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One Health on islands: Tractable ecosystems to explore the nexus between human, animal, terrestrial, and marine health

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Abstract

Islands play a central role in understanding the ecological and evolutionary processes that shape life but are rarely used to untangle the processes that shape human, animal, and environmental health. Islands, with their discrete human and animal populations, and often well-studied ecological networks, serve as ideal natural laboratories for exploring the complex relationships that shape health across biomes. Relatively long coastlines and, in some cases, low lying topography also make islands sentinels for climate change. In this article, we examine the potential of islands as valuable laboratories and research locations for understanding the One Health nexus. By delving into the challenges faced in island settings, we provide valuable insights for researchers and policymakers aiming to globally promote and apply One Health principles. Ultimately, recognizing the interconnected health of humans, animals, and the environment on islands contributes to efforts aimed at promoting global health and sustainability.

Keywords: antimicrobial resistance, oceans, infectious disease, arthropod-borne viruses, aquatic health

The concept of One Health has gained significant attention in recent years as a holistic approach to address the interconnections among human, animal, and environmental health (OHHLEP et al. 2022). The World Health Organization defines One Health as a unifying approach designed to sustainably balance and enhance the health of humans, animals, and ecosystems (WHO 2022). One Health approaches are increasingly used worldwide to address fundamental challenges such as antimicrobial resistance, ecotoxicology, pathogen spillover, and zoonotic pathogen dynamics (Mackenzie et al. 2014). For example, a One Health approach identified and controlled zoonotic schistosomiasis outbreaks in Corsica (Destoumieux-Garzón et al. 2018). Ecologists pinpointed the intermediate host, hybrid status, and Senegalese origin of the parasite; veterinarians confirmed the absence of ruminant reservoirs; and physicians and health authorities improved diagnostics, addressed patient clinical characteristics, and measured the outbreak's extent (Boissier et al. 2016, Destoumieux-Garzón et al. 2018). However, the environmental component of the One Health triad is often neglected, and this impedes progress in the field (Destoumieux-Garzón et al. 2018, Essack 2018, Muhammad-Bashir and Halimah 2022). Successful integration of the environment in One Health requires a reliable measure of ecosystem health. This is complicated because there is no generally accepted definition of ecosystem health (see Penn et al. 2024), and measures such as species richness that can be proxies for environmental health are complicated by the fact that individual species distributions dynamically shift over large areas (e.g., Warren et al. 2015). Simply recording the number of species present at a location is difficult, particularly in the species rich tropics (Wiens 2023).

Although One Health principles have been applied globally, the unique characteristics and biota of islands provide tractable but underused ecosystems for exploring and implementing One Health approaches. Geographic isolation, land-sea interfaces, discrete human and animal populations with limited distributions, and (in some cases) well-studied ecological networks (e.g., Traveset et al. 2013, Cunningham et al. 2018, Harrison et al. 2020, Graham et al. 2023a) make islands ideal locations to better integrate environmental health with human and animal health. The convergence of multiple species—including humans; native and domestic animals; terrestrial, freshwater, and marine organisms-in limited space, creates opportunities for interdisciplinary research and interventions to address health challenges. Moreover, because islands are particularly vulnerable to climate change because of, for example, relatively large coastlines and, in some cases, low elevation (Veron et al. 2019, Leal Filho et al. 2024), they represent priority areas for One Health research.

Islands cover a broad gradient of human population sizes, socioeconomic development stages, and degrees of connectivity, from highly connected and developed countries such as the

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Figure 1. Conceptual figure outlining the One Health connections across islands. (a) Some of the aspects that make islands important laboratories for One Health research (Illustration: BirdCircus.com) and (b) how these island features may interact with One Health management. The plus sign indicates positive impacts (e.g., islands assist in outbreaks being contained), and the minus sign indicates negative impacts (e.g., high pathogen naivety hinders outbreaks being contained).

United Kingdom and Singapore to less developed but highly populated countries (e.g., Java) through to some of the most remote places on Earth (e.g., the Seychelles and the Polynesian islands). Broadly, islands can be classed as continental (i.e., located on a continental shelf) or oceanic (no geological connections to continents). Because the majority of islands have relatively low populations sizes compared with continental land masses (Mologni and Burns 2023), we focus on the less connected smaller marine island countries or states with populations less than 2 million people. This includes examples from both continental and oceanic islands, as well as small island developing states in the tropics that are identified by the United Nations as having distinct sociodemographic and sustainability challenges (UNCD 1994). Even within this subset of islands, development status and access to health resources varies, as do the particular One Health challenges (Mackenzie et al. 2014). Inadequate health resources, workforce capacity, and surveillance are key (and often linked) barriers for One Health approaches to be operationalized in developing islands and continental countries alike (Yopa et al. 2023). However, the isolation of islands magnifies these difficulties, because, for example, communities have to use slower sea transport to receive secondary and tertiary care (figure 1; Binns et al. 2010, Nelson et al. 2015). Public health difficulties such as reduced access to healthcare are well established (Binns et al. 2010, Bell et al. 2022); however, how the specific characteristics of islands make them unique settings for One Health research is not often considered.

