



VKM Report 2021: 20

Assessment of the risk to Norwegian biodiversity from import and keeping of American bison, European bison, domesticated water buffalo and domesticated yak

Scientific Opinion of the Panel on Alien Organisms and Trade in Endangered Species of the Norwegian Scientific Committee for Food and Environment

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17.12.2021

ISBN: 978-82-8259-375-5

ISSN: 2535-4019

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Cover photo: Aleksander Bolbot/Mostphotos.com

Suggested citation: VKM, Erlend Nilsen, Gunnar Austrheim, Tor GjØen, Kjersti Kvie, Martin Malmstrøm, Bjørnar Ytrehus, Kathrine Eldegard, Kjetil Hindar, Johanna Järnegren, Anders Nielsen, Kyrre Kausrud, Lawrence Kirkendall, Eli Rueness, Eva B. Thorstad, Gaute Velle (2021). Assessment of the risk to Norwegian biodiversity from import and keeping of American bison, European bison, domesticated water buffalo and domesticated yak. Scientific Opinion of the panel on Alien Organisms and Trade in Endangered Species (CITES). VKM Report 2021:20, ISBN: 978-82-8259-375-5, ISSN: 2535-4019. Norwegian Scientific Committee for Food and Environment (VKM), Oslo, Norway.

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Preparation of the opinion

The Norwegian Scientific Committee for Food and Environment (Vitenskapskomiteen for mat og miljø, VKM) appointed a project group to draft the opinion. The project group consisted of three VKM members, two VKM staff and one external experts. One referee commented on and reviewed the draft opinion. The VKM Panel on Alien organisms and Trade in Endangered Species (CITES), assessed and approved the final opinion.

Authors of the opinion

The authors have contributed to the opinion in a way that fulfils the authorship principles of VKM (VKM, 2019). The principles reflect the collaborative nature of the work, and the authors have contributed as members of the project group or the VKM Panel on Alien organisms and Trade in Endangered Species (CITES) that assessed and approved the work.

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Acknowledgement

VKM would like to thank Thea Benedicte Blystad Klem (Norwegian Veterinary Institute) for her valuable comments through critical review of the draft opinion. VKM emphasises that the referees are not responsible for the content of the final opinion. In accordance with VKM's routines for approval of a risk assessment (VKM, 2018), VKM received the comments before evaluation and approval by VKM Panel on Alien Species and Trade in Endangered Species (CITES), and before the opinion was finalised for publication.

Competence of VKM experts

Persons working for VKM, either as appointed members of the Committee or as external experts, do this by virtue of their scientific expertise, not as representatives for their employers or third-party interests. The Civil Services Act instructions on legal competence apply for all work prepared by VKM.

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Summary

Key words: VKM, (benefit and) risk assessment, Norwegian Scientific Committee for Food and Environment, Norwegian Food Safety Authority, Norwegian Environment Agency

Background

The Norwegian Scientific Committee for Food and Environment (VKM) was requested by the Norwegian Environment Agency to assess the risk of negative impact on biodiversity in Norway following import and keeping of American bison (*Bison bison*), domesticated water buffalo (*Bubalus bubalis*), domesticated yak (*Bos grunniens*) and European bison (*Bison bonasus*). VKM was asked to separately assess the risks caused by accompanying virus, bacteria or parasites that may affect biological diversity. VKM was also requested to describe effects on ecosystem services.

Among the four species, yak and water buffalo are domesticated. As with other large bodied species, all four species have relatively slow life histories with high survival and low reproductive rates. This life history limits the maximal population growth rate. Moreover, the American bison, yak and water buffalo can be characterized as grazers, whereas the European bison is a mixed feeder. We consider the potential for dietary overlap and competition with wild herbivores to be highest in relation to other grazers in Norway, such as the red deer (*Cervus elaphus*). Habitat suitability for domestic animals is normally modulated by humans to improve animal production, and we considered the possibility to keep these species in Norway both on infields (fenced and cultivated habitats, and to some extent for winter fodder production) and outfields (unfenced areas mainly modified due to extensive livestock grazing and fuel wood cutting). Based on experience from animal husbandry in comparable climatic regions (nemoral, boreal and alpine), all species are expected to thrive in both infields and outfields during summer across Norway. Winter months will be challenging for water buffalo, which normally are kept indoors during winter season in temperate and boreal areas.

New species that are imported to Norway will always include the associated pathogens of the imported species. The full inventory and risk of the “unseen” microbiome import cannot be known. However, based on knowledge of the common pathogens of the imported animals, an evaluation of the most likely scenarios of disease transmission can be conducted. Some of these pathogens only cause disease in closely related species of the Bovidae family (where there is only one wild representative in Norway, the muskox (*Ovibos moschatus*)), whereas other pathogens have the potential to transmit disease to related (red deer, roe deer (*Capreolus capreolus*), moose (*Alces alces*) and reindeer (*Cervus elaphus*)) or distant species (even humans, if the disease is zoonotic). In our assessment of the risk associated with pathogen transmission, we have grouped the potential disease-causing agents into viruses, bacteria and parasites.

Methods

We used a semi-quantitative method to assess the risk of negative impact on biodiversity associated with import and keeping of the four species described above. We independently conducted an identification of potential hazards, characterized their potential impact and assessed the likelihood for a negative impact. The conclusion of the risk assessment is a product of the likelihood of impact from a hazard and the magnitude of potential consequences of that hazard on Norwegian biodiversity. A similar assessment was conducted for disease-causing agents.

Results

A key issue when assessing potential hazards associated with the four target species is the density at which they are kept: number/metabolic biomass of herbivore per net grazeable area. This assessment is based on the assumption that the animals are kept in low to intermediate densities, which should be similar to typical densities at which farm animals are normally kept on outfields in Norway. We have given some general discussion around the concept of density in the report but point out that this is a complex interaction between many ecological factors and outside the scope of this assessment to accurately define.

Considering general ecosystem services, we consider that should these bovid species be kept on outfields, there is a risk that human fear of these species might cause reluctance towards use of these areas, resulting in a reduction in cultural ecosystem services.

Conclusions

Assuming low to intermediate densities, VKM concludes that there is "Low" risk of negative impact on biodiversity in Norway, stemming from import and keeping of domesticated yak, domesticated water buffalo, European bison and American bison. This is based on assessment of five identified hazards: i) escape and establishment in the wild, ii) general grazing effects on biodiversity, iii) grazing effects on red listed species, iv) competition with wild herbivores, and v) interactions with carnivores. VKM notes that this assessment is based on the assumption that the assessed bovids are kept at densities typical for farm animals in Norway. Should the assessed bovids be kept at higher densities, negative effects on biodiversity might occur due to direct and indirect effects of high grazing/browsing pressure.

The risk of negative impact from disease-causing agents was also assessed by VKM. VKM concludes that thirteen species pose a "Moderate" risk to biodiversity in Norway, while six species pose a "Low" risk. Disease-causing agents assessed with a "Moderate" risk is found both among viruses (Bovine herpesvirus-1, Blue Tongue Virus (BTV), Epizootic Haemorrhagic Fever Virus, Bovine Virus Diarrhea Virus (BVDV) and Foot and mouth disease virus (FMDV)), bacteria (*Mycobacterium bovis*, *Mycobacterium avium subspecies paratuberculosis* (MAP), *Mycobacterium capra*, *Brucella abortus*, *Mycoplasma bovis* and *Salmonella spp.*) and parasites (*Ashworthius sidemi* and *Fascioloides magna*). This conclusion is based on the assumptions mentioned above regarding density, and that imported animals originates from

populations subjected to surveillance programs and declared free of certain pathogens listed by the World Organization of Animal Health (OIE).

Sammendrag på norsk

Bakgrunn

Vitenskapskomiteen for mat og miljø (VKM) ble bedt av Miljødirektoratet om å vurdere risiko for negative effekter på biologisk mangfold som følge av import og hold av amerikansk bison (*Bison bison*), domestisert vannbøffel (*Bubalus bubalis*) og domestisert jak (*Bos grunniens*). I tillegg ble VKM bedt om å gjøre en tilsvarende vurdering av europeisk bison (*Bison bonasus*). VKM ble bedt om å vurdere risiko for negative effekter på biologisk mangfold som følge av import og hold av disse artene. Risiko knyttet til sykdomsfremkallende agens som følge av import, er ikke en del av den generelle risikovurderingen. Dersom det er risiko knyttet til sykdomsfremkallende organismer skal likevel dette vurderes, men separat fra vurderingen av negative effekter på biologisk mangfold. VKM ble også bedt om å beskrive eventuelle effekter på økosystemtjenester, men heller ikke dette er en del av den generelle risikovurderingen.

Av de fire vurderte artene har jak og vannbøffel så langt blitt domestisert. De to andre artene er ikke domestiserte. I likhet med andre arter med høy kroppsvekt har disse fire artene høy overlevelse og lav reproduksjon. Dette setter en grense for maksimal bestandsvekst. Amerikansk bison, jak og vannbøffel er karakterisert som grasbeitere (grazer), mens europeisk bison er regnet som kvist- og grasbeiter (mixed feeder). På grunn av overlappende diett anser vi at potensialet for næringskonkurranse er størst i relasjon til andre ville grasbeitere, som for eksempel hjort (*Cervus elaphus*). Habitategnethet for husdyr påvirkes vanligvis av at mennesker forbedrer forholdene, og VKM anser det som mulig å holde de vurderte artene både på inn- og utmark i Norge. Vintermånedene er trolig utfordrende for vannbøffel, som vanligvis holdes innendørs gjennom vinteren i boreale og tempererte områder.

Nye arter som importeres til Norge vil alltid inkludere mikrobiomet til de importerte artene. Det er ikke mulig å få en full oversikt over den «usynlige» risikoen ved mikrobiomet, men basert på kunnskap om de mest vanlige patogenene, har vi likevel vurdert de mest sannsynlige scenarioene knyttet til sykdomsspredning. Noen av de aktuelle patogenene kan utelukkende forårsake sykdom hos nært beslektede kvegarter i familien Bovidae, hvor det kun er moskus (*Ovibos moschatus*) som lever vilt i Norge. Andre patogener har potensiale til å forårsake sykdom hos beslektede arter, for eksempel hjort og villrein (*Rangifer tarandus*), samt ubeslektede arter, inkludert mennesker, dersom sykdommen er zoonotisk. Patogenene er delt inn i virus, bakterier og parasitter i vår vurdering av risiko knyttet til sykdom.

Metoder

Vi har benyttet en semi-kvantitativ metode for å vurdere risiko for negative effekter på biologisk mangfold forårsaket av import og hold av de fire kvegartene. Metoden inkluderer identifisering av potensielle farer (hazards), karakterisering av mulig negativ effekt, samt

vurdering av sannsynligheten for at negativ effekt oppstår. Den samlede risikovurderingen blir da en kombinasjon av disse. En tilsvarende vurdering ble gjort for patogener.

Resultater

Et avgjørende element når man vurderer risiko knyttet til import og hold av disse artene er hvilken tetthet dvs. antall eller biomasse per areal, de forekommer i. I denne vurderingen har vi antatt at dyrene forekommer i lave til moderate tettheter, sammenliknbart med de tettheter som domestiserte beitedyr typisk holdes på i utmark i Norge. Vi har i rapporten diskutert hva tetthet kan innebære, men understreker at dette er et komplekst økologisk spørsmål som ligger utenfor denne rapportens rekkevidde å besvare fullt ut.

Når det gjelder økosystemtjenester vurderer VKM at det er et potensial for negativ effekt på kulturelle økosystemtjenester, ettersom frykt for store dyr kan føre til at enkelte i befolkningen ikke tør å benytte utmarksområder hvor dyrene beiter.

Konklusjon

Under antagelsen om at artene holdes under lave til middels tettheter, konkluderer VKM med at det er lav risiko for negative effekter på biologisk mangfold i Norge som følge av import og hold av domestisert jak, vannbøffel, amerikansk bison og europeisk bison. Dette er basert på en vurdering av fem mulige farer som vi har identifisert i) rømming og etablering av ville bestander, ii) negative effekter på biologisk mangfold forårsaket av beiting generelt, iii) negative effekter på rødlistede arter som følge av beiting, iv) konkurranse med andre ville plantespisere; herbivorer, og v) interaksjon med rovdyr.

VKM bemerker at vurderingene er godt med forbehold om at dyrene holdes i tettheter tilsvarende det som er normalt for andre husdyr i Norge. Dersom artene blir holdt i høye tettheter, vil det kunne ha negative effekter på biologisk mangfold, som følge av direkte og indirekte effekter av høyt beitetrykk.

VKM vurderte også risiko knyttet til negative effekter av sykdomsfremkallende organismer. Under antagelsen om at artene holdes under lave til middels tettheter konkluderer VKM med at seks arter sykdomsfremkallende organismer utgjør lav risiko, mens 13 arter utgjør moderat risiko for biologisk mangfold. Disse 13 omfatter virus ((Bovine herpesvirus-1, Blue Tongue Virus (BTV), Epizootic Haemorrhagic Fever Virus, Bovine Virus Diarrhea Virus (BVDV) og Foot and mouth disease virus (FMDV)), bakterier (*Mycobacterium bovis*, *Mycobacterium avium subspecies paratuberculosis* (MAP), *Mycobacterium capra*, *Brucella abortus*, *Mycoplasma bovis* og *Salmonella* spp.) og parasitter (*Ashworthius sidemi* og *Fascioloides magna*). Konklusjonen om sykdomsfremkallende organismer er basert på forutsetningen at kvegartene holdes i moderate tettheter, og at de importerte dyrene stammer fra populasjoner som overvåkes for sykdomsagens, og som erklæres fri for patogener på listen fra Verdens dyrehelseorganisasjon (OIE).

Background as provided by the Norwegian Environment Agency

The Norwegian Environment Agency, referring to the collaboration agreement between the Norwegian Environment Agency and the Scientific Committee for Food and Environment (VKM), requests VKM to carry out an assessment of the risk of negative effects on biodiversity resulting from import and keeping of American bison, European bison, domesticated water buffalo and domesticated yak.

American bison, domesticated water buffalo and domesticated yak are subject to the requirement for permission to import, release and keeping under regulations related to alien organisms. It is under consideration to exempt these species from the requirement for a permit in accordance with the regulations according to the entry in the §3, 2nd paragraph. Currently, only cattle and zebu are listed under this provision.

Terms of reference as provided by the Norwegian Environment Agency

As a basis for an assessment of how American bison (*Bison bison*), domesticated water buffalo (*Bubalus bubalis*) and domesticated yak (*Bos grunniens*) should be managed in the future by regulations relating to alien organisms, the Norwegian Environment Agency requests the Norwegian Scientific Committee for Food and Environment (VKM) to carry out a scientific assessment of the risk of negative impacts on biological diversity resulting from importing and keeping these species. In addition, a similar assessment of European bison (*Bison bonasus*) should be carried out.

Risks caused by accompanying diseases or parasites shall not be included in the overall assessment of the risk of negative impacts on biological diversity. However, any other relevant accompanying organisms must be included in the overall risk assessment. The reason why diseases and parasites should not be included in the overall risk assessment is that American bison, domesticated water buffalo and domesticated yak are regulated by harmonized EU regulations. If the three species are associated with diseases or parasites that may affect biological diversity, the risk of negative impacts on biological diversity as a result of these shall nevertheless be assessed, but separately from the overall assessment of the risk of negative impacts on biological diversity. The assessment of European bison shall be carried out in the same way as for the other three species.

Any effects on ecosystem services must be stated in the report, even if this is not part of the assessment of negative impacts on biological diversity.

1 Introduction

1.1 Taxonomy and distribution

Bovini is a tribe in the subfamily Bovinae (family Bovidae) that includes several wild and domestic species of cattle, bison, yak, buffalo and saola (Zhang et al. 2020). The phylogenetic relationship within the tribe is not fully resolved, but molecular analyses of ribosomal and mitochondrial DNA indicate separation into three subtribes, i.e., Bovina (comprising the genera *Bison* and *Bos*), Bubalina (genus *Bubalus*) and Pseudorygina (genus *Pseudoryx*) (Zhang et al. 2020; Hassanin and Ropiquet 2004).

The American and European bison, domestic yak and domestic water buffalo are all part of the Bovini tribe (Figure 1.1-1). Sequencing of mitochondrial DNA (Guo et al. 2019; Zhang et al. 2020) and single nucleotide polymorphism (SNP) analysis (Decker et al. 2009) show that European bison, American bison and yak are closely related to each other, and to domestic cattle (*Bos taurus* and *Bos indicus*) (Guo et al. 2019; Zhang et al. 2020), and it has been proposed that these species should be considered as one genus - *Bos* (Douglas et al. 2011). The water buffalo represents a separate clade (subtribe Bubalina) together with the African buffalo (*Syncerus caffer*) and related species (Douglas et al. 2011; Yang et al. 2013; Bao et al. 2016).

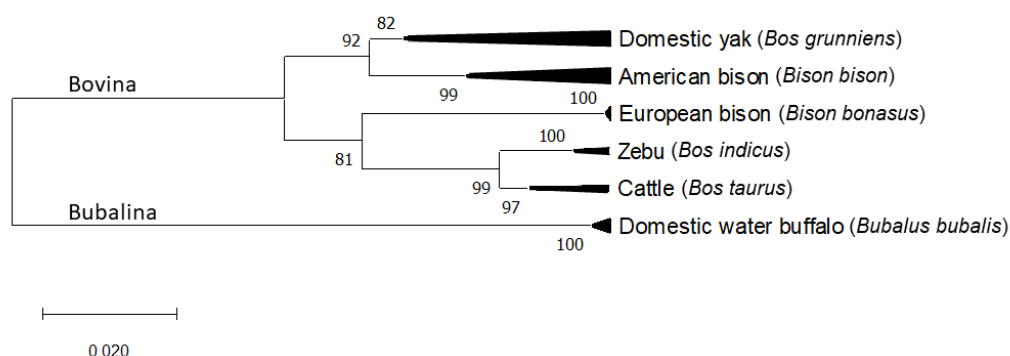


Figure 1.1-1: Evolutionary relationship among six species within tribe Bovini based on mitochondrial DNA (cytochrome *c* oxidase subunit 1). The phylogeny shows a close relationship between the genera *Bos* and *Bison* (subtribe Bovina), while domestic water buffalo (subtribe Bubalina) is placed as an outgroup. Bootstrap support is shown at each node. See Appendix I for data used in the phylogeny.

1.1.1 American bison (*Bison bison*)

American bison (Figure 1.1.1-1) evolved during the last millennia of the Holocene from prehistoric central North American bison species, that had evolved from the first wave of steppe bison (*B. priscus*) that colonised the continent from Eurasia (Zver et al. 2021). American bison went through a severe bottleneck in the 1870s, when intensive hunting

almost eradicated the large herds that once roamed the American prairies. Some authorities divide American bison in two subspecies based on morphology: The larger plains bison (*B. bison bison*) and the smaller wood bison (*B. bison athabascae*) (but, see Shaw 2021 for an alternative interpretation). The plains bison is considered a migratory species adapted to open landscapes and originally distributed from northern Mexico to southwestern Canada, while the wood bison is considered adapted to the boreal forests of north-western Canada. However, studies of the genetic makeup of the populations do not support this division (Cronin et al. 2013). There are currently few large wild populations of bison and most of the total population of around 12,000 mature animals is spread across several smaller populations (Aune et al. 2017). All populations depend on continued conservation efforts and are listed by IUCN as Near Threatened (NT) (IUCN, 2021). Approximately 300,000 American bison are held for commercial purposes at 4000 farms in North America. American bison has not been domesticated.



