Discover Public Health

CASE STUDY Open Access

Bridging eco-exposome and one health approaches to address emerging infectious diseases through the EMERG project

Laurence Delhaes[1,2*], Baptiste Defaye[1,3,4,5], Gautier Chauvin[1,6], Aurélien Mercier[3], Jérôme Moreau[7], Karine Monceau[7], Cristiana Cravo-Laureau[8], Gaelle Gonzalez[9], Jean-Luc Guerin[10], Nicolas Eterradossi[11], Christine Imbert[6], Hélène Agogué[12] and Denis Malvy[5,13] on behalf of the EMERG consortium

*Correspondence:
Laurence Delhaes
laurence.delhaes@u-bordeaux.fr

Full list of author information is available at the end of the article

Abstract

Introduction Emerging or re-emerging infectious diseases (EIDs) are being increasingly reported and represent a significant burden on public health and global economies, as exemplified by COVID-19 pandemic.

Context Given the current EID importance at the territory level in Nouvelle-Aquitaine (NA, a French southwestern region), we designed a project to address this risk. The EMERG project and consortium (for "Microbial exposome and EID risks: the benefits of a One Health management of zoonotic influenza-related issues and beyond") aim at deciphering and anticipating EID risks in NA.

EMERG project design EMERG is a transdisciplinary network for evaluating and predicting EID risk and zoonotic potential. EMERG focuses on highly pathogenic avian influenza, zoonotic arboviral infections due to West Nile and Usutu viruses, and the burden of microbial multidrug resistance in NA. Investigative approaches were developed considering the exposome extended to animals, namely the eco-exposome and specifically the microbial eco-exposome. It brings together specialists in human, animal and environmental health. EMERG aim is to provide up-to-date and region-specific data on major EID risks and their determinants in NA, thereby facilitating local management and anticipation of threatening events, epizootics, and epidemics.

Implications, limitations, and future directions In addition to addressing the multiscale nature of complex ecosystems driving EIDs, this transdisciplinary project supports informed decision-making for an adapted regional (NA) policy and can be integrated into larger (national, international) public health initiatives. While EMERG has several limitations, it represents a practical implementation of the One Health approach and eco-exposome concept, which is essential for preventing future EID risks. Here, we focused on project design and organization, and presented examples to demonstrate EMERG feasibility throughout a case study.

Keywords Emerging infectious diseases, Exposome, Eco-exposome, One health, West nile virus, Avian influenza, Antimicrobial resistance

1 Introduction

Pandemics have always existed and represent a source of danger in the collective imagination, as reinforced by the recent COVID-19 pandemic [1, 2]. Numerous countries, including France, as well as European and international organizations (such as the World Health Organization (WHO) and Earth emergency preparedness and response (HERA)), have promoted a new health ecosystem based on transdisciplinary, multilateral cooperation to mitigate COVID-19 risks and to address the next pandemic or epidemic episode, with the aim of building a more equitable framework for future pandemic response [1–4]. This new ecosystem also promotes a holistic approach to the risk of emerging or reemerging infectious diseases (EIDs), especially by including a One Health (Box 1) dimension and evidence-based analysis to strengthen adopted policies. In this context, the COVARS (*Comité de veille et d'anticipation des risques sanitaires*: a French interdisciplinary committee for monitoring and anticipating health risks) currently represents an independent task force to anticipate, prepare, and manage health crises according to its position at the science-decision interface [1–3, 5, 6]. Among numerous institutions and working groups, COVARS recently highlighted the urgent need for a One Health High-Level Expert Panel approach to EIDs [3, 6]. Here, we present the case study of EMERG, a transdisciplinary project implemented in southwestern France that aims to address EIDs through an integrated One Health approach including eco-exposome (Box 1) analysis. We focused on project design and organization, and presented a few examples to demonstrate EMERG feasibility.

2 Box 1

The One Health approach and the concepts of exposomes, eco-exposomes, and zoonotic spillover events.

The **One Health** framework endorsed by the quadripartite WHO, WOAH, FAO and UNEP is defined as an "integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals, and ecosystems", and explicitly refers to the health of plants as part of the whole interrelated system to consider. Although the ultimate issue is the planet's habitability for humans, the definition introduces the idea that human health is no longer the only priority but that all human, animal, plant and ecosystem health must be balanced and optimized [7]. The meta-concept of sustainably balancing and optimizing the health of people, animals, plants and ecosystems implies that health is considered at the scale of the whole system, not just at the scale of each type of health. In this case, for example, human health may be limited to a degree that preserves the health of animals, plants or ecosystems. At the scientific level, the One Health approach can contribute to the sharing of a scientific culture that inspires a common narrative.

The **exposome** represents all the environmental, specific and nonspecific, biotic and abiotic factors, to which a human is exposed from conception throughout life (climate, pollution, diet, and microorganisms). This concept initially referred to the field of human research [8, 9], but it can be applied to nonhuman living organisms such as animals, leading to the recently proposed **eco-exposome** concept [10]. By analogy to the exposome dedicated to humans, the eco-exposome represents the totality of the specific and nonspecific, biotic and abiotic factors to which a nonhuman organism is exposed throughout its lifetime. All exposure factors can influence human, animal, plant and

environmental health by causing pathological processes, either directly or by impacting the circulation of various pathogens and modulating pathogen virulence or host susceptibility. Exposomes and eco-exposomes appear to be clearly and complexly linked to EIDs, as recently highlighted [6]. At the One Health level, the exposome and eco-exposome must be considered a useful part of the puzzle to address EIDs; characterizing the variability in the eco-exposome component over time will help identify high-risk groups for a given EID [11]. The derived concept of the eco-exposome emphasizes the dynamic balance between ecosystems, humans and animals. It fits perfectly within the One Health approach, as the current and future global changes will mainly bring about changes in exposures (heat, UV, pollution, vector-borne diseases, pollen, zoonoses, etc.) that will impact humans but also animals and the environment, bringing us to the global vision of the environment and health fields as defined in the Helsinki Declaration [12].

Zoonotic spillover events are defined as processes that enable pathogen transmission from a vertebrate animal to a human. All zoonotic pathogens have to overcome a hierarchical series of barriers to cause spillover infections in animals and ultimately in humans, which consequently remain relatively rare. These phenomena remain poorly understood but represent a global planetary health burden [13, 14].

3 Context: emerging infectious diseases and global to regional trends

3.1 Global overview and one health rationale

Multiple international assessments that have addressed the pandemic risks of EIDs converge on similar conclusions. Briefly, EIDs are dominated by zoonotic viral infections transmitted through airborne or vector-borne routes [6]. In France (both mainland and overseas) and across Europe, the priority agents include high-pathogenicity avian influenza viruses (HPAIVs), new coronaviruses, and agents responsible for West Nile fever, Crimean-Congo haemorrhagic fever (CCHF), Rift Valley fever, yellow fever, and acute respiratory infections [6, 15]. Four additional diseases transmitted by mosquitoes, infections with Dengue, Zika, and Chikungunya viruses and, to a lesser degree, malaria, have been identified as potential EIDs in France [6, 16–18]. Several of these diseases have already emerged or pose a high risk in southwestern France, especially in the Nouvelle-Aquitaine (NA) region. Avian influenza viruses (AIVs), especially HPAIVs (such as H5Ny clade viruses according to the international nomenclature in which H refers to haemagglutinin and N to neuraminidase antigens), caused major outbreaks in NA poultry farms during the European waves in 2020-22 [19–21]. Since 2022, West Nile virus (WNV) has spread to the NA region, affecting birds, equines, and humans, mirroring its rise in other European countries [22, 23]. Concurrently, autochthonous dengue and Chikungunya cases—as part of the indigenous transmission chain— have been reported in southern France (including NA) and in several European countries [23]. Apart from the last examples that are related to *Aedes* spp. mosquitoes born arboviral disorders, the reported data are largely congruent with a zoonotic origin of numerous human EIDs. Globally, up to 60% of human infectious diseases are zoonoses, with 72% originating from wildlife (e.g., Ebola or SARS-CoV-2 virus) [10, 24], and these events are zoonotic spillover events (Box 1) [13]. Taken together, these figures highlight the direct involvement of disturbed links between humans, animals, and the environment, exacerbated by global changes such as climate change, deforestation, megafires, and biodiversity loss, a condition also observed in the French NA region [25]. These disturbances, whether local or distant

(such as Amazon deforestation), influence EID risks globally [14]. All these changes, at various scales, are clearly associated with spillover occurrences (for review, see [13]). The holistic One Health approach, which integrates the analysis of the eco-exposome developed in the EMERG project, is essential for understanding these interconnections. As it is impossible to separate human health from animal and environmental health, the analysis of the eco-exposome within a One Health framework provides a unifying perspective. It enables systematic investigations of the links between human, animal, and environmental health, including the emergence of WNV/Usutu virus clusters in NA (linked to *Culex* mosquitoes and driven by human behaviours) as well as the circulation of AIV (associated with bird migration and poultry farming activities). AIV infection of certain hosts may integrate into the eco-exposome of other hosts alongside other biotic and abiotic factors such as the copresence of microbial communities, environmental pollution, or pesticide exposure, which are involved in antifungal resistance [26, 27]. Combining One Health and eco-exposome analysis represents a prerequisite for anticipatory and accepted decision-making, considering the temporal hierarchies of epidemics and pandemics, both in humans and animals [11, 13, 14]. The EMERG project focuses on analysing the microbial eco-exposome in NA, cross-referencing these data with abiotic parameters (pollution, temperature, soil pH, pesticide, etc.) to better understand the complex interplay of environmental, behavioural, and microbial factors [4, 11]. The regional context detailed in the next section highlights characteristics specific to NA that make this region highly vulnerable to the development of EIDs, such as HPAI and WNV.

3.2 Regional context: environmental characteristics of Nouvelle-Aquitaine in relation to EIDs

The NA region has a long history of maritime trade with Africa and the Americas, dating back to the triangular trade era through the port cities of Bordeaux and La Rochelle. As France's largest region since 2016 and the third most populous with more than 6 million inhabitants (2021 estimates, Fig. 1) [28], its extensive trade and activity levels have

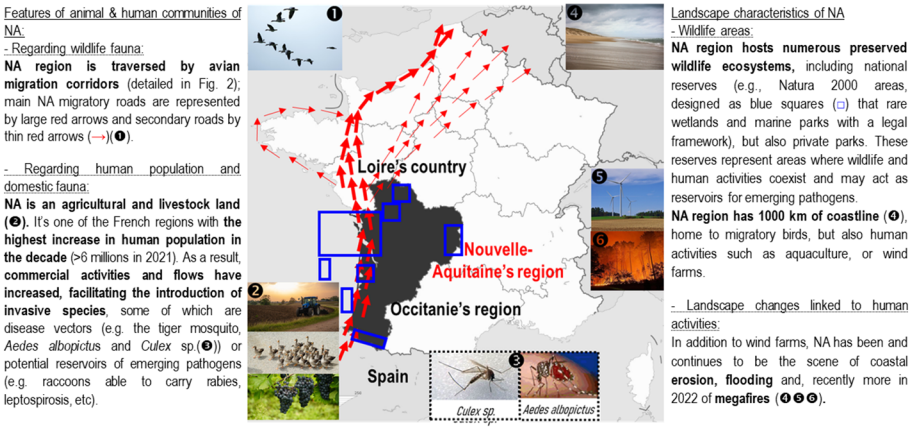

Fig. 1 Environmental characteristics of the Nouvelle-Aquitaine (NA) region in relation to EIDs. NA is represented in black on the map of France; the main characteristics of NA in relation to EIDS are presented as main features associated with animal and/or human population behaviours (points 1 to 3, left text) and environmental scenarios characterizing wildlife preservation or human activities (points 4 to 6, right text). The photos were selected from the Pixabay website (https://pixabay.com/fr/), except for photo number 6, which was provided by Mr Jean-Luc Gleyze (Président du Département de la Gironde & Conseiller Départemental du canton Sud Gironde)

facilitated the introduction of invasive species, including disease agent vectors such as the tiger mosquito (*Aedes albopictus*; Fig. 1) and potential pathogen animal reservoirs such as raccoons which can carry rabies virus, *Leptospira* genus bacteria, sarcoptic mange mites, parvoviruses and canine distemper virus, as well as *Baylisascaris procyonis*, a nematode parasite specific to this species.

The NA region is crossed by major avian migration corridors as detailed in the next section, providing resting areas for birds that spread pathogens across continents (Figs. 1 and 2). The region's diverse ecosystems, such as national reserves, wetlands, and a marine park, where wildlife and human activities coexist, serve as potential pathogen reservoirs. Intensive agriculture and poultry farming, often near natural habitats, increase zoonotic transmission risks [29]. Furthermore, the densely urbanized coastal area (1,000 km of coastline), with its significant shellfish and aquaculture production, faces heightened microbiological risks because of complex human–environment interactions [30].

Climate change exacerbates these risks by disrupting ecosystems in the region [33], promoting invasive species such as raccoons [34, 35], and altering avian migration routes. Extreme events, such as heatwaves (e.g., 2022-23 heatwaves in NA), large-scale wildfires (e.g., 30,000 hectares burned in the county of Gironde (within the boundary of the regional park of *Landes de Gascogne*) in 2022; Fig. 1), and frequent flooding further increase human-wildlife interactions [36, 37], increasing pathogen transmission and EID risks. Rapid urbanization, and intensive agriculture and aquaculture amplify these challenges in NA.