In this article, we aim to examine the application of the One Health approach to islands and to highlight the potential of islands as valuable and tractable systems for understanding connections across health silos. The unique attributes of islands as geographically isolated, with relatively simple ecosystems and high degrees of endemism, have made them model systems in ecology, biogeography, and evolution throughout the history of these fields, with islands often described as tractable "natural laboratories" (e.g., Warren et al. 2015, Whittaker et al. 2017). It has already been argued in previous work that simpler, smaller, isolated insular ecosystems provide ideal laboratories to study arboviral emergence (Tortosa et al. 2012). In the present article, we suggest that islands could represent model systems for One Health research. Moreover, given the ongoing and escalating threat of climate change, increasing One Health research and surveillance on islands is urgently needed and has global implications, with islands acting as potential sentinels as climate change progresses. We present examples from oceanic and continental islands to exemplify the diverse One Health challenges and opportunities across systems. Ultimately, our framework contributes to the growing body of knowledge on One Health and emphasizes the importance of understanding and preserving the health of interconnected ecosystems on islands and beyond.

Islands as tractable systems for One Health research

Islands, due to their limited size and isolation, often have simplified ecological networks that we argue can be model systems for One Health research (figure 1). In particular, the relatively simple ecological networks on islands allow for the relative importance of species in the transmission of multihost neglected zoonotic disease, such as schistosomiasis to be better quantified and more effectively controlled (Webster et al. 2016, Hewitt and Willingham 2019). On Caribbean islands, for example, schistosomiasis has been controlled and eliminated on many of the islands partly as a result of a more complete understanding of reservoirs and the key intermediate hosts: freshwater snails from the genus Biomphalaria (and Biomphalaria glabrata in particular; Pointier and Jourdane 2000, Hewitt and Willingham 2019). The comparison of islands across the region has enabled researchers to identify ecological feedback loops between B. glabrata and competitor snails (e.g., of the Thiaridae group) that reduces B. glabrata abundance and, when coupled with human chemotherapy treatment, land-use change, and molluscicide, can interrupt the transmission and reduce the prevalence of schistosomiasis (Pointier and Jourdane 2000, Hewitt and Willingham 2019).

By understanding the ecological and evolutionary processes that shape island biogeography, researchers can gain insights into the factors influencing disease dynamics and develop effective strategies for disease prevention and control applicable to continental systems. Species richness and diversity on islands are strongly influenced by both island size and isolation (the theory of island biogeography; Macarthur and Wilson 1967). Stochastic processes reduce species richness on small islands, because of the higher chance of extinction in a small area and limited immigration due to geographic isolation (Macarthur and Wilson 1967). Oceans function as a strong filter on species traits limiting dispersal capability for those able to swim, fly, or raft to an island. The more isolated the island from other land masses, particularly from continents, the more limited the taxonomic lineages, resulting in high endemism and adaptive radiation of single lineages, leading to assemblages with low phylogenetic diversity (figure 1; Grant 1968). The small size of islands may also limit the number of trophic levels, whereby smaller areas of vegetation community types or simplified vegetation structures do not support the diversity and abundance of primary producers (plants) and consumers (herbivores) to support tertiary (apex predators) or even secondary (predators) consumers. Therefore, trophic networks may also be restricted (Gravel et al. 2011). Although measuring ecosystem health is challenging (Penn et al. 2024), the simplified and tractable ecosystem dynamics allow for more robust measures of ecosystem health through better understanding of ecological function (e.g., Fukami et al. 2006, Warren et al. 2015).

Another advantage of the discrete nature of islands is that they are sometimes well studied, including being comprehensively mapped, facilitating One Health research (figure 1). For example, the low species diversity of arbovirus (arthropod-borne virus) vector species allow for comprehensive entomological surveys to help uncouple local transmission from long distance spread of viruses such as Chikungunya and Dengue virus (Tortosa et al. 2012). Where affluent human societies live on islands, there are likely to be strong local scientific endeavors and institutions. Isolated volcanic island chains such as the Hawaiian Islands, which are also affluent, being part of the United States, and the Galapagos Islands (Ecuador) are well studied because their extreme isolation has given rise to unique endemic lineages of fauna derived from limited dispersal events. Populated islands offer the relatively close proximity of terrestrial (including freshwater) ecosystems with anthropogenic land uses, including agriculture and urban areas, and unambiguous examples of terrestrial-aquatic-ecosystem links (Fukami et al. 2006), including both disturbed and intact estuarine, coastal, and pelagic ecosystems. The increasing global focus on sustainability opens possibilities to compare traditional with regenerative practices in aquaculture, agriculture, and forestry and how these influence human health, as well as pathogen and antimicrobial resistance transmission. Well-studied islands, with detailed mapping of environmental layers and human impacts, can offer ideal study systems to understand the dissemination of antimicrobial resistance, zoonotic spillover, and pathogen transmission among wild, feral, and domestic animals. For example, although it is still technically challenging, high definition spatial data available in Ireland allowed for mapping of antimicrobial resistance transmission routes and sources, as well as bovine tuberculosis risk across the island (McGrath et al. 2009, Chique et al. 2019).

