Australia’s Faunal Extinction Crisis – Senate inquiry submission

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Disease should be considered a major threatening process leading to Australian fauna declines and extinctions

The following submission relates specifically to Points 1, 3, 4, 8 and 9 of the Committee’s Frame of Reference.

Key points:

- Diseases can be important independent threatening processes for wild animal populations, that directly cause faunal declines and extinctions, with current examples in Australia including chytrid fungus, psittacine beak-and-feather disease and Tasmanian devil facial tumour disease (Section 1)
- Other factors, such as habitat degradation/destruction, climate change and invasive species may act synergistically with disease to cause declines in species (Section 2)
- Known infectious diseases with population-level effects in Australian fauna include chytrid fungus, psittacine beak-and-feather disease, Tasmanian devil facial tumour disease, sarcoptic mange, chlamydiosis, toxoplasmosis and pilchard herpesvirus. The level of understanding of how these diseases affect our wildlife populations varies significantly, but all desperately require further research to effectively protect affected species. Other infectious and non-infectious diseases may play crucial roles in the current and future decline of Australian fauna, however, there is currently insufficient baseline data and surveillance to effectively detect or address these threats and avert future extinctions (Section 3)
- Key actions needed to ensure diseases are appropriately considered to prevent and address faunal declines are (Section 4):
    - Formal inclusion of disease in investigating and managing faunal declines
    - Biosecurity at Australian borders must include significant consideration of prevention of entry of infectious diseases with potential significance for Australian fauna

- Meaningful financial and administrative support for active and passive surveillance of wildlife for presence and impact of disease for the purposes of conservation
- Consistent, meaningful and long-term funding of a collaborative, strategic framework for wildlife health and disease outbreak investigation and response as part of managing species and threatened species programs. This includes recognition of the importance, and funding, of research that addresses the clinical diagnosis, ecological consequences and mitigation options for disease impacting Australia's wildlife.
- Consistent inclusion of veterinary experts on Threatened Species Recovery Teams in recognition that both veterinary and ecological knowledge is required to deliver prudent management solutions.

1. Background

Australia has a long list of Extinct (at least 54) and threatened animal species. Those currently Critically Endangered include eight fish species, five frog species, ten reptile species, seventeen bird species, nine mammal species and 29 "other" species, most of which are insects and molluscs (e.g. snails) (Australian Government, 2018a). The threats facing our wildlife are varied and many, although the underlying problems of habitat destruction, habitat degradation, invasive pest species and, especially into the future, climate change, are likely to significantly affect and modify the effects of all other threatening processes, including disease.

However, while there is a great awareness of the significance of these underlying problems, our understanding of the role of disease as a threatening process in wild animal populations is still very limited. There are dramatic and very recent examples of how disease can devastate wildlife populations. White Nose Syndrome, a fungus introduced to North America from Europe or Asia, has already killed millions of insect-eating bats in North America (e.g.Leopardi et al., 2015). Chytrid fungus is thought to be responsible for the decline of over 500 frog species worldwide, including 43 in Australia (Scheele et al., 2017). Seven of these Australian species, which were unique to our country, have recently been declared, or are likely to be, extinct (Scheele et al., 2017). In 2015, the then locally abundant population of Bellinger River Snapping Turtle (*Myuchelys georgesi*), a freshwater turtle restricted to the Bellinger River Catchment in northern New South Wales, declined dramatically over approximately seven weeks (Zhang et al., 2018). The decline was estimated to be approximately 90% of the population (https://www.abc.net.au/news/2019-05-23/rare-endangered-bellinger-river-turtles-returned-to-wild/11141358), with the majority of adult turtles dying (Spencer et al., 2018). Subsequently, a previously unknown virus (now called Bellinger River Virus) was identified as the cause of this population crash (Zhang et al., 2018). The population was subsequently re-classified as Critically Endangered under the EPBC Act and is now at high risk for extinction. **Despite these and many other examples, there is practically no mention of disease as a threatening process in the federal government's current Threatened Species Strategy (Australian Government, 2015), which has significant implications for the availability of funding in this area. We strongly believe that this is a significant and highly problematic omission, and therefore ask the Environment and Communications References Committee to include disease as significant factor in Australia's faunal extinction crisis**.

