SAREM Series A
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VOLUME 3

INTRODUCED INVASIVE MAMMALS OF ARGENTINA

MAMÍFEROS INTRODUCIDOS INVASORES DE ARGENTINA

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The Argentine Society for the Study of Mammals (Sociedad Argentina para el Estudio de los Mamíferos – SAREM) was created in 1983, and currently has about 300 members from several countries. SAREM is an interdisciplinary society of natural sciences professionals whose main goals are the promotion of scientific and technical research, the consolidation of national collections and research centers, and the publication and diffusion of research on living and/or extinct mammals. SAREM has organized scientific meetings for mammal researchers since 1994, publishes the journals *Mastozoología Neotropical* and *Notas sobre Mamíferos Sudamericanos*, and has edited books on the systematics, distribution and conservation of the mammals of southern South America, including *Libro Rojo de los mamíferos amenazados de la Argentina* (first ed. 2000, second ed. 2012) and *Mamíferos de Argentina. Sistemática y distribución* (2006), as well as contributing to the *Libro Rojo de los mamíferos y aves amenazados de la Argentina* (currently out of print).

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Introduced invasive species are a major driver of local to global environmental change, including important negative impacts on biodiversity, ecosystem processes, economies, health and other social values. At the same time, however, different social actors can hold diverse representations of these species, particularly of introduced invasive mammals (IIMs). Such divergent values and perceptions can lead to conflicts regarding the management of IIMs, but also invite researchers and managers to be reflexive regarding their own work at a more fundamental level. Therefore, it is key that we advance towards a holistic understanding of IIMs and develop strategies to manage them based on solid technical information and plural perspectives regarding their multiple values. Despite a rich history of initiatives in Argentina to study and manage IIMs, until now there has not been an opportunity to assess the state-of-the-art knowledge in our country. This book seeks to provide rigorous, relevant and legitimate information to support research, policymaking and management decisions regarding IIMs in Argentina. With this objective in mind, the book presents a series of chapters selected to highlight priority topics concerning the conceptualization and implementation of IIM research and management. Then, fact sheets are provided for the different IIMs found in Argentina. Finally, beyond the realm of academic inquiry, the timing of this publication is ideal to re-enforce policy and decision-making, such as the recently approved National Invasive Exotic Species Strategy, which seeks to implement actions and enhance institutional capacities related to invasive species management in Argentina, and the Convention on Biological Diversity's new Global Biodiversity Framework, which also addresses biological invasions as part of broader efforts to attain the 2050 Vision for Living in Harmony with Nature.

Dr. Alejandro E.J. Valenzuela
Dr. Christopher B. Anderson
Editors, Vol. III SAREM Series A

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FOREWORD

Biological invasions by introduced species are one of the great changes rapidly transforming the globe today, with innumerable impacts on economics, human health, ecosystem services, and biodiversity. Mammals are among the most impactful of invasive species, transmitting diseases to humans, livestock, and native animals, trampling native grasslands, voraciously devouring vegetation from groundcover to saplings of forest trees, fouling water, causing erosion, and preying on and outcompeting native animals. They were among the first species humans introduced worldwide and in Argentina, both deliberately (*e.g.*, livestock) and inadvertently (*e.g.*, rats and mice). They have been introduced for sport (*e.g.*, deer, boar) and companionship (*e.g.*, cats, dogs), or simply as attractive ornamentals (*e.g.*, squirrels). Some that are meant to be kept in captivity, such as cats, dogs, and squirrels, escape and establish feral populations.

Argentina looms large in the history of biological invasions by introduced mammals. The earliest permanent European settlers of Buenos Aires in 1580 discovered huge herds of feral horses already on the pampas, and soon after, Vázquez de Espinoza described feral horses in Tucumán that were "in such numbers that they cover the face of the earth…". Many sheep were in Tucumán as well at that time, and of course later sheep were enormously numerous in Patagonia, effecting huge changes in the vegetation and driving land degradation and desertification to this day. When Charles Darwin visited the La Plata region in 1832 during the voyage of the Beagle, he reported that "…countless herds of horses, cattle, and sheep, not only have altered the whole aspect of the vegetation, but they have almost banished the guanaco, deer and ostrich. Numberless other changes must likewise have taken place; the wild pig in some parts probably replaces the peccari; packs of wild dogs may be heard howling on the wooded banks of the less-frequented streams; and the common cat, altered into a large and fierce animal, inhabits rocky hills."

Approximately 40 mammals have been introduced to South America, of which 25–30 have established populations; most of these are in the Southern Cone. In Argentina, I count 23 successfully introduced mammal species, including feral cats, dogs, and cows. Many, such as rats, rabbits, boar, and goats, are widely distributed around the world. By contrast, the hairy armadillo has been introduced nowhere else but from the mainland of Patagonia to Tierra del Fuego Island. Strikingly, except for the rats and house mouse, all these mammals were brought to Argentina deliberately; this is very different from, say, introduced insects. A few of these invasive mammals, like the squirrel, were not intended to be released, but I hesitate to term such invaders truly "accidental," because the people who brought them should have realized that escapes or later releases were almost inevitable. Of course, almost all of these mammals were introduced before the late twentieth century, which was when most scientists and the public began to recognize the extent and importance of impacts of introduced species. However, the squirrel and armadillo introductions were recent enough that potential impacts should have been foreseen. Things could be worse, of course—mammals deliberately brought to Argentina that either were released, but did not establish persistent populations or have not yet escaped from hunting preserves include reindeer, silver fox, mule deer, African buffalo, white-tailed deer, Père David's deer, thar, barbary sheep, wisent, mouflon, chamois, and ibex.

The technology of eradicating introduced invasive mammals has made enormous strides in the last thirty years—at least 31 mammal species have been eradicated from islands worldwide, including relatively large islands like South Georgia. Both Norway and ship rats have been eradicated hundreds of times, and house mice about 100 times. Most large mammals, such as deer and horses, are technologically easier eradication targets—many can simply be tracked and shot, for instance. However, mammals more than any other introduced species pose the complication that many people—especially hunters—simply do not want to eradicate them, and many animal welfare advocates, even those recognizing the damage some invaders cause, object to eradicating them by the only currently feasible means—killing them, humanely if possible. Even rat eradication has been impeded on animal rights/animal welfare grounds, and free-ranging dog and cat populations frequently are seen more as animal welfare issues than as conservation problems to broad sectors of some societies. In Argentina, the problem of implementing feasible eradication programs for invasive mammals is epitomized by the rather schizophrenic attitude taken by the National Parks Administration (Administración de Parques Nacionales–APN) towards red deer. The APN's conservation imperative is supported by the section of Law #22,351 that forbids propagating introduced animals, yet red deer, known to damage native species and ecosystems, are managed in Lanín National Park to foster ongoing hunting, and even to improve the size and quality of the deer for better hunting trophies. Additionally, there is often inconsistent and inadequate funding for managing and eradicating invasive mammals in protected areas, almost always constituting a supervening impediment even when a rational and effective goal is stated.

Argentine scientists have participated heavily in the rapid growth of modern invasion science since its inception in the 1980s, and they and overseas colleagues have conducted substantial research on the biology and impacts of many of the introduced invasive mammals in Argentina, as well as other invasive species. Some of the threats posed by these mammals have even become widely known to the general public in Argentina and beyond—the spread of the beaver from Tierra del Fuego to the mainland has been an international news story. *Introduced Invasive Mammals of Argentina* is therefore an exciting and timely addition to the literature on invasions in southern South America for both the Argentine public (and its political representatives and environmental managers) and scientists worldwide. The many authors assembled for this book explore how these biological invasions happened in the first place, how they spread, what they do to biodiversity, ecosystems, and human enterprises, what has been done about them so far, what can be done about them now, and what might be done with them in the future. The editors and authors are to be congratulated for an excellent exposition of the Argentine part of a growing global phenomenon.