Another advantage of islands is the possibility of replicated study—in particular, in archipelagos, where each island functions as a discrete entity with independent ecosystems, which means replication can be achieved that is unattainable in other regions (Fukami et al. 2006). For example, small island clusters with varying densities of feral cats and sheep farming with different degrees of isolation or movement of livestock, combined with an advanced health system, could be a tractable model to study transmission of *Toxoplasma gondii* and its impacts on human, livestock, and wildlife health, which is currently out of reach (Aguirre et al. 2019, Roberts et al. 2020). In the Caribbean, divergent rabies reservoir dynamics (caused by the rabies virus), control efforts, and outbreak histories enable unique interisland comparisons that can facilitate better understanding of globally applicable reservoir management (Seetahal et al. 2018). The unique ability to do comparative One Health research across islands is underused and can help tease apart complex One Health relationships.

Islands as models for advancing global One Health research

Islands are well established sentinels of climate change impacts (e.g., Ansorge et al. 2014, Kane and Fletcher 2020). The complex links between changing climate and animal and human health have been at least partly driven by increasing One Health awareness (Muhammad-Bashir and Halimah 2022). Climate-health feedback loops are crucial for climate change adaption; however, knowledge of these links is geographically skewed and limited, particularly on islands (Zinsstag et al. 2018, Kim et al. 2022). Low lying oceanic islands are particularly vulnerable and among the first to experience the consequences of climate change (e.g., Kane and Fletcher 2020). Unprecedented anthropogenic sea level rise, along with wave-driven flooding and salinization, poses a significant threat to the stability and habitability of some oceanic islands, particularly those located on coral atolls between 1-3 meters above sea level (Kane and Fletcher 2020). Without intervention, atoll islands will face accelerating instability, a loss of potable groundwater and agroforests, and threatened infrastructure, becoming permanently unstable before 2100 as sea levels exceed late-Holocene threshold values (Kane and Fletcher 2020). For these islands, groundwater could be permanently lost within a few decades (Kane and Fletcher 2020). The window to understand the climate-One Health nexus is brief, but the links between climate and health are still rarely quantified on islands (Kim et al. 2022).

Even for islands not located on atolls, the large coastlines relative to land size makes the issues of coastal erosion, inundation, and the increasing frequency of large storm events major challenges (Kulp and Strauss 2019, Walsh et al. 2019, Kim et al. 2022). Events such as cyclones not only threaten health infrastructure and infection control but also have One Health implications, direct and indirect (Graham et al. 2023b). Leptospirosis is a widespread zoonosis with high morbidity rates across the tropics, especially in tropical islands (Pappas et al. 2008, Biscornet et al. 2017, Guernier et al. 2018). Leptospirosis outbreaks are strongly correlated with severe weather events. In New Caledonia, during periods of flooding, both rodent abundance and their Leptospira infection rates increased, which, in turn, was linked to higher human exposure (Perez et al. 2011). More indirectly, the increasing frequency and intensity of storms can also affect environmental health by reducing biodiversity-for example, by increased pressure on forests through storm damage and increased risk of invasive plants (Goulding et al. 2016). For island species occupying higher altitudes, increased temperatures threaten extinction in contrast to continents migration routes are limited (Fernández-Palacios et al. 2021). To what degree these

ecosystem changes will have cascading impact on One Health challenges is an open question.

Climate change will also alter arbovirus dynamics (Mordecai et al. 2020), and islands in the tropics are recognized as arbovirus hotspots (Mavian et al. 2018). Islands in each major ocean frequently experience outbreaks of infections due to arboviruses, such as Dengue, Zika, and Chikungunya viruses. These outbreaks can have implications beyond the islands themselves, because they can facilitate the transmission of these arboviruses to adjacent continental areas, including, for example, from Caribbean islands to the United States (Mavian et al. 2018). An island in the Torres Strait, situated between Australia and Papua New Guinea, served as the first site of Japanese encephalitis virus outbreaks in Australia, with the proximity of human dwellings, domestic pigs, and environment for mosquito breeding leading to detection (Hanna et al. 1996). These outbreaks foreshadowed subsequent occurrences on continental Australia, acting as early indicators of shifting Japanese encephalitis virus dynamics (Hanna et al. 1996).

Demonstrable increases in ocean warming, acidification, and oxygen loss related to climate change are occurring across marine environments (Bindoff et al. 2024). These affect marine life at multiple levels, from molecular processes to organisms and ecosystems (Pörtner 2012) with implications for food production and human communities (Hoegh-Guldberg et al. 2019). Habitat disturbances associated with climate change (e.g., coral reef bleaching, kelp forest, and seagrass meadow contractions) are exacerbated by human activities in coastal ecosystems, such as wetland area declines and increased nutrient runoff (Bindoff et al. 2024). Consequently, food provision from oceans in many regions is already affected and predicted to become more so in the future (Hoegh-Guldberg et al. 2019). For example, it is likely that more than 50% of exploited fishes and invertebrates from the exclusive economic zones of the Pacific Island states will become locally extinct by 2100 (Asch et al. 2018).