Although such a recognition will represent an essential first step in starting to effectively address disease as a significant contributor to extinction events, it is worth noting that even chytridiomycosis and Psittacine Beak and Feather Disease (for details of these disease see sections 3.1 and 3.3), which are both listed as Key Threatening Processes, last received federal Threat abatement project funding in 2011/12 ($40,000) (https://www.environment.gov.au/biodiversity/invasive-species/funded-projects) despite the relevant Threat Abatement Plans and numerous scientific papers (e.g.Skerratt et al., 2016) clearly articulating what actions and funding are needed to save Australian species. The following discussion will briefly outline how disease may cause species and/or population declines including specific examples relevant to Australian wildlife.

2. How can disease cause faunal declines and extinctions?

The population numbers of wild animal populations fluctuate naturally, due to births, deaths, immigration and emigration; this is referred to as population dynamics. Disease may affect all these drivers of population dynamics, but predominantly through causing mortality (i.e. more deaths) and/or affecting reproductive rates (i.e. most often fewer births, although there can be more complex long-term effects). In many cases, any specific disease will only affect a relatively minor portion of the total population, and its effects will contribute to sustainable population dynamics together with other factors such as predation, senescence (resulting in decreased fertility with age, and eventually death) or dispersal. Perhaps because of this, at least in the past, the important role disease may play in population declines has often been underestimated or neglected. In more recent years, however, it has become increasingly clear that disease may be a major driver of faunal declines and extinctions worldwide (Cunningham et al., 2017).

2.1 Factors which may be involved in “unbalancing” the relationship between disease and population dynamics include:

1. Existing disease-causing agent (pathogen) is introduced into a (naïve) population, i.e. the species or population has not evolved with the pathogen, has no immunity to it, and is highly susceptible. This has become a significant occurrence due to global trade and travel and may result in massive mortalities and wide-spread declines. Introduction of disease into naïve populations is also a significant risk in the translocation and reintroduction of threatened species and must be adequately mitigated in such programs.

   Examples: *White Nose Syndrome in North American bats*; C*hytrid fungus in amphibians* (both briefly described above)

2. Populations are already threatened due to other processes, e.g. habitat destruction and/or degradation, climatic changes and extreme events, and pressure from invasive predators and herbivores). Mass mortalities that were previously absorbed within large, generally healthy populations are of much greater significance if the total population size is already significantly diminished. Some of the long-term consequences of this include reductions in the genetic diversity of the population, leading to genetic bottlenecks which may make the population more susceptible to

future threats. In addition to obvious mortality events, disease can have subtle, sub-lethal effects on populations that nonetheless have profound consequences when combined with other pressures (e.g. increased predation and competition from introduced species).

Example: *Saiga antelopes* (Saiga tatarica) *in central Asia* have been pushed towards extinction due to hunting/poaching pressures, with only 300,000 remaining at the start of 2015. In May 2015, 200,000 of these animals died within 10 days due to Pasteurellosis, caused by bacteria that live in the intestines of healthy animals, but which may cause fatal disease under certain adverse environmental conditions (Kock et al., 2018). In the case of the 2015 event, these conditions appear to have been high temperatures and humidity after a harsh winter, which left the animals in poor body condition and thus more susceptible to disease.

3. New pathogen arises, i.e. as a result of random mutation or recombination of existing pathogens, a new pathogen arises which then causes significant disease in the species (one or multiple, depending on the pathogen) it affects. The consequences are further exacerbated if the new pathogen is readily spread within and between populations, and/or if the population is already threatened.

Example: *Tasmanian Devil Facial Tumour Disease 1 (DFTD 1)* was first seen in north-east Tasmania in 1996. DFTD is a transmissible cancer, probably passed on through biting, which originated from a single mutated cell in a female animal. At that stage, the Tasmanian devil (*Sarcophilus harrisii*) was a species of Least Concern; as a direct consequence of the rapid and large-scale spread of this disease, in 2008 the species was listed as Endangered (Australian Government, 2018a) with estimated declines of at least 60% of the overall population, and 90% in the areas where the disease was first observed (McCallum et al., 2009). In 2014, a second cancer type, called DFTD2 was discovered; the significance of this for the population is as yet unknown.

4. Non-infectious disease processes, such as toxicity due to heavy metals or pesticides, lead to direct mortalities or sub-lethal effects that impact animal health, reproduction and/or behaviour.