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RIESGOS DE ENFERMEDAD POR MAMÍFEROS INTRODUCIDOS

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Abstract. Many pathogens brought with introduced species have caused extinctions and dramatic ecosystem changes worldwide. Global literature illustrates how pathogens can facilitate biological invasions by "spilling over" into vulnerable, non-immune native hosts, or by "spillback," whereby introduced species become hosts for native pathogens that then affect local species. Introduced pathogens may even persist where the exotic host species fails. Moreover, if these pathogens establish disease cycles between domestic and wild species, they become virtually impossible to eliminate. Interventions to halt disease in wildlife populations are complex, expensive, controversial and often ineffective. Thus, strong biosecurity and prevention practices are needed to avoid pathogen introduction in the first place. Dealing with this threat requires interdisciplinary expertise and inter-agency coordination. In Argentina, introduced animal diseases are listed as one of the main conservation threats for nearly every threatened native mammal. Yet, current knowledge on whether or how invasive species' pathogens impact and alter ecosystems in the country is scarce. In recent years, disease surveillance in native and introduced wildlife has increased in Argentina. Several targeted and opportunistic investigations are being conducted via an *ad hoc* network reporting to the national veterinary service, thus providing reasonable species and geographic coverage. As more research enables a diagnosis of the present situation and assessment of future risks, systematic monitoring (*e.g.*, via sentinel or easily accessible species) is recommended for early warning and rapid response. Meanwhile, best practices, such as avoiding contact between introduced (wild and/or domestic) and native species, enhanced surveillance, and strict biosecurity, particularly in wildlife strongholds, can buffer against accidental pathogen invasions. With increased connectivity and globalization, introduced pathogens are becoming more prevalent and widespread worldwide. Like all countries, Argentina must strive for healthy wildlife and functional ecosystems, free of introduced invasive species and pathogens. Therefore, readiness for early detection and response must be of the highest priority.

Resumen. Las especies introducidas, y los patógenos asociados a esas especies, son reconocidos factores de pérdida de biodiversidad y cambios ecosistémicos. A nivel mundial, muchos patógenos invasores han causado epidemias severas y extinciones de especies. Según la literatura global, las enfermedades no son solo una consecuencia de las invasiones biológicas. Los patógenos pueden también ser actores clave para que la especie invasora se establezca exitosamente. Hay dos mecanismos comunes de facilitación de la invasión. Uno es el *spillover*, en que la especie invasora trae consigo patógenos nóveles para los cuales las especies locales no tienen inmunidad. El otro es el *spillback*, en que las especies invasoras se convierten en hospederos de patógenos nativos, y así impactan sobre

especies de la fauna local. Incluso, si un patógeno invasor encuentra hospederos locales adecuados, puede establecerse y persistir en el nuevo ambiente, aun cuando su hospedero invasor original no lo logre. Numerosos patógenos de mamíferos introducidos han causado graves trastornos ecosistémicos, modificando la ecología de enfermedades existentes o removiendo especies clave de cadenas tróficas y hábitats sensibles. Es más, muchos han causado importantes pérdidas de servicios ecosistémicos que se traducen en graves pérdidas económicas y de otros beneficios sociales. Cuando los patógenos introducidos logran establecerse en ciclos que incluyen especies domésticas y silvestres, son casi imposibles de eliminar. Peor aún, estos ciclos suelen incluir componentes ambientales que sostienen e incrementan las reinfecciones, limitando todavía más las opciones de control o erradicación. Esto es grave porque las intervenciones en poblaciones silvestres son de por sí complejas, costosas, controversiales y a menudo ineficaces. La clave se centra entonces en la prevención. Y esta depende, en gran medida, de una sólida bioseguridad y una adecuada capacidad de detectar tempranamente las invasiones. Lidiar con esta amenaza requiere colaboración interdisciplinaria y coordinación entre instituciones gubernamentales y de la sociedad civil.

Aunque la Argentina sostiene un número preocupante de especies introducidas invasoras, que se expanden por casi toda su geografía, casi no existen estudios sobre el rol de los mamíferos introducidos como reservorios de patógenos. Es más, considerando que las enfermedades introducidas se señalan como una de las principales amenazas para prácticamente todos los mamíferos amenazados del país, es preocupante este enorme vacío de información. Los estudios existentes muestran que en áreas de solapamiento entre especies introducidas y nativas los problemas de salud pueden ser significativos, principalmente cuando se asocian a cambios ambientales bruscos (antrópicos o naturales) que generan fuerte estrés sobre las poblaciones silvestres. Afortunadamente, en los últimos años se han ido incrementando las investigaciones en salud de fauna silvestre (nativa e introducida) en el país. Además, y siguiendo modelos de otros países, numerosos investigadores contribuyen a la vigilancia de enfermedades por medio de una red de apoyo al servicio oficial de sanidad animal (SENASA). Muchos de estos estudios se basan en muestras colectadas a partir de especies cosechadas para consumo (p.ej. ciervo colorado, *Cervus elaphus*), o programas de control de especies introducidas y cacería deportiva (p.ej. jabalí, *Sus scrofa*), lo cual permite una mayor cobertura de especies y áreas, con costos menores.

Las especies invasoras pueden cambiar la dinámica de las enfermedades en los ecosistemas que colonizan de diversas maneras. Estos cambios pueden tener efectos profundos y altamente costosos para la fauna nativa, pero también para la producción animal (y la seguridad alimentaria) y la salud de las personas. Hasta donde se sabe, la Argentina se encuentra aún mayormente libre de las principales enfermedades problemáticas en especies no domésticas. Por ello, urge generar más conocimiento que permita un mejor diagnóstico de la situación actual y una evaluación informada de futuros riesgos. Se requiere, además, y tal como ocurre para las especies productivas, poner en práctica un monitoreo sistemático (p.ej. usando especies indicadoras o centinela) para la detección y respuesta temprana a posibles invasiones. Al mismo tiempo, es recomendable la implementación de buenas prácticas básicas, como evitar el contacto entre especies exóticas (silvestres y/o domésticas) y especies nativas, particularmente en áreas protegidas (p.ej. restringiendo o eliminando la presencia de ganado y mascotas). También se sugiere mejorar la capacidad para la vigilancia de enfermedades en especies nativas y la aplicación de medidas básicas de bioseguridad, como por ejemplo el uso de «lava pies» en el ingreso de senderos turísticos, para evitar la introducción accidental de patógenos exóticos.

Con la creciente conectividad y globalización, la contaminación por patógenos se está haciendo más prevalente, dispersa y común a nivel mundial. Al igual que otros países, la Argentina debe aspirar a que su fauna esté saludable y sus ecosistemas funcionales, libres de especies y patógenos invasores. Las lecciones aprendidas de otras regiones demuestran que estar adecuadamente preparados y alertas tiene un incalculable valor para proteger a nuestras especies y paisajes nativos, debiendo ser, por ello, de nuestra más alta prioridad.

Introduced pathogen-species association

Biological invasions are well-recognized drivers of biodiversity loss and ecosystem change (CBD, 2007). Similarly impactful, yet notably less acknowledged, are the pathogens often brought with introduced species (Daszak *et al.*, 2000). In this chapter, relevant aspects of the introduced pathogen-species association are described, and global literature is used to exemplify known impacts of introduced pathogens on native species and to summarize information on potentially harmful pathogens linked to introduced mammals in Argentina. Finally, this evidence is used to identify opportunities to enhance local conservation efforts by reducing risk and improving disease management practices.

Pathogens are an intrinsic part of biological diversity and ecological complexity in natural, healthy ecosystems. Furthermore, they are critical natural selection factors by which only the fittest individuals survive (Altizer *et al.*, 2003; Vander Wal *et al.*; 2014). In natural systems, complex host-pathogen co-evolution processes allow for a delicate balance, which keeps infections from necessarily leading to disease. However, when novel agents are introduced, disease-defense mechanisms may be quickly overcome (Roelke-Parker *et al.*, 1996; Hochachka and Dhondt, 2000; Altizer *et al.*, 2003). Introduced pathogens are more likely to produce severe wildlife epidemics than pathogens that locally evolved with their host (Dobson and Foufopoulos, 2001). Yellow fever, introduced to the Americas in association with the commercial practice of trading enslaved Africans, illustrates this fact. Lack of evolution-acquired immunity in New World primates (particularly in the genus *Alouatta*) leads to recurrent and devastating mortalities that have placed some species on the verge of extinction (Holzmann *et al.*, 2010; Moreno *et al.*, 2015; Kowalewski and Oklander, 2017). At the same time, even at sub-lethal levels, diseases can influence reproduction, survival, fitness, and abundance of wildlife populations, and pose a particularly significant risk for threatened and endangered species (Smith *et al.*, 2009; Pedersen *et al.*, 2017).