Figure 1.1.1-1: American bison (*Bison bison*). Photo: Phil Bird/Mostphotos.com

1.1.2 European bison (*Bison bonasus*)

European bison (Figure 1.1.2-1) probably evolved from ancestral bison species during the Late Pleistocene (Zver et al. 2021). The European bison went extinct in the wild about 100 years ago and survived only in zoos (Tokarska et al. 2011). The total global population descends from only twelve individuals (Wang et al. 2017). The species has three subspecies: lowland bison (*Bison bonasus bonasus*), Caucasian bison (*Bison bonasus caucasicus*) and

Carpathian bison (*Bison bonasus hungarorum*), of which the latter went extinct around 1850. The lowland bison was originally distributed across large parts of central and Eastern Europe. It roamed the large deciduous forests but was repelled to small pockets of land as the forests were cut down and the bison killed by the expanding and increasing European human population. In the 17th century, only one herd survived in the protected areas of the Białowieża forest on the Polish-Belarussian border. However, also this herd was killed during World War I. The existing population of lowland bison originates from seven individuals used in a captive breeding program in Białowieża and released into the wild in the same area from 1952 and later (Tokarska et al. 2011). The Caucasian bison was originally found in the area now consisting of Georgia, Abkhazia and the two Russian regions Karachay-Cherkessia and Krasnodar Krai. Only a single bull of this subspecies survived, but he was mated to several lowland bison cows. The current lowland-Caucasian line of the species consists of progeny from five individuals. There are currently about 2500 adult animals in the world, divided among eight subpopulations consisting of more than 150 individuals and a large number of smaller subpopulations. Approximately half of the animals are of the lowland line, and half of the lowland x Caucasian line (Plumb et al. 2020). The species is listed as Near Threatened (NT) by IUCN (IUCN, 2020), and depends on active conservation activities. European bison has not been domesticated.



Figure 1.1.2-1: European bison (*Bison bonasus*). Photo: Wildmedia/Mostphotos.com

Both the American-, and European bison have been introduced to the Nordic countries in enclosures in several small herds¹. This has included 16 European bison introduced to Bornholm in Denmark as a part of a Natura 2000 conservation initiative to increase the number of sites where this red-listed herbivore is present². In 2018, a small herd of European bison was introduced to the Jura mountains in Switzerland, first enclosed but with the plan that they can roam freely from 2023 (Project WisentThal 2018).

1.1.3 Domestic water buffalo (*Bubalus bubalus*)

In 2005, there were around 168 million domestic water buffalo globally (Borghese 2005). The domestic water buffalo originates from the Indian water buffalo (*Bubalus arnee*) and is divided into two subspecies: the swamp (*B. bubalis carabensis*) and the river buffalo (*B. bubalis bubalis*) (Figure 1.1.3-1), although some authors regard the two as different species (Tanaka et al. 1996). The swamp buffalo is much larger than the river buffalo; an adult male swamp buffalo weighs between 450-1000 kg, whereas an adult male river buffalo weighs 325 - 450 kg. The river buffalo is mainly kept for milk production and found in India, Pakistan and Western Asia, while the swamp buffalo are mainly used as draught animals and for combined meat and milk production in China and Southeast-Asia (Borghese 2005). Several breeds from both subspecies are adapted to local environments and local needs. Water buffalo kept in Europe are of the river subspecies (Borghese 2005). In south-eastern Europe, the number of domestic water buffalo has declined because dairy buffalo have been replaced by high-yielding cattle, agriculture is mechanized, and market demands for buffalo products have diminished. In contrast, the water buffalo population in Italy has increased considerably to meet the demand for buffalo milk for mozzarella cheese production (Borghese 2005).

The wild Indian buffalo is only found in small, scattered populations in India, Nepal, Myanmar, Thailand and Cambodia, totalling around 2500 adult individuals. IUCN consider the species as Endangered (EN) (Kaul et al. 2009).

¹ <https://allaboutbison.com/bison-world-news/europe/denmark/>

² <https://naturstyrelsen.dk/naturbeskyttelse/naturprojekter/bison-bornholm/>



Figure 1.1.3-1: Domestic water buffalo (*Babalis bubalis*), the river buffalo type. Photo: tinabasgen/<https://flickr.com/photos/7624089@N02/3131711079>

1.1.4 Domestic yak (*Bos grunniens*)

The yak is endemic to the Tibetan plateau and surrounding high-altitude habitats (Wiener et al. 2003). The domestic yak (*Bos grunniens grunniens*) (Figure 1.1.4-1) originated from wild yaks (*Bos grunniens mutus*) (Shi et al. 2016), from which it was domesticated in prehistoric time. The global population of domesticated yak was estimated at 14 million individuals in 2003 (Shi et al. 2016). Most of these animals are found in Tibet, Qinghai and bordering Chinese provinces, while around one million are found in Nepal, Bhutan, the southern slopes of Himalaya in India, northern Pakistan, eastern Afghanistan, Kyrgyzstan, Tajikistan, Kazakhstan and Mongolia. Apart from zoo collections, there have been few attempts on yak farming in Europe. Wiener et al. (2003) describe only two herds, one in Switzerland and one in Austria, but this appears to be an underestimate. The Swedish Veterinary Institute, describe that there are “a couple of hundred yaks in Sweden” (www.sva.se accessed the 27th of Aug 2021). In North-America there have been around 90 breeders of yak, with a total of less than 2000 animals (Wiener et al. 2003).

The world population of wild yak has been declining for the last century and is now, according to Shi and co-workers, estimated to 22,000 individuals dispersed over several herds within Tibet and Qinghai (Shi et al. 2016). The total population is estimated at 7,500 -

9,999 individuals, and IUCN categorizes wild yak as Vulnerable (VU) (Buzzard and Berger 2016).



Figure 1.1.4-1. Domestic yak (*Bos grunniens*). Photo: Phil Bird/Mostphotos.com.

1.2 Biology and ecology

1.2.1 Morphology and climate tolerance

The American bison persists both in arid locations in Chihuahua in Mexico, snow rich and cold areas in Yellowstone and as far north as Yukon and Alaska (Aune et al. 2017). In winter, the bison uses its head and well-developed vertebral muscles to swipe snow away from the ground to access food. Wood bison has been introduced to Central Yakutia in Russia and seems to thrive well in the cold climate (Safronov et al. 2012).

The European bison was previously considered a forest dwelling species but is now assumed to be adapted to open grassland or mosaic landscape (Kowalczyk et al. 2021) but restricted to suboptimal forest habitats as a refugee species (Kerley et al. 2012). Mysterud et al. found increased mortality in hard winters with much snow (Mysterud et al. 2007). High average temperatures in May and oak masting increased recruitment rates.

Water buffalos are mostly found in the tropic and subtropic areas and are adapted to a hot and humid climate, tolerating temperatures from 0 to well above 30°C (Borghese 2005).

Water buffalos use wallows and water to cope with heat and reduce thermal stress. Different breeds are assumed to have different traits pertaining to hardiness, and there are for example multiple “mountain breeds” in China. Buffalos in Europe are considered to constitute a Mediterranean breed.

Yaks are adapted to a dry and cold climate in alpine grasslands and deserts 3000–6000 meters above sea level. They have a stout and rounded body covered with long and dense guard hairs over a down wool undercoat, minimizing heat loss. Their tracheas are short and wide and their lungs proportionally large compared to other bovids. They also have larger heart stroke volume, faster blood circulation, more red blood cells and higher blood haemoglobin content than other bovids, all factors that facilitate oxygen exchange at high altitudes (Shi et al. 2016). They are, however, large and heavy (200–600 kg) and have relatively small claws, so that deep snow probably would constitute a problem. Yaks are reported to increase their breathing frequency at 13°C, and at 16°C their heart rate and body temperature start to rise. At 20°C, yak will seek to water or shade, and stand still. When it comes to cold hardiness, yaks seem to thrive at temperatures as low as -30 to -40°C (Wiener et al. 2003).

1.2.2 Reproduction

American bison cows normally give birth to their first calf at three years of age. Gestation lasts for around 270 days, and they normally produce one calf each year (Agabriel et al. 1996).

In European bison, age at first reproduction is on average four years and gestation length is around 264 days (Daleszczyk 2011).

In water buffalos, age at first calving is around three years (28 to 40 months). Gestation length is 305–320 days for the river buffalo and 320–340 days for the swamp buffalo. They give birth to one calf at the time, consequently producing 2 calves every three years (Jainudeen 2002).

Yak cows normally have their first calving when they are around three years old. Gestation length is around 260 days, and twins are rare, giving an average production of two calves every three to four years (Wiener et al. 2003).

1.2.3 Suitable habitats in Norway

Habitat suitability for domestic animals is normally modulated by humans to improve animal production. As argued by Mysterud (2010), wild animal management actions, such as harvest pressure and selectivity, fencing, artificial feeding and predator control, might change traits of wild species towards domestication (adaptations to humans and semi-natural/human induced environments) and also extend the range of natural habitat suitability. The short review below assesses the habitat suitability for all four species kept as

part of 1) an animal husbandry system where the farmer and agricultural management system have the responsibility, or 2) introduced as wild species and thus part of the wildlife management.

1.2.3.1 Animal husbandry management

An animal husbandry system implies adaptations to man and a semi-natural/human-modified habitat. In Norway, this could be both on 1) infields (fenced and cultivated habitats, and to some extent for winter fodder production) and 2) outfields (unfenced areas mainly modified due to extensive livestock grazing and fuel wood cutting, but normally not cultivated in terms of tilling, fertilization and addition of seeds for changing the plant community composition).

Based on experience from animal husbandry in comparable climatic regions (nemoral, boreal, alpine), all species are expected to thrive in both infields and outfields during summer all over Norway. Winter months will be challenging for the water buffalo, which normally are kept indoors during winter season in temperate and boreal sites (Borghese 2005).

Yak (Wiener 2006), European bison (Plumb et al. 2020) and American bison (Aune et al. 2017) are adapted to harsher climates than the water buffalo and expected to sustain winter also in northern environments, dependent on the availability of winter fodder, and ability to cope with extreme weather events (e.g., contrasts between warm and wet winter events vs. cold (icing) episodes). However, outfield animal husbandry is expected to be more vulnerable during winter (partly because snow cover the ground in many regions of Norway) and in need of more human support to maintain animal welfare.

1.2.3.2 Wild animal management

Although wild animals are not owned and managed individually, as within the agricultural management systems, the Norwegian wildlife management uses a broad range of human interventions for wild large herbivores, such as hunting and supplementary feeding that affect population abundances and distribution, and ultimately their impact on ecosystems (Myysterud 2010). The large sized non-native muskox was deliberately introduced to the wild in Norway (Dovre, Femunden: Pedersen et al. 2018a). Also, the introduction of moufflon sheep (Vestfold, Telemark³) was deliberate, while the spread of wild boar (*Sus scrofa*) and fallow deer (*Dama dama*) is accidental in areas close to Sweden due to both invasive animals from Sweden (Pedersen et al. 2018b and 2018c) and escapees from Norwegian farms, respectively.

³ <https://www.statsforvalteren.no/siteassets/fm-vestfold-og-telemark/miljo-og-klima/verneomraader/dokumenter/verneomraader-vestfold/fritzoehus-landskapsvernomrade/larvik-fritzoehus-landskapsvernomraade-natur-i-vestfold-2014.pdf>

If introduced as wild animals, three of the four target species in this assessment could be expected to persist within some areas of Norway. Potential natural habitats for wild living European and American bison would be deciduous broadleaf forest and semi natural grasslands, which grows in restricted patches in southeastern and southern Norway. Yak has a typically alpine (arctic) adaptation and could be sustained within the alpine/arctic environment, similar to some populations in North America (Wiener 2006).

1.2.4 Diet

The American bison is mainly a grazer and graminoids seem to contribute to about 80% of its food intake. It also gets important contributions of fatty-acids and proteins from browsing on forbs and shrubs (Hecker et al. 2021). In comparison, the European bison is better characterized as a mixed feeder, and in the Białowieża forests, woody plant species constitute a major part of its diet (Kowalczyk et al. 2019).

Yaks graze on both grass, herbs and shrubs and are assumed to survive well on low-quality feed compared to domestic cattle. They graze rough stems and leaves of sedges. In the winter, they dig through the snow, using both their claws and their head, gaining access to wilted grass and other plants. Yaks are said to reduce grass with a height of 15 cm to between 2.6 cm and 5.2 cm but will in spring normally not graze green shoots down to more than 2–3 cm above the ground (Wiener et al. 2003).

Water buffalo have lower digestibility of organic matter compared to cattle. This is assumed to be related to longer passage time through the post-ruminal gastrointestinal tract in the latter species, while rumen retention actually is higher in buffalo (Borghese 2005). It is, however, often remarked that water buffalos are good at utilizing poor quality roughage and crop residues compared to dairy cattle (Jainudeen 2002). In Italy, a common feeding regime consists of 34% concentrates, 28% maize silage, 25% hay and straw and 13% other feed items (Borghese 2005), indicating a feeding regime that is comparable to Norwegian dairy cow production.

1.2.5 Indoor/outdoor

Domestic water buffalos in Europe are most commonly kept in fenced areas outdoor during the day, and indoors at night. In the northern parts of the distribution, like northern Iran, water buffalos are kept in barns during the winter (Borghese 2005). The other species are kept outdoor also during night and winter.

1.2.6 Regulations and occurrence in Norway

The import of domesticated yak, domesticated water buffalo, European bison and American bison is currently regulated under the "Regulation on alien organisms" ("FOR-2015-06-19-716 - Forskrift om fremmede organismer" in Norwegian), which regulates the import, introduction, trade and release, as well as the unintentional spread of alien organisms. The

purpose of the regulation is to “prevent the introduction, release, and spread of alien organisms that cause, or may cause, adverse consequences for biodiversity”. The four species in question in this report can be imported if granted a permission (according to § 6) as these are not listed on Appendix I of the regulation (prohibited species, following § 5). Nor are the species listed in Appendix II (species that can be imported without permission) or fall under the other exceptions listed in § 7, and each import must therefore currently be applied for and granted by the Norwegian Environment Agency.

Neither of the bison species (*B. bison* or *B. bonasus*) are listed on the CITES Appendices. The Indian water buffalo (*B. arnee*) is listed on CITES Appendix III, but the domesticated river buffalo (*B. bulbalis bulbalis*) is excluded. Similarly, the wild yak (*B. grunniens mutus*) is listed on CITES Appendix I, but the domesticated form (*B. grunniens grunniens*) is excluded. Thus, none of the assessed species are subject to the provisions of the convention.

Of the four species under consideration in this report, two have already been imported to Norway. The domesticated yak and domesticated water buffalo have both been imported in a limited number a few times since 2016. These species have been imported for production of milk and cheese, breeding for meat production and to function as grazers in semi-natural meadows (cultural landscape). We do not know whether these species are still kept in Norway. To the best of our knowledge, no applications have been filed for import and keeping of American or European bison.

1.2.7 Known and potential use

To our knowledge, there is no information on the potential motivation people may have for introduction of bison, yak or water buffalo to Norway. We assume that farmers in areas with large predators might consider swapping traditional livestock, such as sheep and cattle, with any of these species. The species may potentially represent an economically and animal welfare-wise feasible opportunity that can allow continued farming and utilization of uncultivated areas. In addition, some farmers will find such new species interesting, and explore the opportunities of creating niche products. The number of farms engaging in meat production from bison was increasing in Europe when it was last assessed (Agabriel et al. 1996; Bornett-Gauci et al. 2006).

In USA and Canada, there is a large number of commercial herds of American bison used for meat production. The farming is considered economically competitive with traditional livestock production, due to relatively low input costs and willingness among consumers to pay high prizes for bison beef produced without use of growth-promoting agents (Galbraith et al. 2014).

European bison has been introduced into several locations in Europe as a part of the “rewilding movement”, aiming to restore past biodiversity (see for example <https://rewildingeurope.com/>, <https://rewilding.org/> or <https://www.rewildingbritain.org.uk/>). Note, however, that European bison has not been part

of native fauna in Norway (Kuemmerle et al. 2012). More relevant use of European bison in Norway is to let herds graze in semi-natural landscapes in order to restore or maintain meadows and prevent reforestation (Kowalczyk et al. 2021). In several countries, small herds are kept in fenced areas for a combination of meat production and tourism, i.e., the owner arrange so-called bison safaris.

In its native range, yak is mainly kept for meat production and its fat-rich milk. The hides can provide high quality leather and the down wool can be used for textile production. Yaks are used as transport animals and for ploughing in many areas. In Norway, potential use of yak can be meat production based on mountain pastures, requiring minimal investment in infrastructure provided that the animals can graze outdoor during the winter. In addition, yak may be used for landscape restoration, especially in areas that previously had a cultural landscape shaped by mountain dairy farming and harvesting of hay from natural/seminatural meadows and mires.

Domestic water buffalo in Norway could potentially be used for production of fresh cheese products such as mozzarella.

1.3 Impacts of Bison, domestic water buffalo and domestic yak

1.3.1 On biodiversity

Large herbivores are often defined as ecosystem engineers that modify their environment and the associated biodiversity significantly (Nickell et al. 2018). Due to processes such as selective plant defoliation, trampling, and nutrient input in the form of dung and urine, they may modify plant and microbial community composition, nutrient cycling and productivity (Bardgett and Wardle 2003). These processes may sustain structurally diverse vegetation important for a functionally diverse ecosystems, such as the temperate forest (Sandom et al. 2014). However, the impact on biodiversity very much depends on the herbivore pressure (i.e. stocking rate) in relation to habitat productivity with a biodiversity optimum at intermediate densities in productive systems (Milchunas & Lauenroth 1993).

The ecological effects of American bison are well studied within North American grassland ecosystems, and the American bison is considered an ecosystem engineer with strong impacts on several groups of organisms (plants, insects, other herbivores) and ecosystem functions and processes (Sanderson et al. 2008; Nickell et al. 2018).

There are fewer studies on the ecological effects of European bison, but Schwerk et al. (2021) argue that also the European bison could act as an ecosystem engineer in the forest ecosystem by changing important ecological functions and services, and facilitate biodiversity conservation in broad leaf forest ecosystems, e.g., as an effective vector of plant propagules (Jaroszewicz et al. 2008). Being a mixed feeder, European bison is also found to prevent succession of tree species and thus maintain more open forest habitats and woody pastures (Kowalczyk et al. 2021).

Little is known about how these animals affect the northern or upland forest ecosystems should they be introduced. However, temperate and mixed forests in southern parts of Norway may serve as a suitable habitat for both European and American bison. Nevertheless, modelling studies on habitat suitability suggest that the future for bison in the wild lies in eastern Europe (Kuemmerle et al. 2011).

Domestic yak is adapted to alpine ecosystems, and the few small herds kept as livestock in Europe are found in the European alps (Switzerland and Austria). Yak is a grazer like the bison species, and high densities may cause grassland ecosystem degradation due to erosion and development of resistant, unpalatable plant species (Wiener et al. 2003). However, grazers also have a positive effect of keeping the land open by browsing on shrubs and trees and thus facilitate biodiversity by grazing on dominating grass species.

Finally, the domesticated water buffalo is mainly found in the Mediterranean part of Europe. In 2005, 0.5 million animals were kept enclosed in Europe mainly for the production of mozzarella cheese (Borghese & Mazzi 2005). More extensive farming systems with free ranging buffalos are found in more tropical and subtropical regions, e.g., in Bangladesh (Samad 2020). Limited information about the ecological effects caused by domesticated water buffalo is available.

Potential negative effects of large herbivore introductions in the wild are associated with overgrazing (Myrsterud 2006). High densities cause degradation of the ecosystem, such as soil erosion, change towards unpalatable resistant species in the plant community and other groups of organisms, and with indirect negative effects on processes, such as nutrient flow and carbon storage. However, the threshold densities vary with both animal and habitats characteristics, and precautions are needed to avoid development of unsustainable densities. Plant biodiversity is expected to peak at intermediate disturbance (e.g., Grime 1973), which is expected to hold for herbivore densities at intermediate levels (Austrheim et al. 2016).

1.3.2 On ecosystem services

Large herbivores are expected to impact a broad range of ecosystem services including provisioning, regulating, cultural and supporting services through their effects on important ecosystem functions, such as ecosystem resilience/resistance to disturbance, nutrient cycling, carbon cycling, plant regeneration, and primary productivity (Forbes et al. 2019). Dependent on environmental settings and herbivore species, there are normally various synergies and trade-offs among ecosystem services; for example, high densities of animals are found to be traded off against runoff water quality, plant productivity and soil carbon storage (Austrheim et al. 2016). Consequently, provisioning services associated with livestock and the production of other material services are traded off with other services, which is in correspondence with findings in the ecosystem assessment for Europe and Central Asia (IPBES 2018). See also chapter 4.1.