   Examples: Lead toxicity in raptors from ingestion of carcases is a cause of neurological disease and death, but also at sublethal levels has been shown to negatively affect foraging and hunting behaviour and increases mortality risk (Ecke et al., 2017). Long term exposure to organochlorine (OC) pesticides and the more persistent polychlorinated biphenyls (PCBs), which have well-established dose-dependent toxicities to birds, fish and mammals, has been shown to impact populations of orcas and dolphins due to reproductive toxicity (Jepson et al., 2016).

5. Other factors contributing to spread of disease in wildlife populations include: chronic stress (e.g. due to habitat degradation/destruction, climate change, introduced pest species competition, resource shortages) (Hing et al., 2016), invasive species acting as disease reservoirs resulting in persistence of a pathogen in a population and ongoing disease occurrence (typically the reservoir species are introduced directly or indirectly through human activity)

   Example: *Squirrelpox virus* causes a fatal disease in native red squirrels (*Sciurus vulgaris*) in Great Britain; this squirrel species is already threatened due to other factors (habitat loss, competition with introduced grey squirrel (*S. carolinensis*) (Collins et al., 2014). In addition to providing competition for habitat and food, the grey squirrel also acts as reservoir for the squirrelpox virus. Grey squirrels do not tend to show signs of disease when infected but will readily pass on the virus to red squirrels. Presence of grey squirrels infected with the squirrelpox virus results in much higher (at least twenty times) mortality rates in red squirrels than when uninfected grey squirrels are present and have caused serious population declines and local extinctions of red squirrels in Great Britain.

3. What does this mean for Australian fauna?

Australian wildlife is no exception when it comes to the effects of disease on population health, and there are numerous known examples of disease impacts on native species causing significant declines and/or extinctions. Below is a list and short description of the most important diseases we are currently aware of. However, there are massive gaps in our knowledge of the diseases of Australian fauna and, even more importantly, of their role at a population level (i.e. whether these diseases are likely to constitute a significant threat to the conservation of a species). It is thus reasonable to assume that this list is by no means exhaustive, and that some declines and/or extinctions are occurring without us ever realising that disease is or was a significant contributing factor.

3.1. *Chytridiomycosis caused by Chytrid fungus (Batrachochytrium dendrobatidis):* affects amphibians

This disease was recognised by Australian researchers (Dr Lee Berger, Dr Rick Speare and others) in the 1990s (Berger et al., 1998). It is believed to be responsible for dramatic amphibian population declines worldwide from the 1970s onwards, including the extinction of seven Australian frog species such as the northern (*Rheobatrachus vitellinus*) and southern gastric brooding (*R. silus*) frogs, both highly unique species (Scheele et al., 2017). The fungus survives particularly well in cool, humid climates and is a major continuing threat for a number of already threatened frog species, including (among others) the Baw Baw frog (*Philoria frosti*) and spotted tree frog (*Litoria spenceri*) in Victoria; the northern (*Pseudophryne pengilleyi*) and southern corroborree (*P. corroboree*) frog, the yellow-spotted tree frog (*L. castanea*) and spotted tree frog in New South Wales; and the Kroombit tinker frog (*Taudactylus pleione*) in Queensland (Scheele et al., 2017). The disease was formally recognised as a Key Threatening Process by the Commonwealth in 2002 (Australian Government, 2018b), yet there is only fleeting mention of the disease in the Threatened Species Strategy (Australian Government, 2015). Some of the key factors affecting the spread and impact of chytrid in Australian frog populations include: onset of reproductive age (some populations simply persist by replacing themselves every year with new offspring, as the adults die from chytrid disease); populations that are already in decline due to other factors; existence of disease resistant reservoir species (e.g. eastern froglet (*Crinia signifera*)); general water quality and biodiversity in water bodies;

and climate change. Targeted and long-term monitoring has been key to understanding the impacts of chytrid on populations, but this has only been possible for a few key species (Scheele et al., 2017; West, 2015). The impacts on most species are still unknown. Very few options exist to mitigate the threat of chytridiomycosis, and so further research is urgently required to determine if populations can develop resistance to infection, if resistance can be engineered and to investigate alternative options to create safe-havens for susceptible threatened amphibians.