Terrestrial isolation and small populations

The limited terrestrial connectivity with other regions and their smaller human populations makes control of One Health threats-and infectious diseases in general-possible. Limited connectivity and discrete arrival zones such as ports and airports can help with targeted surveillance of pests, diseases, and vector species and can allow for timely and focused intervention strategies (figure 1). For example, rapid SARS-CoV-2 containment measures were more effective in island nations than in the countries with shared land boundaries because of the manageable number of physical entry points (Murphy et al. 2020). Indeed, island states were the countries that experienced the lowest global numbers of SARS-CoV-2 cases and mortalities during the first waves of the pandemic, in large part because their isolation enabled more effective closures of borders (Campbell and Connell 2021, Strøm et al. 2021). Effective border closures allowed some islands, such as the Galapagos, to successfully eradicate classical swine fever (Freire-Paspuel et al. 2020). Advancing One Health research and increasing surveillance capacity in this area represents good value for money as control is possible and easier to achieve than in similar continental regions.

Once an exotic pathogen arrives on an island, however, the trait of geographic isolation may be detrimental to island populations due to higher degrees of immune naivety (figure 1). For example, the accidental introduction of avian malaria, *Plasmodium relictum*, to the islands of Hawaii has led to catastrophic declines in endemic bird species (e.g., Atkinson et al. 1995, Wood-

worth et al. 2005, Neddermeyer et al. 2023). The immunological naivety of Hawaiian birds to the mosquito-borne pathogen is one likely mechanism underlying the declines (Atkinson et al. 1995). Similar patterns have been found in endemic rodent species on Christmas Island with the introduction of a pathogenic trypanosome (Pickering and Norris 1996). This naivety to disease of island species makes the introduction of disease an important extinction threat across taxa (Wikelski et al. 2004).

Increased One Health capacity building and research efforts on islands will benefit the human, animal, and plant populations by mitigating the impacts of climate change, population naivety to disease and provide important global lessons for climate change adaption. Islands are already providing insights into the socioand biophysical challenges of at least 1.5 degree Celsius increase poses for humans (Albert et al. 2018), and increasing One Health research on islands promises to help quantify health–climate links that are globally relevant.

Testing the dilution effect

We argue that simplified and discrete ecological networks on islands provide unique opportunities to explore how species diversity shapes disease outbreaks across the One Health interface via the dilution effect. The dilution effect occurs when adding reservoir-incompetent host species to a community (e.g., by introductions) reduces the transmission of enzootic pathogens maintained by competent reservoir hosts (e.g., Norman et al. 1999, Ostfeld and Keesing 2000). This effect reduces pathogen abundance, decreases persistence likelihood, and has significant implications for public health and land management decisions regarding biodiversity (Keesing et al. 2006). Conversely, disease could be amplified (e.g., increased prevalence) in systems such as islands, where species diversity is low and contact between more taxonomically closely related species is high (Keesing et al. 2006). This amplification effect may underlie the increased prevalence of leptospirosis on Pacific islands and the Seychelles (Derne et al. 2011, Biscornet et al. 2017). Furthermore, the species that have colonized islands recently or are introduced by humans tend to be good dispersers and fast-lived species (i.e., species with rapid growth and short life spans) that may be more competent hosts for some pathogens (e.g., Johnson et al. 2012, Dietrich et al. 2014, Albery and Becker 2021). In Madagascar, it has been reported that endemic small mammals carry Leptospira species different from those in introduced rats, suggesting that endemic versus introduced mammal species harbor different roles in the local epidemiology of leptospirosis (Dietrich et al. 2014). Experimental infections later suggested that endemic mammals show a strong host specificity to their Leptospira (Cordonin et al. 2020) and that Leptospira strains shed by endemic mammals in specific insular ecosystems (Leptospira mayottensis isolated from a tenrec in Mayotte; Leptospira borgpetersenii isolated from a bat in Madagascar) are less pathogenic than the ubiquitous Leptospira interrogans rat-borne isolate (isolated in Reunion Island, Cordonin et al. 2019).

Disease dynamics and the risk of spillover could be altered by the island animal communities often consisting of phylogenetically related species. The high degrees of species endemism often found on islands may protect island faunas from disease; however, reduced species phylogenetic diversity on islands may increase the chances of spillover between species (Fountain-Jones et al. 2018). Briefly, this is because closely related species tend to be more biologically similar and share similar immune

Box 1. Migrating predators and the case of influenza.

Marine predators, including pinnipeds (seals) and marine birds, are potential vectors of disease in the marine environment. Breeding marine birds and mammals on islands tend to form dense aggregations typically covered in excretions that provide ideal outbreak conditions (Vanstreels et al. 2023). Following the breeding months, millions of marine birds and mammals set out on long-distance seasonal migrations (Hindell et al. 2020), crossing hemispheres and participating in food webs on different continents. As an example, short-tailed shearwaters (*Ardenna tenuirostris*) are a pelagic seabird that breed on the islands of Tasmania, Australia, then fly to the Northern Hemisphere to spend the boreal summer in Alaska, Russia, and the Bering Sea (Carey et al. 2014). The species is consumed by humans in Tasmania (Lavers and Bond 2013). Although the role of migratory marine birds as disease vectors is somewhat understudied, there is evidence for transport of various pathogens including *Borrelia* (Comstedt et al. 2011), *Campylobacter* and *Salmonella* (Moré et al. 2017).