1.3.3 On agriculture

More than 75% of farmers in Norway in 2020 had animal husbandry as their main agricultural activity (SSB⁴). Free ranging large herbivores, such as cattle and sheep, are key species for animal husbandry in most of Norway and have modified ecosystem structure, functions and services across most habitats over millennia (Austrheim et al. 2008). In recent decades, new livestock species within both Bovidae (Scottish highland cattle (*Bos taurus*), moufflon sheep (*Ovis gmelini*), Kashmir goat (*Capra hircus*) and Camelidae e.g, lama (*Lama lama*) and (*Lama pacos*) have been introduced for animal husbandry. An introduction of the target herbivores will increase the number of domesticated farm species but will probably not add significantly to the economy of agricultural production except for certain niche products (e.g., buffalo milk, meat) that might be important for the economy of marginal agricultural areas normally used for domestic herbivores.

1.4 Hitchhiking organisms

Import of new species to Norway will always include the microbiome of the imported species and such imports will therefore probably include new microorganisms, as well as the imported animal. The full inventory of this "unseen" import cannot be known but based on knowledge of the common pathogens of the imported animals, an evaluation of the most likely scenarios of disease transmission can be discussed. Some of these pathogens can only cause disease in closely related species of the Bovidae family (where there is only one wild representative in Norway, the muskoxen (*Ovibos moschatus*), which belong to another subfamily, Caprinae), whereas other pathogens have the potential to transmit disease to related (deer, moose, reindeer) or distant species (even humans if the disease is zoonotic). Below follows an overview of common pathogens in bison, water buffalo and yak that may have the potential of transmission to Norwegian wild fauna. These pathogens may be passengers on at least one of the evaluated species and we have not distinguished between these hosts with respect to the most likely carrier. Some of the pathogens are already present in Norway and will as such not constitute new risks to Norwegian wildlife. However, viruses, bacteria and parasites with the same name come in many flavours (strains). New variants of endemic pathogens imported with any of the four species may therefore constitute new risks that are not evaluated in this report

A risk assessment of import of live cattle to Norway from Sweden, Denmark, the Netherlands, France, United Kingdoms, New Zealand and Canada was made by the Norwegian Veterinary Institute for KOORIMP in 2016. The assessment followed the OIE guidelines for import risk analysis of 2016 (OIE, 2016, current version available online⁵). The

⁴ <https://www.ssb.no/jord-skog-jakt-og-fiskeri/faktaside/jordbruk>

⁵ <https://www.oie.int/en/what-we-do/standards/codes-and-manuals/terrestrial-code-online-access/>

report identified 27 pathogens (including “resistant bacteria” and “resistant parasites”) that can affect cattle, and to a lesser degree included pathogen hazards that could be important for humans, other domestic animals, wildlife or environment. Five pathogens were discussed in more depth, though the authors expressed that they were uncertain if these were the most important health hazards (for cattle). These pathogens were *Mycobacterium avium* ss. *paratuberculosis*, *Mycobacterium bovis*, *Mycoplasma bovis*, *Coxiella burnetii* and *Chlamydophila abortus*. The risk for import of one of these pathogens with import of cattle was regarded as high with imports from both Denmark, the Netherlands, France, United Kingdoms, New Zealand and Canada.

Import of non-native animals to new territories involves a risk to the importing country with respect to hitch-hiking pathogens. Known and unknown microorganisms and parasites follows the animals to their new habitat. In case of transmission of new pathogens to immunologically naive native animal populations, epidemic disease may occur before herd immunity and adaption to the new pathogen are established. In addition, both the location (contact with wildlife) and volume of the imports are important when assessing the risks. Impact from animal imports may also be indirect: in the case of confirmed transfer of infectious disease to local animal populations, containment measures, like population regulation or even eradication, may pose a considerable risk to local biodiversity. For a hitch-hiking pathogenic organism to be classified as a hazard to Norwegian biodiversity, the pathogen must be transmissible (some pathogens spread via vectors that may not be present in Norway) and have susceptible hosts in Norwegian wildlife.

We have based our characterization on the general criteria for the inclusion of a disease, *infection* or *infestation* in the OIE list :

- International spread of the pathogenic agent (via live *animals* or their products, *vectors* or fomites) has been proven.

AND

- At least one country has demonstrated freedom or impending freedom from the disease, *infection* or *infestation* in populations of susceptible *animals*, based on the provisions of Chapter 1.4.

AND

- Reliable means of detection and diagnosis exist and a precise *case* definition is available to clearly identify *cases* and allow them to be distinguished from other diseases, *infections* or *infestations*.

AND

- Natural transmission to humans has been proven, and human infection is associated with severe consequences.

OR

- The disease has been shown to have a significant impact on the health of domestic *animals* at the level of a country or a *zone* taking into account the occurrence and severity of the clinical signs, including direct production losses and mortality.

OR

- The disease has been shown to, or scientific evidence indicates that it would, have a significant impact on the health of *wildlife* taking into account the occurrence and severity of the clinical signs, including direct economic losses and mortality, and any threat to the viability of a *wildlife* population.

Introduction of animal pathogens with the import of animals can have negative impacts on biological diversity through:

1. The direct impact of disease on wildlife behavior and/or population performance
2. The indirect impact of measurements installed by the authorities to mitigate or eradicate an introduced pathogen.

For a pathogen to have a direct impact on biological diversity, the pathogen must affect the reproduction or survival of a population to an extent that mortality rate exceeds recruitment rate. In order to do so, the pathogen must be virulent (i.e. cause sufficient damage in the host) and be efficiently transmitted to a sufficient number of susceptible animals so that the prevalence becomes high enough to have a population level impact. Very few pathogens do meet these criteria in robust, large populations of wild animals. Small and vulnerable populations that already are under pressure can, on the other hand, reach tipping points when new and virulent pathogens are introduced.

The animal health authorities can install measurements as eradication or population reduction of a wildlife species to eradicate or minimize spread of a pathogen. This will typically occur if a wildlife species functions as host for a disease that has a profound impact on domestic animal production or human health.

1.4.1 Viruses

1.4.1.1 Bovine herpesvirus-1 (IBR/IPV), Bovine respiratory syncytial virus (BRSV), Parainfluenza-3 (PI-3)

These three viruses are found in bison and may cause bovine respiratory disease (Berezowski et al. 2018). It is often manifested after various stress situations (nutritional, environmental, transport) and spread via aerosols. The disease starts as a low grade viral respiratory infection but may develop into severe viral or bacterial pneumonitis (Makoschey et al. 2021). IBR/IPV has not been detected since the 1960s and Norway is considered free

from this virus (Klem et al. 2021e). Infections with BRSV and PI-3 are common and antibodies against these agents can be found in samples from cattle in Norwegian farms (Gulliksen et al. 2009; Klem et al. 2021e).

1.4.1.2 Bovine Virus Diarrhea Virus (BVDV), Rotavirus, Coronavirus

These viruses cause diseases in the digestive system in bison calf, often in connection with stress situations, like overcrowding, poor nutrition and lack of hygiene. They are transmitted via the oral-faecal route and lead to dehydration, intestinal damage and in some cases to septicaemia and death (Berezowski et al. 2018). BVDV has not been detected in Norway since 2005 and Norway is considered free from this virus (Klem et al 2021c). Infection with rotavirus and coronavirus are common and antibodies against these agents are regularly found in samples from cattle milk in Norwegian farms (Toftaker et al 2016; Falk et al. 2021).

1.4.1.3 Blue Tongue Virus (BTV) and Epizootic Haemorrhagic Fever Virus (EHFV)

Blue tongue virus (BTV, Reoviridae family) causes blue tongue disease in various ruminants and is transmitted via an insect vector (biting midges of the genus *Culicoides*). Symptoms include fever, loss of appetite, oedema and inflammation in mouth and airway mucus membranes (Coetzer & Tustin 2004). In Norway, BTV virus was confirmed in a few bovine production units in 2009 but eradicated within 2 years (Klem et al. 2021b). Despite an extensive surveillance program, sporadic outbreaks of disease have occurred in Europe over the last 20 years (EFSA AHAW Panel, 2017). Control measures, like transport zoning, vaccination and vector control, have not been sufficient to eradicate this virus from European farming.

Epizootic Haemorrhagic Fever Virus (EHFV) is common in Western and south-eastern USA. Most wild and domestic ruminants are susceptible to infection, but in several species (cattle, goat, deer) this may only cause subclinical disease in several species (cattle, goat, deer), indicating that these species can function as reservoirs and silent carriers. According to the World Animal Health Information System (WAHIS) the virus has been detected in both domestic and wild animals throughout Europe the last 10 years⁶. American bison show high prevalence and considerable mortality, while for example infected red deer are seropositive for BTV serotype 8 without showing clinical signs. Likewise, experimental infection of red and roe deer with EHDV serotype 1 did not result in clinical signs (Mellor 2012).

1.4.1.4 Foot and mouth disease virus (FMDV)

This highly contagious infection is caused by an RNA virus in the genus *Aphthovirus* in the Picornaviridae family. Foot and mouth disease was one of the first infectious diseases to be

⁶ <https://wahis.oie.int/>

identified as viral disease (filterable) in the 1870s. The virus infects many animals, particularly domestic and wild ungulates. The infection transmits via contact, aerosols, feed, and animal products such as semen. Infected animals develop fever, blisters in the mouth and feet, and sometimes lethal myocarditis. Episodic outbreaks of this disease have had large economic consequences as thousands of animals have been culled to contain the epidemic. North America, Australia, New Zealand and most of Europe have been declared free of FMD but the disease is endemic in parts of Asia, Africa, the Middle east and South America (Stenfeldt et al. 2020).

1.4.1.5 Bovine leukemia virus (BLV)

BLV is a retrovirus causing enzootic bovine leucosis (EBL). This disease is characterized by persistent lymphocytosis, and may in some cases develop into lymphosarcomas (tumors). The virus normally spreads via contact with bodily fluids containing infected cells, like blood and milk. This virus naturally infects domestic cattle and water buffalos but can experimentally be transmitted to sheep, deer, goats and buffalos among others (OIE 2021) (Johnson & Kaneene 1992). The virus has never been reported in Norway, but several cattle herds tested positive for BLV antibodies in 1995. No new cases have been reported since 1997 and Norway is considered free status by EFTA (Johnson & Kaneene 1992; Klem et al. 2021d). The virus can be found globally but a number of European countries are recognized as officially free from BLV due to extensive surveillance programmes (OIE 2021).

1.4.2 Bacteria

1.4.2.1 Mycobacterium avium subspecies paratuberculosis (MAP)

This bacterium causes Johne's disease, a chronic intestinal infection that is transmitted via food or water and can have an incubation time of up to 10 years. Infection affects the mucosal immune tissues and will over time lead to diarrhea, weight loss and often to death within a year. The bacteria are resistant in the environment and stay infectious in faeces on pasture for more than a year. The bacteria are common in Europe but almost absent in Norway (Waddel et al. 2015; Kampen et al. 2021; Klem et al. 2021a).

1.4.2.2 Mycobacterium bovis /M. capra

This bacterium causes bovine tuberculosis and transmits via direct contact, aerosolized bacteria or contaminated soil/water. Infected animals develop a slow progressing disease of chronic cough and weight loss. The bacteria can infect many animal species including humans, carnivores, rodents, insectivores, lagomorphs and ungulates, and is present throughout the world. In many developed countries, the infection has been eradicated from production animals through stringent eradication programs but are present in wild animals with the possibility of reintroduction into cattle herds. Apart from two cases in 1984 and 1986, the disease has been eradicated from Norwegian cattle farms since 1963 (Klem et al.

2020a). No cases have been observed in wildlife in Scandinavia or Iceland the last decades (Gavier-Widén et al. 2012, Klem et al. 2021a). Infection has been detected in European bison in Poland on several occasions (Didkowska et al. 2021).

1.4.2.3 *Brucella abortus*

Brucella abortus is a gram-negative intracellular bacterium causing Brucellosis (Bang's disease) in many species (including humans). Transmission is via contact with aborted fetal tissues or fomites on the ground, but it can also spread via milk, faeces and seminal fluids. Infected animals develop disease in reproductive organs (abortion in females and testicular inflammation in males) and can become chronic carriers. Brucellosis has a global distribution, but many countries in Western Europe have managed to eradicate this disease, and it has not been observed in Norway since 1953 (Schumaker 2013; Klem et al. 2020b). Wild ruminants can become infected with *B. abortus*, but according to Godfroid (2012), European wildlife species are not able to function as reservoir hosts of the infection without continuous introductions from infected bovids.

1.4.2.4 *Mycoplasma bovis*

Mycoplasma bovis is one of 13 mycoplasmas diagnosed in cattle. It causes respiratory disease, mastitis, arthritis, keratoconjunctivitis in ruminants and spread via contact with infected animals during coughing or contaminated surfaces. Infected animals experience weight loss, mild fever and runny eyes. The disease has spread globally in cattle rearing countries since its first isolation in 1961. Norway and Iceland are the only countries where this bacterium has yet to be detected (Bürki et al. 2015; Klem et al. 2020a).

1.4.2.5 *Salmonella*

The more than 2500 variants of *Salmonella* bacteria can cause intestinal infections (salmonellosis) in a wide range of animals, including humans. It is found in all parts of the world but is most prevalent in areas with intensive animal husbandry. The bacteria are excreted via faeces and infects via contaminated food or water. In bovine species, *S. typhimurium* and *S. dublin* are the most prevalent species. *Salmonella* infections are rare in Norway (Coburn et al. 2007; Heier et al. 2021; Klem et al. 2020a).

1.4.2.6 *Coxiella burnetii*

C. burnetii is the agent of Q-fever in multiple species, including humans (Ruiz-Fons 2012). Infection is usually mild or unapparent, but can cause general infection with for example pneumonia, hepatitis and/or abortion. The importance of wildlife for the epidemiology of the disease is not known, but many species can be infected, probably without major clinical disease. The disease is transmitted with contaminated surfaces or ticks or via contact with infected material like milk, urine, faeces and amniotic fluids. The importance of the disease lies in the costs of abortions storms in livestock and in the zoonotic potential. *C. burnetii*

have never been detected in Norway but is found in most other countries in the world, also in Sweden and Denmark.

1.4.3 Parasites

Like other animals, the bovines share a wide range of parasitic organisms that may cause disease. Many of these are already present in domestic cattle in Norway. As such, an introduction of these parasites with imported bison, yak or water buffalo, may not expose Norwegian wildlife to new pathogens, though imported animals can carry new strains that potentially can be more virulent to Norwegian wildlife hosts than those that they historically have been exposed to. Bovine parasites that already are present in Norway include (List compiled after Bjørn Gjerde's student compendium "Parasitter hos storfe", 13th edition, 2011⁷):

- *Giardia intestinalis*
- *Cryptosporidium parvum*
- *Eimeria bovis*, *E. zuernii*, *E. alabamensis* and others
- *Neospora caninum**
- *Babesia divergens*
- *Fasciola hepatica*
- *Dicrocoelium dendriticum*
- *Taenia saginata**
- *Taenia hydatigena**
- *Ostertagia ostertagi*
- *Trichostrongylus axei*
- *Cooperia oncophora*
- *Nematodirus helvetianus*, *N. battus*
- *Oesophagostomum radiatum**
- *Trichuris* spp.
- *Chorioptes bovis*, *C. texanus*
- *Bovicola bovis*, *Linognathus vituli* and other lice

(* = the distribution of these parasites in Norway is not known, but they are regarded as uncommon)

Other parasites may not currently be present in Norway, but are regarded to be strongly associated with bovids, suggesting that the risk of spillover, spread and impact on biological diversity among non-bovid wildlife after import of a limited number of bison, water buffalo or yak can be regarded as negligible. Import of these parasites may nevertheless be very important in a livestock agriculture context. Among these are *Toxocara vitulorum*, *Parafilaria*

⁷ <http://bk.gjerde.name/index.php/component/phocadownload/file/117-storfepar-2011>

bovicola, *Stephanophilaria stilesi*, *Besnoita besnoiti*, *Sarcoptes scabiei* var. *bovis*, *Hypoderma lineatum* and *H. bovis*.

Toxocara vitulorum is commonly found in bison, buffalos and yaks. The nematode is found in many countries in Europe and has been isolated from European bison herds in Sweden (Vesterholm 2021). It is currently not found in Norway. This gastrointestinal nematode only infects bovids.

Parafilaria bovicola is a filaroid nematode that is common in bovids in Asia, Africa and Southern- and Eastern Europe (Spickler 2020). It is transmitted by *Musca* flies, for example the common face fly *M. autumnalis*, and larvae live in the subcutis and intramuscular connective tissues. Presence of the parasite causes green discoloration of surround muscle, and the females penetrate the skin when laying their eggs, damaging both meat and hides. *Parafilaria bovicola* was imported to Sweden with cattle in 1978 and has spread widely. Major efforts have been performed to hinder spread and lower the prevalence in Swedish cattle (Gibbons et al. 2000). *P. bovicola* does not appear to infect species outside Bovini (Spickler 2016).

Stephanophilaria stilesi is another filaroid nematode transmitted by flies. It causes dermatitis. The horn fly (*Haematobia irritans*), which is believed to be absent from Norway, is important for transmission, though other flies probably can transmit the nematode. *S. stilesi* is not present in Norway but found in many areas of Europe and America. It is believed to only infect bovines.

The protozoan *Besnoita besnoiti* is widely distributed in southern Europe, Asia and Africa and expanding (Frey et al. 2016). It is transmitted by stinging insects and cause a chronic and debilitating disease in young cattle. In endemic situations, 90% of cattle develop a subclinical infection, while 10% suffer severe disease. Cattle are intermediate hosts. The parasite is closely related to *B. tarandi* that infects reindeer and other cervids (Dubey et al. 2004). *B. tarandi* has been found in Finland.

Sarcoptes scabiei var. *bovis* causes highly contagious mange in bovines but does not seem to be transmitted to other species.

Hypoderma lineatum and *H. bovis* are warble flies of cattle that are widespread in Europe and other parts of the world but eradicated in Norway. The warble flies are believed to be relatively species-specific.

Bovids can also host a limited number of parasites that originate from wildlife reservoirs and potentially can have high virulence in Norwegian wildlife hosts. Three relevant parasites that are not present in Norway, but elsewhere in Europe are *Ashworthius sidemi*, *Fascioloides magna* and *Parafasciolopsis fasciolaemorpha*.

***Ashworthius sidemi* (Nematoda, Trichostrongylidae)** was originally isolated from Sika (*Cervus nippon*) and sambar deer (*Cervus unicolor*) in Asia but was introduced into Europe

with imported sika deer. It has spread and is still spreading over large parts of the continent (Drózdź et al. 2003; Kuznetsov 2021; Nosal et al. 2021). Spread is thought to occur both with introduction of animals and with migrating red deer (Drózdź et al. 2003; Demiaszkiewicz et al. 2017). The parasite has been found in a wide range of ruminants, both bovids and cervids. It was found in a Sika deer introduced to Sweden from Hungary and their Swedish-born calf in 2007 (Höglund et al. 2007) but based on ongoing investigations of the cervid nemabiome in Sweden, no evidence suggests spread from this location (pers. comm. Johan Höglund) The nematode has been found in a variety of ruminants: Sika deer, fallow deer, roe deer, red deer, moose, mouflon, chamois, sheep, European bison and domestic cattle (Kuznetsov 2021; Nosal et al. 2021).

A. sidemi is a haematophagous parasite of the abomasum but may in bovids with heavy infections also be found in the most oral part of the intestines. Heavy infections can cause widespread chronic abomasitis with necrosis and fibrosis and loss of abomasal mucin production (Magdalek et al. 2021), resulting in chronic diarrhea. *A. sidemi* can survive winter as larvae in hypobiosis in the abomasal mucosa and is hence thought to be able to establish also in alpine areas (Nosal et al. 2021). *A. sidemi* is prevalent in European bison in Poland (Kołodziej-Sobocińska et al. 2016).