3.2. *Tasmanian Devil Facial Tumour Disease*: affects Tasmanian Devils

Tasmanian Devil Facial Tumour Disease (TDFTD) is an infectious cancer (which is very unique, there is only a handful of them in the world) which has affected Tasmanian devils since 1996 (Obendorf and McGlashan, 2008). It is transmitted through biting, with the most dominant and strongest animals being the best spreaders (because they bite a lot) (Wells et al., 2017). The disease causes extensive tumours, especially around the head region, which may spread to the entire body, and almost inevitably kills the host within a few months. It has now spread almost throughout Tasmania and has reduced the Tasmanian devil population from a very healthy number to less than 40% of the original population across the island. In the regions where the tumour originated, populations are at around 10% of the original population (McCallum et al., 2009). A second infectious cancer was recognised in 2014, but the significance of this is not yet known (Pye et al., 2016). The Tasmanian devil is the apex predator in Tasmania, meaning that its decline, and potential extinction, is likely to have major ramifications for Tasmania’s ecosystem and may in fact result in the decline of additional native fauna. Extensive management and research efforts have established insurance populations and are working towards ways of protecting animals against infection, but continuing work is needed to ensure this species (whose populations were already affected by limited genetic diversity) does not eventually become extinct.

3.3. *Psittacine Beak and Feather Disease Virus*: affects many bird species, with disease primarily in parrots

Psittacine beak and feather disease (PBFD) is caused by beak and feather disease virus (BFDV) and has probably existed in Australian parrot populations for a long time. Not all parrot species are equally susceptible to developing disease when infected. However, those who do develop disease generally succumb within weeks to a couple of years, depending on age at infection (Raidal et al., 2015). Psittacine Beak and Feather Disease was listed as a Key Threatening Process by the Commonwealth in 2001 (Australian Government, 2018b). While the level of infection in some parrot species with healthy population numbers is very high, e.g. in sulfur-crested cockatoos (*Cacatua galerita*), the disease is thought to pose a significant risk for extinction to already threatened species, such as the orange-bellied (*Neophema chrysogaster*) and swift (*Lathamus discolour*) parrots (Raidal and Peters, 2018). Both of these species are on the brink of extinction, believed to be a result of habitat destruction and degradation, with very few individuals still living in the wild. Both populations are thus particularly susceptible to any effects associated infection with BFDV (Australian Government, 2005). Consequences of infection in these threatened populations include premature death, which not only immediately decreases population size, but also reduces the number of potential future offspring because the dead bird will no longer contribute to the reproductive output of the population. Great management and research efforts are going into the conservation of these two species, including captive breeding and release, and work into disease prevention, e.g. through vaccination. However, the real effects of the disease at a population level in threatened and non-threatened parrot species are still very poorly understood. While other species are currently less severely affected by PBFD, it is highly likely that the disease will pose a serious risk to other parrot species undergoing current or future declines. Much work is needed to ensure this disease does not lead or contribute to the decline or extinction of Australian bird species.

3.4. Chlamydiosis (Chlamydia pecorum and *Ch. pneumoniae)*: affects koalas

Chlamydiosis is a widespread infection of koalas (*Phascolarctos cinereus*) throughout Australia, with only a few chlamydia-free populations. The disease is thought to have been introduced to Australia with European settlers (Jelocnik et al., 2013) and causes eye-disease and/or disease of the kidneys, urinary and reproductive tract in koalas, often resulting in infertility (Polkinghorne et al., 2013). Reproductive rates in affected populations are significantly lower than those not infected (McLean and Handasyde, 2006). The prevalence of infection varies significantly between southern Australian (Victoria and South Australia – high koala population densities and lower chlamydia prevalence) and the rest of the country which has koalas (New South Wales and Queensland – lower koala population densities and higher chlamydia prevalence) (Patterson et al., 2015). There appear to be significant differences in how chlamydia affects koalas between the northern and southern populations, with northern populations apparently more severely impacted. However, the reasons for this are still quite poorly understood. We also have no good understanding of how chlamydia affects koalas within free-ranging populations from birth to death, as there is relatively little (in Victoria there is none) long-term data on individuals within populations with regards to infection status, reproductive effort and clinical signs. While there are significant research and management efforts underway to better understand the role and effects of chlamydia in koala populations, and to develop ways of effectively preventing and treating the disease, we are still a long way from knowing enough to be able to reduce the effects of chlamydia on threatened koala populations, especially in the northern populations.