Since October 2021, high-pathogenicity avian influenza (HPAI) H5N1 lineage 2.3.4.4b has swept across the Northern Hemisphere, the Americas, and Africa, resulting in the destruction of more than half a billion poultry and mass mortalities in wild birds and marine mammals (Gamarra-Toledo et al. 2023, Klaassen and Wille 2023, Leguia et al. 2023). At least 356 species of birds experienced mortality (Klaassen and Wille 2023), island populations of wildlife have been decimated (Camphuysen and Gear 2022, Knief et al. 2024) and at least seven humans infected (three fatally in 2023; Bruno et al. 2023). As of September 2024, the only continent free of this panzootic is Australia. HPAI is a clear One Health challenge. Although low-pathogenicity avian influenza is maintained in wildlife species, the emergence of HPAI has been typically linked directly with poultry production (Gilbert et al. 2017). The HPAI H5N1 2.3.4.4b lineage has altered this pattern and the toll of this panzootic con wildlife and ecosystems is enormous and it may take years for us to understand its long-term effects. Likewise, the economic cost is yet to be tallied, but the last major outbreak of HPAI in the United States (2014–2016) led to the deaths of 50 million domestic birds, at a cost of at least US\$1 billion (Seeger et al. 2021). HPAI H5N1 2.3.4.4b has been unprecedented in its rapid spread, carried across oceans, between continents, and onto islands, largely by migratory birds (Caliendo et al. 2022, Lv et al. 2022).

profiles and are therefore susceptibility to infectious disease (Longdon et al. 2011). Outbreaks of high-pathogenicity avian influenza are more likely in wild bird communities with low phylogenetic diversity than in more diverse communities (boxes 1–3; Huang et al. 2019). Higher infectious disease burdens in wildlife have clear implications for human health with, for example, areas of low-phylogenetic diversity of rodents in the United States recording more cases of Lyme disease in humans than in areas with higher diversity (Wang et al. 2023). Whether this is true in island ecosystems remains an open question.

Aquatic connectivity

Although islands are physically isolated, they are connected by the ocean. Ocean connectivity is greater than terrestrial, at least partly because of the physical differences between water and air (McCallum et al. 2003). This connectivity is essential for the life cycles of some marine animals, but it also promotes transmission of pathogens, including those affecting both highly mobile and sessile hosts (McCallum et al. 2003). For example, in 1995 herpes virus spread through mobile pilchard populations in Australia and New Zealand at up to 45 kilometers per day and 11,000 kilometers per year (Jones et al. 1997, Murray et al. 2001) whereas Neoparamoeba invadens, an amoeba pathogenic to sea urchins, had a maximum rate of spread of 986 kilometers per year (Miller and Colodey 1983). Marine currents and paratenic hosts are also implicated in the spread of Toxoplasma gondii, a parasite with a complex cycle involving cats and various mammals or birds, because antibodies against T. gondii in over 1000 pelagic seabirds were detected in seabirds from cat-colonized but also cat-free islands in the Western Indian Ocean (Poulle et al. 2021). Inert materials such as floating plastic debris provide the potential for connectivity between islands and have been proposed as a potential vector for pathogenic bacteria (Bowley et al. 2021). Although a variety of human and animal pathogens have been identified as part of the bacterial communities living on microplastics, their pathogenicity potential or extent to which human and animal

pathogen transmission occurs via this route is unknown (Bowley et al. 2021, Beloe et al. 2022).

Islanders interact with aquatic ecosystems

Island inhabitants often have close connections to their aquatic environments, which occupy a prominent role in cultural and recreational activities, as well as practical roles in transport and food provision. This close link between island communities and their aquatic environments provides an excellent setting for the understanding of ecosystem changes in response to these multiple stressors. Several of the Pacific Islands have relatively large exclusive economic zones. For example, the Pacific Island country of Nauru controls an exclusive economic zone that is 15,000 times larger than its total landmass. Although little research has been devoted to links between human and animal health and the health of the aquatic environment, a One Health approach is equally valid in this setting. Pollution, plastics (including microplastics), overfishing, aquatic pathogens, and climate change are threats to environmental health that are relevant in a One Health context (Norman et al. 2023).

Two examples of this are Vibrio bacteria and harmful algae. Vibrio spp. are ubiquitous in aquatic environments and can be both commensal organisms in marine biota (Egerton et al. 2018) and common pathogens of finfish, shellfish, and shrimp capable of causing large scale mortalities in aquaculture (Worden et al. 2022, Cowan et al. 2023). Increases in the environmental levels of Vibrio related to climate change are well noted (e.g., Baker-Austin et al. 2013). At the same time, the incidence of human vibriosis is rising worldwide (WHO 2020, Trinanes and Martinez-Urtaza 2021). Vibrio vulnificus causes 95% of seafood related mortalities in the United States (Oliver 2015, Heng et al. 2017), and Vibrio parahaemolyticus is a leading cause of seafood related foodborne illness in the many areas of the world (Baker-Austin et al. 2018, WHO 2020). This is particularly important for those island communities that rely more on seafood as a source of protein-for example, the communities from Pacific islands (O'Meara et al. 2023).