The tiger mosquito *A. albopictus*, a competent vector for arboviruses such as Dengue, Chikungunya and Zika virus, exemplifies this trend. These viruses are now actively circulating in temperate areas such as France because of globalization, trade, and global warming after being historically confined to tropical and subtropical (or Mediterranean, in the case of Dengue viruses) regions [38]. Moreover, the vulnerability of NA is evident when the emergence of indigenous zoonotic arboviral events of WNV among autochthonous avian, equine and human populations driven by dense avian migratory routes

Fig. 2 Maps of the main global avian migratory pathway in the Old World and the Nouvelle-Aquitaine (NA) with the main avian stopovers (*) [31, 32]. This is nonexhaustive list of stopovers (the names and geographic coordinates are listed in Supplementary Table 1). Four of the pathways directly impact NA, namely, the dark blue, light blue, green and pink pathways, and indirectly through cross-migration pathways represented in orange (created with QGIS 2.3.8). The green stars in NA represent the various avian stopovers in the region

and climate disruption is considered (Figs. 1 and 2) [23]. Overall, the environmental characteristics of NA, combined with climate change and globalization, create conditions favourable for pathogen emergence and spread, highlighting the relevance for an integrated One Health approach to mitigate EID risk.

3.3 Wild avifauna as key vectors and reservoirs in EID widespread, especially in Nouvelle-Aquitaine

Wild birds are found on every continent and are among the few terrestrial vertebrates capable of travelling long distances across national or continental boundaries. Among the 10,000 bird species described worldwide, 20% are considered to be migratory [31]. Their migrations cover thousands of kilometres and involve diverse habitats, enabling the spread of pathogens across large geographical areas. This has direct implications for animal and human health, including the risk of zoonotic transmission of AIV, WNV, and bacterial infections such as those caused by *Salmonella* and *Campylobacter* [21, 39–41]. Notably, birds (especially sea birds) have been described as reservoirs for indirect transmission of *Candida* species, such as *Candida auris* that may be transmitted to humans through potential host jump mechanisms similar to those involved in avian influenza transmission [42, 43]. Given their natural nature, detecting and monitoring these zoonotic agents as asymptomatic carriers is challenging. Migration facilitates the intercontinental spread of viruses such as HPAIV (e.g., the influenza A virus subtype H5N1 clade) and potentially contributes to the emergence of new pathogen species or strains capable of infecting various animals, including humans [42, 90, 91].

Wild birds transmit pathogens through multiple pathways: infection from contaminated environments (e.g., water or soil) or direct contact with other infected migratory or sedentary birds, particularly at stopover sites (Fig. 2) [32]. Several orders play a pivotal role in the spread of pathogens between wild and domestic faunas and ultimately to humans [21, 42]. Anseriforms (e.g., mallards and mute swans) are natural reservoirs for several AIV types and significantly contribute to the genetic reassortment and adaptability of AIV [45]. Passeriforms (e.g., European robin, Barn swallow) are key players in the dissemination of vector-borne pathogens. For instance, they participate in the transport of WNV between Africa and Europe as well as through central European and Mediterranean routes, enabling mammalian infections that range from mild morbidity to mortality in horses and humans [46]. Their role can also be indirect, as seen with tick-borne pathogens: migratory birds have introduced vectors such as *Hyalomma* ticks, which carry the CCHF virus across geographical barriers such as the Mediterranean Sea [15]. Artic sterns (Charadriiforms) represent the longest migrating bird species and are able to cover more than 80,000 km annually [47]. Although they play a lesser role than Anseriforms do, Charadriiforms still influence the large-scale circulation of health-threatening pathogens such as AIV and HPAIV [48]. This avifauna diversity is observed in the NA region, which hosts numerous migratory routes and significant stopover sites for birds (Fig. 2 and Supplementary Table 1), characterized by a wide variety of environments (Fig. 1). As stated previously, these features, combined with the presence of many poultry farms and nearby wetlands, have contributed to recurrent epizootic outbreaks of AIVs (including HPAI and, H5Ny viruses) in recent years [19]. For example, of the three H5Ny strains isolated in the 2015-16 epidemic, one was from a chicken poultry farm (H5N1 virus), and two were from duck farms (H5N2 and H5N9), all located in the NA

region [19]. Consistent with these trends, WNV infections emerged in horses in 2022 and humans in 2023 [49], both within and beyond the borders of NA, underscoring the role of migratory birds in pathogen transport and the associated risks of EIDs.

4 Design of the EMERG project: a transdisciplinary approach to EIDs in Nouvelle-Aquitaine

4.1 EMERG project and consortium presentation

The EMERG project ("Microbial exposome and EID risks: the benefits of a One Health management of zoonotic influenza-related issues and beyond") aims to decipher and anticipate EID risks in NA. Funded by the regional council of NA under the PSGAR program (Scientific program of great ambition), the project spans five years and focuses on exploring the microbial (viral, bacterial, parasitic, and fungal) eco-exposomes (Box 1 [8–10]), in NA. By studying this microbial eco-exposome in NA samples from the environment, migratory birds, poultry farms, horses, and humans, it addresses the One Health approach. By combining, for the first time in NA, the microbial eco-exposome as the research concept with a One Health approach as the research process, the key objectives of EMERG are as follows:

- Investigate the links between the human and animal microbial eco-exposome and the risk of EIDs, such as HPAIVs, and their zoonotic potential;
- Analyse how the microbial eco-exposome is affected by environmental changes driven by anthropogenic activities (e.g., pollution and anthropization) in relation to AI epizootics and other epidemic risks such as zoonotic arboviral (WNV and USUV) infections;
- Assess the impacts of climate change on NA biotopes, bird migration and microbial spread;
- Identify potential bioindicators to monitor environments conducive to the emergence of HPIAV, WNV/USUV, and/or other emerging trends, such as microbial multidrug resistance.

For the first time in NA, the project integrates the One Health approach (methodological framework) and the eco-exposome (research concept), bringing together a transdisciplinary consortium. This consortium includes many researchers—ecologists, microbiologists, epidemiologists, physicians, veterinarians, specialists in systems biology, legal experts, bioinformaticians, and EID modellers— and, public and private stakeholders (companies and government institutions) involved in EID management (Fig. 3).

By promoting an inclusive approach and coconstruction, the consortium *(i)* provides up-to-date, regional data on major EID risks, *(ii)* strengthens the prevention and management of epizootics in NA, and *(iii)* supports regional policy decisions while aligning with other public health initiatives, such as the national COVARS initiative. This represents an innovative application of the One Health approach to the study of the eco-exposome, which is consistent with recent national and international recommendations to prevent future EID risks [3, 6]. Preliminary results of the EMERG project led to the production of a flyer sensitizing NA citizens to EID risks, the establishment of regular meetings with the regional council of NA and its president, and participation in the task-force focused on EID risks and the One Health approach coordinated by the regional council. In parallel, deep-sequencing tools as well as prediction tools based on artificial

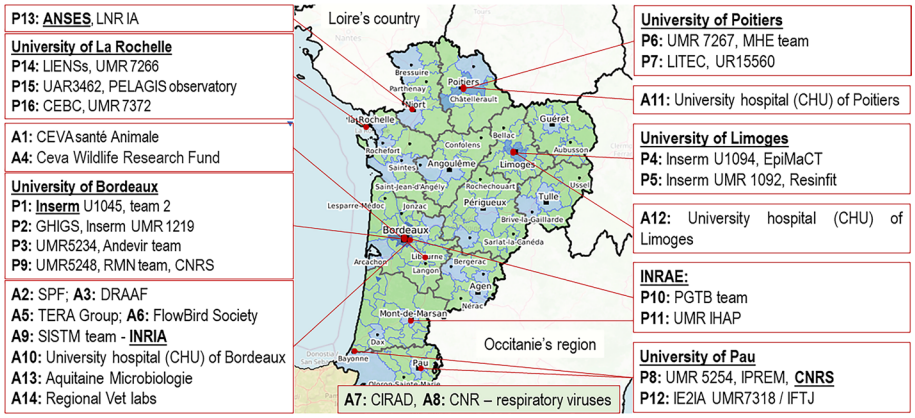

Fig. 3 EMERG consortium composition (P: Partner, refers to institutionally granted teams; A: Actor, i.e., institutional groups or private societies without grant and possibly with service) **P1**: L. Delhaes, T Trian, B. Defaye, E. Enaud & P. Berger (Inserm U1045 - Team 2); **P2**: D. Malvy, A. Duvignaud, J. Poublan & L. Altman (GHIGS-Inserm UMR 1219/ IRD EMR 271); **P3**: M-L. Andreola & M. Métifiot (UMR5234 - Andevir Team); **P4**: A. Mercier & H. Yéra (Inserm U1094/ IRD UMR270: EpiMaCT, CHU Limoges); **P5**: S. Hantz & S. Alain (Inserm UMR 1092, Resinfit team); **P6**: C. Imbert, G. Chauvin, M. Girardot, E. Perraud & L. Deroche (UMR 7267 - MHE team, CHU de Poitiers); **P7**: C. Bodet, N. Lévêque & M. Garcia (LITEC - UR15560, CHU de Poitiers); **P8**: C. Cravo-Laureau (IPREM - UMR 5254); **P9**: A. Loquet & M. Berbon (UMR5248, RMN team); **P10**: O. Lepais & E. Guichoux (PGTB team - Inrae); **P11**: J-L. Guérin, T. Vergne & G. Le Loc'h (UMR IHAP - Inrae); **P12**: A. Bourrel, P. Zavoli (IE2IA - UMR 7318, IFTJ); **P13**: N. Eterradossi, G. Salvat (ANSES, LNR IA); **P14**: H. Agogué, (A) L. Lacerda, M. Paoletti, P. Pineau & J. Jourde (LIENSs, UMR 7266); **P15**: J. Spitz & S. Wund (UAR3462, PELAGIS observatory); **P16**: J. Moreau & K. Monceau (CEBC, UMR7372); **A1**: G. Dauphin, H. Karembe & V. Kaltsatos (CEVA santé animale); **A2**: L. Filleul & S. Bertrand-Stoekel (Santé Public France (SPF) department); **A3**: V. Alavoine (DRAFF); **A4**: H. Karembe (Ceva Wildlife Research Fund); **A5**: P. Kaluzni (Tera Group); **A6**: J. Stefanello (FlowBird society); **A7**: C. Hautefeuille (CIRAD); **A8**: (B) Lina, L. Josset, V. Escuret (National Reference Center (CNR) for respiratory viruses); **A9**: M. Alvalos Fernandez (SISTM team - INRIA); **A10**: D. Malvy, D. Nguyen, T. Pistone, P. Perreau, S. Burrel, M-E. Lafon, L. Delhaes & S. Imbert (University Hospital of Bordeaux); **A11**: University Hospital of Poitiers; **A12**: University Hospital of Limoges; **A13**: F. M'Zali (Aquitaine Microbiologie society); and **A14**: Regional Vet Lab of counties N°24, 40, 64 & 79. The names of the regional public institutions involved in scientific research are in bold underlined; non-regional research institutions with a recognized expertise in EMERG research field are associated as actor (**A7**, **A8**) with their names framed in green

intelligence are under development by the EMERG consortium, especially regarding HPAI risk and the corresponding microbiome eco-exposome.

4.2 Main research topics addressed in the EMERG project

4.2.1 From AIV to HPAIV in Nouvelle-Aquitaine

Avian influenza (AI) is a highly contagious viral infection affecting all species of birds, whether wild, captive, or farmed [50]. AIVs are RNA-viruses with a segmented genome (genus *Alphainfluenzavirus*, family *Orthomyxoviridae*) that undergo frequent mutations and reassortment events, leading to high diversity [20]. As a result, AIVs exist as a variety of genotypes, which are grouped into subtypes defined by the combination of their surface antigens: AI haemagglutinin (H1 to H16 in birds) and neuraminidase (N1 to N9 in birds) antigens. Reflecting their genetic diversity, AIVs also vary in their pathogenicity for birds, ranging from low-pathogenicity AI to high-pathogenicity AI (HPAIV), with the latter essentially limited to the H5 and H7 subtypes and capable of causing mass mortality. Since 1996, AI ecology has been characterized by the panzootic diffusion of H5Ny HPAIV; the current most widespread descent is the 2.3.4.4b H5 lineage. The major epidemiological changes linked with the H5 HPAIV panzootic include the following:

(i) The multiplication and geographical shift of epizootics caused by H5Ny viruses of decreasing Gs/Gd from Asia in 2003-04 to Europe, Africa, North America, and most recently (2023-24), South America and even Antarctica [51, 52];

(ii) A seasonal shift in HPAIV epizootics with the virus becoming entrenched in nonmigratory birds (including those of waterfowl) or in domestic poultry species that may maintain the HPAIV risk for introduction into or circulation even during intermigratory seasons, as observed in France and NA (Fig. 4);

(iii) Introduction of HPAIV in colony-bred seabirds, even in remote ecological environments, with a possible devastating ecological impact on biodiversity and sometimes endangered animal species [18, 53];

(iv) Since 2022, increased exposure of mammals through contact with infected birds, either in wild mammals preying on or scavenging diseased birds (e.g., foxes, bears) or sharing the habitat of contaminated birds (e.g., sea lions), or in mammalian species exposed to the virus through the contaminated farming environment [21].