3.5. Koala Retrovirus (KoRV): affects koalas

There are different strains of KoRV, the best described strains being KoRV A and KoRV B. KoRV A is ubiquitous in koalas from Queensland and New South Wales, but less common in Victorian koalas. The health effects of infection with KoRV are not well understood, but it appears that infection with KoRV A in Victorian koalas, but not those in Queensland or New South Wales, is associated with a greater likelihood of suffering from chlamydial disease (see above) (Legione et al., 2017). On the other hand, while no cases of infection with KoRV B have been documented from Victorian koalas, those koalas in Queensland and New South Wales infected with KoRV B also had a higher chance of suffering from chlamydial disease (Waugh et al., 2017). Retroviruses in other species may be associated with suppression of the immune system and development of cancer, and thus there has long been speculation that a similar mechanism may be true for KoRV. There is some evidence that KoRV may potentially be associated with common koala cancers such as lymphoma and leukaemia (Tarlinton et al., 2005). Our northern koala populations are threatened (Vulnerable, according to EPBC List (Australian Government, 2018a)), and, alongside predation and habitat destruction, disease is likely to be a major factor in their decline. We urgently need to gain a better understanding of the complex disease interactions that appear to be occurring in koala populations. Without these, it will be impossible to design effective conservation and management strategies, or to work towards protecting already threatened populations from the additional effects of disease. Long term funding and research is needed.

3.6. Mucormycosis (Mucor amphibiorum) in platypus: **affects platypus in Tasmania**

This disease is caused by a fungus which is common in northern Australia and may also cause disease in amphibians, but used to be exotic to Tasmania (Connolly, 2015). While it is not clear how the fungus came to Tasmania, it is responsible for causing skin ulceration leading to disease of internal organs and, ultimately, death in affected Tasmanian platypus (*Ornithorhynchus anatinus*). The distribution of the disease across Tasmania, and the prevalence in Tasmanian platypus, is not fully understood due to a lack of specific surveillance, but it may have originated from the Tamar River catchment spreading towards north-west (Macgregor et al., 2010). There are significant knowledge gaps as to the significance of this infection in Tasmanian platypus, and how great a risk it poses to the Tasmanian platypus population. Active research and diagnostics are needed to address this. It is also not known whether spread of the fungus to southern mainland Australia could potentially be a threat to those platypus populations.

3.7. Toxoplasmosis (Toxoplasma gondii): **affects all warm-blooded animals, marsupials may be particularly susceptible:**

Toxoplasmosis is the disease caused by the protozoan parasite *Toxoplasma gondii*. *Toxoplasma* is a parasite of cats and is shed into the environment in the faeces of infected felines. All warm-blooded animals (i.e. mammals and birds) can be infected with *T. gondii* and act as intermediate hosts. Intermediate hosts typically develop a chronic infection, with *T. gondii* forming cysts within their tissues (predominantly in muscle and the central nervous system). The organism survives in these tissue cysts and remains infectious. Cats are infected when they consume tissues from an infected intermediate host; other carnivorous species can also be infected in this way and will develop tissue cysts. Most intermediate hosts do not experience significant disease, unless they are young or immunosuppressed. Australian marsupials are an exception to this rule, however, and it is thought that they are particularly susceptible to this disease as they did not evolve in the presence of cats and their parasites (e.g.Canfield et al., 1990). Native rodents may also be at an increased level of risk because of their isolation from cats and *Toxoplasma* in recent evolutionary history. Both marsupials and native rodents may develop acute disease after their first exposure to the parasite, or they may develop disease later due to the release of the organism from 'reactivated' tissue cysts. Outbreaks of fatal toxoplasmosis have been reported in a number of our native species, including, but not limited to, bare-nosed (common) wombats (*Vombatus ursinus*) (Donahoe et al., 2015), and the critically-endangered eastern barred bandicoot (*Perameles gunnii*) (Obendorf and Munday, 1990) . Toxoplasmosis has been implicated as a contributory factor in the decline of a number of native small mammal species, although much of this evidence is circumstantial (Hillman et al., 2016). *Toxoplasma gondii* infection has also been detected in marsupials not showing signs of disease, however, it is thought that such chronic infections reduce longevity in the wild. The parasite is known to increase 'risky' behaviours in mice (Berdoy et al., 2000), and, if present in marsupials, these behavioural changes probably reduce survival by increasing the likelihood of other causes of death, such as predation and road trauma. Stress is also highly likely to play a role in the reactivation of *Toxoplasma* from tissue cysts, and therefore other stressors such as habitat degradation and limited food availability may increase the impact of this disease. In order to understand the role of *Toxoplasma* as a cause of disease and its contribution to population declines in Australian fauna, extensive further research is required. In particular, long-term studies measuring the survival and reproductive success of wild, infected individuals are essential to understand how this disease effects Australian native species at the population level.