Fascioloides magna, also known as the giant liver fluke, is an American trematode species that was introduced to Central Europe with imported wapiti in the 20th century. It is currently found in focal areas of Austria, Hungary, the Czech Republic, Slovakia, Croatia, Serbia and Italy, and is spreading along the Danube River, in Poland and into Germany (Malcicka 2015; Rehbein et al. 2021). The intermediate hosts of the trematode are freshwater snails in the Lymnea family, for example the species *Galba truncatula*, which is widespread in Europe, also at high latitudes (Malcicka 2015). Definitive hosts (hosts in which the parasite can reach adult stage and reproduce) include cervids, like white-tailed deer, mule deer, wapiti, caribou and red deer. Other ungulates are also infected in endemic areas. In definitive hosts, the flukes migrate through the liver tissues until they find a mate and thereafter reside in pseudocysts connected to the biliary duct system. The definitive hosts tolerate low-grade infections. However, the migration tracts are associated with local destruction of liver tissue, rupture of the pseudocysts can cause peritonitis and large amounts of eggs can cause occlusion of biliary ducts (Pybus, 2001). Infection with high numbers of flukes can cause extensive liver damage and there are several reports of declining condition of red deer in areas with increasing loads of *F. magna* (see Rehbein et al. 2021, for an overview). Severe clinical signs and mortality are seen in aberrant hosts, such as roe deer, sheep and goats, in which the flukes not are enclosed in pseudocysts, but continue to migrate within the liver and other tissues. Low number of mature flukes (5-6) can hence cause major tissue damage and death (Pybus 2001; Rehbein et al. 2021). Moose, cattle, horses and pigs are regarded as dead-end hosts for *F. magna*, i.e., the mature flukes become encysted in capsules without communication to the bile duct, and the eggs consequently not are excreted with faeces. While one study proposed that giant liver fluke infection caused a decline in the moose population (Murray et al. 2006), this has been rejected by other studies (Lankester & Foreyt 2011; Wünschmann et al. 2015). We have not found scientific information about *F. magna* in

European bison, yak or water buffalo, but American bison is proposed to have low susceptibility (Foreyt and Drew 2010)

Parafasciolopsis fasciolaemorpha is a liver fluke with moose as its primary host. The distribution of the parasite was limited to areas of Poland and Western Russia, but it seems to have spread to red deer in Hungary (Majoros 2000).

The fluke occurs with high prevalence in Polish moose, and the infestation levels are high. More than 100,000 flukes have been found within the liver of a single moose. The mature flukes reside in the bile ducts, and an infected moose may show severe and extensive liver lesions characterized by formation of ductal biliary cysts and fibrosis (Filip-Hutsch et al. 2019). The remaining liver tissue may, however, not be severely affected. Although affected animals might show diarrhea and fatal emaciation, they do not show signs of liver failure (Filip et al. 2016; Filip-Hutsch et al. 2019; Filip-Hutsch et al. 2021). Obligate intermediate host for *P. fasciolamorpha* is the Greater Ramshorn snail (*Planorbis corneus*). This snail is introduced to several locations in Norway, but do not show major spread from these (Kjærstad et al. 2018). The fluke has been isolated from European bison in Poland (Karbowski et al. 2014).

1.5 Interactions between kept and wild animals

1.5.1 Between bovids and other ungulates

Interactions between the bovid species considered here and other wild ungulates can occur through different mechanisms. First, direct competition for food might occur in areas where wild ungulates have dietary overlap with the introduced bovid species. Dietary overlap between herbivore species have received attention in the literature (see e.g. Myrnes 2000), and the specific diet of yak, water buffalo and American and European bison is discussed in chapter 1.2.4 of this assessment. In short, the American bison is mainly a grazer, the European bison is also a grazer but has more mixed diet including browse, the yak is mainly a grazer whereas the water buffalo has a more mixed diet (see chapter 1.2.4 and 1.4.1). If these bovids are introduced to the outfields, the probability for dietary overlap is highest with mixed feeders, such as red deer and to some extent the roe deer (which is closer to the browser end of the continuum) (Andersen et al. 1998; Myrnes 2000; Spitzer et al. 2020). The effects of such dietary overlap will strongly depend on food availability and might only be a considerable factor if there is shortage of food. Local overgrazing by introduced bovids might therefore have local effects on wild ungulates due to shared food resources.

There is also potential for other types of interactions with wild ungulates. For instance, in high elevation habitats in southern Norway, it is well known that wild reindeer is disturbed and avoid areas with high or even moderate human activity (Panzacchi et al. 2015; Reimers et al. 2003). If so, avoidance behaviour could also manifest directly or indirectly because the bovid herd is at least periodically looked after by the owners. The extent of such effects is

unknown, but will likely depend both on the habitat overlap, on the density of domestic bovids and the frequency of herder visits. Such disturbance effects might also be relevant for other wild forest-dwelling ungulates (red deer, roe deer and moose), but these species are less affected by human disturbance.

1.5.2 Interactions between bovids and other wildlife

There are several types of interactions between bovids and other wildlife species. First, predation might occur in outfields or in the wild in areas with large predators, such as wolves (*Canis lupus*), lynx (*Lynx lynx*), wolverine (*Gulo gulo*) or brown bear (*Ursus arctos*). However, it is not expected that predation on adult bovids will be common for lynx, wolverine or brown bear (Gervasi et al. 2015; Gervasi et al. 2012). To the extent that predation from these species will occur, it is expected that calves will be targeted (Gervasi et al. 2015). It is however known that wolf predation on adult American bison does occur, in particular in late winter when the bison might be in poor condition, or on subadult individuals (Smith et al. 2000). Studies from Bialowieza Primeval Forest, Poland, where wolves and European bison co-occur, have shown that predation from wolves is not common (Churski et al. 2021; Jedrzejewski et al. 1992). From parts of China where yak and wolves are sympatric, wolf predation on yak can be substantial in some cases (Liu & Jiang 2003). We are not aware of cases on wolf predation on domestic water buffalo.

Other interactions with wildlife are expected to be more indirect. As with wild ungulates, dietary overlap and potential scramble competition might be a factor between bovids and other herbivorous prey (e.g., hare (*Lepus timidus*), small rodents and grouse species). However, the strength of the competition is strongly contingent on the density of bovids relative to food availability and habitat productivity (see e.g., Myrnerud 2006 for a discussion about overgrazing). Other interactions between bovids and wildlife are also likely to be indirect and caused by potential knock-on effects due to grazing and trampling, as described in 1.4.1 and 1.4.2.

1.6 Influence of climate change

While alien and invasive species are more likely to migrate to new areas due to climate change and increasing temperatures (Bellard et al. 2013), it is less clear if climate change will affect the likelihood of entry - or the interest to import – the species considered here into Norway.

The climate tolerance of each species, as described in chapter 1.2.1, indicate considerable variation in the climate tolerance and preferences among the species when kept outdoor. For instance, the American bison have their main distribution in cold and snow rich areas, but also persist in arid locations in Mexico. The domestic yak is adapted to cold and dry alpine climate but will probably strive in deep snow and will seek water and shade at temperatures above 20°C. The European bison have elevated mortality (in wild) during snow rich winters, and the water buffalo is adapted to tropic and subtropic areas with hot and humid climate.

Thus, the climatic suitability of different parts of Norway might vary currently for the species considered here and might likewise change due to changing climatic conditions.

Due to climate change, both temperatures and precipitation are expected to increase in most parts of Norway, and in some areas, the increased precipitation will result in more snow (Hanssen-Bauer et al. 2017). These changes might make certain areas more or less suitable for the species considered here. However, the animals can be kept indoor during parts of the year, and supplemental feeding can make harsh winter conditions benign. Thus, more snow rich winter do not need to represent an obstacle. Warmer summers might be a problem for the domestic yak in some areas, but access to shade and water might reduce the potential negative effect of increased temperature.

Also, the risk associated with hitchhiking organisms and pathogens could be expected to change due to climate change (Cohen et al. 2020), but this is not considered here.

2 Methodology and data

2.1 Methodology for risk assessment

We have used a semi-quantitative risk assessment approach. VKM assess each potential hazard in four standardized steps: Hazard identification, hazard characterization, likelihood, and risk characterization, as judged by the project-group experts. Table 2.1-1 describes the ratings for the level of confidence the project group has in the assessments.

Under "**Hazard identification**" we describe the specific hazard and why this hazard is considered in the current assessment. Examples include specific species relevant for import, competition with native species or a hitchhiking disease-causing organism. The known effects of the hazard are presented and referenced examples of the known impacts from other countries are usually included.

Under "**Hazard characterization**" the specific potential effects of the hazard in question are described under Norwegian conditions. Examples include which areas/habitats that a species can thrive in, which species the invading species would compete with (or predate on) and what species that can be infected by the hitchhiking organism. The potential magnitude of the specific hazard is then characterized from "Minimal" to "Major" as described in Table 2.1-2.

Under "**Likelihood**" we assess how likely it is that the characterized hazard occurs. Likelihood intervals range from "Very unlikely" to "Very likely", as described in Table 2.1-3. Depending on the nature of the hazard this assessment included different aspects like likelihood of entry, establishment and spread, which may include additional, independent, assessments.

Finally, under "**Risk characterization**" the risk to biodiversity in Norway, posed by the specific hazard, is characterized as either "Low", "Medium" or "High", based on the magnitude of potential impact of that hazard and the likelihood of this occurring. This characterization follows the matrix presented in Figure 2.1-1.

Table 2.1-1 Ratings used for describing the level of confidence of the assessments.

Rating	Descriptors
Very low	There are no published data on the topic. Only expert judgement used.
Low	Available information on the topic is limited, and mostly expert judgements are used.
Medium	Some published information exists on the topic, but expert judgements are still used.
High	There is sufficient published information, and expert judgements are in concurrence.
Very high	The topic is very well debated in peer-reviewed journals, and international reports. Expert judgements are in concurrence.

Table 2.1-2 An adapted versions of the descriptors from Appendix E in (EFSA Panel on Plant Health (PLH) 2015) used for rating the magnitude of the impacts in the assessment.

Rating	Descriptors
Minimal	No known impact on local biodiversity
Minor	Potential impact on local biodiversity, but only occasional deaths of individuals
Moderate	Impact may cause moderate reduction in viability and adaptability of native populations
Major	Impact may cause severe reductions in local populations with consequences for local biodiversity and ecosystem functions and services
Massive	Impact may cause severe reductions in local biodiversity (local extinctions), with severe consequences for ecosystem functions and services

Table 2.1-3 An adapted versions of the descriptors from Appendix E in (EFSA Panel on Plant Health (PLH) 2015) used for rating the likelihood of the impacts in the assessment.

Rating	Descriptors
Very unlikely	Negative consequences would be expected to occur with a likelihood of 0-5%
Unlikely	Negative consequences would be expected to occur with a likelihood of 5-10%
Moderately likely	Negative consequences would be expected to occur with a likelihood of 10-50%
Likely	Negative consequences would be expected to occur with a likelihood of 50-75%
Very likely	Negative consequences would be expected to occur with a likelihood of 75-100%

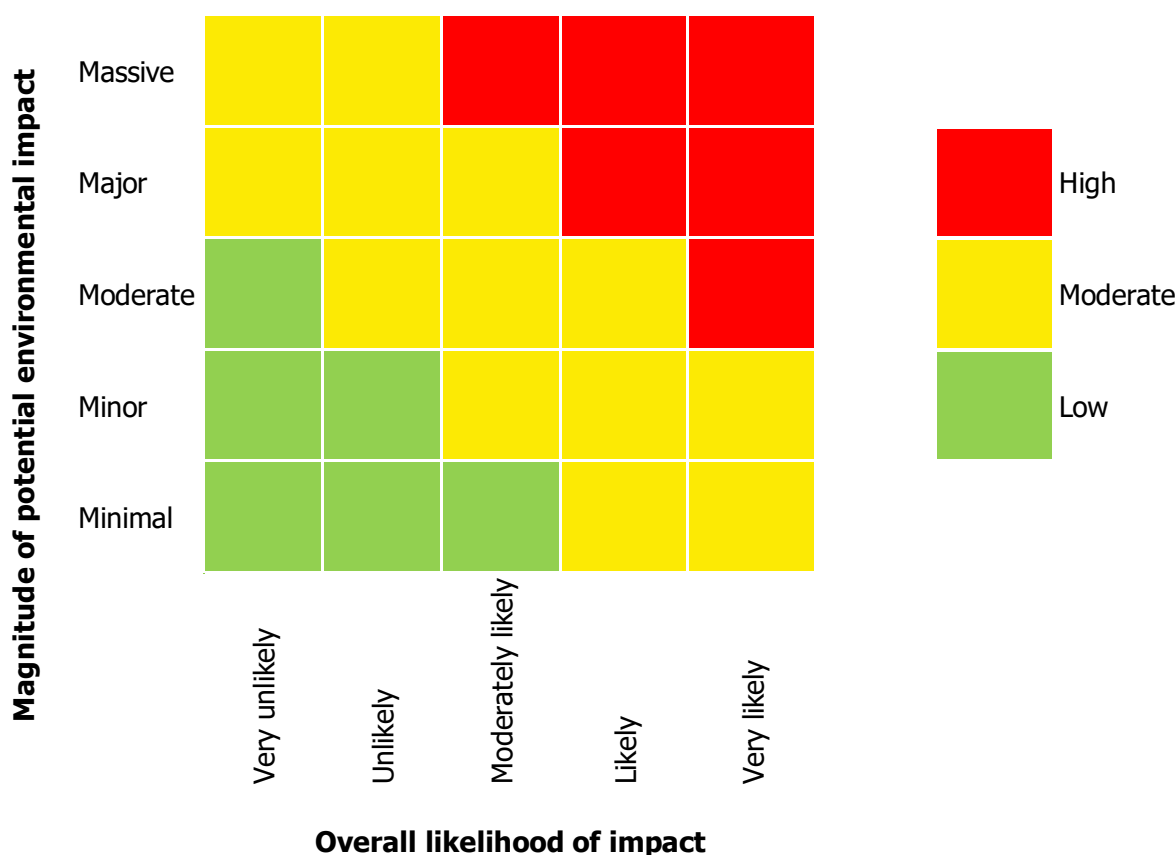


Figure 2.1-1: The conclusion of the risk assessments (low, moderate, or high) is based on the overall likelihood of the impact and the magnitude of the potential consequences of that impact on Norwegian biodiversity.

2.2 Information gathering and literature search

We have used ISI Web of Science core collection as primary source of scientific information. In addition, we performed general searches in Google Scholar. The searches included species name (or synonyms or common name) AND specific terms, such as "invasiveness", "invasive", "alien", "non-native", "introduced", "disease", "parasite", "pathogen", "virus", "bacteria" in combination with both common and scientific names of the four species.

We conducted general Google searches using some of the same terms as mentioned above. These searches sometimes revealed webpages or grey literature with relevant information. Finally, the involved experts used their extensive databases of relevant scientific literature.

3 Potential hazards

A key issue when assessing potential hazards associated with the four target species is the density at which they are kept, i.e., the number/metabolic biomass of herbivore per net grazeable area/available forage (stocking rate). General grazing effects on biodiversity (3.2.1) and on red-listed species (3.2.2.) will depend on herbivore density. Also, effects on biodiversity through competition with wild herbivores (3.2.3.) and in relation to wild carnivores (3.2.4.), will depend on the density of the actual herbivore. Finally, risk of transmitting viral (3.3.1.) and bacterial pathogens (3.3.2.) and parasites (3.3.3.) will all depend on the total number of animals in a given area. However, the actual *ecological impact* depends on several habitat- and management properties (Myserud 2006; Ross et. al 2016), of which we mention the most important here. Firstly, productive habitats in terms of biomass production can sustain higher herbivore densities compared to low productive habitats (Bråthen et al. 2007). Second, the length and timing of the grazing season impact the potential to tolerate grazing (lower resilience to winter grazing and trampling compared to summer) and grazing free periods during the growing season increases the potential to recover after grazing. Third, the use of supplementary fodder reduces grazing pressure but might also cause heavy trampled/disturbed patches close to the feeding stations. The same applies to the use of salt stones. Fourth, the density of wild herbivores adds to the total grazing pressure. An assessment of sustainable densities must take all these properties into account when recommending a density that will reduce the likelihood of a hazard. This implies sufficient availability of land and resources. Often an adaptive management is required to quantify a minimum area for a given number of animals.

To exemplify, we can consider two likely alternative scenarios for animal husbandry of the four species. In the first scenario, the import of a small herd of animals (e.g., < 10 individuals) in each case will have limited space requirements. This scenario is relevant for more small-scale pilot studies and for small scale meat or milk production or to attract visitors, and potential hazards are considered to be as assessed in the following subsections (*i.e.*, assuming that the animals are kept at low to intermediate (sustainable) densities, as practiced for other farm animals). As a second scenario, large herds imported for large scale meat (yak, bison) or milk production (water buffalo) which are in need of extensive areas and intensive herding to avoid local overgrazing, are expected to constitute an elevated risk (in terms of more severe potential impact and higher likelihood) for all cases assessed below.

The second scenario is not explicitly assessed in this report, and all risk assessment is based on scenario one where the animals are kept at low to intermediate densities.

3.1 General hazards

3.1.1 Escape and establishment in the wild

3.1.1.1 HAZARD IDENTIFICATION

Even in cases where animals are kept as domestic animals, either on fenced areas or free ranging in the wild, there is a risk of escapement and establishment in the wild (see chapter 1.2.3.2). The associated risks with respect to effects on wider biodiversity are identified later. However, regardless of associated effects on biodiversity from such escaped individuals, this is undesired because it may result in alien species becoming established in Norwegian nature.

3.1.1.2 HAZARD CHARACTERIZATION

If the species escape and establish a viable population in the wild, this may change the legal status of the animals as they are no longer considered the property of someone. Potential effects from escapement and establishment of feral populations in the wild on wider biodiversity is assessed below (chapter 3.2). However, unintended establishment in the wild by escaped animals is considered as a negative consequence in itself. We consider the negative impact from escapement as "Minimal", and the negative impact from establishment in the wild as "Moderate". The hazard characterization is assessed with "Low" to "Medium" confidence.

3.1.1.3 LIKELIHOOD

Based on the biology and life history of the assessed species (yak, water buffalo, American bison and European bison), we have assessed the likelihood for escape as "Moderate likely" if kept in unfenced areas, and "Unlikely" if kept in fenced areas. However, due to slow life histories and therefore slow population growth rates, we assess the likelihood of unintended establishment of feral populations in the wild as "Very unlikely". The likelihood is assessed with "Medium" confidence.

3.1.1.4 RISK CHARACTERIZATION

If kept at low to intermediate densities, VKM assesses that the risk associated with both escaping and potential establishment is "Low" for all four species (Medium to low confidence).

3.2 Behavioural impacts

3.2.1 General effects on biodiversity from grazing and trampling

3.2.1.1 HAZARD IDENTIFICATION

All target species are herbivores feeding selectively on specific graminoids and herbs (main diet) and to a minor extent on small woody species. At high densities, some plant species might be at risk for population declines and local extinctions. However, too low densities of grazing herbivores might also cause population declines for species associated with semi-natural habitats, highlighting the need of adapting intermediate grazing levels relative to habitat productivity (avoid under and overgrazing). The four species, but water buffalo in particular, can also have negative effects on the same organism, through trampling.

3.2.1.2 HAZARD CHARACTERIZATION

In Norway, the negative impact of grazing and trampling on biodiversity is most relevant for semi-natural habitats with high species richness of vascular plants and fungi, as well as pollinating insects and other invertebrates associated with for example plants and fungi. Trampling in wet habitats (beach meadows, deltas and wetlands) can potentially develop into a more severe problem even before densities are very high. Overall, the potential magnitude of this hazard is considered to be "Minor", with "High" confidence.

3.2.1.3 LIKELIHOOD

The likelihood of overgrazing and trampling causing loss of biodiversity is considered "Unlikely" given that the target herbivores are managed with access to sufficient grazing area. The likelihood is assessed with "Medium" confidence.