Box 2. Fiji: A model of One Health research in the Pacific.

Fiji, an archipelago nation of over 300 oceanic islands in the South Pacific, faces a myriad of One Health threats due to its geographic and environmental characteristics. Situated in a tropical climate zone, Fiji's diverse ecosystems support a rich marine biodiversity. Fiji considers itself to be a "large ocean state" as its exclusive economic zone is 70 times larger than its landmass and includes more than 10,000 km² of coral reefs. This results in a high level of biodiversity with more than 12,000 species of fish, 800 species of mollusks and 350 species of hard coral. Comparatively, the terrestrial fauna is much less diverse than continental locations at the same latitude with 76 vertebrate species (including five mammal species; Pernetta and Watling 1978). The Republic of Fiji, with a Human Development Index (HDI) of .743, ranks among the largest economies in the South Pacific. Approximately 75% of the Fijian population lives in coastal zones on Viti Levu Island (Swail et al. 2019).

Terrestrial ecosystems and One Health threats in Fiji

Leptospirosis is a widespread zoonosis in the Pacific Islands, with some epidemiological heterogeneity within and between islands that needs to be better understood (Guernier et al. 2018). In Fiji for example, human leptospirosis presents a significant health concern, attributed to its specificities, including a tropical climate and frequent heavy rainfall, which provide ideal conditions for the survival and transmission of Leptospira bacteria (e.g., Lau et al. 2016, Reid et al. 2017, Naing et al. 2019). The disease is notably prevalent in rural and periurban areas of Fiji, where agricultural activities are common, and individuals have frequent contact with contaminated water sources (Lau et al. 2016). Community-level exposure to livestock, especially pigs and cows, also seems to be a strong predictor of the risk of leptospirosis infection (Lau et al. 2017). Flooding events, exacerbated by climate change, further propagate the spread of pathogenic Leptospira through contaminated water and soil, heightening the risk of infection for both humans and animals (e.g., Lau et al. 2010). Socio-economics and poor living conditions have also been linked to higher risk of infection (Lau et al. 2016). Limited access to healthcare services in remote regions of Fiji exacerbates the impact of leptospirosis, highlighting the urgent need for targeted public health interventions to mitigate its transmission (Lau et al. 2016). Mosquito-borne viruses such as Dengue, Zika, and Chikungunya viruses pose ongoing threats to public health, particularly in urban areas where population density is high (Roth et al. 2014). Antibiotic resistance is also a growing concern, with antimicrobial surveillance programs providing valuable insights into the prevalence and distribution of resistant bacteria (World Health Organization 2014). Remote areas of the Fiji Islands may experience lower levels of antimicrobial resistance compared with urban centres, highlighting the importance of understanding regional variations in resistance patterns (Robbins et al. 2024).

Aquatic ecosystems and One Health threats in Fiji

Many islanders around the world rely heavily on the health of their marine environment, especially its reefs, which are vital for traditional ways of life, artisanal fishing as well as being the dominant source of protein in some communities. This is the case in Fiji. But poisoning due to consumption of fish containing natural toxins has significantly increased in Fiji and could be associated with marine heatwaves (Holbrook et al. 2022). Thirty-four species of reef fish were identified as potentially toxic mostly because of the presence of tetrodotoxins, palytoxin, or ciguatoxin, particularly under warmer conditions (Lako et al. 2023). Also, the ocean is a reservoir of antibiotic resistant genes (Hatosy and Martiny 2015), and around Fiji, pharmaceutical residues detrimental to marine life, including antibiotics, have been detected in seawater samples even in coastal areas with low population (Dehm et al. 2021). Currently, there is a lack of information on ocean antimicrobial resistance from Pacific Island countries (Loftus et al. 2020, Xu et al. 2023). Similarly, there is little information on infection of fish from Fiji by zoonotic parasites, making risk assessment for zoonosis due to seafood consumption difficult.

Primary production from phytoplankton is the basis of food chains in aquatic systems. Significant interest has been focused on those algae able to produce marine biotoxins (Hallegraeff et al. 2021b), a range of lipophilic and hydrophilic metabolites that potentially play a role in avoiding zooplankton grazing pressure (Turner 2014). These biotoxins accumulate in the food chain—notably, amnesic, diarrhetic, or paralytic shellfish toxins in bivalve shellfish, carnivorous mollusks, and crustacea (e.g., Hallegraeff et al. 2021b) or ciguatoxins in finfish (Chinain et al. 2020). Depending on the toxin group, a range of human illnesses can result (FAO 2004). However, marine biotoxins can also cause mass mortality events of marine animals across multiple trophic levels (Starr et al. 2017, Hallegraeff et al. 2021a, Rolton et al. 2022) or can affect the neurological, physiological, and behavioral responses of bivalves (Kvitek et al. 1991, Bricelj et al. 2011) and marine invertebrates, notably affecting metabolism, immune responses, fecundity, and juvenile survival and growth (Haberkorn et al. 2010, Goïc et al. 2013, Navarro et al. 2016) and, therefore, also ecosystem health.