The close link between introduced invasive species and pathogens is revealed in the IUCN's list of the world's 100 worst introduced invasive species (Lowe *et al.*, 2000). Several of the fourteen mammal species on that list are notable for their roles in transmission of infectious diseases to native wildlife, livestock, or humans (*e.g.*, wild boar, *Sus scrofa*; red deer, *Cervus elaphus*; red squirrel, *Sciurus vulgaris*; brushtail possum, *Trichosurus vulpecula*; black rat, *Rattus rattus*; Lowe *et al.*, 2000; Dunn and Hatcher, 2015). Moreover, some have been responsible for species extinctions and dramatic ecosystem changes. Several examples worth highlighting include the extinction of the endemic Christmas Island rat (*Rattus macleari*) at the turn of the 20th century, due to the introduction of black rats hosting a pathogenic trypanosome carried by their fleas (Wyatt *et al.*, 2008). Also noteworthy is the morbillivirus, which caused rinderpest and was introduced to Africa from India with cattle (*Bos primigenius taurus*) to feed invading Italian troops in 1887. Rapidly spilling over to wild ungulates, in two years it exterminated 95% of buffalo (*Syncerus caffer*) and wildebeest (*Connochaetes* spp.), in addition to causing incalculable loss of farmed cattle and famine in humans, as it spread across the entire continent (Mack, 1970). The effects of rinderpest were so severe that it modified the distribution of several native ruminants and shattered human pastoral civilizations (Mariner *et al.*, 2012).

Disease is not only a consequence of biological invasion; pathogens can be key players in the success of the invasion itself. That is, introduced invasive species' pathogen loads are part of the mechanisms that enable their successful establishment in a new area (Vilcinskas, 2015). A common mechanism described in the ecology of biological invasions is that of the "novel weapon," also termed "spillover" of a co-invasive pathogen or pathogen pollution (Daszak *et al.*, 2000; Morand *et al.*, 2015; Vilcinskas, 2015). That is, the invasive species benefits from carrying pathogens that are harmless to the invasive host, but lethal to native species. For example, in the United Kingdom (UK), native red squirrels (*Sciurus vulgaris*) are being rapidly replaced by the invasive North American gray squirrel (*S. carolinensis*) because the latter carries a poxvirus which causes fatal disease only in the native species (Tompkins *et al.*, 2003). Red squirrel declines and replacement are up to 25 times higher in areas where squirrel poxvirus is present in gray squirrel populations (Rushton *et al.*, 2006). Similarly, introduced species can also "spillback" pathogens when they become part of an existing local pathogen cycle, amplifying its impact on the native host (Kelly *et al.*, 2009; Dunn *et al.*, 2012). While several examples of this mechanism exist for invasive plants, fish and marine invertebrates, there appears to be limited evidence for mammals (Kelly *et al.*, 2009).

Upon introduction, such pathogens rely on many host-dependent parameters, including rates of encounter, transmission, co-infection, mortality, and recovery, for their establishment and spread (Telfer and Brown, 2012). Worryingly, however, if native species prove to be competent hosts, some pathogens may persist even where the introduced host species fails. Such is the case of West Nile virus (WNV), which arrived in the United States of America (USA) in 1999 with an unknown carrier. Regardless of its original host, the virus quickly became established in local passerine birds and mosquitoes and within four years had reached nearly every corner of the USA and southern Canada (Sejvar, 2003). Despite the dominant role that avian species play in WNV transmission (McLean *et al.*, 2001), dozens of mammal species have since been exposed to the virus in North America (Root, 2013). Yet only a few, such as the fox squirrel (*Sciurus niger*), become viremic enough to be competent hosts (Root, 2013). Also, wild boar have been proposed as sentinels for WNV, since they are commonly exposed, are regularly available for sampling from control operations, and are widespread, particularly in rural areas where practicality of surveillance via report of dead birds is limited (Gibbs *et al.*, 2006).

An invasive species may also act as a facilitator for the subsequent invasion of an introduced pathogen. In Svalbard, Norway, the establishment of the tapeworm (*Echinococcus multilocularis*), which causes a rare, but potentially lethal human disease, known as alveolar echinococcosis, was enabled by the preceding introduction of the sibling vole (*Microtus* *levis*) (Henttonen *et al.*, 2001). This small mammal filled the previously inexistent role of intermediate host in the parasite cycle, which has the Arctic fox (*Vulpes lagopus*) or domestic dog (*Canis lupus familiaris*) as definitive hosts (Fuglei *et al.*, 2008).

Impacts of introduced pathogens on native species

Many introduced mammal pathogens have led to major ecosystem disruptions, modifying the ecology of an existing disease, or removing key species from food chains and habitats. For example, it is thought that the profound ecological and social changes following rinderpest's devastating path led to a massive epidemic that caused over 250,000 human deaths from African sleeping sickness in Uganda alone (Fèvre *et al.*, 2004). When tsetse flies (*Glossina* spp.), which are vectors of the deadly trypanosome parasite that causes sleeping sickness, were left without their primary food source (*i.e.*, cattle and wild ruminants), they turned to humans (Mariner *et al.*, 2012). This was facilitated by the colonization of tsetse flies as depopulated pasturelands reverted to shrubs and by large-scale restocking with trypanosome-infected livestock from remote locations (Fèvre *et al.*, 2004). Also of note, the arrival of *Rattus* spp., one of the most widespread introduced mammals, to the USA onboard ships in the late 1890s drove significant and lasting changes to prairie ecosystems. With the rats came fleas infected with the bubonic plague bacterium (*Yersinia pestis*) (Kugeler *et al.*, 2015). Plague, possibly the deadliest disease of all times, is considered to have shaped modern civilization through three massive pandemics (*i.e.*, Europe lost 60% of its population in the 14th century), according to the Center for Disease Control and Prevention from USA. Fortunately, plague's human death toll in the USA was halted by the timely discovery that it was treatable with antibiotics in the 1920s (Kugeler *et al.*, 2015). By then, however, plague had already reached the prairie dog (*Cynomis* spp.), its most emblematic native mammal victim. Completely vulnerable to plague, prairie dogs suffered about 98% reductions in population size and range during the 20th century, worsened by persecution as agriculture pests. Then, in a typical negative cascading effect, black-footed ferrets (*Mustela nigripes*) became the next casualty, both directly from plague infection and indirectly through mortality of prairie dogs, which is their main prey-base. The effect was devastating, and black-footed ferrets were declared extinct in the wild in 1987. They are currently listed as endangered and are supported by massive reintroduction efforts from captive populations (IUCN, 2012). The plague-prairie dog-ferret example illustrates the cascading, ecosystem-level impacts of an introduced pathogen removing a keystone species (*i.e.*, those with a much larger role in the structure and function of the ecosystem than would be expected from their abundance) (Walsh *et al.*, 2016). Moreover, loss of many grassland-dependent ecosystem services has recently been linked to prairie dog absence (Martínez-Estévez *et al.*, 2013). Invasive species can also directly disrupt ecosystem services linked to health, such as disease regulation. Wild boar in Hawaii are known to create breeding habitat for introduced mosquitoes by hollowing out ferns they feed upon, thus favoring vector-borne diseases, such as avian malaria and dengue fever that impact both wildlife and humans (Pejchar and Mooney, 2009). Likewise, the death of over seven million bats in the USA since 2006, due to the introduced fungal disease white-nose syndrome (WNS) (presumably introduced by scientists studying caves), entails massive losses in pest control services. It is estimated that one million little brown bats (*Myotis lucifugus*), the species most affected by WNS, can consume up to 1,320 metric tons of insects a night (when multiplied by seven the result is stunning). In financial terms, the value of this bat-dependent pest suppression plus concomitant reduction in pesticide use has been estimated to reach $53 billion US dollars per year (Boyles *et al.*, 2011; Kunz *et al.*, 2011).