Given the ability of some AIV subtypes (e.g., H9, H7, H5, and H10) to be occasionally transferred to mammals [54–56] and given that their high genetic variability contributes to virus–host transmission [19, 57], increased fitness of AIV for new mammalian hosts may occur, potentially in NA. Recently, this transmission was observed in dairy cows in the USA, where the B3.13 genotype of the H5 2.3.4.4b HPAIV was supposedly introduced in a single event on a dairy farm, in late 2023 or early 2024, as supported by phylogenetic evidence. This genotype was then likely spread between cows via shared milking equipment and movements of infected cows, up to more than 860 dairy farms (as of December 2024), resulting in human and cat cases exposed to infected bovines or raw milk [21, 58, 59].

These repeated introductions or sustained transmissions of AIVs in mammalian populations may ultimately result in an AIV-derived virus circulating in the new host population, with limited preexisting immunity (as is currently the case with H5Ny viruses, since this subtype does not normally infect mammals). Finally, the threatening event addresses the debatable risk of importing HPAIV variants to Europe during North Pole waterfowl migration, which represents the only avian migration route connecting the American continent to Europe. This situation has been proposed as a potential risk for a

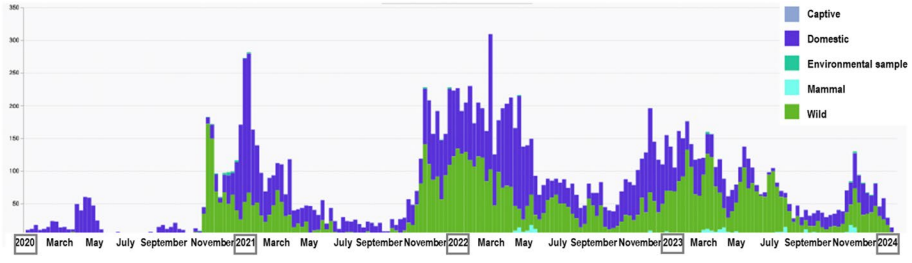

Fig. 4 Timeline of the number of HPAIV outbreaks from 2020 to the present, coloured by type of animal and environmental sample. This includes the outbreaks reported to the World Organization for Animal Health (WOAH) via the World Animal Health Information System (WAHIS) platform and to national authorities as gathered by the Food and Agricultural Organization Emergency Prevention System Interface (EMPRES-i) (https://www.offlu.org/wp-content/uploads/2024/02/February2024-VCM-OFFLU-Avian.pdf). Note, *(i)* the seasonal pattern linked with inc reasing reports in domestic and wild birds (dark blue and green, respectively) during the fall and winter months, corresponding to the AIV season in the Northern Hemisphere; *(ii)* the significant global increase in summer reports starting with summer 2021; and *(iii)* the increasing number of reports in mammals (light blue) since summer 2021

new pandemic [56]. Given the importance of human and veterinary public health, infections in poultry caused by HPAIV are notifiable and regulated worldwide. Currently, the massive epizootics caused by clade 2.3.4.4b H5 HPAIV have attracted increasing interest for vaccination, which was introduced under European Regulation 2016/429 [60] and guided by surveillance protocols established in Delegated Regulation 2023/361 [61]. In France, vaccination against H5 2.3.4.4b virus in duck farms was adopted in October 2023; a strategy that combined biosecurity measures to limit poultry exposure to wild bird viruses has helped reduce the disease burden compared with that in previous years, especially in NA [62].

The NA region is included in three major overlapping migratory flyways of the western Palearctic (Fig. 2) and hosts more than 50% of French duck farms, with a significant proportion being bred with free range access for several weeks. The implementation of the EMERG project in the NA region, therefore, provides a unique opportunity to investigate AIV circulation at the human–poultry–environment interface and to evaluate how recently introduced vaccination strategies may influence the ecology of H5 HPAIV in this context.

4.2.2 West nile and Usutu viruses: two viruses newly emerged in Nouvelle-Aquitaine

WNV and USUV are two zoonotic avian orthoflaviviruses that are maintained in enzootic cycles between birds and mosquitoes, posing threats to both public and veterinary health in Europe, and recently, in NA. Native to Africa, they were introduced in Europe through import corridors driven by migratory birds [23, 63, 64]. Both viruses overlap in terms of geographic range, mosquito vector species and the amplification of resident avian hosts [23, 41, 65, 66]. As incidental dead-end hosts, humans and horses do not develop viremia with a sufficient viral load to spread the disease. Although WNV has a greater public health impact than USUV does (due to its higher incidence of severe human disease, broader geographical spread, and possibly better-established surveillance and reporting systems), both viruses can be transmitted to humans through mosquito bites, which can lead to neuroinvasive and potentially fatal diseases. Notably, WNV can also be transmitted through blood donations and organ transplants. The high proportion of asymptomatic infections caused by these viruses and their cryptic enzootic circulation make their early detection in the environment challenging. In France, both the European and African genotypes of USUV and lineages 1 and 2 of WNV are now circulating in endemic cycles mainly in the circum-Mediterranean basin, occasionally causing infections in humans, equids, and birds. By the end of the summer of 2022, WNV unexpectedly emerged on the Atlantic coast of France (NA), first in equids, indicating substantial WNV and USUV circulations [23, 49, 67]. Hence, serological evidence of WNV circulation was reported in Gironde County in the NA region, with the detection of an acute infection (the presence of IgM- and IgG-specific antibodies) in 3 symptomatic horses in October 2022, coincident with a human case of USUV with no travel history outside the region. To monitor the spread of WNV and USUV in NA, studies were conducted to assess the seroprevalence levels in horses and the prevalence of viral genomes in birds and mosquitoes before the 2023 transmission season. The equine seroprevalence study revealed a heterogeneous distribution of specific anti-WNV IgG antibodies across the territory [68], with an average prevalence of 6.4%, close to that

reported in equids after the 2000 outbreak that occurred in the historical circulation area of Camargue in the southeastern Mediterranean region of France [69].

The ecological factors underlying the emergence of WNV and USUV in the NA region remain partly unresolved. A link with the migration of birds (Figs. 1 and 2), which are reservoirs for these viruses, can reasonably be suggested and will be documented through the EMERG project. The largest forest megafire that has ever been recorded in the NA area, in 2022 (Fig. 1), may have destroyed natural buffer zones and displaced bird populations [36, 37]. Although early findings were limited to a few confirmed equine cases, this unexpected EID event challenged prior assumptions that virus circulation in France was restricted to the Mediterranean Basin. This date clearly marked a turning point in the epidemiology of these viruses in France and foreshadowed an increase in cases the following year. By 2023, the newly recognized epidemic cluster of the NA region included 15 symptomatic human cases (two severe neuroinvasive infections), 26 asymptomatic infections identified among blood donors, and 31 equine cases (including two deaths). Interestingly, phylogenetic analysis revealed that the strains detected in NA belonged to WNV Lineage 2 and were distinct from strains isolated in Provence-Alpes-Côte d'Azur [69]. WNV sequences from NA exhibit significant phylogenetic diversity, indicating two possible scenarios: *(i)* the virus may have circulated cryptically in the region for several years before its first detection in 2022, or *(ii)* it has been repeatedly introduced from another area where it is locally maintained. Notably, WNV strains of NA are genetically similar to the strains that circulated in southern Spain in 2024, suggesting a potential route of introduction into that neighbouring country. These strains were associated with the Spanish first autochthonous human case of neuroinvasive disease caused by WNV Lineage 2 [70]. Even more recently, the WNV sub-lineage 2 strains of NA were evidenced to be causative of the cluster that occurred in Ile-de -France region and Paris in summer 2025 [71]. By 2025, transdisciplinary EMERG program efforts were prioritized to gain an understanding of multiple potential factors, such as climate and ecological changes, urban fringes and landscape uses, migratory bird routes, host and vector abundances, microbial eco-exposome, and factor dynamics, as well as of weak epidemiological signalling significance for mitigation [72]. This effort was implemented in the context of global changes and of the always-heavy burden in neighbouring southern European settings where endemic-epidemic transmission continues despite substantial resource allocation [16, 73].

4.2.3 Antimicrobial resistance: a one health concern focused on fungal resistance

Among microorganisms, fungi have recently emerged as critical pathogens, with species such as *C. auris* raising concerns because of their emerging nature and multidrug resistance profile. Several yeasts and moulds (*Candida albicans*, *C. auris*, and *Aspergillus fumigatus*) were ranked as critical priority pathogens by the WHO in 2022 [74]. In 2024, human mycoses accounted for 9% of acquired nosocomial infections in NA, which may be related to the fungicide exposure in NA, since open source data indicate that Gironde (part of NA) is the French region with the highest pesticide consumption; 3,038 tons of phytosanitary products –primary fungicides (e.g., sulphur and fosetyl-aluminium)– are being purchased, potentially because of its high concentration of vineyards. The One Health approach proposed by the project is essential for understanding the emergence of these fungal species, their relationships with other microorganisms as part of the

microbial eco-exposome, and addressing antimicrobial resistance (AMR), a global issue referred to as a "silent pandemic" [75]. AMR complicates the treatment of infections in humans and animals, increasing the risk of disease spread, severe illness and death [75, 76]. Fungal antimicrobial resistance (fAMR) has become a growing concern for human and animal health and food safety [26, 27, 77].

During the past decade *C. auris* has emerged as a pathogenic yeast [78] and exhibits multidrug resistance regardless of clade or geographical location [27, 79]. However, its environmental cycle remains poorly explored and understood, despite its remarkable genomic plasticity under stressors such as high salinity (10% NaCl) or elevated temperature (42 °C) [43, 80, 81]. Recent studies suggest that global temperature changes may have enabled species such as *C. auris* to adapt and thrive in warmer climates [82]. Therefore, in the context of NA, identifying potential environmental niches and reservoirs such as birds is crucial for developing effective epidemiological and management strategies. Although other *Candida* species (*C. albicans*, *C. parapsilosis*, *C. glabrata*, and *C. tropicalis*) are frequently isolated from various samples (soils, plants, water, and animals, including migratory birds) [43], the links between their environmental cycles and pathogenicity remain underexplored while they may exhibit fAMR traits [27, 77].

fAMR has also emerged in filamentous fungi, particularly *A. fumigatus*, with increasing resistance to azole antifungals, a concern under the One Health framework, as aspergillosis affects both humans and animals [26, 27, 83]. Monitoring fAMR has become a major issue, potentially linked to environmental exposure from fungicide use, which represents a dual-use antifungal challenge (i.e., shared azoles in agriculture and medicine leading to cross-resistance) [26, 27].

As new fungal species may emerge and several viral coinfections have been described (e.g., virus-associated pulmonary aspergillosis (VAPA)) [84, 85], exploring the pathogenicity factors of *Candida* and *Aspergillus* across diverse habitats (aquatic, terrestrial, anthropized, animal, or human environments) is critical. Certain environments may promote fungal persistence, diverse exposure routes (fungal eco-exposomes), and the expression of resistance genes and well-known pathogenicity factors (e.g., adherence and biofilm formation). The project and consortium aim to document the emergence and links between *Candida* and *Aspergillus* isolates circulating in NA among humans, animals and environments and their corresponding fAMR profiles. It is characterizing strains from the EMERG biocollection (samples from coastal wetlands, saltworks, air samples, and migratory birds crossing the NA region; Fig. 5), exploring factors directly or indirectly related to fAMR (e.g., biofilm formation, thermotolerance, protease and phospholipase activities) and analysing the minimal inhibitory concentrations of antifungal agents used in human and veterinary medicine as well as agriculture. Potential links between other EIDs, especially viral EIDs, and fungal eco-exposomes are also being investigated.

Taken together, these research efforts address the circulation of multiple pathogens (from viruses to fungi) and EID risk in a transdisciplinary way, which may help provide stakeholders and national surveillance systems with knowledge at the community–level to optimize prevention and control strategies.

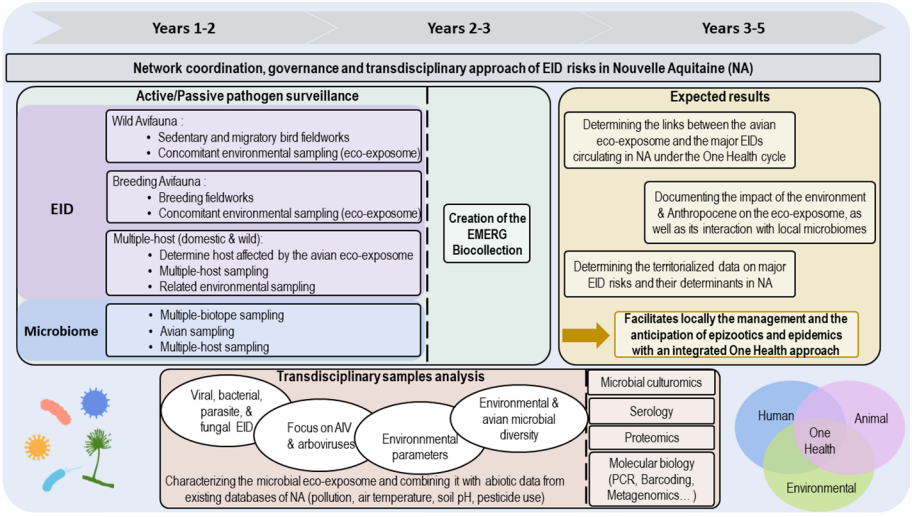

Fig. 5 Schematic representation of the specific scientific actions planned for the EMERG project, expected results, and timeline (in year) for reaching the milestones along with the biological methods deployed for transdisciplinary sample analysis

5 Implications, limitations, and future directions

5.1 Implications and achievements

France has launched national and local surveillance initiatives to respond to threatening EIDs, but gaps persist in data dissemination between national and local levels. Beyond the formal labels of academic frameworks (One Health, Planetary Health or Eco-Health), strengthening coordination is essential to shift from reactive to proactive responses, enabling early implementation of measures to protect human, animal and environmental health. Operational research must prioritize transdisciplinary approaches to support this paradigm shift.