3.2.1.4 RISK CHARACTERIZATION

If kept at low to intermediate densities, VKM assesses that the risk of potential negative impact on biodiversity, posed by grazing and trampling, is "Low" for all four species ("Medium" to "High" confidence).

3.2.2 Grazing on red listed species

3.2.2.1 HAZARD IDENTIFICATION

Twenty-four percent of all red-listed species in Norway including vascular plants, fungi and invertebrates (wasps, beetles, butterflies) are associated with semi-natural habitats in either outfields or infields. Although their habitat maintenance is dependent on grazing, the four target herbivores might increase their vulnerability if the grazing pressure is too high.

3.2.2.2 HAZARD CHARACTERIZATION

Overgrazing and trampling at high densities may be detrimental for rare species in semi-natural habitats relevant for the four target species. As outlined in section 1.2.3 (suitable habitats in Norway), a wide range of semi-natural habitats could be suitable for the four herbivores, and no specific red-listed species could be identified as vulnerable due to herbivore pressure for any specific herbivore species. Overall, the potential magnitude of this hazard is considered to be "Minor", with "High" confidence.

3.2.2.3 LIKELIHOOD

The likelihood of overgrazing (and trampling) causing loss of red listed species is considered "Unlikely" given that the target herbivores are managed with access to sufficient grazing area. The likelihood is assessed with "Medium" confidence.

3.2.2.4 RISK CHARACTERIZATION

If kept at low to intermediate densities, VKM assesses that the risk of potential negative impact on red listed species, posed by grazing, is "Low" for all four species ("Medium" to "High" confidence).

3.2.3 Competition with wild herbivores

3.2.3.1 HAZARD IDENTIFICATION

Competition for food with wild herbivores is a relevant hazard, as discussed in chapter 1.6. The effects of such competition due to dietary overlap will strongly depend on food availability, and density of the bovid population and might only be a considerable factor when there is shortage of food. Local overgrazing by introduced bovids might have local effects on wild herbivores due to shared food resources.

3.2.3.2 HAZARD CHARACTERIZATION

Based on the available evidence, we consider the potential negative impact to be "Minimal" if the animals are kept in fenced infields. However, if allowed to graze outside fenced areas, the potential for competition with wild herbivores increases. Local overgrazing by introduced bovids might have local effects on wild herbivores due to shared food resources. In such cases, we consider the potential magnitude of this hazard to be "Minor" (assessed with "Medium" confidence).

3.2.3.3 LIKELIHOOD

If kept at low to intermediate densities, VKM consider the likelihood for negative effects as "Very unlikely" (assessed with "Medium" confidence).

3.2.3.4 RISK CHARACTERIZATION

Overall, VKM assesses that the risk of potential negative impact on biodiversity in Norway, posted by competition with native herbivores, is “Low” for all four species (“Medium” confidence).

3.2.4 Effects on wild carnivores

3.2.4.1 HAZARD IDENTIFICATION

As discussed in chapter 1.6, predation on three of the species (yak, American bison and European bison) might be expected, in particular from wolves in parts of Norway inside the wolf zone. Moreover, it is expected that calves and younger individuals are more vulnerable to predation. Predation events might both shift the habitat use of the involved carnivores, with potential negative effects associated with more frequent use of habitats close to humans. These areas might be associated with a higher risk of mortality for the carnivores (more roads etc), and a shift in habitat use might therefore have negative consequences.

3.2.4.2 HAZARD CHARACTERIZATION

If the presence of the bovid species assessed in this report is affecting the space use patterns of the relevant carnivore species (in particular wolves), there is a potential for negative side effects. In particular, if the bovids are grazing in unfenced areas close to human settlements, this might cause the predators to spend more time close to human settlements, which potentially is related to higher mortality risk (e.g., due to road accidents). We consider the potential magnitude of this hazard on biodiversity to be “Minor” (assessed with “Low” confidence).

3.2.4.3 LIKELIHOOD

Based on existing knowledge about carnivore space use, we consider the likelihood for changes in carnivore space use, and potential negative effects related to such a shift (e.g., spending more time close to human settlements) as “Unlikely” (assessed with “Low” confidence). It is expected that even though the bovid species discussed here might be preyed by wolves, it is unlikely that they will be distributed to an extent that they affect the habitat use patterns of the predators.

3.2.4.4 RISK CHARACTERIZATION

If kept at low to intermediate densities, VKM assesses that the risk of potential negative impact on biodiversity in Norway, posted by interactions with native carnivores, is “Low” for all four species (“Low” confidence).

3.3 Introduction of disease-causing agents

In the current report, we have focused on pathogens that potentially can be transmitted from bovids to cervids and/or lagomorphs. We have further concentrated on pathogens that are known or thought to occur in areas from which it is plausible that buffalo and yak can be imported from, i.e., northern and central Europe.

Import of American bison, yak and water buffalo is regulated under "forskrift om dyrehelsemessige betingelser for innførsel og utførsel av storfe" [regulation on zoosanitary conditions for import and export of cattle]⁸. The regulation states that imported animals should originate from a population subjected to surveillance programs and declared free for tuberculosis, brucellosis and enzootic bovine leucosis⁹ and declared free from bovine herpesvirus 1 (infectious bovine rhinotracheitis)¹⁰. Animals that originate from areas without approved surveillance and eradication programs according to this legislation, shall be held in isolation facilities approved by the Norwegian Food Authority for six months. The isolation facilities shall be "sufficiently fenced with respect to prevention of contact with cervids"¹¹.

The animal production association's coordinating unit for pathogen transmission protection during imports (KOORIMP) recommend additional requirements¹². These are voluntary, but animal producers can be met with sanctions if they do not fulfill the requirements¹¹. Important requirements with regard to the risk of introduction of pathogens with a potential impact on biodiversity are (translated and abbreviated from KOORIMP's web page – see this for a full description):

- To minimize the risk of introduction of vector-diseases as bluetongue and Schmallenberg's disease, imports shall only occur between the 1st of November and the 1st of april.
- animals shall not be imported from herds that themselves have imported live animals
- the ten oldest animals in the herd shall be tested for paratuberculosis according to the described procedures and the herd shall not be vaccinated against paratuberculosis
- animals in the export herd shall not have showed clinical signs consistent with ringworm *or* be vaccinated against ringworm the last three years
- the export herd shall not have diagnosed digital dermatitis or besnoitosis

⁸ <https://lovdata.no/forskrift/2002-03-25-305>

⁹ <https://eur-lex.europa.eu/legal-content/DA/TXT/PDF/?uri=CELEX:02003D0467-20210101&qid=1616416883790&from=EN>

¹⁰ <https://eur-lex.europa.eu/legal-content/DA/TXT/PDF/?uri=CELEX:02004D0558-20210101&qid=1616416212874&from=EN>

¹¹ <https://lovdata.no/dokument/INS/forskrift/2006-02-14-199>

¹² <https://www.animalia.no/no/Dyr/koorimp---import/tilleggskrav-ved-import/tilleggskrav-levende-storfe/>

- the imported animals shall be born in the export country
- the imported animals shall be isolated the last 30 days before the transport and tested against salmonella (not animals from Sweden or Finland), *Mycoplasma bovis*, Q-fever, bovine virus diarrhoea, bluetongue (if the country is not free) and examined for contagious claw disease as digital dermatitis.
- the imported animals shall be treated against endo- and ectoparasites before transport to Norway
- the animals shall be treated with disinfectant foot bath with documented effect against contagious claw diseases before and after arrival to Norway
- the animals shall be tested or treated against *Parafilaria bovicolis* before and after arrival to Norway
- the animals shall not be sold or held on pasture together with or otherwise have contact with cattle from other herds before they have been in Norway for 24 months and all animals in the herd are more than four years old

Consequently, for transmission to wildlife of a pathogen with potential impact on biodiversity to occur, the following factors have to be present (modified from Mørk et al. 2016).

1. The export herd has to be infected
2. The pathogen has to remain undiscovered before export
3. The pathogen has to survive transport and eventual isolation (or escape from isolation)
4. An infective dose of the pathogen has to be exposed to a susceptible wild animal and establish an infection.

This emphasizes that, as long as the above-mentioned preventive measures are followed, the pathogens that pose the highest risk, are those that are prevalent in the area where the animals are exported from *and* that they survive for a long period in the bovine host without causing major clinical signs and/or being detectable with the routinely performed diagnostics. A low infective dose of the pathogen will also facilitate transmission to wildlife.

3.3.1 Viral pathogens

3.3.1.1 HAZARD IDENTIFICATION

As described above in 1.5.1 there are a number of pathogenic viruses that may be introduced with import of the four bovid species described in this report.

These viruses may therefore be considered hazards if an infected bison, yak or water buffalo were to be imported. The ability to diagnose disease caused by these viruses or test for their presence in the exporting herd will vary, but they can all be considered potential hazards. Transmission can occur via close contact with wild animals, vectors or via uptake of environmentally stable viruses via feeding in the same area.

3.3.1.2 HAZARD CHARACTERIZATION

In the case of transfer of the viral pathogens that can be found in bison, yak or water buffalo to susceptible wildlife in Norway, transmission for some of the diseases must be expected. Without pre-existing immunity to these viruses in Norwegian wildlife, the potential for negative effects will range from minor to major, dependent on the type of virus. Many of the disease agents that infect and cause disease in cattle, may only cause unapparent or mild disease in wildlife (Thomson et al. 2003). In such cases (an example would be import of FMDV), an impact on biodiversity will only ensue if the veterinary authorities install disease eradication/mitigation measures that include wildlife population regulation. With limited literature on the impact of these viruses on wildlife the magnitude of hazard can be characterized with "Medium" or "High" confidence as follows:

Virus	Magnitude of hazard	Confidence
Bovine herpesvirus-1	Major	Medium
Bovine respiratory syncytial virus (BRSV)	Minimal	Medium
Parainfluenza-3 (PI-3)	Minor	Medium
Bovine Virus Diarrhea Virus (BVDV)	Major	Medium
Rotavirus	Minimal	Medium
Coronavirus	Minimal	Medium
Blue Tongue Virus (BTV)	Major	Medium
Epizootic Haemorrhagic Fever Virus	Major	High
Foot and mouth disease virus (FMDV)	Major	High
Bovine leucemia virus (BLV)	Minor	Medium

3.3.1.3 LIKELIHOOD

The likelihood that the imported species will be a carrier of the discussed viruses depends on the prevalence of disease in the exporting units and the quality of the diagnostic system used in the exporting country. Underreporting of lack of diagnosis may lead to low prevalence estimates. The quarantine regime employed for the imports will also affect the likelihood of transfer. With a good diagnostic system, accurate reporting and appropriate quarantine routines, the likelihood of pathogen import is "Very unlikely" with "Medium" confidence.

3.3.1.4 RISK CHARACTERIZATION

Although some viruses can have a profound impact on biodiversity should they enter Norway and be transmitted to susceptible hosts, the likelihood of this occurring is determined to be very unlikely. Therefore, the following viral pathogens are characterized with a "Moderate" risk; Bovine herpesvirus-1, Blue Tongue Virus (BTV), Epizootic Haemorrhagic Fever Virus, Bovine Virus Diarrhea Virus (BVDV) and Foot and mouth disease virus (FMDV).

Coronavirus, Rotavirus, Bovine leukemia virus (BLV), Bovine respiratory syncytial virus (BRSV), and Parainfluenza-3 (PI-3) have been assessed to pose a “Low” risk to biodiversity in Norway.

3.3.2 Bacterial pathogens

3.3.2.1 HAZARD IDENTIFICATION

As outlined above, bison, yak and water buffalo carry numerous pathogenic bacteria that may have the potential to infect Norwegian wildlife.

Bovine tuberculosis caused by *M. bovis*/*M. capra* is able to establish persistent infection that in some cases is difficult to detect in a live animal due to lack of clinical signs and relatively low sensitivity of diagnostic tests (Gavier-Widén et al. 2012). The agent can establish infection in multiple wildlife hosts and has for example been isolated from farmed and free-living cervidae (Clifton et al. 1991). Likewise, *Brucella abortus* has been documented in both bison and elk in the Yellowstone national park, suggesting that the bacteria can be transferred to- and from these species (Kamath et al. 2021; Godfroid 2017)

3.3.2.2 HAZARD CHARACTERIZATION

In the case of transfer of any of the bacterial pathogens found in bison, yak or water buffalo to susceptible wildlife in Norway, transmission for some of the diseases must be expected. Without pre-existing immunity to these bacteria in Norwegian wildlife today, the potential for negative effects must be considered to be “Moderate” to “Major”. *Mycobacterium bovis* is highly resistant in the environment and may therefore be transmitted to deer, moose and reindeer grazing in the same area. For example, red deer, wild boar and badgers (*Meles meles*) can function as maintenance hosts, and establishment in these species would prevent eradication in livestock. If the disease become established in Norwegian wildlife, a direct impact on survival and condition of the infected populations can be expected, at least where host species are found in high densities and the transmission is efficient. Predators in such areas, for example lynx, can also have a high probability of infection, adding a concern for potential impact on these species. The zoonotic aspects and the economic impact of transmission to livestock may in addition stimulate to disease control programs that have an impact on biodiversity. A herd of European bison was for example eradicated by Polish authorities in 2005 due to persistent tuberculosis (Didkowska et al. 2021) and British and Irish authorities have culled badgers in order to minimize prevalence of bovine tuberculosis in cattle (Gavier-Widén 2012). The potential magnitude of these hazards is assessed with “Medium” to “High” confidence.

Bacteria	Magnitude of hazard	Confidence
<i>Mycobacterium avium subspecies paratuberculosis</i> (MAP)	Moderate	Medium
<i>Mycobacterium bovis</i>	Major	High

Bacteria	Magnitude of hazard	Confidence
<i>Mycobacterium capra</i>	Moderate	Medium
<i>Brucella abortus</i>	Moderate	Medium
<i>Mycoplasma bovis</i>	Moderate	Medium
<i>Salmonella spp.</i>	Moderate	Medium

3.3.2.2 LIKELIHOOD

The likelihood that the imported species will carry any of the discussed bacteria depends on the prevalence of disease in the exporting units, the quality of the diagnostic system used in the exporting country and the preventive measures taken in Norway. The highest risk is associated with disease agents that can persist in the imported animals for a long period without causing major clinical signs, that resist treatment and/or escape detection with routine tests. Mycobacterial infections (*M. bovis*, *M. avium* ss. *paratuberculosis*) fall in this group.

Provided that all animal health regulations are followed and KOORIMP's additional requirements fulfilled, we regard the likelihood of an introduction of bacterial pathogens with a major impact on biodiversity as unlikely with "Medium" confidence

3.3.2.3 RISK CHARACTERIZATION

Although some bacterial pathogens can have a profound impact on biodiversity should they enter the country and be transmitted to susceptible hosts, the likelihood of this occurring is unlikely. Therefore, all bacterial pathogens assessed here are considered to pose a "Moderate" risk to biodiversity in Norway (assessed with "Medium" confidence).

3.3.3 Parasites

3.3.3.1 HAZARD IDENTIFICATION

Most of the described parasites found in bison, yak and/or water buffalo are already present in Norway (see chapter 1.5.3).

These parasites will therefore not lead to a significantly increased risk for negative impact on Norwegian biodiversity. However, some species known to infect Bovine animals have not yet been detected in Norway:

- *Parafilaria bovicola*
- *Toxocara vitulorum*
- *Stephanophilaria stilesi*
- *Besnoita besnoiti*
- *Sarcoptes scabiei* var. *bovis*
- *Hypoderma lineatum* and *H. bovis*

- *Ashworthius sidemi*
- *Fascioloides magna*
- *Parafasciolopsis fasciolaemorpha*

Parafilaria bovicola, *Toxocara vitulorum*, *Stephanophilaria stilesi*, *Besnoita besnoiti*, *Sarcoptes scabiei* var. *bovis*, *Hypoderma lineatum* and *H. bovis* are presumed unable to establish life cycles in species outside the family Bovidae. With the exception of the introduced muskox, that tend to become infected with any parasites present in its environment (Alendal & Helle, 1983; Davidson et al. 2014), there are no native bovid wildlife in Norway, and these parasites are not identified as a hazard for biological diversity.

The bovids can, however, act as definitive hosts for a limited number of parasites that are able to establish long-lasting infections that are difficult to detect both in bovids, cervids and perhaps also in lagomorphs and other species. In the current report, we have identified *Ashworthius sidemi* and *Fascioloides magna* as such parasites. *Parafasciolopsis fasciolamorpha* is not regarded as an important hazard, though it has been found in European bison, since its obligate intermediate host, the greater ramshorn snail, has only a limited distribution in Norway.

3.3.3.2 HAZARD CHARACTERIZATION

Ashworthius sidemi and *Fascioloides magna* can potentially be present in export herds and in the exported animals without being detected, and they are probably able to resist and survive the preventive measures normally taken during import of bovids to Norway. With the high densities of susceptible hosts (cervids) that are found in Norway, it is suspected that an incident with transmission from buffalo, bison or yak to wildlife will lead to efficient transmission and further spread within a cervid reservoir with spill over to domestic animals. Once established, the parasites will be difficult to eradicate. These parasites may have major impact on Norwegian biodiversity. This potential magnitude of these hazards is assessed with "Medium" to "High" confidence.

Parasite	Magnitude of hazard	Confidence
<i>Ashworthius sidemi</i>	Major	High
<i>Fascioloides magna</i>	Major	High
<i>Parafasciolopsis fasciolaemorpha</i>	Minor	Medium

3.3.3.3 LIKELIHOOD

The likelihood of introducing *Ashworthius sidemi* and *Fascioloides magna* to Norway with bison, water buffalo or yak will depend on the prevalence of these infection in the area the export herd live in. Given the presumed absence of these parasites in the Nordic countries and the patchy distribution elsewhere in Europe, we regard the likelihood of the introduction

as “Unlikely”. The level of confidence for this judgement is “Low”, as there is little available information.

3.3.3.4 RISK CHARACTERIZATION

In areas with high host (cervid) density and conditions that support efficient transmission, some animals can be infected with high intensities of these parasites. This may potentially cause moderate reduction in viability of native populations, and thus biodiversity. Overall, VKM assesses that the parasites *Ashworthius sidemi* and *Fascioloides magna* pose a “Moderate” risk to biodiversity, while the risk is “Low” for *Parafasciolopsis fasciolaemorpha*.

There is, however, little information available about the population impact of *Ashworthius sidemi* and *Fascioloides magna*, so the confidence in these assessments is “Low”.

4 Other impacts

4.1 Impact on ecosystem services

Several cultural/non-material services and disservices might also be associated with the four target herbivores (Section 1.4.2). While humans often appreciate the appearance of large herbivores, both livestock and wild, as part of cultural/non-material services, human fear and risk of animal attacks could be seen as a disservice when animals are roaming in outfields also used by humans (and where humans have the right of public access). Examples for Norway are everything from herds of cattle to muskox which are causing accidents/incidents every year. For European bison in Denmark, people are told to keep distance to the animals to avoid interferences¹³.

4.2 Impact on agriculture

The domesticated yak and domesticated water buffalo have both been imported in limited number a few times each from 2016 and onwards. Arguments for introducing new livestock are partly commercial (food production, tourism), but also related to maintaining open semi-natural habitats such as heathland and grasslands, and wooded meadows¹⁴. These arguments are also the main arguments for introducing European and American bison to Norway. However, none of the four target species assessed in this report represents known ecological functions and services needed for the ecological sustainability of nature in Norway, which is not supported by species and breeds already present among large herbivores.

¹³ <https://bornholm.info/en/meet-a-buffalo/>

¹⁴ <https://rewildingeuropa.com/impact-stories/european-bison/>

5 Uncertainties

A substantial uncertainty is associated with the density at which the considered species will be kept. Our assessment assumes that they are kept at low to moderate densities. However, based on the available information, VKM is not able to assess with any precision at what density biodiversity effects will be evident, and our assessment is partly based on general ecological theory (see chapter 1 and chapter 3). Because no information about the motivation to keep yak, American bison, European bison or water buffalo in Norway is available, VKM is uncertain of the most likely scenarios for animal husbandry based on the assessed bovid species. All target species may at certain densities act as ecosystem engineers, i.e., modify their environment and the associated biodiversity significantly (Nickell et al. 2018). However, we have limited knowledge on how yak, American bison, European bison or water buffalo in Norway could affect abundance and diversity of organisms associated with different trophic levels (primary producers, other herbivores, predators and decomposers) due to complex bottom-up and top-down interactions induced by the herbivore (Kuijper et al. 2015; Nickell et al. 2018).