Diseases associated with livestock are worth highlighting for two interrelated reasons. First, food animals are both vectors and victims of introduced pathogens, many of which are shared with native and introduced wildlife (*e.g.*, brucellosis, tuberculosis, influenza; Miller *et al.*, 2013). Second, in productive systems, perceived or actually failing yields from disease often lead to heightened conflict at the wildlife-livestock-human interface. Retaliatory killing of wild animals and, in the best-case scenario, controlled culling operations, are often the unfortunate result of disease-mediated livestock wildlife interactions (Miller *et al.*, 2013; Gortázar *et al.*, 2015). Moreover, once bidirectional transmission of pathogens between domestic and wild species is established, they become almost impossible to eliminate. Even well-designed or well-intended disease management efforts have suffered from the inherent complications of such shared cycles, particularly since interventions in wildlife populations are complex, expensive, controversial, and often ineffective (Gortázar *et al.*, 2015; Woodroffe *et al.*, 2016). Furthermore, these wildlife-livestock cycles often include a persistent environmental component by which re-infection continuously occurs. The badger (*Meles meles*)-cattle-tuberculosis (TB) triangle in the UK is a contemporary example of such a situation. Recent studies suggest that infectivity of pastures is so high and prolonged, that even with reciprocal cattle-to-cattle transmission control, badger culls to reduce wildlife-to-cattle transmission repeatedly fail to lessen disease burdens (Woodroffe *et al.*, 2016). Furthermore, localized reactive badger culling triggers both badger movement and changes in TB infection prevalence, increasing risk of new infections in cattle farms by 27% within a 1 to 5 km radius (Bielby *et al.*, 2016). Thus, contrary to expectations, these unfruitful attempts nurture generalized dissatisfaction, leading to intensified frustration in the farming sector and reactive distrust and antagonism in the observing public (*The Guardian*, 2016). A somewhat less contentious scenario exists in New Zealand, where TB is sustained by a suite of hosts, yet uniquely centered on an introduced marsupial, the brushtail possum (*Trichosurus vulpecula*) (Warburton and Livingstone, 2015). Since the 1950s, before possums were acknowledged as a wildlife vector of TB, they had already been recognized as a significant conservation pest and were under targeted control (Warburton and Livingstone, 2015). Despite its aggressive culling approach and the many impacted wildlife species (target and non-target casualties), the "TB-free New Zealand" campaign has been highly effective, is socially accepted, and shows promise for eradication of the disease in the next few decades (Warburton and Livingstone, 2015). Notwithstanding this success, control of livestock-threatening diseases can be even more challenging if the introduced pathogen accompanies a widespread, well-established, and culturally-valued invasive species, such as the wild boar (Keuling *et al.*, 2016; Ballari *et al.*, this volume). A current open-ended example is the ongoing and seemingly unstoppable expansion of African swine fever (ASF) across Europe and Asia (Gaudreault *et al.*, 2020). ASF is highly contagious and causes death from hemorrhagic disease in domestic and feral pigs, with mortality rates up to 100% (Gavier-Widén *et al.*, 2015). Originating from a food-borne geographic jump (food scraps from a ship from southern Africa were fed to pigs in the country of Georgia) in early 2007, pig-boar contact kick-started the ongoing epidemic (Sánchez-Vizcaino *et al.*, 2013). ASF quickly spread to neighboring countries, reached the European Union (EU) in 2104 and had affected at least eight EU countries by 2018 (Chenais *et al.*, 2018). In August 2018, the virus was also found in China and within the next year and a half had spread to 11 additional countries in Asia (Mighell and Ward, 2021). By 2021, the Asian outbreak had resulted in the death or culling of more than five million pigs (over 10 percent of the total pig population in China, Mongolia and Vietnam) and huge economic and food security consequences (Gaudreault *et al.*, 2020; You *et al.*, 2021). Of relevance for this chapter are the different pathways by which the disease is expanding. While in Asia it is mostly linked to pig farms and products (the latter oftentimes illegally transported by humans), in Europe the epidemic spread is closely linked to wild boar (Bosch *et al.*, 2017; Chenais *et al.*, 2018). Recent risk analyses for Europe suggest that wild boar habitat (contaminated by infected carcasses) and wild boar presence are the most important factors enabling the geographic spread of the disease. Concurrently, contact between wild boar and domestic pigs allows for repeated introductions of the virus (Bosch *et al.*, 2017; Chenais *et al.*, 2018). Under very different conditions, it took over 30 years to eradicate ASF from a previous introduction to Europe in the 1960s (Bosch *et al.*, 2017). In the current scenario, it is unlikely that such a success will occur anytime soon. The only effective containment and eradication of ASF thus far was achieved by the Czech Republic through a combination of quick reaction to the initial (small) outbreak, intensive surveillance and proper disposal of dead wild boar, and strict biosecurity to avoid transmission to domestic pig (State Veterinary Administration, Czech Republic, 2019). In the absence of a vaccine, early detection of infected wild boar remains the most relevant measure to stop ASF spread, in addition to quick removal of carcasses and strict control of pig and by product (including feed) movement (Guinat *et al.*, 2017; Cwynar *et al.*, 2019). In July 2021, ASF was detected in the Americas, specifically in Haiti and Dominican Republic, raising alarms for the region and activating a strong response to control the spread of the disease (World Organization for Animal Health, 2021). As will be discussed later in this chapter, expertise and multi-sectorial collaborations for surveillance are essential for timely detection and prevention of diseases that affect both wild and domestic animals.

Diseases of free-roaming pets or their feral counterparts, namely cats (*Felis sylvestris catus*) and dogs (*Canis lupus familiaris*), may reach native wild populations by mechanisms as straightforward as incursions of unvaccinated animals into wildlife heavens, or by intricate ecosystem changes, facilitating high environmental pathogen loads and consequent wildlife exposure. Canine distemper virus (CDV) has caused massive die-offs in endangered African wild dogs (*Lycaon pictus*) and no-longer-abundant African lions (*Panthera leo*) in the Serengeti ecosystem in Tanzania (Roelke-Parker *et al.*, 1996; Goller *et al.*, 2010). The Ethiopian wolf (*Canis simensis*), the rarest canid species in the world and the most threatened carnivore in Africa, is almost extinct due to the combined effects of rabies and CDV infections (Gordon *et al.*, 2015). In all the above cases, viral strains were backtracked to dog populations and were associated with poor healthcare and lack of vaccination. Irresponsible pet ownership is an all-too-common condition in human dwellings adjoining wildlife reserves (often intensified by poverty), which not only implies health risks, but also leads to wildlife losses from predation. Locally in Argentina, Ferreyra *et al.* (2009) found CDV—which was 97% identical to non-vaccine dog viral strains—killing crab-eating foxes (*Cerdocyon thous*) in the Parque Nacional El Palmar. The exact origin of the fox-killer virus remains unconfirmed, but at the time of the outbreak hunters with dogs had been allowed into the park as part of an introduced invasive species control program for wild boar and axis deer (*Axis axis*). Incursions of stray dogs from neighboring towns into the park might have been an alternative or additional entry options for the disease. In any case, while control of dog movements is known to be nearly impossible in vast areas with permeable boundaries, red flags should be raised whenever domestic species are purposely introduced to or placed in close proximity with wildlife in protected areas of any kind.

A contrasting, convoluted introduced-to-native wildlife pathogen pathway is exemplified by the feline protozoan *Toxoplasma gondii* infections in endangered southern sea otters (*Enhydra lutris nereis*) in California, USA. In a complex setting of intertwined land-use changes, this terrestrial cat-originated parasite ended up in a main sea otter food item (marine turban snails, *Tegula* spp.), exposing the highly specialized and voracious otters to life-threatening *T. gondii* loads (Conrad *et al.*, 2005; Mazzillo *et al.*, 2013). Investigations by several authors revealed a situation in which human population growth and urban development of coastal areas lead to unfiltered runoff and sewage heavily contaminated with *T. gondii* ending up in the sea. VanWormer *et al.* (2016) estimated a 44% increase in oocyst (the infective form of the parasite) delivery from land to sea between 1990 and 2010. The loss of estuarine wetlands is thought to have further contributed to the problem by eliminating natural filtering mechanisms. Shapiro *et al.* (2010) projected that erosion of 36% of vegetated coastal wetlands may increase the flux of oocysts by more than two orders of magnitude and that total loss of wetlands would result in a number three times higher. Sadly, a similar scenario seems to be unfolding in Hawaii, where at least 13 endangered Hawaiian monk seals (*Neomonachus schauinslandi*) have died from toxoplasmosis since 2001 (National Oceanic and Atmospheric Administration, 2022). *T. gondii* is only shed by felids. Thus, infection reduction can only be achieved by controlling feline sources of the parasite. A decade-old estimate reports a daunting 60 to 100 million feral cats in the USA (Loyd and DeVore, 2010).