A pilot initiative of the EMERG program in 2023 illustrated how the NA region transitioned the effort from a concept to an operational strategy in response to emerging zoonotic arboviral diseases. By bringing together regional and national partners, each expert in their own fields, to produce integrated scientific data in the human, veterinary, entomological and environmental fields, this effort aimed to support evidence-based decision-making to mitigate the spread of WNV. Innovative entomological and environmental surveillance tools (specific mosquito traps [67, 69]) successfully identified hidden WNV circulation and viral genetic identity in NA, accelerating the detection of infection hotspots and enabling targeted public health interventions.

Other events in NA, such as the circulation of HPAIVs/AIVs since 2020 and norovirus outbreaks linked to intense rainfall on NA seaboards by late 2023, highlight the complex interactions among climate change, ecological shifts, and pathogen emergence. The detection of HPAIV H5N1 in sub-Antarctic and Antarctic regions underscores the global threat to biodiversity locally and the pandemic risk internationally [86]. Norovirus clusters in 2023 further illustrated the impact of extreme weather on sewage treatment systems and pollution in coastal areas, including oyster farms [30, 33].

In response to these events, the EMERG project is an integrated regional research initiative designed to characterize pathogen emergence from viruses to fungi, explore the role of the microbial eco-exposome, and understand the determinants of EID dynamics. Researchers from diverse fields (Fig. 3) collaborate to promote transdisciplinarity.

Teams studying HPAIV, arboviruses, *Toxoplasma*, bacteria, archaea, and fungi have expanded the number of candidate animal species as natural reservoirs for these pathogens, contributing to the debate on biodiversity–disease relationships. A first pilot study focused on wild avifauna and environmental samples along migratory corridor of NA (i.e., first step of eco-exposome analysis) was performed between April and July 2024, and screened for WNV/USUTUV, AIV, and fungal carriage (Table 1). All captured birds were negative for WNV/USUTUV and for AIV screening based on anti-WNV immunoglobulin G antibodies detection on blood samples [67] and on M gene for pan-AIV detection by rt-PCR performed on faeces or cloacal samples [50], respectively. Soil samples were concomitantly sampled and screened negative for AIV using pan-AIV rt-PCR [50]. Both, avifauna and environmental samples were screened for fungal growth using culturomics method with Maldi-Tof identification [87]. Several faeces and cloacal samples were positive for fungal detection: *Candida auris* was not isolated in this avifauna population captured in NA in 2024, neither in the soil samples. Eight birds (all belonging to order of Passeriformes) were colonized with *Aspergillus fumigatus* as well as nine soil samples (those isolates being currently investigated for fAMR) (Table 1). From this pilot study, another larger study has been designed and is currently ongoing.

5.2 Challenges and limitations

This consortium emphasizes the role of regional climatic dynamics in EID, including vector-borne diseases, food/water-driven infections, AMR and interactions with coastal/continental avian migration routes, while environmental and demographic factors are considered.

In practice, the diverse environment of NA, which is impacted by anthropogenic pressures and climatic disruption, makes it a critical region for pathogen emergence. The EMERG project and consortium combine the One Health approach with the microbial eco-exposome concept to decipher current and future EIDs, with a focus on human–animal–environment interactions (Fig. 5). Considering spillover management activities from the perspective of the One Health cycle, as recently proposed [88], they analyse EID risks using the classic model of zoonotic disease prevention: detection, control, and early prediction (Fig. 6), all of which are linked to the eco-exposome concept [6]. Fieldwork will integrate data from wild and farmed avifauna (e.g., faeces and feather samples, as well as parameters specific to migratory birds such as bird age, morphology, migratory roads and hotspots, and breeding areas), environmental samples (microbial eco-exposome of soil, water, and air samples), and surveillance databases (pollution, temperature, and fungicide indices in NA). Biological methods, including culturomics and proteomics for fungal and bacterial isolations, secured viral cultures, and molecular techniques (PCR, metagenomics), will be employed to study a variety of EIDs. This will enable the consortium to study and compare EID risks in avifauna (AIV-HPAIV infections) and other animals (horses in WNV/USUV investigations) in their close environments (e.g., deciphering VAPA relevance in the One Health context) and ultimately in humans. The methods employed are mastered by at least one member of the consortium and are presented in Fig. 5, which summarizes the specific actions, expected results, and main timelines of the project. The project will translate operational research findings into policies, control measures and biosecurity actions at the local level. A tiered alert system facilitates prompt decision-making among health authorities, veterinary

Table 1 Viral and fungal analysis of blood, faeces and cloacal samples from avifauna (each bird was captured between April and July 2024, and identified by its reference ring) and of environmental (soil) samples collected at the end of May 2024 along the bird migration corridor of Nouvelle Aquitaine (NA)

Type of samples	Coordinates (Latitude; Longitude)	Blood sample	Faeces or cloacal sample	
		WNV/ USUTUV detection by serology	AIV detection by rt-PCR	Fungal detection by cultures after incubation at 30 °C & 37 °C quantified as CFU/mL or CFU/g*
Avifauna analysis: Type of sampled birds grouped in orders and species with (Migratory behaviour), number of captured birds				
Bucerotiformes				
Upupa epops (Migratory), *n*=1	49.3140652; 0.4670513	/	Negative	At 30 °C: Moulds (50 CFU/mL) - At 37 °C: Yeasts (*Metshnikowia pulcherima*: 50 CFU/mL)
Columbiformes				
Columba palumbus (Migratory), *n*=2	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
Streptopelia decaocto (Sedentary), *n*=3	46.1631972; −0.2974212	/	Negative	At 30 °C: Moulds (*Aspergillus pseudoglaucus*: 50 CFU/mL) & Yeasts (*Rhodotorula mucilaginosa*: 100 CFU/mL) - At 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
Streptopelia turtur (Migratory), *n*=1	46.1631972; −0.2974212	/	Negative	At 30 °C: Moulds (*Aureobasidium pullulans*: 650 CFU/mL) & Yeasts (*R. mucilaginosa*: 100 CFU/mL) At 37 °C: Negative
Passeriformes				
Anthus trivialis (Migratory), *n*=1	46.2374047; −0.3480075	/	Negative	At 30 °C & 37 °C: Negative
Carduelis carduelis (Migratory), *n*=6	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.2353984; −0.4099026	/	Negative	At 30 °C & 37 °C: Negative
	46.2353984; −0.4099026	/	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	46.1745396; −0.4541719	Negative	Negative	At 30 °C & 37 °C: Negative
Emberiza cirlus (Sedentary), *n*=5	46.2374047; −0.3480075	/	Negative	At 30 °C: Negative – At 37 °C: Moulds (*Aspergillus fumigatus*: 150 CFU/mL)
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	46.1745396; −0.4541719	Negative	Negative	At 30 °C: Moulds (*Cladiosporium cladoporiodes*: 50 CFU/mL) - At 37 °C: Yeasts (*Meyerozyma guillermondii*: 50 CFU/mL)
	46.1745396; −0.4541719	/	Negative	At 30 °C & 37 °C: Negative

Table 1 (continued)

Type of samples	Coordinates (Latitude; Longitude)	Blood sample	Faeces or cloacal sample	
		WNV/ USUTUV detection by serology	AIV detection by rt-PCR	Fungal detection by cultures after incubation at 30 °C & 37 °C quantified as CFU/mL or CFU/g*
	46.1631972; −0.2974212	Negative	Negative	At 30 °C & 37 °C: Negative
Erithacus rubecula (Migratory), *n*=12	46.1967223; −0.4190926	Negative	Negative	At 30 °C & 37 °C: Negative
	46.2274946; −0.4816043	/	Negative	At 30 °C & 37 °C: Negative
	46.1745396; −0.4541719	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.2595794; −0.3466615	/	Negative	At 30 °C: Moulds (*Penicillium sizovae*: 50 CFU/mL) - At 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.2148443; −0.5534316	/	Negative	At 30 °C & 37 °C: Negative
	46.2274946; −0.4816043	/	Negative	At 30 °C: Moulds (Mucor sp.: 50 CFU/mL) - At 37 °C: Negative
	46.2274946; −0.4816043	/	Negative	At 30 °C: Negative - At 37 °C: Yeasts (*M. guillermondii*: 50 CFU/mL)
Hirundo rustica (Migratory), *n*=2	46.1631972; −0.2974212	/	Negative	At 30 °C: Moulds (*Mucor circinelloides*: >1000 CFU/mL) - At 37 °C: Moulds (*M. circinelloides*: 1000 CFU/mL) & Yeasts (*M. guillermondii*: 50 CFU/mL)
	46.1631972; −0.2974212	/	Negative	At 30 °C: Moulds (*M. circinelloides*: >1000 CFU/mL) - At 37 °C: Moulds (*M. circinelloides*: 1000 CFU/mL)
Passer domesticus (Sedentary), *n*=22	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative

Table 1 (continued)

Type of samples	Coordinates (Latitude; Longitude)	Blood sample	Faeces or cloacal sample	
		WNV/ USUTUV detection by serology	AIV detection by rt-PCR	Fungal detection by cultures after incubation at 30 °C & 37 °C quantified as CFU/mL or CFU/g*
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.1875362; −0.2536718	Negative	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
Phylloscopus collybita (Migratory), *n*=1	46.1875362; −0.2536718	/	Negative	At 30 °C: Moulds (*Mucor hiemalis*: 550 CFU/mL) - At 37 °C: Negative
Prunella modularis (Migratory), *n*=7	46.1745396; −0.4541719	/	Negative	At 30 °C & 37 °C: Negative
	46.2353984; −0.4099026	/	Negative	At 30 °C & 37 °C: Negative
	46.2299425; −0.5845503	/	Negative	At 30 °C & 37 °C: Negative
	46.2020843; −0.3206741	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.1875362; −0.2536718	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
Sylvia atricapilla (Migratory), *n*=28	46.1745396; −0.4541719	Negative	Negative	At 30 °C & 37 °C: Negative
	46.2374047; −0.3480075	/	Negative	At 30 °C & 37 °C: Negative
	46.2374047; −0.3480075	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.2353984; −0.4099026	/	Negative	At 30 °C & 37 °C: Negative
	46.2299425; −0.5845503	/	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	46.1875362; −0.2536718	/	Negative	At 30 °C & 37 °C: Negative
	46.2020843; −0.3206741	/	Negative	At 30 °C & 37 °C: Negative
	46.2020843; −0.3206741	/	Negative	At 30 °C & 37 °C: Negative
	46.2353984; −0.4099026	/	Negative	At 30 °C & 37 °C: Negative
	46.2274946; −0.4816043	/	Negative	At 30 °C & 37 °C: Negative
	46.2274946; −0.4816043	/	Negative	At 30 °C & 37 °C: Negative

Table 1 (continued)

Type of samples	Coordinates (Latitude; Longitude)	Blood sample	Faeces or cloacal sample	
		WNV/ USUTUV detection by serology	AIV detection by rt-PCR	Fungal detection by cultures after incubation at 30 °C & 37 °C quantified as CFU/mL or CFU/g*
	46.2274946; −0.4816043	/	Negative	At 30 °C & 37 °C: Negative
	46.2274946; −0.4816043	/	Negative	At 30 °C & 37 °C: Negative
	46.2374047; −0.3480075	/	Negative	At 30 °C & 37 °C: Negative
	46.1745396; −0.4541719	/	Negative	At 30 °C & 37 °C: Negative
	46.1745396; −0.4541719	Negative	Negative	At 30 °C & 37 °C: Negative
	46.1745396; −0.4541719	/	Negative	At 30 °C & 37 °C: Negative
	46.1745396; −0.4541719	/	Negative	At 30 °C & 37 °C: Negative
	46.1745396; −0.4541719	Negative	Negative	At 30 °C & 37 °C: Negative
	46.1745396; −0.4541719	/	Negative	At 30 °C & 37 °C: Negative
	46.2353984; −0.4099026	Negative	Negative	At 30 °C: Moulds (450 CFU/mL) - At 37 °C: Negative
	46.2353984; −0.4099026	Negative	Negative	At 30 °C: Negative - At 37 °C: Moulds (*A.* fumigatus: 450 CFU/mL)
	46.2353984; −0.4099026	Negative	Negative	At 30 °C & 37 °C: Negative
	46.1875362; −0.2536718	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
Sturnus vulgaris (Migratory), *n*=5	46.2274946; −0.4816043	/	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
Sylvia communis (Migratory), *n*=1	46.2299425; −0.5845503	/	Negative	At 30 °C & 37 °C: Negative
Turdus merula (Partial migratory), *n*=55	46.1745396; −0.4541719	/	Negative	Insufficient quantity to perform cultures
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	46.2274946; −0.4816043	/	Negative	At 30 °C & 37 °C: Negative
	46.2274946; −0.4816043	/	Negative	At 30 °C & 37 °C: Negative
	46.2274946; −0.4816043	/	Negative	At 30 °C & 37 °C: Negative

Table 1 (continued)

