delay a suspicion report?". Master 2 OHMHP, MSc *Public Health*, Université Claude Bernard – Lyon 1, France.

C. Beslay, M. Bouix, H. Fauroux, A. Gautier, F. Luposella, J.-M. Pillon, **T. Porphyre**, M. Schell, N. Soleau (2023) « Un lavage, c'est un lavage ». Des chauffeurs bovins face aux consignes sanitaires [in French]. *Les mondes du Travail* 29 :147-163.

A. Jennings, K. Adams, **T. Porphyre** (2021) Pig keepers in Lilongwe, their biosecurity practices, and African swine fever. A technical report for the Malawi Department of Animal Health and Livestock Development (DAHLD).

C. Kyle, L.-A. Sutherland, **T. Porphyre** (2021) Understanding attitudes to biosecurity in small scale pig keepers. A technical report produced by EPIC Centre of Expertise on Animal Disease Outbreaks to the Animal Health and Welfare Division (AHWD) of the Scottish Government. <https://www.epicotland.org/resources/reports-by-epic-members/>

Role of individual decision-making processes on disease spread

Although farmers' decisions and compliance to regulations (either on livestock trading, biosecurity, reporting and/or disease control) may well vary with changes in commodity prices and their own expectations on revenue forgone, they also markedly depend on cultural aspect and can be disrupted by various triggers such as disease outbreaks, introductions of animals with undesired characteristics, and farm relocation (Hidano et al., 2019). This later is consistent with recent economic research suggest that people depart from rational decision-making process (based only maximizing gains/utility) even in 'normal time' (DellaVigna, 2009): they have non-standard preference (e.g., reference dependence), non-standard belief or cognitive limitation (e.g., limited attention, emotion). In particular, how do people change their behaviour following a sudden and unforeseen change in the environment or facing tail events (Barberis, 2013) is an open question. For example, how do they adapt their beliefs about the probabilities of infecting their herd after receiving new information? What is the role of emotion, experience or stress in their decision making? Likewise, what does the effect of new (untested) constraints imposed by authorities to mitigate outbreaks on their behaviour? Answering some of these questions will likely improve our understanding of the dynamic nature of decision-making and therefore improve, once integrated, the prediction ability of epidemiological models.

Most studies on farmers' compliance and behaviour have been focused on qualitative surveys or perspectives of farmers collected from questionnaires (Delgado et al., 2012; Jemberu et al., 2015; Pham et al., 2017). However, these methods are limited to clarify and measure real-time individual decision-making or may suffer from recall biases at best. Experimental economics is the method of using controlled experiments to study important questions in economics and thus provides a way to clarify what impact people's individual choices. The idea is that, by performing experiments to test hypothesis, new insights can be generated, and people's individual choices could be integrated into models in a more realistic way. Obviously, this work is intrinsically transdisciplinary and will be built on work and collaborations already initiated with experimental and behavioural economist (B. Tarroux, UMR GATE, Lyon2; and J. Rosaz, Burgundi School of Business) as part of a PhD project (S. Kramer, Claude Bernard University Lyon1).

In this project, we are looking at changes in animal trading behaviour patterns when farmers are facing various level of disease risk. To reach this goal, a financial double auction market experiment is being conducted to simulate the dynamics of animal trading and evaluate how observed variations in prices and trade flows (product of the real-time trading decisions of participants) may relate to the introduction of a given disease and affect its spread. This experiment is currently very simple but offers exciting research perspectives, especially testing different hypothesis related to farmers' decision during animal trading when facing disease-related risks. The outcomes of our experiments (i.e. prices and trade flows) would then be integrated into a simple modelling framework for pathogen spread that considers farmers' dynamic decision-making regarding animal trade. Together with the modelling framework, this experiment represents a transdisciplinary framework that can be easily modified to test other trading hypothesis and collect much needed data for improving our epidemiological simulation models and assess the effectiveness of implemented mitigation strategies (Bedson et al., 2021; Verelst et al., 2016).