From food reserves for shipwrecked sailors to sprouting businesses based on fur-bearing or agriculture animals, over the course of history humans have managed to re-arrange the natural distribution of animal species on every corner of the planet (McNeely, 2001). Recognizing the previously inadvertent impacts from such actions, current trade restrictions and biosecurity protocols are modern tools used by governments to prevent new invasions. International bodies, such as the World Organization for Animal Health (WOAH), set standards for the health of traded agriculture animals to which most countries adhere (WOAH, 2022). Yet no method has succeeded in yielding zero risk (Early *et al.*, 2016), and food mammals can still become invasive. For example, in Brazil the water buffalo (*Bubalus bubalis*) is thriving in feral populations and may be involved in the transmission of zoonotic and livestock-relevant pathogens (Barbosa da Silva *et al.*, 2014; Minharro *et al.*, 2016). Of additional concern is the shift in the drivers for non-agriculture animal movement worldwide. Today, demand for vertebrate wildlife species in the pet trade is exponentially increasing as more countries achieve higher wealth and living standards (Ding *et al.*, 2008). The current scale of the legal and illegal global wildlife trade is in the billions of animals and tens of billions of US dollars annually (Smith *et al.*, 2009; Rosen and Smith, 2010; Scheffers *et al.*, 2019). Beyond its impact on species extinctions and abundance, there is an underlying, but poorly recognized, risk of the pet trade becoming a source of introduced invasive species and diseases (Rosen and Smith, 2010; García-Diaz *et al.*, 2016; Lockwood *et al.*, 2019). Lockwood *et al.* (2019) provide several examples of pet trade-originated invasive reptiles, amphibians, birds and fish in North America and the EU. Moreover, Hulme *et al.* (2008) determined that pet escapes were the source of establishment for several introduced taxa in the EU, including mammals. Likewise, Ikeda *et al.* (2004) blame irresponsible ownership and release of pet raccoons (*Procyon lotor*) for their naturalization in Japan. The recent finding of raccoon roundworm (*Baylisascaris procyonis*), which causes serious disease in humans with a >40% case fatality rate (Sapp *et al.*, 2018), adds to the danger of this popular pet. The gravity of wildlife trade lies in the inadequacy of current regulations to detect the diversity of wildlife imported and assess the risk they pose as potential invasive species or hosts of harmful pathogens. In an analysis of the USA imports from 2000–2006, the majority of shipment records did not contain the appropriate level of taxonomic information, nor did they undergo mandatory testing for pathogens before or after shipment (Smith *et al.*, 2009).

A recent study showed that most countries have limited capacity to predict, detect, and act against invasions (Early *et al.*, 2016). This is particularly worrying in the context of increased trade and commerce, since successful prevention (via rapid eradication) hugely depends on early detection as well as rapid response to newly discovered invasions (Early *et al.*, 2016). It is also worth highlighting that once established, eradication of pathogens is just as complex, or likely much more, than that of any other introduced invasive species. Proof of this fact is that despite huge expense, technological progress, high social relevance, and concerted effort, only two diseases have been eradicated worldwide since the advent of modern medicine, namely smallpox in humans (in 1979; World Health Organization) and rinderpest in animals (in 2011; WOAH).

As shown in the global literature, the pervasive impacts of invasive pathogens (alone or in association with their introduced host) span the full spectrum from native to domestic species, natural to agriculture ecosystems, food security to human health and wellbeing. Importantly also, introduced pathogens place a substantial financial burden on the global economy, costing many hundreds of billions of US dollars each year (Pimentel *et al.*, 2001).

Links between potentially harmful pathogens and introduced mammals in Argentina

Despite bewildering numbers, broad geographic presence, and recognition of their likely impact on native wildlife health, very few studies have assessed the role of introduced mammals as disease hosts in Argentina. This is particularly notable for non-reportable diseases (*i.e.*, those not listed by the WOAH as mandatory due to their lower significance for international trade). The main exception is regular testing for a few pathogens of public health concern in species consumed by humans (*e.g.*, trichinellosis in wild boar, brucellosis in European hare, *Lepus europaeus*).

A non-comprehensive list of potential health hazards posed by introduced mammals and feral/free-roaming pets and livestock in Argentina is presented in Table 1. A focus was placed on pathogens linked to species previously identified as probable health risks (see Valenzuela *et al.*, 2014; Ballari *et al.*, 2016), as well as those known or suspected to be of concern for conservation, agriculture, or public health in other parts of the world. While not exhaustive, this table allows for a quick glimpse of latent risks based on reports from other countries or regions and locally, when available. It also permits a visualization of existing knowledge gaps and data restrictions, which abound. Diseases of non-feral livestock and domestic animals transmissible to wild mammals were purposely not included, as they are too vast to discuss in this chapter and can be found in specialized literature.

It is worth mentioning that livestock diseases are broadly believed to have had a significant role in the decline of several native ungulates. Such is the case for the Pampas deer (*Ozotoceros bezoarticus*) and the Patagonian huemul (*Hippocamelus bisulcus*), presumably affected by foot-and-mouth disease (FMD) and other cattle and sheep illnesses (summarized in Pastore and Vila, 2001; Uhart *et al.*, 2003; Uhart and Chang Reissig, 2006). While many historical reports were based on empirical observation, and diagnoses were not always confirmed, nowadays some of these risks are likely mitigated given active national plans for control of reportable diseases, such as FMD, brucellosis and tuberculosis in livestock (SENASA, 2017). Notwithstanding, forced sympatry with livestock in most areas where these endangered cervids remain is a matter of concern and should be proactively addressed to avoid pathogen spillover. Regardless of scale, livestock rearing and/or grazing concessions have been repeatedly acknowledged as a problem requiring immediate attention in national parks in Argentina (Martinez, 2008; Chang Reissig *et al.*, 2010). An urgent and timely call to action stems from several viral, bacterial, and parasitic livestock-origin diseases currently affecting the huemul in Chile. Vila *et al.* (2019) reported on severely incapacitating foot lesions caused by a parapoxvirus closely related to bovine papular stomatitis virus (BPSV) and pseudocowpoxvirus (PCPV) in Parque Nacional Bernardo O'Higgins. Likewise, huemul affected by ovine caseous lymphadenopathy (LAC – *Corynebacterium pseudotuberculosis*) require frequent medical interventions and suffer occasional mortality at Reserva Nacional Cerro Castillo (Morales *et al.*, 2017). Recently, a huemul killed by LAC in this protected area was found with lung cysts from a livestock strain of *Echinococcus granulosus*, a parasite spread by carnivores and responsible for hydatid disease in humans (Hernández *et al.*, 2019). But not only cervids are affected by livestock diseases. Between 2014 and 2019, sympatric populations of vicuña (*Vicugna vicugna*) and guanaco (*Lama guanicoe*) from Parque Nacional San Guillermo in Argentina were decimated by an epidemic of sarcoptic mange (Ferreyra *et al.*, 2022). It is hypothesized that this debilitating skin disease was introduced to the area by infected llamas (*Lama glama*) given to farmers near the national park in the context of a governmental livestock incentive program. Mange nearly extirpated the native camelids from the protected area, which had profound cascading ecological impacts,

Table 1. **(A)** Mammal species introduced to Argentina (* refers to species native to the mainland that have been introduced to Tierra del Fuego); **(B)** Pathogen transmission to environment and/or native species; **(C)** Impact area: relevant for wildlife (conservation concern); relevant for agriculture; relevant for public health. Impacts are either potential, known, unknown, or considered not relevant; **(D)** Reports of pathogen in alien species host in America and/or Argentina; **(E)** Reports of pathogen in native species in Argentina (disease, infection or exposure). Pathogens are either reported (reference) or not reported.