Type of samples	Coordinates (Latitude; Longitude)	Blood sample	Faeces or cloacal sample	
		WNV/ USUTUV detection by serology	AIV detection by rt-PCR	Fungal detection by cultures after incubation at 30 °C & 37 °C quantified as CFU/mL or CFU/g*
	46.2374047; −0.3480075	/	Negative	At 30 °C & 37 °C: Negative
	46.2374047; −0.3480075	/	Negative	At 30 °C & 37 °C: Negative
	46.2374047; −0.3480075	/	Negative	At 30 °C: Moulds (*A. fumigatus*: 150 CFU/mL) - At 37 °C: Moulds (*A. fumigatus*: 100 CFU/mL)
	46.1967223; −0.4190926	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.2353984; −0.4099026	/	Negative	At 30 °C & 37 °C: Negative
	46.2353984; −0.4099026	/	Negative	At 30 °C & 37 °C: Negative
	46.2353984; −0.4099026	/	Negative	At 30 °C & 37 °C: Negative
	46.2299425; −0.5845503	/	Negative	At 30 °C & 37 °C: Negative
	46.2299425; −0.5845503	/	Negative	Insufficient quantity to perform cultures
	46.1631972; −0.2974212	/	Negative	At 30 °C: Moulds (*A. fumigatus*: 50, *Penicillium sp.*: 50, *Talaromyces purpureogennus*: 50 CFU/mL) - At 37 °C: Moulds (*T. purpureogennus*: 50 & Talaromyces soli 50 CFU/mL)
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C: Moulds (*Purpureocillium lilacinum*: 50 CFU/mL & Yeasts (*Yarrowia lipolytica*: 350 CFU/mL) - At 37 °C: Yeasts (*Candida parapsilosis*: 50 CFU/mL)
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	Insufficient quantity to perform cultures
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.1875362; −0.2536718	/	Negative	At 30 °C & 37 °C: Negative
	46.1875362; −0.2536718	/	Negative	At 30 °C & 37 °C: Negative
	46.1631972; −0.2974212	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.2595794; −0.3466615	/	Negative	At 30 °C & 37 °C: Negative

Table 1 (continued)

Type of samples	Coordinates (Latitude; Longitude)	Blood sample	Faeces or cloacal sample	
		WNV/ USUTUV detection by serology	AIV detection by rt-PCR	Fungal detection by cultures after incubation at 30 °C & 37 °C quantified as CFU/mL or CFU/g*
	46.2595794; −0.3466615	/	Negative	At 30 °C & 37 °C: Negative
	46.2595794; −0.3466615	/	Negative	At 30 °C & 37 °C: Negative
	46.2595794; −0.3466615	/	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	/	Negative	At 30 °C & 37 °C: Negative
	46.2353984; −0.4099026	/	Negative	At 30 °C & 37 °C: Negative
	46.2148443; −0.5534316	/	Negative	At 30 °C & 37 °C: Negative
	46.2274946; −0.4816043	/	Negative	At 30 °C: Moulds (*A. fumigatus*: 150 CFU/mL) - At 37 °C: Moulds (*A. fumigatus*: 50 CFU/mL)
	46.2274946; −0.4816043	/	Negative	At 30 °C: Negative - At 37 °C: Moulds (*A. fumigatus*: 2000 CFU/mL)
	46.1745396; −0.4541719	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
	46.1967223; −0.4190926	Negative	Negative	At 30 °C & 37 °C: Negative
	46.1875362; −0.2536718	Negative	Negative	At 30 °C & 37 °C: Negative
	46.1875362; −0.2536718	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C: Moulds (*M. circinelloides*: 100 CFU/mL) & Yeasts (*Candida albicans* 150, *Y. lipolytica*: 200, *R. muciloginosa*: 650 CFU/mL) - At 37 °C: Moulds (*M. circinelloides*: 50 CFU/mL) & Yeasts (*Pichia kluyveri*: 50, *R. muciloginosa*: 50 CFU/mL)
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C & 37 °C: Negative
	49.3140652; 0.4670513	Negative	Negative	At 30 °C: Yeasts (*M. pulcherrima*: 2000, *Hanseniaspora uvarum*: 2000, *P. kluyveri*: 2000 CFU/mL) - At 37 °C: Yeasts (*M. pulcherrima*: 200, *P. kluyveri: 14*000 CFU/mL)
	49.3140652; 0.4670513	Negative	Negative	At 30 °C: Negative - At 37 °C: Yeasts (*M. pulcherrima*: 100, *H. uvarum* 150 CFU/mL)
	46.2595794; −0.3466615		Negative	At 30 °C: Negative - At 37 °C: Moulds (*A. fumigatus*: 100 CFU/mL)
Turdus philomelos (Migratory), *n*=2	46.1745396; −0.4541719	Negative	Negative	At 30 °C: Yeasts (200 CFU/mL) - At 37 °C: Moulds (*A. fumigatus*: 50 CFU/mL)
	46.2274946; −0.4816043		Negative	At 30 °C & 37 °C: Negative

Table 1 (continued)

Type of samples	Coordinates (Latitude; Longitude)	Blood sample	Faeces or cloacal sample	
		WNV/ USUTUV detection by serology	AIV detection by rt-PCR	Fungal detection by cultures after incubation at 30 °C & 37 °C quantified as CFU/mL or CFU/g*
Eco-exposome analysis: Soil samples collected concomitantly along the bird migration corridor of Nouvelle Aquitaine (NA)				
S1: Gamarde-les-bains	43.716167; −0.8591667	/	Negative	At 30 °C: Moulds (*A. fumigatus*: 7000, *Aspergillus welwitschiae*: 1500, *M. circinelloides*: 1500 CFU/g) & Yeasts (3450, *C. tropicalis:* 50 CFU/g) At 37 °C: Moulds (*A. fumigatus*: 20500, *A. welwitschiae*: 500 CFU/g)
S3: Orgambidesca pass	43.0436667; −1.026	/	Negative	At 30 °C: Moulds (250 CFU/g) - At 37 °C: Moulds (3000 CFU/g)
S4: Iraty campground natural area	43.0372222; −1.0493889	/	Negative	At 30 °C: Moulds (*Penicillium sp*: 500, *M. hiemalis*: 150, other moulds 100 CFU/g) - At 37 °C: Moulds (*Aspergillus niger*: 50, *Penicillium sp*: 50, other moulds 1300 CFU/g)
S5: Miramar beach	43.4848056; −1.5589445	/	Negative	At 30 °C: Moulds (*Fusarium sp*: 50 CFU/g) & Yeasts: 650 CFU/g - At 37 °C: Negative
S6: Tarnos dunes	43.5553611; −1.5031111	/	Negative	At 30 °C: Moulds (*Aspergillus tubingensis*: 100, *M. circinelloides*: 50, other moulds 2700 CFU/g) & Yeasts (*M. guilliermondii*: 200, other yeasts: 50 CFU/g) At 37 °C: Moulds (*A. fumigatus*: 250, *A. flavus/orizae*: 100, other moulds: 2100 CFU/g)
S7: Around Orx Marshes national nature reserve	44.4325556; −1.3869722	/	Negative	At 30 °C: Moulds (*A. terreus*: 100, *Aspergillus subgen. Circumdati*: 250, other moulds: 250 CFU/g) At 37 °C: Moulds (*A. terreus*: 150, *Aspergillus alabamensis*: 50 CFU/g)
S8: Moliets beach	43.8533611; −1.3926389	/	Negative	At 30 °C: Moulds (250 CFU/g) - At 37 °C: Moulds (*A. fumigatus*: 50, other moulds: 50 CFU/g)
S9: Courant d'Huchet nature reserve	43.8870556; −1.3192222	/	Negative	At 30 °C: Moulds (*Penicillium sp.*: 1100, other moulds: 150) & Yeats (350 CFU/g) At 37 °C: Moulds (*A. alabamensis*: 100, *Penicillium sp.*: 200, other moulds: 1800) & Yeats (100 CFU/g)
S10: Mimizan beach	44.20875; −1.2993611	/	Negative	At 30 °C: Moulds (*Aspergillus insulicola*: 50, other moulds: 450 CFU/g) & Yeasts (150 CFU/g) At 37 °C: Negative

Table 1 (continued)

Type of samples	Coordinates (Latitude; Longitude)	Blood sample	Faeces or cloacal sample	
		WNV/ USUTUV detection by serology	**AIV detection by rt-PCR**	**Fungal detection by cultures after incubation at 30 °C & 37 °C quantified as CFU/mL or CFU/g***
S11: Aureilhan lake	44.222; −1.2058889	/	Negative	At 30 °C: Moulds (*Aspergillus brasiliensis*: 50 CFU/g) & Yeasts (250 CFU/g) At 37 °C: Moulds (*A. fumigatus*: 50, *A. welwitschiae*: 50, other moulds 250 CFU/g) & Yeasts (1100 CFU/g)
S12: Cazaux Sanguinet lake	44.4325556; −1.1783611	/	Negative	At 30 °C: Moulds (600 CFU/g) & Yeasts (100 CFU/g) At 37 °C: Moulds (500 CFU/g)
S13: Petit Nice beach	44.5605556; −1.2414722	/	Negative	At 30 °C: Moulds (*A. fumigatus*: 20, *Penicillium murcianum*: 20 CFU/g) - At 37 °C: Negative
S14: Salie beach	44.522; −1.25325	/	Negative	At 30 °C: Moulds (*Aspergillus felis*: 100, *P. murcianum*: 850, other moulds: 204050 CFU/g) At 37 °C: Moulds (*A. felis*: 100, other moulds: 104900 CFU/g)
S15: Teich bird sanctuary	44.6417778; −1.0201944	/	Negative	At 30 °C: Moulds (*A. fumigatus*: 5000, *Penicillium sp.*: 6000, other moulds: 5000) & Yeasts (1000 CFU/g) At 37 °C: Moulds (>500 CFU/g)
S16: Andernos pier beach	44.7397778; −1.1012778	/	Negative	At 30 °C: Moulds (*A. flavus*: 40, *Penicillium sp.*: 200, Mucorales: 20 CFU/g) & Yeasts (30 CFU/g) At 37 °C: Moulds (*Penicillium sp.*: 20 CFU/g) & Yeasts (40 CFU/g)
S17: Cap-Ferret beach	44.64875; −1.2443333	/	Negative	At 30 °C: Moulds (*A. fumigatus*: 100, *Penicillium coralligerum*: 100, other moulds: 500 CFU/g) & Yeasts (150 CFU/g) - At 37 °C: Negative
S18: Lacanau beach	45.0015833; −1.2024167	/	Negative	At 30 °C: Moulds (*Cladosporium allicinum*: 50 CFU/g) - At 37 °C: Negative
S19: Hourtin lake	45.0702222; −1.1408611	/	Negative	At 30 °C: Moulds (*Penicillium sp.*: 500, other moulds: 1050 CFU/g) & Yeasts (200 CFU/g) At 37 °C: Moulds (*T. soli*: 50, other moulds 100 CFU/g) & Yeasts (100 CFU/g)
S20: Cousseau pond	45.05025; −1.1241111	/	Negative	At 30 °C and 37 °C: Moulds (>500 CFU/g)
S21: Soulac-sur-mer beach	45.5183056; −1.1260278	/	Negative	At 30 °C: Moulds (*Penicillium sp.*: 400, other moulds: 150 CFU/g) - At 37 °C: Negative
S22: Royan beach	45.6079444; −1.00925	/	Negative	At 30 °C: Moulds (*Penicillium sp.*: 450, other moulds: 200 CFU/g) - At 37 °C: Negative
S23: Estuary of the Seudre river	45.79775; −1.1490556	/	Negative	At 30 °C: Moulds (*Aspergillus insuetus*: 300, *Penicillium sp.*: 150, other moulds: 1900 CFU/g) At 37 °C: Negative
S24: Embellie beach	45.7925; −1.2161944	/	Negative	At 30 °C: Moulds (*Penicillium sp.*: 350, other moulds: 350 CFU/g) & Yeasts (50 CFU/g) - At 37 °C: Negative

Table 1 (continued)

Type of samples	Coordinates (Latitude; Longitude)	Blood sample	Faeces or cloacal sample	
		WNV/ USUTUV detection by serology	AIV detection by rt-PCR	Fungal detection by cultures after incubation at 30 °C & 37 °C quantified as CFU/mL or CFU/g*
S25: Brouages marshes	45.8676111; −1.0721667	/	Negative	At 30 °C: Moulds (*M. hiemalis*: 500, other moulds 4500 CFU/g) & Yeasts (2000 CFU/g) - At 37 °C: Moulds (*A. alabamensis*: 50, *A. terreus*: 100, *A. fischeri*: 100, other moulds 1000 CFU/g) & Yeasts (50 CFUL/g)
S26: Mininimes beach	46.1417778; −1.1717222	/	Negative	At 30 °C: Moulds (*Penicillium sp.*: 100, other moulds: 350 CFU/g) & Yeasts (50 CFU/g) - At 37 °C: Negative
S27: Saint-Hilaire d'Arçais marshes	46.2761111; −0.7178056	/	Negative	At 30 °C: Moulds (*M. hiemalis*: 1000, *Penicillium sp.* 1500, other moulds 4500 CFU/g) & Yeasts (2000 CFU/g) At 37 °C: Moulds (*A. fumigatus*: 250, *M. circinelloides*: 150, other moulds 100 CFU/g)

*Micromycetes identification was performed using culturomics, with Maldi-Tof and MSI-2 database identification [86] (in absence of clear MSI-2 identification fungus was classified according to the macroscopy and microscopy characteristics at the genus level or as yeast or mould; quantification was estimated in Colony Unit Formans per mL of faeces or cloacal samples (CFU/mL) or per g of soil samples (CFU/g)