Growing aquaculture production is seen as an important component in world food security (Azra et al. 2021, Garlock et al. 2022), and small island developing states are increasingly looking to aquaculture for economic development (FAO 2017). More broadly, marine environmental health is essential to the health of coastal communities relying on the ocean for their food, shelter, livelihoods, and other resources (Fleming et al. 2019). Mental health and well-being has been associated with closeness to coastal areas as a result of lower stress, physically active lifestyles and social interactions (Garrett et al. 2019, Britton et al. 2020, Nash et al. 2022). At the same time, human activities can adversely affect the marine environment and, as a result, can affect human health. This illustrates the interdependence of human and environmental health and the significance of a One Health approach for investigating environmental, animal, and human health issues.

Box 3. One Health on the continental island of Tasmania.

A contrasting system to Fiji, but one that also offers exceptional opportunity to apply a One Health approach is the temperate continental island of Tasmania (situated 42 degrees south, 68,401 square kilometers), part of and situated south of the world's smallest continent, Australia. Tasmania has the advantage of being a high HDI country that is exceptionally well studied and mapped, including well-studied ecological networks of terrestrial mammal fauna (Cunningham et al. 2018). It also has threats deriving from the human activity of all major land uses (agriculture, forestry, mining, fishing and aquaculture) and its high level of endemicity in the biota. Tasmania's biota, both endemics and representatives of most taxa on the adjacent mainland, reflects both its significant isolation as well as frequent connection with the supercontinent of Sahul during the glacial maxima and its proximity (240 kilometers).

Tasmania is climatically and environmentally diverse, and has both a high proportion of intact landscapes (approximately 50% reserves) concentrated in the western half of the island and the oldest and most fragmented agricultural landscape in Australia (Midlands agricultural region 87% cleared; Davidson et al. 2021). High abundance of rabbits and rodents, as well as the concomitant decline of the apex terrestrial predator and scavenger, the Tasmanian devil (*Sarcophilus harrisii*), have contributed to high densities of feral cats (Hollings et al. 2014, Cunningham et al. 2018, Hamer et al. 2021). Those herbivorous preys also feed native carnivores (Andersen et al. 2017, Hamer et al. 2021). Such close contact between wildlife, invasive and domestic species could cause for pathogen spillover and spillback. As an example of disease cascade, high cat densities in areas of Tasmanian devil decline have been associated with high prevalence of Toxoplasma gondii in the native herbivore rufous-bellied pademelon (*Thylogale billardierii*; Hollings et al. 2014).

A warming climate is increasing spillover of several viruses in this temperate island Macropods and as reservoir hosts for the Ross River virus, Tasmania's most significant mosquito-borne virus (Harley et al. 2001, Koolhof and Carver 2017). Ross River virus is endemic throughout Australia, with occasional epidemics occurring in the South Pacific, leading to manifestations of fatigue and polyarthritis (Harley et al. 2001). Although cases are presently rare and confined to the east coast of Tasmania, rising temperatures are expected to facilitate an increase in the transmission of Ross River virus by increasing mosquito survival (Shocket et al. 2018). Another mosquito-borne virus, the Japanese encephalitis virus, is currently undetected on the island but is at its doorstep in south-eastern Australia (van den Hurk et al. 2022). Similarly to Ross River virus, climate change and increased temperature are likely to favor the emergence of the Japanese encephalitis virus in new territories due to increased mosquito survival and changing wild bird migrations (Brinkhoff 2023).

Salmonella serotype Mississippi infections are very common in Tasmania, representing 80% of Australian notifications (Ashbolt and Kirk 2006). Infection sources include Tasmanian wildlife such as skinks, eastern quolls (Dasyurus viverrinus) and kangaroos (Macropus giganteus tasmaniensis), with 50% of 120 eastern quolls sampled infected with Salmonella, of which 97% was Mississippi (Ball 1991). The Tasmanian reservoir of Salmonella Mississippi appears to be the native animal population, which contaminates water supplies leading to sporadic human infections: Salmonella was detected in 1.6% of 500 reticulated drinking water sources and 8.2% of 250 natural fresh water sources of which 53% were Mississippi (Ashbolt and Kirk 2006).