GENERAL CONCLUSION

The intersection of science and policy is a challenging space, perhaps highlighted most clearly in the world's efforts to address COVID-19 and leverage rapidly evolving scientific information. In this context, my research focused on characterizing epidemiological processes driving emerging TADs epidemics and modelling their spread, to inform policy-makers and industrial stakeholders on how to best, most cost-efficiently, implement mitigation protocols on the field. This work is in essence transdisciplinary as it demands involvement of multiple experts from different discipline (i.e. population ecology, maths, statistics, data management and visualisation sciences, political sciences, social sciences, economics, etc...) to take into account multiple dimensions, from eco-epidemiological to social and economic, involved in epidemics spread and mitigation, and ensure that an efficient dialogue, where involved disciplines benefit in the research, is carried out. Such an openness for cross-disciplinary interactions with colleagues in ecology, economics and social sciences, gave me opportunities to integrate their perspectives and develop common conceptual modelling frameworks to further answer important questions on TADs to prepare challenges ahead.

In that regard, my research is in line with the "3P" approach (combining Process, Pattern and Participatory models, **Figure 27**), promoted by Scoones and colleagues (Scoones et al., 2017), for understanding the complex, non-linear, multi-component systems impacting infectious (in Scoones's cases zoonotic) diseases dynamics and offering novel insight to identify appropriate prevention and management measures. Such an approach contributes to the "One Health" agenda by providing a framework for transdisciplinary data-driven work and places modeling efforts at the heart of research implementing the "One Health" concept. It also offers the opportunity to develop novel teaching programmes to train future experts who will be able to promote the dialogue between evidence-providers and field operators, thereby ensuring actions against complex health issues are tangible and practical for all stakeholders and sectors of Health.

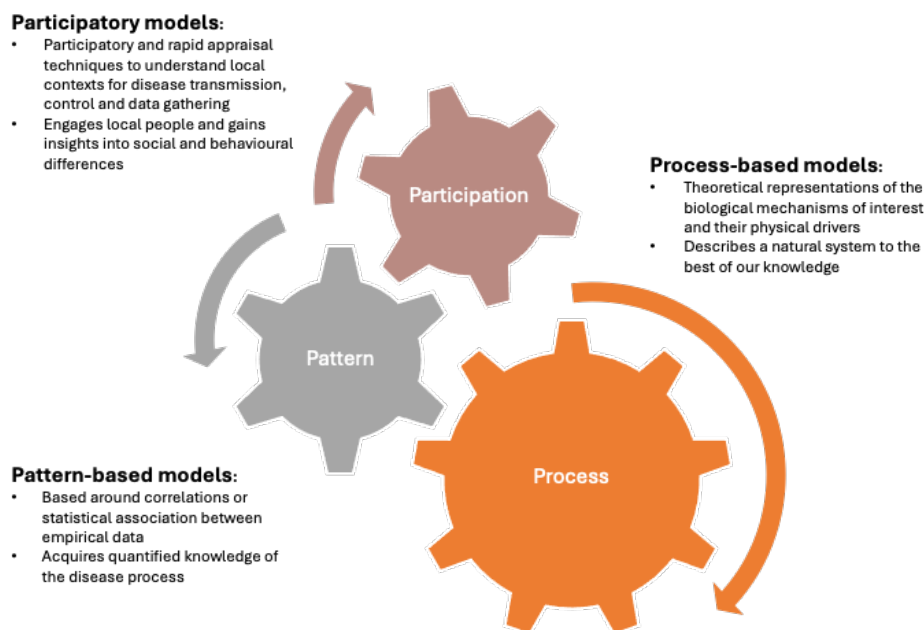


Figure 27. The "3P" approach as a way to integrate a transdisciplinary dialogue between modelling approach. Adapted from Scoones et al. (2017).

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