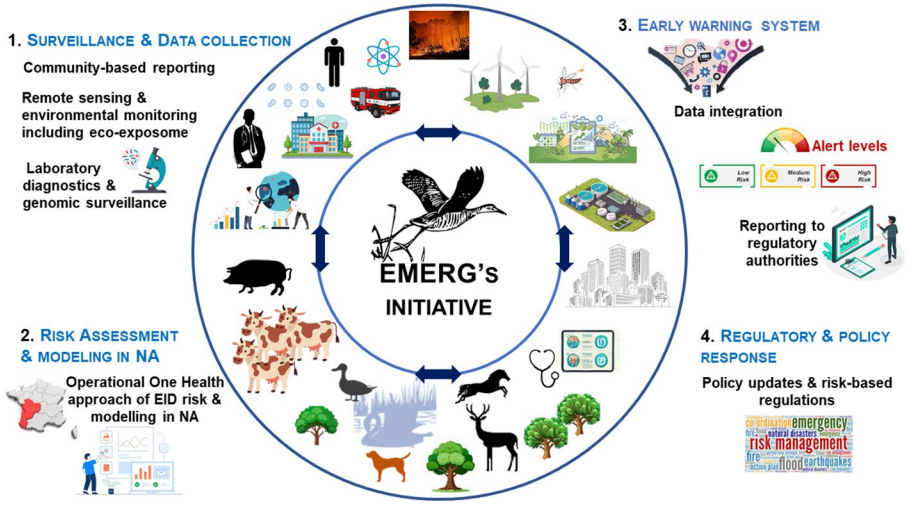

Fig. 6 Enhancing local management of EIDs through the EMERG initiative in Nouvelle-Aquitaine. The EMERG initiative leverages an integrated, community-based surveillance system for early case detection across humans, animals, and the environment. This approach facilitates real-time data sharing and predictive modelling, enabling swift identification and intervention before outbreaks escalate. Strengthening local One Health governance, with robust coordination between community-level stakeholders and national surveillance institutions, will ensure more effective disease prevention and control

services, and environmental agencies (Fig. 6). By fostering across-sector collaborations and risk-based regulations, it aims to mitigate health risks and develop long-term resilience against zoonotic and environmental threats. It will also establish a stakeholder consortium that includes academia, national and local institutions, and civil society (Fig. 3) and implement robust coordination between community-level stakeholders and national surveillance institutions which will lead to better EID preparedness (Fig. 6).

The EMERG project has several limitations. Its holistic approach requires the integration of multiple data sources that are not easy to merge, which will be addressed with support from the INRIA's bioinformatic partner. Strong transdisciplinary collaboration among national institutions, academia, stakeholders, and civil society is essential, but divergent priorities and institutional silos may hinder progress. In addition, aligning human, veterinary, and environmental agencies (each with distinct mandates) has the risk of fragmented efforts. To overcome these challenges, the consortium has defined leadership roles, established legal frameworks, and created data-sharing protocols to ensure secure, efficient exchanges while respecting privacy concerns at the human–animal–environmental interface (Fig. 5). This facilitates real-time EID monitoring and enhances regional response capabilities (Fig. 6). Wet laboratory limitations include restricted sample volumes and time constraints, particularly for wild avifauna. However, the EMERG biocollection and its standardized workflow among partners will help mitigate these issues (Fig. 5). While the microbial eco-exposome represents only a fraction of the overall exposome, the project focuses on microbial aspects because of their dual role in influencing EID transmission and putatively harbouring emerging pathogens [11].

5.3 Future directions

As experienced during the COVID-19 pandemic, EIDs can cause severe economic, societal, and health impacts when all four transmission steps are completed (introduction, interanimal transmission, animal-to-human transmission, and human-to-human transmission (Fig. 7)). However, public knowledge of zoonotic disease transmission remains limited, hindering education and global effort improvements [88]. Filling this knowledge gap is a major challenge, which the consortium will address by considering the multiple specificities of the NA region and sharing the knowledge acquired among scientists but also with the citizens of NA (Figs. 5, 6 and 7).

Finally, the scientific insights gained from this regional initiative may reshape surveillance and preparedness policies, particularly through operational research for early EID detection, such as zoonotic arboviral emergence and circulation in France, the Iberian Peninsula, and Europe. Local differences in management, health care infrastructure, climate, and human resources may pose challenges. For example, modelling WNV/USUV circulation in Spain has been limited by frequent unclear morphological identifications of *Culex sp* [89]. However, an initiative similar to the EMERG project but at a larger scale (at the European level, for example) may improve EID risk management.

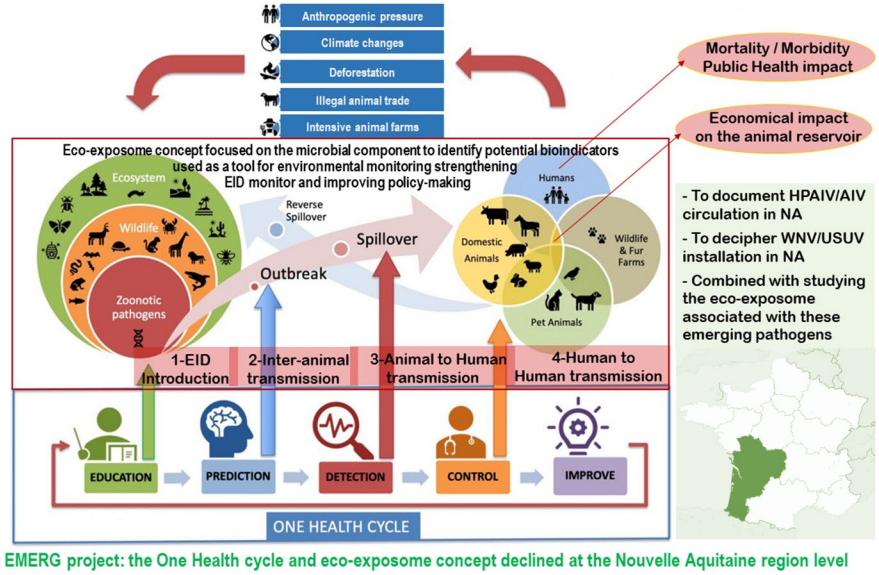

Fig. 7 EMERG project: The One Health cycle and eco-exposome concept adapted at the level of the Nouvelle-Aquitaine (NA) region (adapted from [88]). The EMERG project is focused on EID risk monitoring in NA based on an integrated One Health approach (including all the One Health cycle steps from education to improvement) combined with microbial eco-exposome analysis. By promoting transdisciplinary collaboration, it will enhance surveillance systems of EIDs (such as HPAIV/AIV circulation and WNV/USUTUV installation), enable early outbreak detection (e.g., outbreak prediction and spillover detection), improve understanding of pathogen circulation, and support informed policy decisions for effective EID control measures to limit the economic and public health impact of EIDs. The phenomenon of cross-species spillover is promoted by successive multiscale processes that enable an animal pathogen to pass from EID introduction to transmission between animals, then between animals and humans, and last, between humans leading to human infection, which remains a relatively rare event. This spillover probability is determined by multiscale interactions that are mainly nonlinear and dynamic in space and time. Human behaviours, such as intensive animal farms, illegal animal trade, deforestation, climate change, and other anthropogenic pressures, may increase this probability and, consequently, the risk of infection as exemplified by avian influenza [13, 14, 88]. The EMERG approach will strengthen the monitoring of EIDs and improve policy-making.

Abbreviations

AI	Avian influenza
AIV	Avian influenza virus
AMR	Antimicrobial resistance
CCHFV	Crimean-Congo haemorrhagic fever virus
COVID-19	Coronavirus disease 2019
EIDs	Emerging or reemerging infectious diseases
EMPRES-i	Emergency Prevention System Interface
fAMR	Fungal antimicrobial resistance
FAO	Food and Agriculture Organization
HERA	Earth emergency preparedness and response
HPAIV	High-pathogenicity avian influenza virus
NA	Nouvelle-Aquitaine
SARS-CoV-2	Severe acute respiratory syndrome coronavirus-2
USUV	Usutu virus
VAPA	Virus associated with pulmonary aspergillosis
WAHIS	World Animal Health Information System
WOAH	World Organization for Animal Health
WHO	World Health Organization
WNV	West Nile virus
RNA	Ribonucleic acid

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12982-026-01452-w.

Supplementary Material 8

Acknowledgements
The EMERG program is funded by the Region Nouvelle-Aquitaine (the PSGAR-MIE "EMERG" research grant). The EMERG consortium is composed of R. Enaud, T. Trian, P. Berger (Inserm U1045); M-L. Andreola & T. Métifiot (UMR5234 équipe Andevir); D. Malvy, A. Duvignaud & L. Altman (GHIGS-Inserm UMR 1219/IRD EMR 271); C. Imbert, L. Girardot, E. Perraud & L. Deroche (Equipe MHE – UMR 7267, CHU de Poitiers); C. Bodet, N. Lévêque & M. Garcia (LITEC - UR15560, CHU de Poitiers); D. Malvy, D. Nguyen, T. Pistone, P. Perreau, S. Burrel, M-L. Lafon, L. Delhaes & S. Imbert (CHU de Bordeaux); O. Lepais & E. Guichoux (PGTB); J-L. Guérin, T. Vergne & G. Le Loc'h (UMR IHAP); H. Agogué, A. L. Lacerda, M. Paoletti & J. Jourde (LIENSs, UMR 7266); J. Spitz & S. Wund (UAR3462); J. Moreau & K. Monceau (CEBC, UMR7372); C. Cravo-Laureau (IPREM - UMR 5254); M. Alvalos Fernandez (équipe SISTM); A. Loquet & M. Berbon (UMR5248, équipe RMN); A. Bourrel (IE2IA - UMR 7318); P. Zavoli (IFTJ); (A) Mercier & H. Yéra (Inserm U1094/IRD UMR 270, EpiMaCT, CHU Limoges); S. Hantz & S. Alain (Inserm UMR 1092); G. Salvat & N. Eterradossi (ANSES); C. Hautefeuille (CIRAD); (B) Lina (CNR Grippe); L. Filleul & S. Bertrand-Stoekel (SPF); V. Alavoine (DRAFF); Regional Vet Lab of department N°24, 40, 64 & 79; J. Stefanello (FlowBird); P. Kaluzni (Tera Group); F. M'Zali (Aquitaine Microbiologie); G. Dauphin, H. Karembeu & V. Kaltsatos (CEVA santé animale); H. Karembeu (Fondation CEVA). The authors would like to thank Mr Jean-Luc Gleyze (Président du Département de la Gironde & Conseiller Départemental du canton Sud Gironde) for his consent to use his photo of the 2022 megafire of Landiras & La Teste-de-Buch, Gironde County, and Dr Fabiola Silva-Angulo (Institut Pasteur de Lille) for proofreading and editing of the article, and Maeva Lamarques and Dania Vieira-Gois-Fernandes for their technical assistance in microbial-fungal analysis.

Author contributions
The EMERG consortium is composed of R. Enaud, T. Trian, P. Berger (Inserm U1045); M-L. Andreola & T. Métifiot (UMR5234 équipe Andevir); D. Malvy, A. Duvignaud & L. Altman (GHIGS-Inserm UMR 1219/IRD EMR 271); C. Imbert, L. Girardot, E. Perraud & L. Deroche (Equipe MHE – UMR 7267, CHU de Poitiers); C. Bodet, N. Lévêque & M. Garcia (LITEC - UR15560, CHU de Poitiers); D. Malvy, D. Nguyen, T. Pistone, P. Perreau, S. Burrel, M-L. Lafon, L. Delhaes & S. Imbert (CHU de Bordeaux); O. Lepais & E. Guichoux (PGTB); J-L. Guérin, T. Vergne & G. Le Loc'h (UMR IHAP); H. Agogué, A. L. Lacerda, M. Paoletti & J. Jourde (LIENSs, UMR 7266); J. Spitz & S. Wund (UAR3462); J. Moreau & K. Monceau (CEBC, UMR7372); C. Cravo-Laureau (IPREM - UMR 5254); M. Alvalos Fernandez (équipe SISTM); A. Loquet & M. Berbon (UMR5248, équipe RMN); A. Bourrel (IE2IA - UMR 7318); P. Zavoli (IFTJ); (A) Mercier & H. Yéra (Inserm U1094/IRD UMR 270, EpiMaCT, CHU Limoges); S. Hantz & S. Alain (Inserm UMR 1092); G. Salvat & N. Eterradossi (ANSES); C. Hautefeuille (CIRAD); (B) Lina (CNR Grippe); L. Filleul & S. Bertrand-Stoekel (SPF); V. Alavoine (DRAFF); Regional Vet Lab of department N°24, 40, 64 & 79; J. Stefanello (FlowBird); P. Kaluzni (Tera Group); F. M'Zali (Aquitaine Microbiologie); G. Dauphin, H. Karembeu & V. Kaltsatos (CEVA santé animale); H. Karembeu (Fondation CEVA).

Funding
The EMERG project is funded by the research program PSGAR-MIE of Nouvelle-Aquitaine, France.

Data availability
All data generated or analysed during this study are included in this published article [and its supplementary information files].

Declarations

Competing interests
The authors declare no competing interests.