3.8 Trypanosomes (Trypanosoma spp): **mammals, birds and amphibians**

Trypanosomes are a type of parasite that may infect a wide range of vertebrates, with several species occurring worldwide. They are very common in Australian wildlife, and although they are capable of causing severe disease and death, most of the Australian species of this parasite observed have not been described (Averis et al., 2009). The path of transmission between animals includes a "vector" (an animal that is infected by the parasite, allows the parasite to multiply within, and then passes it on to another animal species – typically these are invertebrate species such as leeches, biting flies or mosquitoes). The vector(s) for trypanosome infection in Australian wildlife are largely unknown. However, it is thought that trypanosomes played a significant part in the recent decline of the now Endangered woylie (*Bettongia penicillate ogilbyi*) (Australian Government, 2018a) in Western Australia (Thompson et al., 2014), and the extinction of the native Maclear's rat (*Rattus macleari*) on Christmas Island, subsequent to introduction of exotic species of rodents to the island (Wyatt et al., 2008). There are massive knowledge gaps in our understanding of how common this parasite is in Australian fauna and of the effects of infection at the individual and population levels.

3.9. Sarcoptic mange (Sarcoptes scabiei): affects mammals, including wombats and koalas

Sarcoptic mange is caused by a parasitic mite, which may be transmitted between animals (and humans) through direct contact or from contact with mites in nests or burrows (after they have fallen off an infected animal) (Skerratt et al., 1998). This mite was introduced to Australia, probably either through red foxes (*Vulpes vulpes)* or domestic dogs, and all mammals are potentially susceptible. The mite causes severe itchiness and widespread thickening and crusting of skin, which results in secondary infections, weakening, and ultimately may lead to death. Wombats are especially susceptible to the disease: it causes their entire body to be covered in scabs, they are seen out feeding during the day time, have major loss of body condition and ultimately often succumb to the infection (Skerratt et al., 1998). The disease is seen commonly in bare-nosed wombats (*Vombatus ursinus*) and occasionally in southern-hairy nosed wombats (*Lasiorhinus latifrons*). While bare-nosed wombats are still relatively common overall, there are many small local populations with high prevalence of sarcoptic mange that are highly susceptible to decline or extinction due to infection (Martin et al., 1998). In Tasmania, the disease has recently caused a 94% decline of bare-nosed wombats at Narawntapu National Park, with all infected wombats succumbing to disease (Martin et al., 2017). Wombats are a very charismatic species, and ill wombats are highly visible to the public, causing significant public distress. There have been a number of treatment trials run both through research groups (e.g. University of Tasmania, University of Sydney) and community groups, however, so far there is no effective way of treating sarcoptic mange at the population level. Extensive research is needed to investigate potential ways of preventing and treating infection beyond the individual animal level, and to prevent further local or widespread declines or extinctions. Sarcoptic mange is also increasingly observed in koalas, and it is unknown whether this is an emerging problem that may spread through a significant portion of the koala population (Speight et al., 2017).

3.10. Pilchard Herpesvirus: affects Australasian pilchards

In 1995 the introduction of a novel herpesvirus resulted in large scale mortalities of Australasian pilchards (*Sardinops sagax neopilchardus*), with subsequent secondary impacts to piscivorous birds such as penguins and gannets, which experienced increased mortality and lower breeding success (Whittington et al., 2008). Pilchard mortality was as high as 75%. Similarly, devastating outbreaks were repeated in 1998 and 1999, significantly impacting commercial fisheries, which take approximately 40,000 tonnes of pilchards annually. The virus now appears to have become permanently established in the Australian pilchard population.