If the bovid species assessed here are imported and kept at higher densities, one viable and robust option would be to develop an adaptive monitoring scheme focusing on potential effects on biodiversity due to grazing and interactions with wildlife, as well as the potential spread of pathogens.

6 Conclusions (with answers to the terms of reference)

In agreement with the terms of reference, VKM has assessed the risks associated with import and keeping of American bison, European bison, domesticated water buffalo and domesticated yak in Norway. VKM's conclusions (with answers to the terms of reference) of the assessment of the impacts on biodiversity follows in chapter 6.1.

VKM was moreover asked to provide a similar assessment and conclusion for the effects of accompanying risk causing agents on biodiversity. This assessment is not part of the overall assessment of risks to biodiversity and is presented in chapter 6.2. Effects on ecosystem services are described in chapter 4.

VKM did not assess the possible risks associated with reduced animal welfare in relation to importing and keeping of the above bovid species.

6.1 Impact on biodiversity

Although the risks associated with the four animal species assessed here vary in terms of the potential level of impact and the likelihood of these hazards occurring, VKM concluded that the risk for negative impacts on biodiversity is low for all assessed bovid species for all the hazards we identified. These hazards relate to both direct and indirect effects of grazing, as well as other interactions with wildlife. This assessment is based on the assumption that the animals are kept in low to intermediate densities as outlined in chapter 3. We have given some general considerations about what "reasonable densities" might imply and highlight that this is a complex interaction between many ecological factors and outside the scope of this assessment to accurately define. VKM note that should the assessed bovinds be kept at higher densities, negative effects on biodiversity might occur due to direct and indirect effects of high grazing and/or browsing pressure.

Assuming low to intermediate densities, VKM concludes that there is "Low" risk of negative impact on biodiversity in Norway, stemming from import and keeping of domesticated yak, domesticated water buffalo, European bison and American bison.

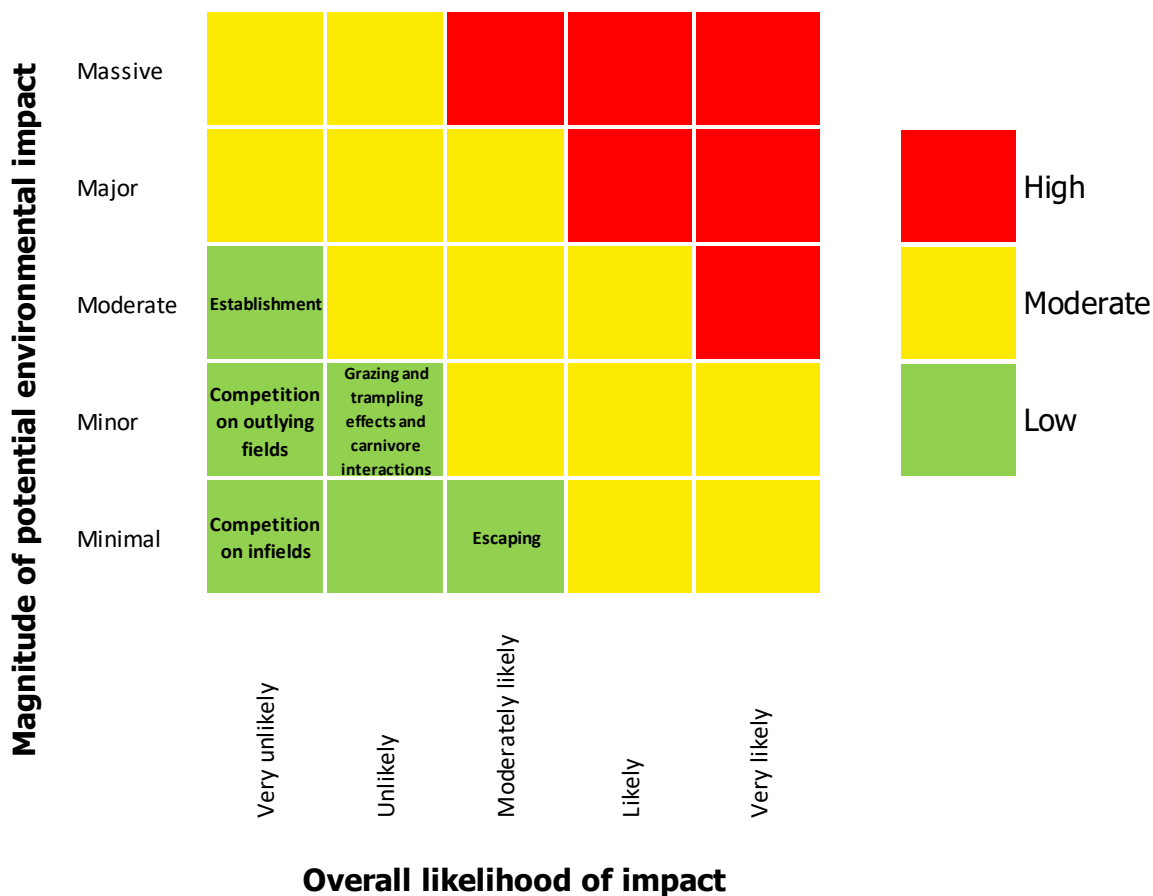


Figure 6.1-1: Summarized risks to biodiversity in Norway from keeping domesticated yak, domesticated water buffalo, European bison and American bison, assuming low to intermediate densities.

6.2 Risks associated with pathogens

Concerning the hitchhiking organisms associated with domesticated yak, domesticated water buffalo, European bison and American bison discussed in this report, VKM concludes that thirteen species pose a “Moderate” risk to biodiversity in Norway, while seven species pose a “Low” risk (see Figure 6.2-1 – 6.2-3 for viral-, bacterial- and parasitic pathogens, respectively). This conclusion is based on the assumptions mentioned above under 3.3, namely that imported animals should originate from a population subjected to surveillance programs and declared free of certain pathogens listed by the World Organization of Animal Health (OIE).

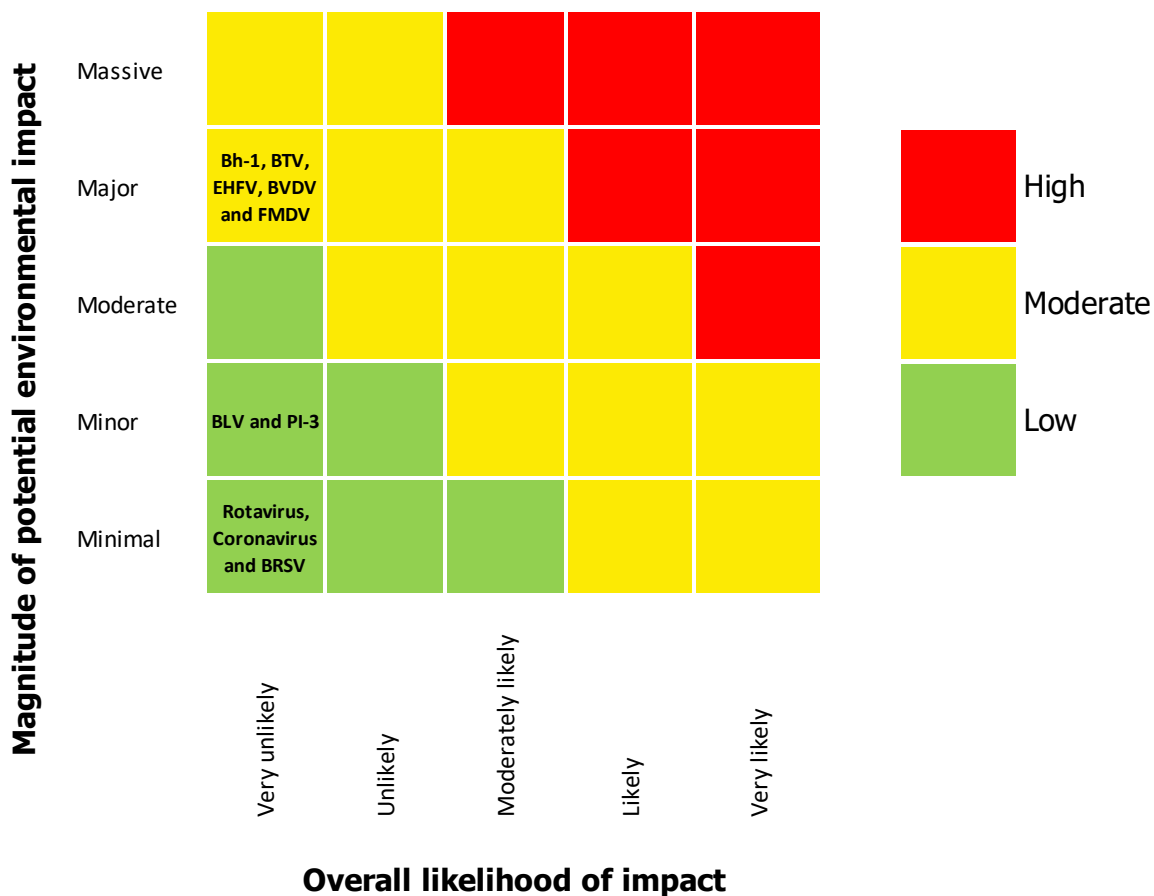


Figure 6.2-1: Summarized risks to biodiversity in Norway through spread of viral pathogens following import and keeping domesticated yak, domesticated water buffalo, European bison and American bison, assuming low to intermediate densities. Abbreviations: Bh-1 = Bovine herpesvirus-1, BTV = Blue Tounge Virus, EHFV = Epizootic Haemorrhagic Fever Virus, BVDV = Bovine Virus Diarrhea Virus, FMDV = Foot and mouth disease virus, BLV = Bovine leucemia virus, PI-3 = Parainfluenza-3, BRSV = Bovine respiratory syncytial virus.

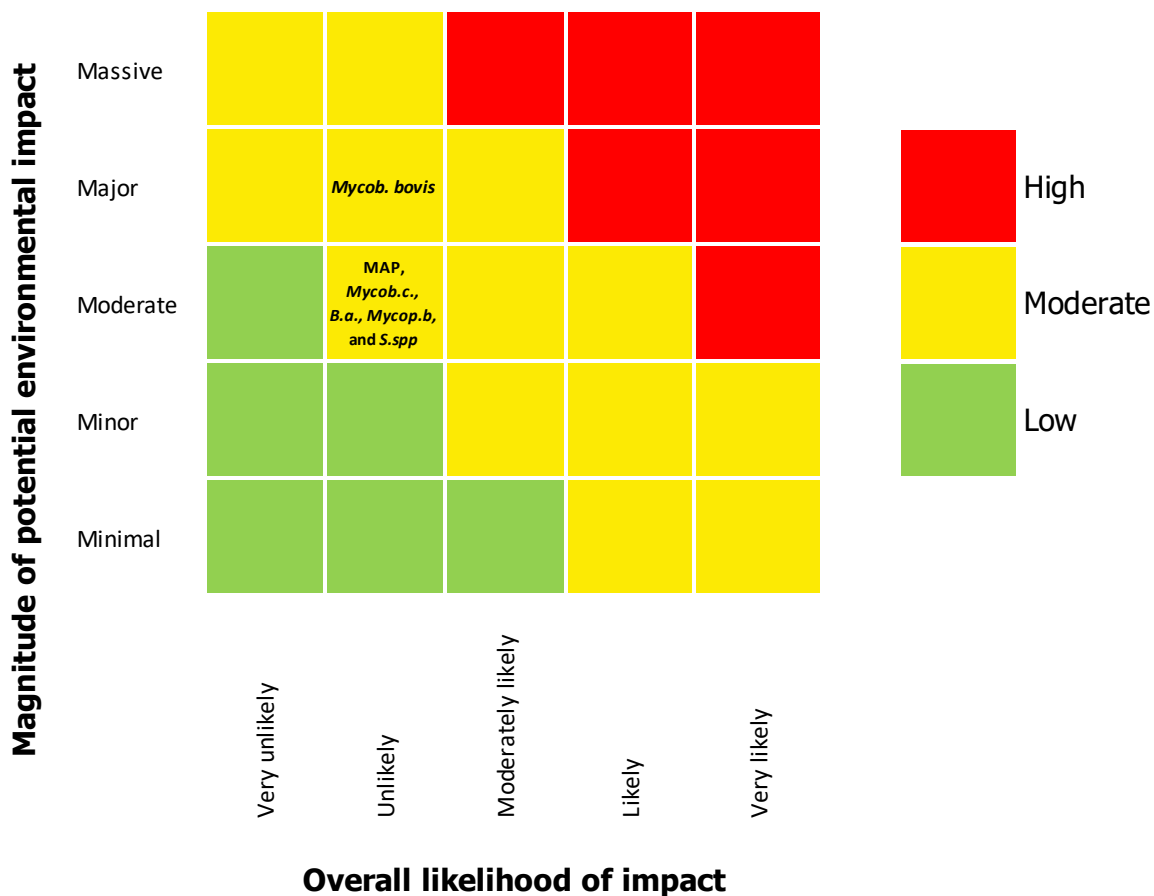


Figure 6.2-2: Summarized risks to biodiversity in Norway through spread of bacterial pathogens following import and keeping domesticated yak, domesticated water buffalo, European bison and American bison, assuming low to intermediate densities. Abbreviations: *Mycob. Bovis* = *Mycobacterium bovis*, MAP = *Mycobacterium avium* subspecies *paratuberculosis*, *Mycob.c.* = *Mycobacterium capra*, *B.a.* = *Brucella abortus*, *Mycop.b* = *Mycoplasmas bovis*, *S.spp* = *Salmonella* species.

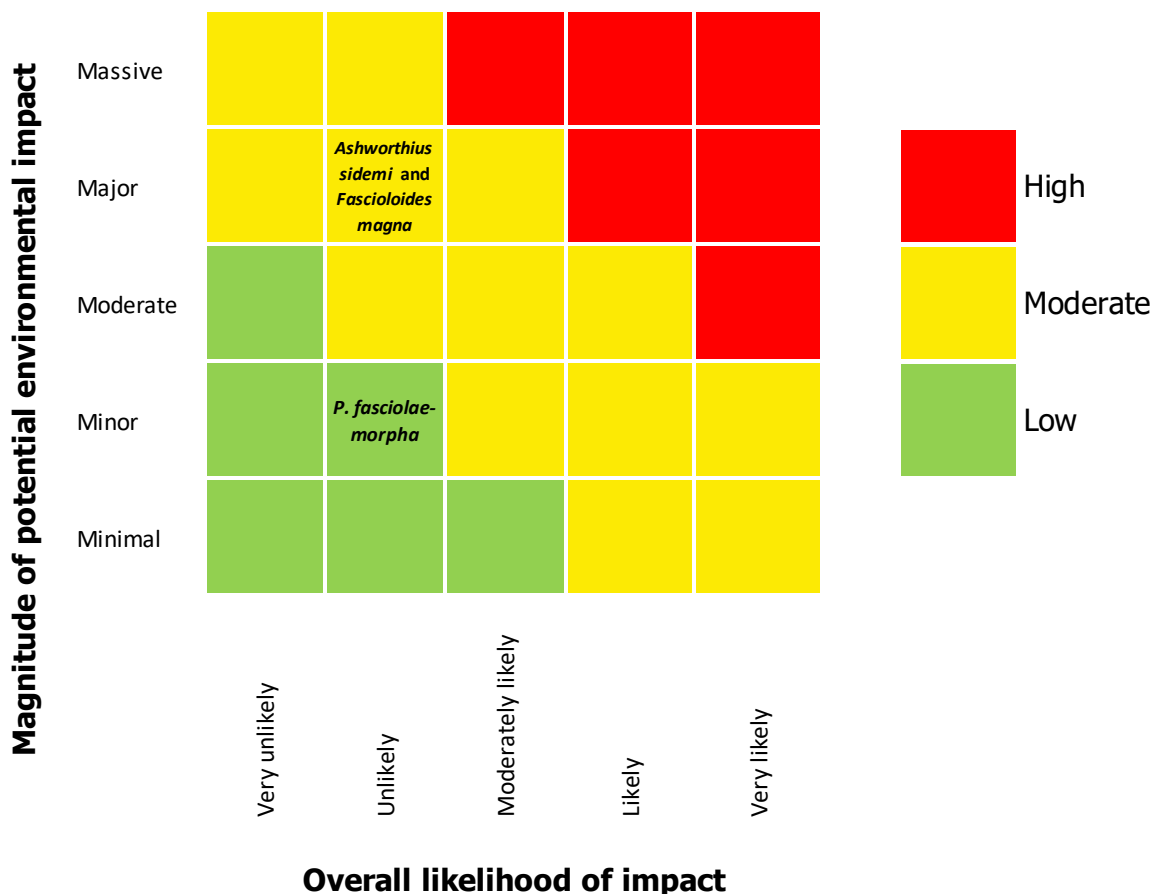


Figure 6.2-3: Summarized risks to biodiversity in Norway through spread of parasites following import and keeping domesticated yak, domesticated water buffalo, European bison and American bison, assuming low to intermediate densities. *P. fasciolaemorpha* = *Parafasciolopsis fasciolaemorpha*.

Animals not subjected to disease surveillance or from areas free of certain pathogens must be held in isolation, as described in section 3.0. This risk also depends on the number of imported animals, their stocking densities and degree of contact with Norwegian wildlife (how the animals are kept). Therefore, the conclusion on moderate risk is highly dependent on these measures to reduce the likelihood of pathogen import. In case of introduction, several of the viruses (Bh-1, BTV, BFDV), bacteria (*M. ovis*, *M. avium paratuberculosis*) or parasites can be expected and result in a major negative impact on Norwegian biodiversity. This impact can be direct through transmission, or indirect due to preventive culling of animals to protect wildlife or farmed animals. The parasites *Ashworthius sidemi* and *Fascioloides magna* can probably have a moderate impact on Norwegian cervids. There are also additional risks due to the presence of undescribed infectious agents not presented here. New strains of commensals, pathogens and parasites in the four Bovidae species discussed here may be more virulent to Norwegian wildlife than strains already present and may as such cause unexpected effects.

7 Data gaps

The distribution and prevalence of pathogens in bison, water buffalo and yak are not always known, and there is often even less information about the occurrence in sympatric wildlife. There is also a lack of knowledge of the susceptibility of infection in Norwegian wildlife species and consequently both the potential role of the wildlife species in the epidemiology of the pathogen and the potential impact the pathogen may have on biodiversity.

8 References

- Agabriel, J., Bony, J. & Micol, D. (1996). Management of an American bison herd [Bison bison]. *Productions Animales*.
- Alendal, E. & Helle, O. (1983). Helminth parasites of muskoxen *Ovibos moschatus* in Norway incl. Spitsbergen and in Sweden, with a synopsis of parasites reported from this host. *Fauna Norvegica. Ser. A*, 4, 41-52.
- Andersen, R., Duncan, P. & Linnell, J.D. (1998). *The European roe deer: the biology of success*. Scandinavian university press Oslo.
- Aune, K., Jørgensen, D. & Gates, C. (2017). Bison bison (errata version published in 2018). *The IUCN Red List of Threatened Species 2017*: e.T2815A123789863.
- Austrheim, G., Solberg, E.J., Mysterud, A., Daverdin, M. & Andersen, R. (2008). Hjortedyr og husdyr på beite i norsk utmark i perioden 1949–1999. *Rapport zoologisk serie*, 2, 2008.
- Austrheim, G., Speed, J.D., Evju, M., Hester, A., Holand, Ø., Loe, L.E., Martinsen, V., Mobæk, R., Mulder, J. & Steen, H. (2016). Synergies and trade-offs between ecosystem services in an alpine ecosystem grazed by sheep—An experimental approach. *Basic and Applied Ecology*, 17, 596-608.
- Bao, P., Guo, X., Pei, J., Liang, C., Ding, X., Min, C., Wang, H., Wu, X. & Yan, P. (2016). Complete mitogenome sequencing and phylogenetic analysis of PaLi yak (*Bos grunniens*). *Mitochondrial DNA A DNA Mapp Seq Anal*, 27, 4590-4591.
- Bardgett, R.D. & Wardle, D.A. (2003). Herbivore-mediated linkages between aboveground and belowground communities. *Ecology*, 84, 2258-2268.
- Bellard, C., Thuiller, W., Leroy, B., Genovesi, P., Bakkenes, M. & Courchamp, F. (2013). Will climate change promote future invasions? *Global change biology*, 19, 3740-3748.
- Berezowski, J., Hunter, D., Love, D., Toomey, P. & Woodbury, M. (2018). *Bison diseases field guide*.
- Borghese, A. (2005). *Buffalo production and research*. REU technical series.
- Borghese, A. & Mazzi, M. (2005). *Buffalo population and strategies in the world*. *Buffalo production and research*, 67, 1-39.
- Bornett-Gauci, H., Martin, J. & Arney, D. (2006). The welfare of low-volume farm animals during transport and at slaughter: a review of current knowledge and recommendations for future research. *ANIMAL WELFARE-POTTERS BAR THEN WHEATHAMPSTEAD-*, 15, 299.