As with most places on the globe, antimicrobial resistance is an important issue for Tasmania and surveillance is reasonably comprehensive given the size of the island (Australian Commission on Safety and Quality in Health Care 2014). Tasmania has the lowest proportion of resistance in priority antimicrobial resistance pathogens in Australia (Australian Commission on Safety and Quality in Health Care 2023). This includes lowest reported rates of methicillin-resistant *Staphylococcus aureus*, ceftriaxone-, gentamicin-, and ciprofloxacin-resistant *Escherichia* coli from bloodstream infections, the lowest state notifications of critical antibiotic resistances reported to the CARAlert program, such as carbapenem-resistant Enterobactereales, *Pseudomonas aeruginosa* and *Acinetobacter baumanii*, and an absence of *Candida auris* and ceftriaxone-resistant Salmonella infections. These findings are also mirrored in community surveillance; for example, urinary *Escherichia* coli had much lower levels of antimicrobial resistance compared with mainland Australia (Meumann et al. 2015). If the lower levels of antimicrobial resistance either a product or a function of relative isolation compared with continental Australia or mediated by environment and climate (e.g., Li et al. 2023) is unknown. Reduced resistance, however, may facilitate more tractable analyses of antimicrobial resistance spread form environmental and animal sources (Bengtsson-Palme et al. 2023)

Aquatic ecosystems and One Health threats in Tasmania

Globally, due to climate change, the marine environment is undergoing measurable changes to key physical parameters such as temperature, salinity, and acidity, with an increase in the frequency of marine heat waves and storm events (Whetten et al. 2015). In Tasmania, changes are occurring on the ecological level that are altering marine ecology (e.g., changing species distributions; Pecl et al. 2014), including invasions of introduced species such as the long-spined sea urchin *Centrostephanus rodgersi* (Johnson et al. 2011) or the loss of giant kelp habitat (Layton al. 2020 et al. 2020). Such ecological changes can be associated to the emergence of new health threats. During the 2016 marine heat wave, the oyster herpes virus (ostreid herpesvirus 1) was detected for the first time in Tasmania, causing over \$12 million in industry losses through oyster mortalities, and the first human health outbreak of vibriosis associated with consumption of Tasmanian oysters was recorded (Harlock et al. 2022). Another example is the impact of recurrent toxic algal blooms on Tasmania east coast since 2012, causing fisheries closures across multiple species (McLeod et al. 2017, Seger et al. 2020) and several human hospitalizations (Edwards et al. 2018).

Islands as One Health sentinels: Surveillance opportunities

For a genuine One Health model to succeed in any system, having a surveillance system that spans humans, domestic and wild animals, and the environment is essential. Although multisector coordination can be logistically simpler on islands, as with most One Health approaches, environmental surveillance is the weakest component or is missing altogether (e.g., Iossa and White 2018). Such surveillance is necessary for understanding patterns of antimicrobial resistance in environmental reservoirs of resistance (Iossa and White 2018, Chique et al. 2019). Notably, water bodies can facilitate the spread of antimicrobial resistance (e.g., Singh et al. 2022); therefore, water monitoring is important for understanding antimicrobial resistance dynamics on islands (figure 1). Bacterial genera and their resistance genes are regularly shared across biomes from air, soil, and water, so monitoring across systems is crucial but is rarely achieved (BIOHAZ et al. 2021, Luiken et al. 2022). Emerging metagenomic frameworks using Oxford Nanopore Technologies' sequencing, such as ARGpore2 (Wu et al. 2022), offer exciting and cost-effective possibilities for surveillance of water, soil, and dust samples (Eltokhy et al. 2021, Li et al. 2021). Moreover, metagenomic surveillance spanning terrestrial and marine systems promises a better understanding of the complex interactions that shape ecosystems (Clarke et al. 2020). As small, discrete units, islands offer an ideal living laboratory to apply a metagenomic surveillance regime that represents key ecosystems, animal species, and human population centers. Existing projects such as the World Network of Island and Coastal Biosphere Reserves (https://core.unesco.org/en/project/526GLO2012) promise to integrate strategies for ecosystem restoration that will also have One Health relevance. Integrated insular surveillance systems will not only lead to better management of health threats on islands but will also have implications and benefits for larger continental areas.

The opportunities and importance of One Health on islands underscore the need for geographically tailored strategies. Islands, characterized by diverse connectivity and development statuses, can serve as tractable systems for understanding disease dynamics because of their simplified ecological networks and well-studied ecosystems. Reduced connectivity (in most circumstances) and smaller populations enhance the manageability of targeted surveillance and intervention strategies, and this can lead to successful containment measures. However, the effects of isolation also shape species diversity and evolutionary relationships, contributing to the intricate interplay between island ecology and disease dynamics. Connectivity between anthropogenic impacts on the land to the sea is important for islands, given their relatively larger exclusive economic zones compared with their total land mass and greater reliance on natural resource harvest from the sea for human sustenance. A holistic approach is needed to address the interconnectedness of human, animal, and environmental health because of the close relationship between island communities.

Author contributions

Nicholas M Fountain-Jones: conceptualization, figure creation, writing—original draft, writing—review and editing; Kate S Hutson: figure creation, writing—original draft, writing—review and editing; Menna Jones: writing—original draft, writing review and editing; Barbara F Nowak: writing—original draft, writing—review and editing; Alison Turnbull: writing—original draft, writing—review and editing; Jane Younger: writingoriginal draft, writing—review and editing; Malgorzata O'Reilly: writing—original draft, writing—review and editing; Emma Watkins: writing—original draft, writing—review and editing; Vanina Guernier-Cambert, Louise Cooley: writing—original draft, writing—review and editing; Rodrigo Hamede: conceptualization, writing—review and editing.

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