Author details
[1]INSERM U1045, Bronchial Remodeling Team, CTCB, University of Bordeaux, Bordeaux, France
[2]Parasitology-Mycology Department, National Reference Center for Chronic Aspergillosis, University Hospital Center, Bordeaux, France
[3]INSERM U1094, IRD UMR270, Univ. Limoges, CHU Limoges, EpiMaCT - Epidemiology of Chronic Diseases in Tropical Zone, Institute of Epidemiology and Tropical Neurology, OmegaHealth, Limoges, France
[4]INSERM U1092, Univ. Limoges, CHU Limoges, RESINFIT, Limoges, France
[5]Bordeaux Population Health Center, UMR Inserm 1219 & EMR IRD 271, University of Bordeaux, Bordeaux, France
[6]University of Poitiers, UMR CNRS 7267, Ecology and Biology of Interactions, Poitiers, France
[7]Centre d'Etudes Biologiques de Chizé, UMR 7372 CNRS-La Rochelle Université, La Rochelle, France
[8]Université de Pau et des Pays de l'Adour, UPPA, CNRS, IPREM, Pau, France
[9]ANSES, INRAE, ENVA, UMR Virology, ANSES Animal Health Laboratory, F-94700 Maisons-Alfort, France
[10]UMR IHAP, INRAE, ENVT, Université de Toulouse, Toulouse, France
[11]ANSES French Agency for Food, Environmental and Occupational Heath Safety, Laboratoire de Ploufragan-Plouzané-Niort, Ploufragan, France
[12]UMR 7266 LIENSs (Littoral Environnement et Sociétés), CNRS – La Rochelle Université, La Rochelle, France
[13]Department of Infectious and Tropical Diseases, University Hospital Center, Bordeaux, France

Received: 15 June 2025 / Accepted: 21 January 2026
Published online: 16 February 2026

References

1. Sachs JD, Karim SSA, Aknin L, Allen J, Brosbøl K, Colombo F, et al. The Lancet Commission on lessons for the future from the COVID-19 pandemic. Lancet. 2022;400(10359):1224–80. https://doi.org/10.1016/S0140-6736(22)01585-9.
2. Cueni T. Lessons learned from COVID-19 to stop future pandemics. Lancet Lond Engl. 2023;401(10385):1340. https://doi.org/10.1016/S0140-6736(23)00507-X.

3. Lefrançois T, Lina B, Autran B. One health approach at the heart of the French Committee for monitoring and anticipating health risks. Nat Commun. 2023;14:7540. https://doi.org/10.1038/s41467-023-43089-2.
4. Boudreau LeBlanc A, Pelletier J, Aenishaenslin C, Beauchet O, Boiteux M, Bouchard M, et al. Bridging one health and sustainability: the anatomy of a socioethical issue. Bioscience. 2025. https://doi.org/10.1093/biosci/biaf008. biaf008.
5. Lefrançois T, Malvy D, Atlani-Duault L, Benamouzig D, Druais P-L, Yazdanpanah Y, et al. After 2 years of the COVID-19 pandemic, translating one health into action is urgent. Lancet. 2023;401(10378):789–94. https://doi.org/10.1016/S0140-6736(22)01840-2.
6. Avis du COVARS sur l'Évaluation des Risques de Situations Sanitaires Exceptionnelles majeures pour la santé humaine en France au cours des années 2025–2030 [Internet]. Enseign.-Rech. 2024. https://www.enseignementsup-recherche.gouv.fr/fr/avis-du-covars-sur-l-evaluation-des-risques-de-situations-sanitaires-exceptionnelles-majeures-pour-95700. Accessed 8 Dec 2024.
7. Tripartite and UNEP support OHHLEP's definition of 'One Health' [Internet]. https://www.who.int/news/item/01-12-2021-tripartite-and-unep-support-ohhlep-s-definition-of-one-health. Accessed 10 Dec 2024.
8. Wild CP. Complementing the genome with an 'exposome': the outstanding challenge of environmental exposure measurement in molecular epidemiology. Cancer Epidemiol Biomarkers Prev. 2005;14(8):1847–50. https://doi.org/10.1158/1055-9965.EPI-05-0456.
9. Wild CP. Invited perspective: the exposome—an exciting opportunity for collaboration, not competition. Environ Health Perspect. 2024;132(9):091302. https://doi.org/10.1289/EHP15504.
10. Escher BI, Hackermüller J, Polte T, Scholz S, Aigner A, Altenburger R, et al. From the exposome to mechanistic understanding of chemical-induced adverse effects. Environ Int. 2017;99:97–106. https://doi.org/10.1016/j.envint.2016.11.029.
11. Andrianou XD, Pronk A, Galea KS, Stierum R, Loh M, Riccardo F, et al. Exposome-based public health interventions for infectious diseases in urban settings. Environ Int. 2021;146:106246. https://doi.org/10.1016/j.envint.2020.106246.
12. WMA - The World Medical. Association-WMA Declaration of Helsinki – Ethical Principles for Medical Research Involving Human Participants [Internet]. https://www.wma.net/policies-post/wma-declaration-of-helsinki/. Accessed 8 Nov 2025.
13. Plowright RK, Parrish CR, McCallum H, Hudson PJ, Ko AI, Graham AL, et al. Pathways to zoonotic spillover. Nat Rev Microbiol. 2017;15(8):502–10. https://doi.org/10.1038/nrmicro.2017.45.
14. Carlson CJ, Brookson CB, Becker DJ, Cummings CA, Gibb R, Halliday FW, et al. Pathogens and planetary change. Nat Rev Biodivers. 2025;1(1):32–49. https://doi.org/10.1038/s44358-024-00005-w.
15. Ukoaka BM, Okesanya OJ, Daniel FM, Ahmed MM, Udam NG, Wagwula PM, et al. Updated WHO list of emerging pathogens for a potential future pandemic: implications for public health and global preparedness. Infez Med. 2024;32(4):463. https://doi.org/10.53854/liim-3204-5.
16. González MA, Chaskopoulou A, Georgiou L, Frontera E, Cáceres F, Masia M, et al. Mosquito management strategies in European rice fields: environmental and public health perspectives. J Environ Manage. 2024;370:122534. https://doi.org/10.1016/j.jenvman.2024.122534.
17. Toma L, Mancuso E, d'Alessio SG, Menegon M, Spina F, Pascucci I, et al. Tick species from Africa by migratory birds: a 3-year study in Italy. Exp Appl Acarol. 2021;83(1):147–64. https://doi.org/10.1007/s10493-020-00573-4.
18. Authority EFS, European Centre for Disease Prevention and Control, Influenza EURL for A, Adlhoch C, Fusaro A, Gonzales JL, et al (2022) Avian influenza overview June – September 2022. EFSA J. 2022;20(10):e07597. https://doi.org/10.2903/j.efsa.2022.7597
19. Briand F, Niqueux E, Schmitz A, Martenot C, Cherbonnel M, Massin P, et al. Multiple independent introductions of highly pathogenic avian influenza H5 viruses during the 2020–2021 epizootic in France. Transbound Emerg Dis. 2022;69(6):4028–33. https://doi.org/10.1111/tbed.14711.
20. Fusaro A, Zecchin B, Giussani E, Palumbo E, Agüero-García M, Bachofen C, et al. High pathogenic avian influenza A(H5) viruses of clade 2.3.4.4b in Europe—why trends of virus evolution are more difficult to predict. Virus Evol. 2024;10(1):veae027. https://doi.org/10.1093/ve/veae027.
21. Peacock T, Moncla L, Dudas G, VanInsberghe D, Sukhova K, Lloyd-Smith JO, et al. The global H5N1 influenza panzootic in mammals. Nature. 2024. https://doi.org/10.1038/s41586-024-08054-z.
22. The European Union One Health 2022 Zoonoses Report. EFSA J. 2023;21(12):e8442. https://doi.org/10.2903/j.efsa.2023.8442.
23. Frasca F, Sorrentino L, Fracella M, D'Auria A, Coratti E, Maddaloni L, et al. An update on the entomology, virology, pathogenesis, and epidemiology status of West Nile and Dengue viruses in Europe (2018–2023). Trop Med Infect Dis. 2024;9(7):166. https://doi.org/10.3390/tropicalmed9070166.
24. Malvy D, McElroy AK, Clerck H, Günther S, Griensven J. Ebola virus disease. Lancet. 2019;393(10174):936–48. https://doi.org/10.1016/S0140-6736(18)33132-5.
25. Ay J-S, Chakir R, Doyen L, Jiguet F, Leadley P. Integrated models, scenarios and dynamics of climate, land use and common birds. Clim Change. 2014;126(1–2):13–30. https://doi.org/10.1007/s10584-014-1202-4.
26. Verweij PE, Lucas JA, Arendrup MC, Bowyer P, Brinkmann AJF, Denning DW, et al. The one health problem of azole resistance in *Aspergillus fumigatus*: current insights and future research agenda. Fungal Biol Rev. 2020;34(4):202–14. https://doi.org/10.1016/j.fbr.2020.10.003.
27. Fisher MC, Burnett F, Chandler C, Gow NAR, Gurr S, Hart A, et al. A one health roadmap towards Understanding and mitigating emerging fungal antimicrobial resistance: fAMR. Npj Antimicrob Resist. 2024;2(1):1–10. https://doi.org/10.1038/s44259-024-00055-2.
28. L'essentiel sur… la Nouvelle–Aquitaine | Insee [Internet]. https://www.insee.fr/fr/statistiques/4482442.Accessed 19 Dec 2024.
29. Vizzari M, Hilal M, Sigura M, Antognelli S, Joly D. Urban-rural-natural gradient analysis with CORINE data: an application to the metropolitan France. Landsc Urban Plan. 2018;171:18–29. https://doi.org/10.1016/j.landurbplan.2017.11.005.
30. Morand S, Lajaunie C. Loss of biological diversity and emergence of infectious diseases. Biodivers Health. 2018;29–47. https://doi.org/10.1016/B978-1-78548-115-4.50003-2.
31. Kirby JS, Stattersfield AJ, Butchart SHM, Evans MI, Grimmett RFA, Jones VR, et al. Key conservation issues for migratory land- and waterbird species on the world's major flyways. Bird Conserv Int. 2008;18(S1):S49–73. https://doi.org/10.1017/S0959270908000439.