Introduced species (A)	**Associated pathogen**	**Relevance (B)**	**Impact area (C)**			**Reports of the pathogen/s (D)**		
			Conservation	**Agriculture**	**Public health**	**Americas**	**Argentina**	**Native species (E)**
American mink (*Neogale vison*)	*Leptospira* spp.	Potential source of waterborne pathogens	Unknown	Known	Known	Reported Chile[1]	Reported serology[2]	Not reported
	Canine distemper virus	Potential source for native mustelids and carnivores	Known	Not relevant	Not relevant	Reported Chile[3]	Not reported	Not reported
	Aleutian disease virus	Potential source for native mustelids and carnivores	Potential	Not relevant	Potential	Reported Canada[4]	Reported serology[2]	Not reported
	Toxoplasma gondii	May infect multiple hosts	Known	Known	Known	Reported Chile[5,6]	Reported serology[2]	Not reported
	Bovine tuberculosis (*Mycobacterium bovis*)	May infect multiple hosts; potential transmission to predators or native herbivores	Potential	Known	Known	Not reported	Reported serology[2]	Not reported
	Brucella abortus	May infect multiple hosts; potential transmission to predators or native herbivores	Known	Known	Known	Not reported	Reported serology[2]	Not reported
	Neospora caninum	Potential source for native carnivores	Known	Known	Not relevant	Reported USA[7]	Reported[2]	Not reported
	SARS-CoV-2	May infect multiple hosts; transmission to and from humans	Potential	Known	Known	Reported USA[8]	Not reported	Not reported
North American beaver (*Castor canadensis*)	*Giardia* spp., *Cryptosporidium* spp.	Potential source of waterborne pathogens	Unknown	Known[77]	Known	Reported USA[9,10]	Not reported	Not reported
Chital (*Axis axis*)	Bovine tuberculosis (*Mycobacterium bovis*)	May infect multiple hosts; potential transmission to predators or native herbivores	Potential	Known	Known	Reported USA[11,12]	Reported[13]	Not reported
	Leptospira spp.	Potential source of waterborne pathogens	Unknown	Known	Known	Reported USA serology[14]	Reported serology[15,16]	Reported serology pampas deer[17], marsh deer[18,19]

Table 1. (Continued).

Introduced species (A)	Associated pathogen	Relevance (B)	Impact area (C)			Reports of the pathogen/s (D)		
			Conservation	**Agriculture**	**Public health**	**Americas**	**Argentina**	**Native species (E)**
Fallow deer (*Dama dama*)	Bovine tuberculosis (*Mycobacterium bovis*)	May infect multiple hosts; potential transmission to predators or native herbivores	Potential	Known	Known	Reported USA[11,12]	Not reported	Not reported
Red deer (*Cervus elaphus*)	Paratuberculosis (*Mycobacterium avium* ssp. *paratuberculosis*)	May infect multiple hosts; potential transmission to predators or native herbivores	Known	Known	Potential	Reported USA[20,21]	Reported[22]	Not reported
	Bovine tuberculosis (*Mycobacterium bovis*)	May infect multiple hosts; potential transmission to predators or native herbivores	Potential[23]	Known	Known	Reported USA & Canada[12]	Not reported	Not reported
	Leptospira spp.	Potential source of waterborne pathogens	Known	Known	Known	Reported USA serology[78]	Reported serology[24]	Not reported
Wild boar (*Sus scrofa*)	Bovine tuberculosis (*Mycobacterium bovis*)	May infect multiple hosts; potential transmission to predators or native herbivores	Known[23]	Known	Known	Not reported	Reported[25]	Not reported
	Herpesvirus (Pesudorabies or Aujezky)	Potential source for wild carnivores	Known[23]	Known	Not relevant	Reported USA[26,27]	Reported serology[28,29,30]	Not reported
	Leptospira borgpetersenii	Potential source of waterborne pathogens	Unknown	Known	Known	Reported Brazil[31]	Reported[32]	Reported white-eared opossum[31]
	Leptospira spp.	Potential source of waterborne pathogens	Unknown	Known	Known	Reported Brazil[33]	Reported serology[29,34]	Not reported
	Trichinella spiralis	Potential source for carnivores and rodents	Unknown	Known	Known	Reported Chile[35,36]	Reported[37,38]	Reported puma, South American sea lion, opossum, armadillo[39,40,38,41]
	Toxoplasma gondii	May infect multiple hosts	Known	Known	Known	Reported USA[42]; reported Brazil[43]	Reported serology[44]	Not reported
	Brucella spp.	May infect multiple hosts	Known	Known	Known	Reported USA[45,46]	Not reported	Not reported
	Brucella suis	May infect multiple hosts	Known	Known	Known	Reported USA[47]	Not reported	Not reported

Table 1. (Continued).

Introduced species (A)	Associated pathogen	Relevance (B)	Impact area (C)			Reports of the pathogen/s (D)		
			Conservation	Agriculture	Public health	Americas	Argentina	Native species (E)
European hare (*Lepus europaeus*)	*Brucella* spp.	Potential source for other species	Unknown	Known	Known	Not reported	Reported[48,49]	Not reported
	Paratuberculosis (*Mycobacterium avium* ssp. *paratuberculosis*)	May infect multiple hosts; potential transmission to predators or native herbivores	Known	Known	Potential	Reported Chile[50]	Reported serology[48]	Reported serology mara[48]
	Neospora caninum	Potential source for native carnivores	Known	Known	Not relevant	Not reported	Reported serology[51]	Not reported
Mice and rats (*Mus* spp.; *Rattus* spp.)	*Yersinia pestis*	Source for wildlife; wild felids and other carnivores are highly susceptible	Known	Known camel, llama, goat, sheep[52]	Known	Reported USA[52]	Not reported	Not reported
	Trichinella spiralis	Potential source for carnivores and rodents	Unknown	Known	Known	Reported[53]	Reported rat[39]	Reported puma, South American sea lion, opossum, armadillo[39,40,38,41]
Muskrat (*Ondatra zibethicus*)	*Giardia* spp. *Cryptosporidium* spp.	Potential source of waterborne pathogens	Unknown	Known	Known	Reported USA[54,55]	Not reported	Not reported
	Toxoplasma gondii	May infect multiple hosts	Known	Known	Known	Reported USA[42]	Not reported	Not reported
	Alveolar echinococcosis (*Echinoccocus multilocularis*)	Potential source for humans and wildlife	Unknown	Not relevant	Known Europe[56]	Not reported	Not reported	Not reported
Feral cattle (*Bos primigenius taurus*)	Bovine tuberculosis (*Mycobacterium bovis*)	May infect multiple hosts; potential transmission to predators or native herbivores	Known	Known	Known	Reported USA[57]	Not reported	Not reported
	Brucella abortus	May infect multiple hosts; potential transmission to predators or native herbivores	Known	Known	Known	Not reported	Not reported	Not reported

Table 1. (Continued).

Introduced species (A)	Associated pathogen	Relevance (B)	Impact area (C)			Reports of the pathogen/s (D)		
			Conservation	Agriculture	Public health	Americas	Argentina	Native species (E)
Feral cat (*Felis sylvestris catus*)	Feline leukemia virus	Potential source for native carnivores	Known Florida panther (*Puma concolor coryi*)[58]	Known	Not relevant	Reported USA and Canada[58,59]	Reported serology[60]	Not reported
	Toxoplasma gondii	May infect multiple hosts	Known	Known	Known	Reported USA[61]; reported serology Brazil[62]	Reported serology[60]	Reported Geoffroy's cat[60], armadillo[63]
Feral dog (*Canis lupus familiaris*)	Canine distemper virus	Potential source for native carnivores and mustelids	Known	Not relevant	Not relevant	Reported Chile free-roaming and rural dogs[64,65]	Not reported	Reported mortality crab-eating fox[66,67]
	Rabies	Potential source for humans, domestic dogs and wildlife	Potential	Not relevant	Known	Reported USA[68,69] and Brazil[70]	Not reported	Reported bats[71,72], red fox[73]
Pampa fox* (*Lycalopex gymnocercus*)	Hydatid disease (*Echinococcus granulosus*)	Potential source for humans and wildlife	Unknown	Known	Known	Reported Chile[74]	Reported[75]	Not reported
Large hairy armadillo* (*Chaetophractus villosus*)	Brucellosis (*Brucella suis*)	Potential source for other species	Unknown	Known	Known	Not reported	Not reported	Reported[76]