- Bråthen, K.A., Ims, R.A., Yoccoz, N.G., Fauchald, P., Tveraa, T. & Hausner, V.H. (2007). Induced shift in ecosystem productivity? Extensive scale effects of abundant large herbivores. *Ecosystems*, 10, 773-789.
- Buzzard, P. & Berger, J. (2016). *Bos mutus*. The IUCN Red List of Threatened Species 2016: e.T2892A101293528. <https://dx.doi.org/10.2305/IUCN.UK.2016-2.RLTS.T2892A101293528.en>. Downloaded on 27 August 2021.
- Bürki, S., Frey, J. & Pilo, P. (2015). Virulence, persistence and dissemination of *Mycoplasma bovis*. *Veterinary microbiology*, 179, 15-22.
- Churski, M., Spitzer, R., Coissac, E., Taberlet, P., Lescinskaite, J., van Ginkel, H.A., Kuijper, D.P.J. & Cromsigt, J.P.G.M. (2021). How do forest management and wolf space-use affect diet composition of the wolf's main prey, the red deer versus a non-prey species, the European bison? *Forest Ecology and Management*, 479, 118620.
- Clifton-Hadley, R. & Wilesmith, J. (1991). Tuberculosis in deer: a review. *The Veterinary Record*, 129, 5-12.
- Coburn, B., Grassl, G.A. & Finlay, B. (2007). Salmonella, the host and disease: a brief review. *Immunology and cell biology*, 85, 112-118.
- Coetzer, J. & Tustin, R. (2004). *Infectious diseases of livestock*. Volume three.
- Cohen, J.M., Sauer, E.L., Santiago, O., Spencer, S. & Rohr, J.R. (2020). Divergent impacts of warming weather on wildlife disease risk across climates. *Science*, 370.
- Cronin, M.A., MacNeil, M.D., Vu, N., Leesburg, V., Blackburn, H.D. & Derr, J.N. (2013). Genetic Variation and Differentiation of Bison (*Bison bison*) Subspecies and Cattle (*Bos taurus*) Breeds and Subspecies. *Journal of Heredity*, 104, 500-509.
- Daleszczyk, K. (2011). Some factors influencing reproductive parameters of European bison cows. *European Bison Conservation Newsletter*, 4, 45-54.
- Davidson, R.K., Amundsen, H., Lie, N.O., Luyckx, K., Robertson, L.J., Verocai, G.G., Kutz, S.J. & Ytrehus, B. (2014). Sentinels in a climatic outpost: Endoparasites in the introduced muskox (*Ovibos moschatus wardi*) population of Dovrefjell, Norway. *International Journal for Parasitology: Parasites and Wildlife*, 3, 154-160.
- Decker, J.E., Pires, J.C., Conant, G.C., McKay, S.D., Heaton, M.P., Chen, K., Cooper, A., Vilkki, J., Seabury, C.M., Caetano, A.R., Johnson, G.S., Brenneman, R.A., Hanotte, O., Eggert, L.S., Wiener, P., Kim, J.J., Kim, K.S., Sonstegard, T.S., Van Tassel, C.P., Neibergs, H.L., McEwan, J.C., Brauning R., Coutinho, L.L., Babar, M.E., Wilson, G.A., McClure, M.C., Rolf, M.M., Kim, J.W., Schnabel, R.D. & Taylor, J.F. (2009). Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. *Proceedings of the National Academy of Sciences*, 106, 18644-18649.

Demiaszkiewicz, A.W., Merta, D., Kobielski, J., Filip, K.J. & Pyziel, A.M. (2017). Expansion of *Ashworthius sidemi* in red deer and roe deer from the Lower Silesian Wilderness and its impact on infection with other gastrointestinal nematodes. *Acta Parasitol*, 62, 853-857.

Didkowska, A., Orłowska, B., Krajewska-Wędzina, M., Augustynowicz-Kopeć, E., Brzezińska, S., Żygowska, Wiśniewski, J.M., Kaczor, S., Welz, M. & Olech-Piasecka, W. (2021). Microbiological and molecular monitoring for bovine tuberculosis in the Polish population of European bison (*Bison bonasus*). *Annals of Agricultural and Environmental Medicine*.

Douglas, K.C., Halbert, N.D., Kolenda, C., Childers, C., Hunter, D.L. & Derr, J.N. (2011). Complete mitochondrial DNA sequence analysis of *Bison bison* and bison–cattle hybrids: Function and phylogeny. *Mitochondrion*, 11, 166-175.

Drózdź, J., Demiaszkiewicz, A.W. & Lachowicz, J. (2003). Expansion of the Asiatic parasite *Ashworthius sidemi* (Nematoda, Trichostrongylidae) in wild ruminants in Polish territory. *Parasitol Res*, 89, 94-97.

Dubey, J., Sreekumar, C., Rosenthal, B., Vianna, M., Nylund, M., Nikander, S. & Oksanen, A. (2004). Redescription of *Besnoitia tarandi* (Protozoa: Apicomplexa) from the reindeer (*Rangifer tarandus*). *International journal for parasitology*, 34, 1273-1287.

EFSA AHAW Panel (EFSA Panel on Animal Health and Welfare). (2017). Scientific opinion on bluetongue: control, surveillance and safe movement of animals. *EFSA Journal* 2017; 15(3):4698, 126 pp. doi:10.2903/j.efsa.2017.4698. In: *EFSA Journal*, p. e04698.

Falk, M., A., R., Wolff, C., Sviland, S., Jonsson, M., Press, M.M., Heier, B. T., Lundberg, H. & Hofshagen, M (red). (2021). *Dyrehelserapporten 2020*.

Filip-Hutsch, K., Czopowicz, M., Barc, A. & Demiaszkiewicz, A.W. (2021). Gastrointestinal Helminths of a European Moose Population in Poland. *Pathogens*, 10, 456.

Filip-Hutsch, K., Hutsch, T., Kolasa, S. & Demiaszkiewicz, A.W. (2019). First description of histopathological lesions associated with a fatal infection of moose (*Alces alces*) with the liver fluke *Parafasciolopsis fasciolaemorpha* Ejsmont, 1932. *Journal of veterinary research*, 63, 549 - 554.

Filip, K.J., Pyziel, A.M. & Demiaszkiewicz, A.W. (2016). A massive invasion of *Parafasciolopsis fasciolaemorpha* in elk (*Alces alces*) in Lublin Province, Poland. *Annals of parasitology*, 62.

Forbes, E.S., Cushman, J.H., Burkepile, D.E., Young, T.P., Klope, M. & Young, H.S. (2019). Synthesizing the effects of large, wild herbivore exclusion on ecosystem function. *Functional Ecology*, 33, 1597-1610.

Foreyt, W.J. & Drew, M. (2010). Experimental infection of liver flukes, *Fasciola hepatica* and *Fascioloides magna*, in bison (*Bison bison*). *Journal of wildlife diseases*, 46, 283-286.

- Frey, C.F., Regidor-Cerrillo, J., Marreros, N., García-Lunar, P., Gutiérrez-Expósito, D., Schares, G., Dubey, J.P., Gentile, A., Jacquet, P. & Shkap, V. (2016). *Besnoitia besnoiti* lytic cycle in vitro and differences in invasion and intracellular proliferation among isolates. *Parasites & vectors*, 9, 1-14.
- Galbraith, J., Rodas-González, A., López-Campos, Ó., Juárez, M. & Aalhus, J. (2014). Bison meat: Characteristics, challenges, and opportunities. *Animal Frontiers*, 4, 68-73.
- Gavier-Widén, D., Chambers, M., Gortázar, C., Delahay, R., Cromie, R. & Lindén, A. (2012a). *Mycobacteria Infections*. In: *Infectious Diseases of Wild Mammals and Birds in Europe*. Wiley-Blackwell, West Sussex, UK, pp. 265-292.
- Gervasi, V., Nilsen, E.B. & Linnell, J.D. (2015). Body mass relationships affect the age structure of predation across carnivore–ungulate systems: a review and synthesis. *Mammal Review*, 45, 253-266.
- Gervasi, V., Nilsen, E.B., Sand, H., Panzacchi, M., Rauset, G.R., Pedersen, H.C. Kindberg, J., Wabakken, P., Zimmermann, Barbara. & Odden, J. (2012). Predicting the potential demographic impact of predators on their prey: a comparative analysis of two carnivore–ungulate systems in Scandinavia. *Journal of Animal Ecology*, 81, 443-454.
- Gibbons, L., Zakrisson, G. & Uggla, A. (2000). Redescription of *Parafilaria bovicola* Tubanguai, 1934 (Nematoda: Filarioidea) from Swedish Cattle. *Acta Veterinaria Scandinavica*, 41, 85.
- Godfroid, J. (2012). *Brucellosis*. In: *Infectious Diseases of Wild Mammals and Birds in Europe*, pp. 318 - 328.
- Godfroid, J. (2017). Brucellosis in livestock and wildlife: zoonotic diseases without pandemic potential in need of innovative one health approaches. *Archives of Public Health*, 75, 1-6.
- Grime, J.P. (1973). Competitive exclusion in herbaceous vegetation. *Nature*, 242, 344-347.
- Gulliksen, S., Jor, E., Lie, K., Løken, T., Åkerstedt, J. & Østerås, O. (2009). Respiratory infections in Norwegian dairy calves. *Journal of dairy science*, 92, 5139-5146.
- Guo, X., Wu, X., Bao, P., Chu, M., Ding, X., Xiong, L., Liang, C., Pei, J. & Yan, P. (2019). Characterization of the complete mitochondrial genome of the Seron yak (*Bos grunniens*). *Mitochondrial DNA B Resour*, 4, 2256-2257.
- Hanssen-Bauer, I., Førland, E., Haddeland, I., Hisdal, H., Mayer, S., Nesje, A. Nilsen, J., Sandven, S., Sandø, A., Sorteberg, A. (2017). *Climate in Norway 2100 – a knowledge base for climate adaptation*, Norwegian Centre for Climate Services. Norwegian Centre for Climate Services, pp. 1 - 47.

- Hassanin, A. & Ropiquet, A. (2004). Molecular phylogeny of the tribe Bovini (Bovidae, Bovinae) and the taxonomic status of the Kouprey, *Bos sauveli* Urbain 1937. *Molecular Phylogenetics and Evolution*, 33, 896-907.
- Hecker, L.J., Coogan, S.C., Nielsen, S.E. & Edwards, M.A. (2021). Latitudinal and seasonal plasticity in American bison *Bison bison* diets. *Mammal Review*, 51, 193-206.
- Heier, B.T., Hopp, P., Mork, J. & Bergsjø, B. (2021). The surveillance programme for *Salmonella* spp. in live animals, eggs and meat in Norway 2020. Surveillance program report. Veterinærinstituttet 2021.
- Höglund, J., Christensson, D., Holmdahl, J., Mörner, T., Osterman, E. & Uhlhorn, H. (2007). The first record of the nematode *Ashworthius sidemi* in Sweden. In: Proc 21st Int Conf of WAAVP. Ghent, Belgium.
- IPBES (2018): Summary for policymakers of the regional assessment report on biodiversity and ecosystem services for Europe and Central Asia of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services. Fisher, M., Rounsevell, M., Torre-Marín, Rando, A., Mader, A., Church, A., Elbakidze, M., Elias, V., Hahn, T., Harrison, P.A., Hauck, J., Martín-López, B., Ring, I., Sandström, C., Sousa Pinto, I., Visconti, P., Zimmermann, N.E., Christie, M. (eds.). IPBES secretariat, Bonn, Germany. 48 pages.
- Jainudeen, M. (2002). BUFFALO HUSBANDRY | Asia. *Encyclopedia of dairy sciences*, 186.
- Jaroszewicz, B.J.B., Pirożnikow, E. & Sagehorn, R. (2008). The European bison as seed dispersers: the effect on the species composition of a disturbed pine forest community. *Botany*, 86, 475-484.
- Jędrzejewski, W., Jędrzejewska, B., Okarma, H. & Ruprecht, A.L. (1992). Wolf predation and snow cover as mortality factors in the ungulate community of the Białowieża National Park, Poland. *Oecologia*, 90, 27-36.
- Johnson, R. & Kaneene, J.B. (1992). Bovine leukemia virus and enzootic bovine leukosis. *VETERINARY BULLETIN*, 62, 287-312.
- Kamath, P.L., Foster, J.T., Drees, K.P., Luikart, G., Quance, C., Anderson, N.J., Clarke, P.R., Cole, E.K., Drew, M.L. & Edwards, W.H. (2016). Genomics reveals historic and contemporary transmission dynamics of a bacterial disease among wildlife and livestock. *Nature communications*, 7, 1-10.
- Kampen, A.H., Tessema, G.T., Moldal, T., Valheim, M. & Er, C. (2021). The surveillance programme for paratuberculosis in Norway 2020. Surveillance program report. Veterinærinstituttet 2021. © Norwegian Veterinary
- Karbowiak, G., Demiaszkiewicz, A., Pyziel, A., Wita, I., Moskwa, B., Werszko, J., Bień, J., Goździk, K., Lachowicz, J. & Cabaj, W. (2014). The parasitic fauna of the European bison

(*Bison bonasus*)(Linnaeus, 1758) and their impact on the conservation. Part 1 The summarising list of parasites noted. *Acta Parasitol*, 59, 363-371.

Kaul, R., Williams, A.C., Rithe, K., Steinmetz, R. & Mishra, R. (2009). *Bubalus arnee*. The IUCN Red List of Threatened Species 2019: e.T3129A46364616. <https://dx.doi.org/10.2305/IUCN.UK.2019-1.RLTS.T3129A46364616.en>. Downloaded on 30 August 2021.

Kerley, G.I.H., Kowalczyk, R. & Cromsigt, J.P.G.M. (2012). Conservation implications of the refugee species concept and the European bison: king of the forest or refugee in a marginal habitat? *Ecography*, 35, 519-529.

Kjærstad, G., Jensen, T. & Johnsen, S.I. (2018, 5. juni). *Planorbarius corneus*, vurdering av økologisk risiko. Fremmedartslista 2018. Artsdatabanken. Hentet (2021, 25. november) fra <https://www.artsdatabanken.no/fab2018/N/1066>.

Klem, B.T., Nilssen, N.R., Nordstoga, A.B., Kampen, A.H., Hopp, P., Søilverød, L.T., Lindheim, D. & Klevar, S. (2020a). Overvåkingsprogram 2019 - Smittemessige konsekvenser av økt grovfôrimport i 2018. © Veterinærinstituttet 2020.

Klem, B.T., Tarpai, A. & Tessema, G.T. (2021a). The surveillance programme for bovine tuberculosis in Norway 2020. Surveillance program report. Veterinærinstituttet 2021. © Norwegian Veterinary Institute.

Klem, B.T., Åkerstedt, J. & Klevar, S. (2021b). The surveillance programme for bluetongue in Norway 2020. Surveillance program report. Veterinærinstituttet 2021. © Norwegian Veterinary Institute.

Klem, B.T., Åkerstedt, J. & Klevar, S. (2021c). The Surveillance programme for bovine virus diarrhoea (BVD) in Norway 2020. Surveillance program report. Veterinærinstituttet 2021. © Norwegian Veterinary Institute.

Klem, B.T., Åkerstedt, J. & Klevar, S. (2021d). The surveillance programme for enzootic bovine leukosis (EBL) in Norway 2020. Surveillance program report. Veterinærinstituttet 2021. © Norwegian Veterinary Institute.

Klem, B.T., Åkerstedt, J. & Klevar, S. (2021e). The surveillance programme for infectious bovine rhinotracheitis (IBR) and infectious oestrous vulvovaginitis (IPV) in Norway 2020. Surveillance program report. Veterinærinstituttet 2021. © Norwegian Veterinary Institute.

Klem, T.B., Tarpai, A. & Klevar, S. (2020b). The surveillance programme for *Brucella abortus* in cattle in Norway in 2019. Surveillance program report. © Norwegian Veterinary Institute 2020.

Kołodziej-Sobocińska, M., Demiaszkiewicz, A.W., Lachowicz, J., Borowik, T. & Kowalczyk, R. (2016). Influence of management and biological factors on parasitic invasions in the wild–

Spread of the blood-sucking nematode *Ashworthius sidemi* in European bison (*Bison bonasus*). *International Journal for Parasitology: Parasites and Wildlife*, 5, 286-294.

Kowalczyk, R., Kamiński, T. & Borowik, T. (2021). Do large herbivores maintain open habitats in temperate forests? *Forest Ecology and Management*, 494, 119310.

Kowalczyk, R., Wójcik, J.M., Taberlet, P., Kamiński, T., Miquel, C., Valentini, A., Craine, J.M. & Coissac, E. (2019). Foraging plasticity allows a large herbivore to persist in a sheltering forest habitat: DNA metabarcoding diet analysis of the European bison. *Forest Ecology and Management*, 449, 117474.

Kuemmerle, T., Hickler, T., Olofsson, J., Schurgers, G. & Radeloff, V.C. (2012). Reconstructing range dynamics and range fragmentation of European bison for the last 8000 years. *Diversity and Distributions*, 18, 47-59.

Kuemmerle, T., Radeloff, V.C., Perzanowski, K., Kozlo, P., Sipko, T., Khoyetskyy, P., Bashta, A.T., Chikurova, E., Parnikoza, I., Baskin, L., Angelstam, P. & Waller, D.M. (2011). Predicting potential European bison habitat across its former range. *Ecological Applications*, 21, 830-843.

Kuijper, D.P.J., te Beest, M., Churski, M. & Cromsigt, J.P.G.M. (2015). Bottom-up and top-down forces shaping wooded ecosystems: lessons from a cross-biome comparison. In: *Trophic Ecology: Bottom-up and top-down interactions across aquatic and terrestrial Systems*. eds. Hanley, T. C. & La Pierre, K.J. Ecological reviews, Cambridge University Press, pp. 107-133.

Kuznetsov, D. (2021). The First Detection of Abomasal Nematode *Ashworthius sidemi* in Fallow Deer (*Dama dama*) in Russia. *Acta Parasitol.*

Lankester, M.W. & Foreyt, W.J. (2011). Moose experimentally infected with giant liver fluke (*Fascioloides magna*). *Alces: A Journal Devoted to the Biology and Management of Moose*, 47, 9-15.

Liu, B. & Jiang, Z. (2003). Diet composition of wolves *Canis lupus* in the northeastern Qinghai-Tibet Plateau, China. *Acta Theriologica*, 48, 255-263.

Magdálek, J., Makovický, P. & Vadlejch, J. (2021). Nematode-induced pathological lesions and alterations of mucin pattern identified in abomasa of wild ruminants. *International Journal for Parasitology: Parasites and Wildlife*, 14, 62-67.

Majoros, G., Erdélyi, K. & Sztojkov, V. (2000). Occurrence of *Parafasciolopsis fasciolaemorpha* (Trematoda: Digenea) in Hungary. *Magyar Állatorvosok Lapja*, 122, 469-474.