32. Jourdain E, Gauthier-Clerc M, Bicout DJ, Sabatier P. Bird migration routes and risk for pathogen dispersion into Western mediterranean wetlands. Emerg Infect Dis. 2007;13(3):365–72. https://doi.org/10.3201/eid1303.060301.
33. Baills A, Garcin M, Bulteau T. Assessment of selected climate change adaptation measures for coastal areas. Ocean Coast Manag. 2020;185:105059. https://doi.org/10.1016/j.ocecoaman.2019.105059.
34. Bellard C, Bertelsmeier C, Leadley P, Thuiller W, Courchamp F. Impacts of climate change on the future of biodiversity. Ecol Lett. 2012. https://doi.org/10.1111/j.1461-0248.2011.01736.x.
35. Roy HE, Pauchard A, Stoett P, Renard Truong T, Bacher S, Galil BS et al. IPBES Invasive Alien Species Assessment: Summary for Policymakers [Internet]. Zenodo; 2024. https://doi.org/10.5281/zenodo.11254974
36. Ummenhofer CC, Meehl GA. Extreme weather and climate events with ecological relevance: a review. Philos Trans R Soc Lond B Biol Sci. 2017;372(1723):20160135. https://doi.org/10.1098/rstb.2016.0135.
37. Weilnhammer V, Schmid J, Mittermeier I, Schreiber F, Jiang L, Pastuhovic V, et al. Extreme weather events in europe and their health consequences – a systematic review. Int J Hyg Environ Health. 2021;233:113688. https://doi.org/10.1016/j.ijheh.2021.113688.
38. Reiter P. *Aedes albopictus* and the world trade in used tires, 1988–1995: the shape of things to come? J Am Mosq Control Assoc. 1998;14(1):83–94.
39. Munster VJ, Baas C, Lexmond P, Waldenström J, Wallensten A, Fransson T, et al. Spatial, temporal, and species variation in prevalence of influenza A viruses in wild migratory birds. PLoS Pathog. 2007;3(5):e61. https://doi.org/10.1371/journal.ppat.0030061.
40. Hughes LA, Shopland S, Wigley P, Bradon H, Leatherbarrow AH, Williams NJ, et al. Characterisation of *Salmonella* enterica-serotype Typhimurium isolates from wild birds in northern England from 2005–2006. BMC Vet Res. 2008;4(1):4. https://doi.org/10.1186/1746-6148-4-4.
41. García-Bocanegra I, Franco JJ, León CI, Barbero-Moyano J, García-Miña MV, Fernández-Molera V, et al. High exposure of West Nile virus in equid and wild bird populations in Spain following the epidemic outbreak in 2020. Transbound Emerg Dis. 2022;69(6):3624–36. https://doi.org/10.1111/tbed.14733.
42. Casadevall A, Kontoyiannis DP, Robert V. On the emergence of *Candida auris*: climate change, azoles, swamps, and birds. mBio. 2019;10(4):e01397-19. https://doi.org/10.1128/mBio.01397-19.
43. Akinbobola AB, Kean R, Hanifi SMA, Quilliam RS. Environmental reservoirs of the drug-resistant pathogenic yeast Candida auris. PLoS Pathog. 2023;19(4):e1011268. https://doi.org/10.1371/journal.ppat.1011268.
44. Stallknecht D, Brown J. Wild birds and the epidemiology of avian influenza. J Wildl Dis. 2007;43:S15–20.
45. Brown JD, Stallknecht DE. Wild Bird Surveillance for the Avian influenza virus. In: Spackman E, editor. Avian influenza virus. Totowa, NJ: Humana; 2008. pp. 85–97. https://doi.org/10.1007/978-1-59745-279-3_11.
46. McVey DS, Wilson WC, Gay CG. West nile virus. Rev Sci Tech Int Off Epizoot. 2015;34(2):431–9. https://doi.org/10.20506/rst.34.2.2369.
47. Egevang C, Stenhouse IJ, Phillips RA, Petersen A, Fox JW, Silk JRD. Tracking of Arctic terns sterna Paradisaea reveals longest animal migration. Proc Natl Acad Sci. 2010;107(5):2078–81. https://doi.org/10.1073/pnas.0909493107.
48. Olsen B, Munster VJ, Wallensten A, Waldenström J, Osterhaus ADME, Fouchier RAM. Global patterns of influenza a virus in wild birds. Science. 2006;312(5772):384–8. https://doi.org/10.1126/science.1122438.
49. Communiqué de presse - Point de situation sur la circulation du virus du Nil occidental (virus West-Nile) en Gironde (33) au 8 août 2023 [Internet]. 2023. https://www.nouvelle-aquitaine.ars.sante.fr/communique-de-presse-point-de-situation-sur-la-circulation-du-virus-du-nil-occidental-virus-west. Accessed 10 Dec 2024.
50. Swayne DE, Suarez DL, Sims LD. Influenza. Dis poult. John Wiley & Sons, Ltd; 2013. pp. 181–218. https://doi.org/10.1002/9781119421481.ch6.
51. Banyard AC, Bennison A, Byrne AMP, Reid SM, Lynton-Jenkins JG, Mollett B, et al. Detection and spread of high pathogenicity avian influenza virus H5N1 in the Antarctic region. Nat Commun. 2024;15(1):7433. https://doi.org/10.1038/s41467-024-51490-8.
52. Jimenez-Bluhm P, Siegers JY, Tan S, Sharp B, Freiden P, Johow M, et al. Detection and phylogenetic analysis of highly pathogenic A/H5N1 avian influenza clade 2.3.4.4b virus in Chile, 2022. Emerg Microbes Infect. 2023;12(2):2220569. https://doi.org/10.1080/22221751.2023.2220569.
53. Molini U, Aikukutu G, Roux J-P, Kemper J, Ntahonshikira C, Marruchella G, et al. Avian influenza H5N8 outbreak in African penguins (*Spheniscus demersus*), Namibia, 2019. J Wildl Dis. 2020;56(1):214–8.
54. Shichinohe S, Itoh Y, Nakayama M, Ozaki H, Soda K, Ishigaki H, et al. Comparison of pathogenicities of H7 avian influenza viruses via intranasal and conjunctival inoculation in cynomolgus macaques. Virology. 2016;493:31–8. https://doi.org/10.1016/j.virol.2016.03.007.
55. Edenborough KM, Lowther S, Laurie K, Yamada M, Long F, Bingham J, et al. Predicting disease severity and viral spread of H5N1 influenza virus in ferrets in the context of natural exposure routes. J Virol. 2016;90(4):1888–97. https://doi.org/10.1128/JVI.01878-15.
56. Abdelwhab EM, Mettenleiter TC. Zoonotic animal influenza virus and potential mixing vessel hosts. Viruses. 2023;15(4):980. https://doi.org/10.3390/v15040980.
57. Suttie A, Deng Y-M, Greenhill AR, Dussart P, Horwood PF, Karlsson EA. Inventory of molecular markers affecting biological characteristics of avian influenza A viruses. Virus Genes. 2019;55(6):739–68. https://doi.org/10.1007/s11262-019-01700-z.
58. Nguyen T-Q, Hutter C, Markin A, Thomas M, Lantz K, Killian ML et al. Emergence and interstate spread of highly pathogenic avian influenza A(H5N1) in dairy cattle [Internet]. bioRxiv; 2024. p. 2024.05.01.591751. https://doi.org/10.1101/2024.05.01.591751
59. Caserta LC, Frye EA, Butt SL, Laverack M, Nooruzzaman M, Covaleda LM, et al. Spillover of highly pathogenic avian influenza H5N1 virus to dairy cattle. Nature. 2024;634(8034):669–76. https://doi.org/10.1038/s41586-024-07849-4.
60. Union PO of the E. Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016 on transmissible animal diseases and amending and repealing certain acts in the area of animal health (Animal Health Law) (Text with EEA relevance)Text with EEA relevance [Internet]. Publ. Off. EU. Publications Office of the European Union; 2021. https://op.europa.eu/en/publication-detail/-/publication/b23b91af-9c5a-11eb-b85c-01aa75ed71a1. Accessed 25 Dec 2024.
61. Delegated regulation – 2023/361 - EN. - EUR-Lex [Internet]. https://eur-lex.europa.eu/eli/reg_del/2023/361/oj/eng. Accessed 25 Dec 2024.

62. Guinat C, Fourtune L, Lambert S, Martin E, Gerbier G, Pellicer AJ et al. Promising effects of duck vaccination against highly pathogenic avian influenza, France 2023-24 [Internet]. bioRxiv; 2024. p. 2024.08.28.609837. https://doi.org/10.1101/2024.08.28.609837.
63. Hubálek Z, Halouzka J. West nile fever–a reemerging mosquito-borne viral disease in Europe. Emerg Infect Dis. 1999;5(5):643–50. https://doi.org/10.3201/eid0505.990505.
64. Weissenböck H, Kolodziejek J, Url A, Lussy H, Rebel-Bauder B, Nowotny N. Emergence of Usutu virus, an African mosquito-borne flavivirus of the Japanese encephalitis virus group, central Europe. Emerg Infect Dis. 2002;8(7):652–6. https://doi.org/10.3201/eid0807.020094.
65. Nikolay B. A review of West nile and Usutu virus co-circulation in europe: how much do transmission cycles overlap? Trans R Soc Trop Med Hyg. 2015;109(10):609–18. https://doi.org/10.1093/trstmh/trv066.
66. Roesch F, Fajardo A, Moratorio G, Vignuzzi M. Usutu virus: an arbovirus on the rise. Viruses. 2019;11(7):640. https://doi.org/10.3390/v11070640.
67. Gonzalez G, Migné CV, Duvignaud A, Martin-Latil S, Bigeard C, Touzet T, et al. Paradigm shift toward 'one health' monitoring of Culex-borne arbovirus circulation in France: the 2022 inaugural spotlight on West Nile and Usutu viruses in Nouvelle-Aquitaine. Open Forum Infect Dis. 2025;12(5):ofaf243. https://doi.org/10.1093/ofid/ofaf243.
68. Seroprevalence of West Nile, Usutu and Tick borne encephalitis viruses in equids from southwestern France in 2023 [Internet]. Sciety. 2024. https://sciety.org/articles/activity/10.21203/rs.3.rs-4688411/v1. Accessed 25 Dec 2024.
69. Bigeard C, Pezzi L, Klitting R, Ayhan N, L'Ambert G, Gomez N et al. Molecular xenomonitoring (MX) allows real-time surveillance of West nile and Usutu virus in mosquito populations [Internet]. bioRxiv; 2024. p. 2024.04.10.588707. https://doi.org/10.1101/2024.04.10.588707
70. Lara M, Casimiro-Soriguer CS, Pedrosa-Corral I, Gómez-Camarasa C, Lorusso N, Navarro-Marí JM, et al. First autochthonous transmission of West Nile virus (WNV) lineage 2 to humans in Spain. One Health. 2025;20:101036. https://doi.org/10.1016/j.onehlt.2025.101036.
71. Hassold-Rugolino N, Jaquet P, Da Silva D, Papa E, Calmettes J, Henry C, et al. Two cases of autochthonous West Nile virus encephalitis, Paris, France, 2025. Emerg Infect Dis. 2025;31(11):2172–4. https://doi.org/10.3201/eid3111.251220.
72. Serres K, Erazo D, Despréaux G, Vincenti-González MF, Van Bortel W, Arsevska E, et al. Integrating indicator-based and event-based surveillance data for risk mapping of West Nile virus, Europe, 2006 to 2021. Euro Surveill Bull Eur Sur Mal Transm Eur Commun Dis Bull. 2024;29(44):2400084. https://doi.org/10.2807/1560-7917.ES.2024.29.44.2400084.
73. Angelou A, Schuh L, Stilianakis NI, Mourelatos S, Kioutsioukis I. Unveiling spatial patterns of West Nile virus emergence in northern Greece, 2010–2023. One Health. 2024;19:100888. https://doi.org/10.1016/j.onehlt.2024.100888.
74. WHO Fungal Priority Pathogens List to Guide Research. Development and public health action. 1st ed. Geneva: World Health Organization; 2022.
75. Ahmed SK, Hussein S, Qurbani K, Ibrahim RH, Fareeq A, Mahmood KA, et al. Antimicrobial resistance: impacts, challenges, and future prospects. J Med Surg Public Health. 2024;2:100081. https://doi.org/10.1016/j.glmedi.2024.100081.
76. Action against antimicrobial resistance. requires a One Health approach [Internet]. https://www.who.int/europe/publications/i/item/WHO-EURO-2024-9510-49282-73655. Accessed 9 Dec 2024.
77. Fisher MC, Alastruey-Izquierdo A, Berman J, Bicanic T, Bignell EM, Bowyer P, et al. Tackling the emerging threat of antifungal resistance to human health. Nat Rev Microbiol. 2022;20(9):557–71. https://doi.org/10.1038/s41579-022-00720-1.
78. Desoubeaux G, Coste AT, Imbert C, Hennequin C. Overview about *Candida auris*: what's up 12 years after its first description? J Med Mycol. 2022;32(2):101248. https://doi.org/10.1016/j.mycmed.2022.101248.
79. Silva I, Miranda IM, Costa-de-Oliveira S. Potential environmental reservoirs of *Candida auris*: a systematic review. J Fungi. 2024;10(5):336. https://doi.org/10.3390/jof10050336.
80. Bravo Ruiz G, Ross ZK, Holmes E, Schelenz S, Gow NAR, Lorenz A. Rapid and extensive karyotype diversification in haploid clinical *Candida auris* isolates. Curr Genet. 2019;65(5):1217–28. https://doi.org/10.1007/s00294-019-00976-w.
81. Allert S, Schulz D, Kämmer P, Großmann P, Wolf T, Schäuble S, et al. From environmental adaptation to host survival: attributes that mediate pathogenicity of *Candida auris*. Virulence. 2022;13(1):191–214. https://doi.org/10.1080/21505594.2022.2026037.
82. Smith DFQ, Casadevall A. Disaster microbiology-a new field of study. mBio. 2022;13(4):e0168022. https://doi.org/10.1128/mbio.01680-22.
83. Imbert S, Normand AC, Cassaing S, Gabriel F, Kristensen L, Bonnal C, et al. Multicentric analysis of the species distribution and antifungal susceptibility of cryptic isolates from Aspergillus section Fumigati. Antimicrob Agents Chemother. 2020;64(12):e01374-20. https://doi.org/10.1128/AAC.01374-20.
84. Aerts R, Autier B, Gornicec M, Prattes J, Lagrou K, Gangneux J-P, et al. Point-of-care testing for viral-associated pulmonary aspergillosis. Expert Rev Mol Diagn. 2024;24(3):231–43. https://doi.org/10.1080/14737159.2023.2257597.
85. Feys S, Carvalho A, Clancy CJ, Gangneux J-P, Hoenigl M, Lagrou K, et al. Influenza-associated and COVID-19-associated pulmonary aspergillosis in critically ill patients. Lancet Respir Med. 2024;12(9):728–42. https://doi.org/10.1016/S2213-2600(24)00151-6.
86. Wille M, Dewar ML, Claes F, Thielen P, Karlsson EA. A call to innovate Antarctic avian influenza surveillance. Trends Ecol Evol. 2024. https://doi.org/10.1016/j.tree.2024.11.005.
87. Gangneux J-P, Brandao J, Segal E, Arikan-Akdagli S, Barac A, et al. Knowledge and regulation on fungal contamination of sand and water: progress report and perspectives. Med Mycol. 2024;62(2):myad137. https://doi.org/10.1093/mmy/myad137.
88. Spanjol K, Zucca P. 7 Biophilia, one health, and humane education: Mitigating global risk through embracing humanity's interconnection with the natural world. 2023. pp. 109–30. https://doi.org/10.1515/9783110731217-007
89. Cuervo PF, Artigas P, Mas-Coma S, Bargues MD. West nile virus in spain: forecasting the geographical distribution of risky areas with an ecological niche modelling approach. Transbound Emerg Dis. 2022. https://doi.org/10.1111/tbed.14398.
90. Bonilla-Aldana DK, Calle-Hernández DM, Ulloque-Badaracco JR, Alarcón-Braga EA, Hernández-Bustamante EA, Cabrera-Guzmán JC, et al. Highly pathogenic avian influenza A(H5N1) in animals: A systematic review and meta-analysis. New Microbes New Infect. 2024;60–61:101439. https://doi.org/10.1016/j.nmni.2024.101439}

91. Bi Y, Yang J, Wang L, Ran L, Gao GF. Ecology and evolution of avian influenza viruses. Curr Biol CB. 2024;34(15):R716–21. https://doi.org/10.1016/j.cub.2024.05.053}

Publisher's note