3.11. White Nose Syndrome (Pseudogymnoascus destructans): **affects insect-eating bats**

Insectivorous bats play an essential role in the ecosystem. They each consume thousands of insects per night, and American estimates of their economic value for pest control are from 3.5 – 53 billion USD per year (Boyles et al., 2011). White Nose Syndrome was introduced to North America around 2006, most likely from Europe or Asia (Zukal et al., 2016). It is believed that it has since killed millions insect-eating bats in North America, where the disease is rapidly spreading north and west from where it was originally discovered in New York State. In affected caves, often more than 90% of all bats are killed (typically many thousand) (Turner et al., 2011). So far, eleven North American bat species are confirmed to have been affected by White Nose Syndrome, including two Endangered and one Threatened species (White-Nose Syndrome Response Team, 2018). Another six species may carry the fungus but do not appear to become ill. Those who are susceptible are typically hibernating and cave-dwelling bats (Wilder et al., 2011). Cave-dwelling bats accumulate very densely in large numbers, which favours transmission between bats; further, the microclimate of caves appears to favour survival of the fungus. Hibernating bats typically become infected before onset of hibernation. Infection causes repeated arousal during winter, which uses up significant energy reserves that are intended to last through the entire hibernation period. This results in bats flying out of the cave to find food and water (which is almost impossible in North American winter) and eventually becoming so emaciated that they die from starvation and dehydration (Verant et al., 2014).

A risk assessment for White Nose Syndrome in Australia found that the introduction of the fungus into Australia was very likely over the next ten years (Holz et al., 2016), although, due to climatic differences compared to North America (notably the absence of very cold winters), fewer of our bat species would be likely to be significantly affected. Nevertheless, there are six species of cave-dwelling Australian insect-eating bats living within climatic zones where cave temperatures would allow for survival of the fungus. In addition, these bats go into torpor, a milder form of hibernation, and some have a naturally limited distribution, which makes these populations extremely susceptible to the effects of significant mortality events. One of these species is the southern bent-wing bat (*Miniopterus orianae bassanii*), which is already Critically Endangered (Australian Government, 2018a); another is the eastern bent-wing bat (*Miniopterus orianae oceanensis*), which is listed as Vulnerable in New South Wales (NSW Government, 2018). The risk assessment deemed that the risk from White Nose Syndrome for southern bent-wing bats was Moderate, and the likely overall impact to the Australian bat population was High (consequences were assessed both at the species and subsequent Australian bat population levels) (Holz et al., 2016). However, there are major knowledge gaps, which are essential to gain a true understanding of the risk of White Nose Syndrome to Australia. Firstly, while an initial survey has failed to find *P. destructans* in southern and eastern bent-wing populations (Holz et al., submitted for publication), this is based on relatively small numbers of individuals and caves. More potentially susceptible species across a wider geographic range need to be surveyed to be certain whether the fungus is currently in the country. Secondly, our understanding of Australian bat behaviour and physiological processes during torpor is very limited and needs further research to be able to predict with more certainty the likely effects of infection with *P. destructans* in these species.

3.11. Other diseases

There is a long list of other diseases of Australian fauna with a potential to cause or contribute to wildlife declines (e.g. see https://www.wildlifehealthaustralia.com.au/FactSheets.aspx) . In addition to these, as mentioned earlier, there are without doubt hundreds of other pathogens and diseases we do not know about, because the associated animal species have been poorly studied (e.g. many invertebrates, fish, amphibians and reptiles), or there have been no visible signs of disease in populations prompting investigation. Clearly, we need to start taking disease seriously when addressing faunal declines, instead of treating it as an afterthought.

4. What action is needed?

The common thread in wildlife health is that our understanding of how diseases affect individuals and populations, under which circumstances they are likely to become a significant conservation threat and, importantly, how to address this threat, is very limited. Most disease investigations into wildlife populations are short term and very limited in scope, often only possible as opportunistic surveys associated with other studies. In consequence, there is little baseline data to go back to when disease outbreaks occur, making it difficult to assess the significance of these events. It also makes it almost impossible to detect outbreaks early on, when there is still time to act and to prevent significant declines, unless the affected species is already closely monitored.

A significant reason for this is a lack of dedicated, long-term funding for wildlife health research, aside from a few high-profile examples (e.g. Tasmanian Devil Facial Tumour Disease), and a lack of a cohesive, collaborative strategic framework for wildlife health and disease surveillance. Unlike diseases of human and agricultural/livestock significance, there are no industry bodies with an interest in funding in this field, and research in this area therefore largely relies on philanthropic funding and relatively small and unpredictable amounts of government funding. The OIE recognises that "*Surveillance of wildlife diseases must be considered equally as important as surveillance and control of diseases in domestic animals*" (OIE, 2018), and addressing wildlife disease through a 'One Health' approach not only benefits conservation of Australian fauna, but also domestic animal and human health.