References: [1]Barros *et al.*, 2014; [2]Martino *et al.*, 2017; [3]Sepúlveda *et al.*, 2014; [4]Nituch *et al.*, 2012; [5]Sepúlveda *et al.*, 2011; [6]Barros *et al.*, 2018; [7]Almería 2013; [8]Shriner *et al.*, 2021; [9]Dunlap and Thies, 2002; [10]Fayer *et al.*, 2006; [11]Waters *et al.*, 2011; [12]Griffin and Mackintosh, 2000; [13]Mc Cormick *et al.*, 2018; [14]Pedersen *et al.*, 2018; [15]Petrakovsky *et al.*, 2015; [16]Tammone *et al.*, 2018; [17]Uhart *et al.*, 2003; [18]Brihuega *et al.*, 2008; [19]Orozco *et al.*, 2020; [20]Jessup and Williams, 1999; [21]Williams, 2001; [22]Paolicchi *et al.*, 2001; [23]Gortázar *et al.*, 2007; [24]Brihuega *et al.*, 2003; [25]Winter *et al.*, 2016; [26]Pedersen *et al.*, 2013; [27]Witmer *et al.*, 2003; [28]Serena *et al.*, 2015; [29]Abate *et al.*, 2015; [30]Carpinetti *et al.*, 2017; [31]Jorge *et al.*, 2012; [32]Brihuega *et al.*, 2017; [33]Vieira *et al.*, 2016; [34]Abate *et al.*, 2021; [35]Landaeta-Aqueveque *et al.*, 2015; [36]Hidalgo *et al.*, 2019; [37]Cohen *et al.*, 2010; [38]Lauge *et al.*, 2015; [39]Ribicich *et al.*, 2010; [40]Castaño Zubieta *et al.*, 2014; [41]Pasqualetti *et al.*, 2018; [42]Ahlers *et al.*, 2015; [43]Santos Brandão *et al.*, 2019; [44]Winter *et al.*, 2019; [45]Leiser *et al.*, 2013; [46]Pedersen *et al.*, 2017; [47]Pedersen *et al.*, 2014; [48]Marull *et al.*, 2004; [49]Fort *et al.*, 2012; [50]Salgado *et al.*, 2011; [51]Baldone *et al.*, 2009; [52]Abbott and Rocke, 2012; [53]Ortega-Pierres *et al.*, 2000; [54]Kirkpatrick and Benson, 1987; [55]Bitto and Aldras, 2009; [56]Umhang *et al.*, 2013; [57]Miller and Sweeney, 2013; [58]Cunningham *et al.*, 2008; [59]Gibson *et al.*, 2002; [60]Uhart *et al.*, 2012; [61]Conrad *et al.*, 2005; [62]Costa da Silva *et al.*, 2014; [63]Kin *et al.*, 2015; [64]Garde *et al.*, 2013; [65]Acosta-Jamett *et al.*, 2015; [66]Megid *et al.*, 2009; [67]Ferreyra *et al.*, 2009; [68]Bergman *et al.*, 2009; [69]Velasco-Villa *et al.*, 2018; [70]Carnieli *et al.*, 2013; [71]Piñero *et al.*, 2012; [72]Torres *et al.*, 2014; [73]Ibañez Molina and Chang Reissig, 2019; [74]Aguilera, 2001; [75]Zanini *et al.*, 2006; [76]Kin *et al.*, 2014; [77]Gow and Waldner, 2006; [78]Bender and Briggs Hall, 1996.

affecting native predators, scavengers and the entire ecosystem (Monk *et al.*, 2022). This outbreak reinforced the fact that conservation and agriculture sectors can no longer operate independently and that there are serious, potentially irreversible, consequences to pathogen introductions to naïve wildlife populations. In contrast, and outside protected areas, several private initiatives have promoted wildlife-friendly livestock husbandry practices and responsible pet ownership, including adequate health care and disease prevention, albeit with fluctuating continuity and implementation success (Miñarro *et al.*, 2007; Marino *et al.*, 2008). Revitalizing such programs should be encouraged and recommended.

The few health evaluations available for native species in Argentina, such as guanaco (*L. guanicoe*) (Karesh *et al.*, 1998; Marull *et al.*, 2012; Rago *et al.*, 2022), Pampas deer (Fondevila *et al.*, 1999; Uhart *et al.*, 2003), marsh deer (*Blastocerus dichotomus*) (Orozco *et al.*, 2020). Vizcacha (*Lagostomus maximus*) (Ferreyra *et al.*, 2007), mara (*Dolichotis patagonum*) (Marull *et al.*, 2004), Geoffroy's cat (*Leopardus geoffroyi*) (Uhart *et al.*, 2012), maned wolf (*Chrysocyon brachyurus*) (Orozco *et al.*, 2014a), capybara (*Hydrochoerus hydrochaeris*) (Corriale *et al.*, 2013), and wild carnivores and marsupials (Orozco *et al.*, 2014b) show varying degrees of exposure to common domestic animal pathogens, in nearly all cases not obviously linked to disease in the species studied. The major caveat for these surveys is, however, that they are mostly based on antibody detection, which does not allow for recognition of current infection and can produce unreliable results if tests are not validated for the target species or pathogen (Gardner *et al.*, 1996). Nevertheless, wildlife disease surveillance via serological assays is a valuable tool in the absence of other options and allows for assessing the health history of a population. This information is essential to evaluate change over time (especially in relation to human activities and disturbance) and is of particular relevance for conservation strategies requiring animal movements, such as reintroductions and translocations (Gilbert *et al.*, 2013).

There are comparatively more reports on parasites of introduced mammals, in some cases including sympatric native species like mara, huemul and Pampas deer (Marull *et al.*, 2004; Kleiman *et al.*, 2004; Caporossi *et al.*, 2008; Chang Reissig *et al.*, 2010; Flueck and Smith-Flueck, 2012; Flores and Brugni, 2013; Gozzi *et al.*, 2013; Chang Reissig *et al.*, 2016). Several of these studies suffer from limitations like incomplete identification of pathogens (*i.e.*, parasites only identified to genera level from egg taxonomy). This shortcoming restricts interpretation of their significance for the host species' health and/or their likelihood of being shared between native and introduced species. To counteract these problems, in recent years more studies are using molecular diagnostics, which allow deeper understanding of the pathogens found, including genetic proximity between host species, origin, transmission, and evolution (Hernández *et al.*, 2019; see also Lizarralde *et al.*, this volume). Notwithstanding these advances, the majority of the studies referenced above do not report morbidity or mortality associated with parasite findings. Conversely, pathological levels of sheep parasite infestations were found in dead guanaco during a severe mortality event in Chubut province (Beldoménico *et al.*, 2003). Similarly, high loads of likely domestic cat-derived parasites were observed in Geoffroy's cats which died following a prolonged drought and prey decline period in central Argentina (Beldoménico *et al.*, 2005). Likewise, extremely high livestock parasite burdens were documented in marsh deer during several die-offs in Iberá wetlands in Corrientes province and in the Lower Delta of the Paraná River in Buenos Aires province (Orozco *et al.*, 2013; Orozco *et al.*, 2020). These examples underpin that while interaction with introduced species' parasites might be tolerated by native fauna under normal circumstances, introduced pathogens can become significant morbidity and mortality factors when local wildlife is subject to other stressors and adverse environmental conditions.

Considering that introduced animal diseases are listed as one of the main conservation threats for pretty much every threatened native large mammal in Argentina (SAyDS and SAREM, 2019), it is both striking and worrying that so little is known about them. While accessing rare native species is inherently complex and often not an option, indirect assessments are oftentimes possible, yet seldom conducted. In this way, studying pathogens in red deer, wild boar and feral cattle, which are more readily accessible and regularly harvested, would allow for some understanding of risks for overlapping endangered native southern pudu (*Pudu puda*) and Patagonian huemul. Even opportunistic and passive (non-invasive) gathering of samples (*i.e.*, feces, saliva) would fill in current basic knowledge gaps, over time enabling better informed management and conservation decisions. For example, by examining feces from Pampas deer, sheep, cattle and axis deer in Samborombón Bay (Buenos Aires province), Caporossi *et al.* (2008) showed that five parasite genera were shared between the first three, and one by all four species. These data allowed for targeted interventions in livestock to minimize risk for the endangered native deer (Marull and Uhart, 2008), and provided baseline knowledge for future monitoring.