Makoschey, B. & Berge, A.C. (2021). Review on bovine respiratory syncytial virus and bovine parainfluenza – usual suspects in bovine respiratory disease – a narrative review. *BMC Veterinary Research*, 17, 261.

- Malcicka, M. (2015). Life history and biology of *Fascioloides magna* (Trematoda) and its native and exotic hosts. *Ecology and evolution*, 5, 1381-1397.
- Mellor, P. (2012). Orbivirus infections. In: *Infectious Diseases of Wild Mammals and Birds in Europe*. Gavier-Widén, D., Duff, J.P. and Meredith, A. Wiley-Blackwell, West Sussex, UK, 2014, pp. 119 - 127.
- Milchunas, D.G. & Lauenroth, W.K. (1993). Quantitative effects of grazing on vegetation and soils over a global range of environments: Ecological Archives M063-001. *Ecological monographs*, 63, 327-366.
- Murray, D.L., Cox, E.W., Ballard, W.B., Whitlaw, H.A., Lenarz, M.S., Custer, T.W., Barnett, T. & Fuller, T.K. (2006). Pathogens, nutritional deficiency, and climate influences on a declining moose population. *Wildlife Monographs*, 166, 1-30.
- Mysterud, A. (2000). Diet overlap among ruminants in Fennoscandia. *Oecologia*, 124, 130-137.
- Mysterud, A. (2006). The concept of overgrazing and its role in management of large herbivores. *Wildlife Biology*, 12, 129-141, 113.
- Mysterud, A. (2010). Still walking on the wild side? Management actions as steps towards 'semi-domestication' of hunted ungulates. *Journal of Applied Ecology*, 47, 920-925.
- Mysterud, A., Bartoń, K., Jędrzejewska, B., Krasiński, Z., Niedziałkowska, M., Kamler, J., Yoccoz, N.G. & Stenseth, N.C. (2007). Population ecology and conservation of endangered megafauna: the case of European bison in Białowieża Primeval Forest, Poland. *Animal conservation*, 10, 77-87.
- Nickell, Z., Varriano, S., Plemmons, E. & Moran, M.D. (2018). Ecosystem engineering by bison (*Bison bison*) wallowing increases arthropod community heterogeneity in space and time. *Ecosphere*, 9, e02436.
- Nosal, P., Kowal, J., Wyrobisz-Papiewska, A. & Chovancová, G. (2021). *Ashworthius sidemi* Schulz, 1933 (Trichostrongylidae: Haemonchinae) in mountain ecosystems – a potential risk for the Tatra chamois *Rupicapra rupicapra tatica* (Blahout, 1971/1972). *International Journal for Parasitology: Parasites and Wildlife*, 14, 117-120.
- Panzacchi, M., Van Moorter, B., Strand, O., Loe, L.E. & Reimers, E. (2015). Searching for the fundamental niche using individual-based habitat selection modelling across populations. *Ecography*, 38, 659-669.
- Pedersen, H.K., Swenson, J.E. & Syvertsen, P.O. (2018a, 5. juni). Dama dama, vurdering av økologisk risiko. Fremmedartslista 2018. Artsdatabanken. Hentet (2021, 25. november) fra <https://www.artsdatabanken.no/fab2018/N/156>.

- Pedersen, H.K., Swenson, J.E. & Syvertsen, P.O. (2018b, 5. juni). *Ovibos moschatus*, vurdering av økologisk risiko. Fremmedartslista 2018. Artsdatabanken. Hentet (2021, 25. november) fra <https://www.artsdatabanken.no/fab2018/N/2474>.
- Pedersen, H.K., Swenson, J.E. & Syvertsen, P.O. (2018c, 5. juni). *Sus scrofa*, vurdering av økologisk risiko. Fremmedartslista 2018. Artsdatabanken. Hentet (2021, 25. november) fra <https://www.artsdatabanken.no/fab2018/N/161>
- Plumb, G., Kowalczyk, R. & Hernandez-Blanco, J. (2020). *Bison bonasus*. The IUCN red list of threatened species, 2020-2023.
- Plumb, G., Kowalczyk, R. & Hernandez-Blanco, J.A. (2020). *Bison bonasus*. The IUCN Red List of Threatened Species 2020: e.T2814A45156279. <https://dx.doi.org/10.2305/IUCN.UK.2020-3.RLTS.T2814A45156279.en>. Downloaded on 03 September 2021.
- Pybus, M.J. (2001). Liver flukes. In: Parasitic diseases of wild mammals (eds. Samuel, WM, Pybus, MJ & Kocan, AA) Iowa State Press, Iowa., pp. 121–149
- Rehbein, S., Visser, M., Hamel, D. & Reindl, H. (2021). Occurrence of the giant liver fluke, *Fascioloides magna*, in sympatric wild ungulates in one area in the Upper Palatinate Forest (northeastern Bavaria, Germany). *Parasitology Research*, 120, 553-561.
- Reimers, E., Eftestøl, S. & Colman, J.E. (2003). Behavior responses of wild reindeer to direct provocation by a snowmobile or skier. *The Journal of wildlife management*, 747-754.
- Rice, J., Carrasco-Medina, L., Hodgins, D. & Shewen, P. (2007). *Mannheimia haemolytica* and bovine respiratory disease. *Animal Health Research Reviews*, 8, 117-128.
- Ross, L.C., Austrheim, G., Asheim, L.-J., Bjarnason, G., Feilberg, J., Fosaa, A.M., Hester, A.J., Holand, Ø., Jónsdóttir, I.S. & Mortensen, L.E. (2016). Sheep grazing in the North Atlantic region: A long-term perspective on environmental sustainability. *Ambio*, 45, 551-566.
- Ruiz-Fons, F. (2012). *Coxiella burnetii* Infection. In: *Infectious Diseases of Wild Mammals and Birds in Europe*, pp. 409-412.
- Safronov, V.M., Smetanin, R.N. & Stepanova, V.V. (2012). Introduction of the wood bison (*Bison bison athabasca* rhoads, 1897) in Central Yakutia. *Russian Journal of Biological Invasions*, 3, 34-48.
- Samad, M. (2020). A systematic review of research findings on buffalo health and production published during the last six decades in Bangladesh. *J Vet Med OH Res*, 2, 1-62.
- Sanderson, E.W., Redford, K.H., Weber, B., Aune, K., Baldes, D., Berger, J. Carter, D., Curtin, C., Derr, J., Dobrott, S., Fearn, E., Fleener, C., Forrest, S., Gerlach, C., Gates, C., C., Gross, J. E., Gogan, P., Grassel, S., Hilty, J. A., Jensen, M., Kunkel, K., Lammers, D., List, R.,

- Minkowski, K., Olson, T., Pague, C., Robertson, P. B. & Stephenson, B. (2008). The ecological future of the North American bison: conceiving long-term, large-scale conservation of wildlife. *Conserv Biol*, 22, 252-266.
- Sandom, C.J., Ejrnæs, R., Hansen, M.D.D. & Svenning, J.-C. (2014). High herbivore density associated with vegetation diversity in interglacial ecosystems. *Proceedings of the National Academy of Sciences*, 201311014.
- Schumaker, B. (2013). Risks of *Brucella abortus* spillover in the Greater Yellowstone area. *Revue scientifique et technique (International Office of Epizootics)*, 32, 71-77.
- Schwerk, A., Klich, D., Wójtowicz, E. & Olech, W. (2021). Impact of European Bison Grazing (*Bison bonasus* (L.)) on Species and Functional Traits of Carabid Beetle Assemblages in Selected Habitats in Poland. *Biology*, 10, 123.
- Shaw, J.H. (2021). Neither stable nor pristine: American bison populations were long influenced by humans. *THERYA*, 12, 171-175.
- Shi, Q., Guo, Y., Engelhardt, S.C., Weladji, R.B., Zhou, Y., Long, M. & Meng, X. (2016). Endangered wild yak (*Bos grunniens*) in the Tibetan plateau and adjacent regions: Population size, distribution, conservation perspectives and its relation to the domestic subspecies. *Journal for Nature Conservation*, 32, 35-43.
- Smith, D.W., Mech, L.D., Meagher, M., Clark, W.E., Jaffe, R., Phillips, M.K. & Mack, J.A. (2000). Wolf–bison interactions in Yellowstone National Park. *Journal of Mammalogy*, 81, 1128-1135.
- Spickler, A.R. (2016). Toxocariasis. Retrieved from <http://www.cfsph.iastate.edu/DiseaseInfo/factsheets.php>.
- Spickler, A.R. (2020). Parafilaria. Retrieved from <http://www.cfsph.iastate.edu/DiseaseInfo/factsheets.php>.
- Spitzer, R., Felton, A., Landman, M., Singh, N.J., Widemo, F. & Cromsigt, J.P. (2020). Fifty years of European ungulate dietary studies: a synthesis. *Oikos*, 129, 1668-1680.
- Stenfeldt, C. & Arzt, J. (2020). The carrier conundrum; a review of recent advances and persistent gaps regarding the carrier state of foot-and-mouth disease virus. *Pathogens*, 9, 167.
- Tanaka, K., Solis, C.D., Masangkay, J.S., Maeda, K.-i., Kawamoto, Y. & Namikawa, T. (1996). Phylogenetic relationship among all living species of the genus *Bubalus* based on DNA sequences of the cytochrome b gene. *Biochemical Genetics*, 34, 443-452.
- Thomson, G., Vosloo, W. & Bastos, A. (2003). Foot and mouth disease in wildlife. *Virus research*, 91, 145-161.

- Toftaker, I., Sanchez, J., Stokstad, M. & Nødtvedt, A. (2016). Bovine respiratory syncytial virus and bovine coronavirus antibodies in bulk tank milk–risk factors and spatial analysis. *Preventive veterinary medicine*, 133, 73-83.
- Tokarska, M., Pertoldi, C., Kowalczyk, R. & Perzanowski, K. (2011). Genetic status of the European bison *Bison bonasus* after extinction in the wild and subsequent recovery. *Mammal Review*, 41, 151-162.
- Vesterholm, V. (2021). Förekomst och kontroll av *Toxocara vitulorum* med ivermektin hos svenska bisonkalvar.
- Waddell, L., Rajić, A., Stärk, K. & McEwen, S. (2015). The zoonotic potential of *Mycobacterium avium* ssp. *paratuberculosis*: a systematic review and meta-analyses of the evidence. *Epidemiology & Infection*, 143, 3135-3157.
- Wang, K., Wang, L., Lenstra, J.A., Jian, J., Yang, Y., Hu, Q., Lai, D., Qiu, Q., Ma, T. & Du, Z. (2017). The genome sequence of the wisent (*Bison bonasus*). *Gigascience*, 6, gix016.
- Wiener, G. (2006). Yak in nontraditional environments. In: *The Yak* FAO Regional Office for Asia and the Pacific, pp. 337 - 345.
- Wiener, G., Jianlin, H. & Long, R. (2003). *The Yak*. Regional Office, FAO Regional Office for Asia and the Pacific.
- Wünschmann, A., Armien, A.G., Butler, E., Schrage, M., Stromberg, B., Bender, J.B., Firshman, A.M. & Carstensen, M. (2015). Necropsy findings in 62 opportunistically collected free-ranging moose (*Alces alces*) from Minnesota, USA (2003–13). *Journal of Wildlife Diseases*, 51, 157-165.
- Yang, C., Xiang, C., Qi, W., Xia, S., Tu, F., Zhang, X., Moermond, T. & Yue, B. (2013). Phylogenetic analyses and improved resolution of the family Bovidae based on complete mitochondrial genomes. *Biochemical Systematics and Ecology*, 48, 136-143.
- Zhang, K., Lenstra, J.A., Zhang, S., Liu, W. & Liu, J. (2020). Evolution and domestication of the Bovini species. *Anim Genet*, 51, 637-657.
- Zver, L., Toškan, B. & Bužan, E. (2021). Phylogeny of Late Pleistocene and Holocene Bison species in Europe and North America. *Quaternary International*, 595, 30-38.

9 Appendix I

A.9.1 Evolutionary relationship among six bovid species

Methods

A total of 50 cytochrome *c* oxidase subunit 1 (COI) sequences was downloaded from the NCBI (NCBI, <https://www.ncbi.nlm.nih.gov/>)- and the BOLD (Ratnasingham and Hebert 2006, <http://www.barcodinglife.org>) websites, and trimmed down to 657 base pairs (Table A.9.1). A neighbor-joining analysis (Saitou & Nei 1987) was performed in MEGA X (Kumar et al. 2018) and evolutionary distances computed using the Kimura 2-parameter method (Kimura 1980), with all sites included, the complete deletion option, assuming homogenous pattern among lineages, and uniform substitution rates among sites. Bootstrap values (Felsenstein 1985) were calculated in MEGAX using 10 000 iterations.

Table A.9.1. Sequences (COI) downloaded from the NCBI- and BOLD systems websites; species, accession numbers (NCBI), sequence id`s (BOLD), and references for the sequences that have been published in scientific journals.

Species	Accession nb. NCBI	Sec.id BOLD	Published
Bison bison	EU177871	GBMA19407-19	Achilli et al. 2008
Bison bison	KX451363	GBMA24308-19	Forgacs et al. 2016
Bison bison	KX451362	GBMA24307-19	Forgacs et al. 2016
Bison bison	KX451361	GBMA24306-19	Forgacs et al. 2016
Bison bison	KX451364	GBMA24309-19	Forgacs et al. 2016
Bison bison	KX451352	GBMA24371-19	Forgacs et al. 2016
Bison bison	KX451353	GBMA24372-19	Forgacs et al. 2016
Bison bison	KX451354	GBMA24373-19	Forgacs et al. 2016
Bison bison	KX451355	GBMA24374-19	Forgacs et al. 2016
Bison bison	KX451356	GBMA24375-19	Forgacs et al. 2016
Bos grunniens	GQ464250	GBMA19414-19	Wang et al. 2010
Bos grunniens	GQ464251	GBMA19415-19	Wang et al. 2010
Bos grunniens	GQ464252	GBMA19416-19	Wang et al. 2010
Bos grunniens	GQ464253	GBMA19417-19	Wang et al. 2010 ³
Bos grunniens	GQ464254	GBMA19418-19	Wang et al. 2010
Bos grunniens	GQ464255	GBMA19419-19	Wang et al. 2010
Bos grunniens	GQ464261	GBMA19425-19	Wang et al. 2010
Bos grunniens	GQ464262	GBMA19426-19	Wang et al. 2010
Bos grunniens	GQ464271	GBMA19435-19	Wang et al. 2010
Bos grunniens	GQ464279	GBMA19443-19	Wang et al. 2010
Bison bonasus	HM045017	GBMA24350-19	Zeyland et al. 2012
Bison bonasus	JN632602.1	GBMA24352-19	Hassanin et al. 2012

Bison bonasus	NC_014044	GBMA24353-19	Zeyland et al. 2012
Bison bonasus	EU623450	GBMA1880-08	
Bison bonasus	KY055664	GBMA24368-19	Wecek et al. 2017
Bison bonasus	JF444283	GBMA24354-19	
Bison bonasus	HQ223450	GBMA19408-19	
Bison bonasus	KX553932	GBMA24339-19	Wecek et al. 2017
Bison bonasus	KX553931	GBMA24338-19	Wecek et al. 2017
Bison bonasus	KX553930	GBMA24337-19	Wecek et al. 2017
Bubalus bubalis	KX758300	GBMA23976-19	Wang et al. 2017
Bubalus bubalis	KX758311	GBMA23987-19	Wang et al. 2017
Bubalus bubalis	KX758315	GBMA23991-19	Wang et al. 2017
Bubalus bubalis	KX758323	GBMA23999-19	Wang et al. 2017
Bubalus bubalis	KX758325	GBMA24001-19	Wang et al. 2017
Bubalus bubalis	KX758336	GBMA24012-19	Wang et al. 2017
Bubalus bubalis	KX758344	GBMA24020-19	Wang et al. 2017
Bubalus bubalis	KX758360	GBMA24036-19	Wang et al. 2017
Bubalus bubalis	KX758366	GBMA24042-19	Wang et al. 2017
Bubalus bubalis	KX758370	GBMA24046-19	Wang et al. 2017
Bos taurus	MF281256	GBMNA16686-19	
Bos taurus	MF663792	GBMNA16697-19	
Bos taurus	MF663793	GBMNA16698-19	
Bos taurus	MF663794	GBMNA16699-19	
Bos taurus	MF925711	GBMNA16703-19	
Bos indicus	KX575711	GBMNA16671-19	Srirattana et al. 2017
Bos indicus	MF667929	GBMNA16693-19	
Bos indicus	MF667930	GBMNA16694-19	
Bos indicus	MF667931	GBMNA16695-19	
Bos indicus	MF667932	GBMNA16696-19	

A.9.2 References

- Achilli, A., Olivieri, A., Pellecchia, M., Uboldi, C., Colli, L., Al-Zahery, N. Accetturo, M., Pala, M., Kashani, B. H. & Perego, U. A. (2008). Mitochondrial genomes of extinct aurochs survive in domestic cattle. *Current Biology*, 18, R157-R158.
- Felsenstein, J. (1985). Confidence Limits on Phylogenies: An Approach Using the Bootstrap. *Evolution*, 39, 783-791.
- Forgacs, D., Wallen, R.L., Dobson, L.K. & Derr, J.N. (2016). Mitochondrial genome analysis reveals historical lineages in Yellowstone bison. *PLoS One*, 11, e0166081.
- Hassanin, A., Delsuc, F., Ropiquet, A., Hammer, C., van Vuuren, B.J., Matthee, C. Ruiz-Garcia, M., Catzeflis, F., Areskoug, V. & Nguyen, T.T. (2012). Pattern and timing of diversification of Cetartiodactyla (Mammalia, Laurasiatheria), as revealed by a comprehensive analysis of mitochondrial genomes. *Comptes rendus biologiques*, 335, 32-50.
- Kimura, M. (1980). A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *J Mol Evol*, 16, 111-120.
- Kumar, S., Stecher, G., Li, M., Knyaz, C. & Tamura, K. (2018). MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. *Mol Biol Evol*, 35, 1547-1549.
- NCBI. National Center for Biotechnology Information (NCBI). Bethesda (MD): National Library of Medicine (US), National Center for Biotechnology Information; [cited 2021 Oct 03]. Available from: <https://www.ncbi.nlm.nih.gov/>.
- Ratnasingham, S. & Hebert, P.D.N. (2007). bold: The Barcode of Life Data System (<http://www.barcodinglife.org>). *Mol Ecol Notes*, 7, 355-364.
- Saitou, N. & Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution*, 4, 406-425.
- Srirattana, K., McCosker, K., Schatz, T. & John, J.C.S. (2017). Cattle phenotypes can disguise their maternal ancestry. *BMC genetics*, 18, 1-11.
- Wang, S., Chen, N., Capodiferro, M., Zhang, T., Lancioni, H., Zhang, H. et al. (2017). Whole mitogenomes reveal the history of swamp buffalo: initially shaped by glacial periods and eventually modelled by domestication. *Scientific reports*, 7, 1-8.
- Wang, Z., Shen, X., Liu, B., Su, J., Yonezawa, T., Yu, Y. Guo, S., Ho, S.Y.W., Vila, C. & Hasegawa, M. (2010). Phylogeographical analyses of domestic and wild yaks based on mitochondrial DNA: new data and reappraisal. *Journal of Biogeography*, 37, 2332-2344.

Węcek, K., Hartmann, S., Pajmans, J.L., Taron, U., Xenikoudakis, G., Cahill, J.A. Heintzman, P.D., Shapiro, B., Baryshnikov, G. & Bunevich, A.N. (2017). Complex admixture preceded and followed the extinction of wisent in the wild. *Molecular biology and evolution*, 34, 598-612.

Zeyland, J., Wolko, Ł., Lipiński, D., Woźniak, A., Nowak, A., Szalata, M. Bocianowski, J. & Słomski, R. (2012). Tracking of wisent–bison–yak mitochondrial evolution. *Journal of applied genetics*, 53, 317-322.