Currently, there is little investment in wildlife disease surveillance for the purposes of conservation and more emphasis needs to be placed on outbreak investigation and response in wild animal populations, including both new and endemic (already present) diseases. For example, better strategic resourcing in these areas might have enabled early stamping out of Tasmanian Devil Facial Tumour, thus saving many millions of dollars. Other countries, such as Canada, are leading the way in this area, and adapting a framework like the Canadian Wildlife Health Cooperative (http://www.cwhc-rcsf.ca/) would provide Australia with a more proactive, instead of just reactive, approach to wildlife health. This will ultimately not only save taxpayer money, but also significantly reduce the potential conservation impact of wildlife disease on Australian fauna.

Australia has great capacity to address these problems, with expertise at many levels including universities and government departments, and many dedicated and passionate workers keen to contribute.

We therefore urge the Environment and Communications Reference Committee to consider the following suggestions (referring to the Points of Reference of the Senate inquiry):

1. The ongoing decline in the population and conservation status of Australia's nearly 500 threatened fauna species
    a. **Disease needs to be consistently and pro-actively considered as a possible factor in population declines, and appropriately investigated**
    b. **Better baseline data on diseases of Australian fauna need to be established**
    c. **Surveillance of wildlife for disease, as well as outbreak investigation and response via a co-ordinated strategic framework is essential for early disease detection and to prevent population and species declines**
    d. **Research is required to provide more sustainable and effective solutions to disease threats**
3. The international and domestic obligations of the Commonwealth Government in conserving threatened fauna
    a. **Many Australian species are unique to this country and/or region, which makes them highly susceptible to diseases introduced from other geographic regions; it is therefore essential to include diseases with significance to wildlife conservation in all Biosecurity assessments and policies**
    b. **Australian fauna and their diseases do not respect state borders, the Commonwealth Government is thus best placed to ensure a consistent and effective approach to addressing and protecting wildlife health**
4. The adequacy of Commonwealth environment laws, including but not limited to the Environment Protection and Biodiversity Conservation Act 1999, in providing sufficient protections for threatened fauna and against key threatening processes
    a. **It is important that diseases continue to be considered as Key Threatening Processes were appropriate**

   b. **Where diseases are listed as Key Threatening Processes, this needs to be followed up with appropriate management actions and funding streams**

7. The use of traditional knowledge and management for threatened species recovery and other outcomes as well as opportunities to expand the use of traditional knowledge and management for conservation
   a. **Funding and training for indigenous rangers to contribute to the surveillance of native fauna and enabling early detection of disease and mortalities**
8. The adequacy of existing funding streams for implementing threatened species recovery plans and preventing threatened fauna loss in general
   a. **Funding for co-ordinated disease surveillance, field and laboratory investigation and management must consistently and meaningfully be included in threatened species programs**
   b. **Long term funding streams must be available to allow for long term surveillance and data collection, collation and dissemination, and is the only way to reliably identify disease effects at the population level**
9. The adequacy of existing monitoring practices in relation to the threatened fauna assessment and adaptive management responses
   a. **Monitoring for disease, both baseline data in apparently health populations, and during disease outbreaks, must be included in all monitoring of threatened fauna**
   b. **Veterinary expertise is essential for monitoring of populations for disease, as well as to interpret findings and place them in the greater context of significance to the wildlife population. Veterinarians with expertise in wildlife diseases (both research and clinical) should always be included in Threatened Species Recovery Teams, without exception.**
   c. **Close and mutually respectful collaboration between ecologists and veterinarians in multi-disciplinary teams is essential to achieving a good outcome for threatened fauna and to prevent further declines**

The Wildlife Health Research Group at the Melbourne Veterinary School has a large and unique group of wildlife population health and conservation veterinarians, researchers with expertise in wildlife diseases, microbiology and other experts with national and international scientific collaborations and standing, such as our epidemiology group which regularly works at the interfaces of wildlife with livestock industries and human population health. We co-ordinate Wildlife Health Victoria: Surveillance (WHV:S), and enjoy strong links with Wildlife Health Australia, Zoos Victoria, Phillip Island Nature Park and many other conservation bodies. We would be delighted to offer our expertise and further input into the outcomes of your consultation in relation to disease and disease surveillance aspects of Australian faunal conservation.

Thank you for considering our submission.

Yours faithfully,

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