Fortunately, and following methods applied in other countries for wildlife disease surveillance, increasing numbers of investigations are being conducted on samples collected opportunistically via an *ad hoc* network of wildlife researchers reporting to the Argentine national veterinary service (SENASA, A. Marcos personal communication). Moreover, several ongoing studies rely on samples collected by recreational hunters and/or culling and harvest operations, further broadening the reach of disease surveillance in terms of species and geographic coverage (*e.g.*, Tammone *et al.*, 2018, 2021). Importantly as well, there are new examples of participatory surveillance for wildlife disease morbidity and mortality events, such as that implemented by Orozco *et al.* (2020) for marsh deer, which are based on a network of researchers, field partners (veterinarians, park rangers, and local community), and decision-makers.

Opportunities to enhance local conservation by improving disease management

Recently, it has been pointed out that policies to control diseases caused by introduced invasive species that affect wildlife, ecosystems and their services must be enhanced, as they are lagging in comparison to efforts directed towards those diseases directly impacting humans, livestock and plants (Roy *et al.*, 2016). These authors also emphasize that dealing with this threat requires interdisciplinary expertise and inter-agency coordination. Based on the information conveyed in the preceding sections of this chapter, it seems like this is both wise and timely advice.

As previously described, introduced invasive species can change the dynamics of disease in colonized ecosystems in several ways. Rare local pathogens can become more common, if they can be amplified by the new invading host species. Alternatively, introduced species can bring associated introduced pathogens that find naïve hosts and propagate. These changes in the disease landscape can have profound and often costly impacts on native fauna, as well as on livestock, food security and public health (Bright, 1999; Charles and Dukes, 2007; Marbuah *et al.*, 2014; Monk *et al.*, 2022).

Currently, knowledge is scarce about whether or how invasive species pathogens impact and alter ecosystem processes in Argentina. Clearly, more research is needed to diagnose the present situation and assess future risks. Mirroring global priorities highlighted by Roy *et al.* (2016), the top of the list with regards to recommendations would be the collection of baseline information on the distribution and dynamics of introduced pathogens, hosts and vectors. Moreover, efforts should extend to developing methods for predicting host shifts, pathogen-host dynamics and the evolution of introduced pathogens, so that proper prevention, mitigation, and control can be implemented. Acknowledging that many suggestions have been made in earlier segments, below are a few additional summary recommendations specific to introduced and invasive mammals in Argentina:

Research. Many extant reports of disease impacts on native species are anecdotal. Also, risk appraisals are often based on generalizations (*i.e.*, all diseases of cats and dogs can be a threat for native carnivores). While valuable for context, there is a need to pinpoint exactly what the existing problems are so that they can be tackled, recognizing that resources (and oftentimes opportunities) are limited. Therefore, it is suggested that researchers need to:

- Carry out studies to learn if and how introduced pathogens disturb the health dynamics of endangered, indicator or special interest native species.
- Conduct such studies on invasive species, with a focus on pathogens that could pose a threat for sympatric native fauna.
- Create a curated database and sample biobank that can be accessed for research and surveillance, including prospective and long-term investigations.

Monitoring. Too often alarms ring when it is too late to act. Monitoring should allow for the detection of subtle changes, thereby providing an opportunity to react accordingly and in a more timely manner. Following the canary in the coal mine metaphor, researchers and managers could work together to:

- Use proven health indicators (*e.g.*, stress hormones, Alford *et al.*, 2007; hematological parameters and body condition, Beldoménico *et al.*, 2008, 2009) to anticipate declines and/or a collapse in diminishing populations.
- Systematically gather health data to define baseline conditions and learn about the natural history of wild species, particularly for those of highest conservation concern.

Management. Even simple interventions can have deep and long-lasting effects. The task may seem daunting, but starting basic and progressively increasing in complexity can provide a realistic pathway for effective progress and success in the context of logistical and budgetary constraints. Keep in mind that best practices are often enough to greatly reduce risk (Simons and De Poorter, 2009). Some possible actions include:

- Restrict/avoid contact between domestic animals and native fauna to decrease opportunities for pathogen spillover by:
  - Aiming for livestock-free protected areas. If livestock are allowed in protected areas, frequent health controls and mandatory preventive health plans (including vaccines and deworming) should be applied to minimize the possibility of disease transmission to wildlife. This should be extended to working dogs used on farms.
  - Enforcing extant regulations on pet possession in protected areas (*e.g.*, APN, 2013).
  - Encouraging responsible pet ownership and husbandry best practices in communities, particularly in the immediate vicinity of protected areas.
  - Establishing and enforcing plans for dealing with free-roaming and feral dogs.
- Restrict/avoid contact between introduced invasive species and native wildlife to decrease opportunities for pathogen spillover by:
  - Preventing introductions of new species, as well as limiting the geographic spread of invasive species already present in the country (*i.e.*, keeping red deer out of Santa Cruz province).
  - Ensuring good sanitation and effective separation of native wildlife from introduced species kept in enclosures (*i.e.*, those used for trophy hunting in game reserves).
  - Reinforcing regulations on imports of species and/or subproducts (*i.e.*, hunting lure) to avoid inadvertent pathogen introductions.
  - Avoiding supplementary feeding or any similar practice that might favor aggregation and close contact between native and introduced mammals.
- Improve wildlife disease surveillance by:
  - Favoring communication and coordination efforts between institutions and sectors (veterinary service, public health, veterinarians, biologists, national parks administration, wildlife experts) to enable an effective, functional and nation-wide wildlife disease surveillance system (Stephen *et al.*, 2018).
  - Using all ethical and planned culling and harvest opportunities to systematically monitor the health of introduced species and/or feral animals.
  - Setting up mechanisms that allow proper investigations of wildlife morbidity and mortality events (which often go undiagnosed), so that similar events can be prevented in the future (*e.g.*, Orozco *et al.*, 2020).
  - Extending surveillance in the face of climate change to detect introduction or range-expansion of disease vectors (*e.g.*, insects) of concern.
- Avoid accidental human introduction of pathogens by:
  - Implementing simple biosecurity measures in vulnerable protected areas that receive tourism. For example, the installation of footbaths in hiking trails could reduce the risk of tourists accidentally introducing pathogens attached to shoes when visiting an area with Patagonian huemul or other endangered fauna.
  - Following best practices and enforcing biosecurity routines for work/research involving native wildlife (mainly for park rangers and researchers). In general, avoiding unnecessary contact with humans (*e.g.*, restrict visitation to sensitive areas),

maintaining adequate hygiene when handling wild animals, avoiding touching sick or dead animals without suitable protective gear and training, and immediately reporting the finding of dead or sick animals to the authorities.

- Strictly enforcing regulations on garbage and waste removal and avoiding contamination of water sources (*i.e.*, do not feed wildlife).

There is an intentional bias in this list towards actions aimed at prevention. The reason is that preventing the introduction of diseases into susceptible populations is, and has always been, the most effective method of disease management (Wobeser, 2002). Moreover, Argentina is fortunately still mostly free (or blissfully ignorant) of diseases of concern (*i.e.*, those which are harmful to conservation, human health or the livestock trade) in wildlife species. This situation heavily contrasts with that of the USA, for example, where a number of reportable diseases, namely bovine tuberculosis, paratuberculosis, brucellosis, rabies, and cattle fever tick, have a wildlife reservoir; and where the complexities of this wildlife component are a recognized impediment to eradication (Miller *et al.*, 2013). Years of unfruitful trials in many countries (*e.g.*, USA, Canada, South Africa, UK, New Zealand) have shown that while bovine tuberculosis may be controlled when restricted to livestock, it is almost impossible to eradicate once it has spread into ecosystems with free-ranging maintenance hosts (Miller and Sweeney, 2013). Another example is brucellosis, which is expanding among Rocky Mountain elk (*Cervus canadensis nelsoni*) in the USA's Greater Yellowstone Ecosystem and re-emerging in cattle from this area after short-lived nationwide eradication from cattle in 2008. Recent studies have shown that despite billions of US dollars spent in control efforts, there is ongoing interspecific transmission of *Brucella abortus* between elk, bison, and cattle, and contrary to previous assumptions, elk have been the source of several outbreaks in cattle since 2002 (O'Brien *et al.*, 2017).

In closing, the axiom “an ounce of prevention is worth a pound of cure” is at the essence of ensuring healthy wildlife and functional ecosystems, free of introduced invasive species and pathogens. With increased connectivity and globalization, pathogen “pollution” is becoming more prevalent and widespread. Lessons from other parts of the world lend proof to the incalculable value of adequate preparedness and early response. Therefore, this must be among the highest priorities for environmental management and conservation.

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