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Norwegian Scientific Committee for Food and Environment

Update on assessment of risk of introduction of *Echinococcus multilocularis* to mainland Norway

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Scientific Opinion of the Panel on Biological Hazards of the Norwegian Scientific Committee for Food and Environment

The VKM Panel on Biological Hazards has assessed the validity of the conclusions given in the 2012 report in present situation and updated the knowledge regarding introduction and establishment of the parasite *Echinococcus multilocularis* (EM) in mainland Norway.

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Update on assessment of risk of introduction of *Echinococcus multilocularis* to mainland Norway

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 four VKM members and two VKM staff. Two referees commented on and reviewed the draft opinion. The Committee, by the Panel on biological hazards 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, 2023). The principles reflect the collaborative nature of the work, and the authors have contributed as members of the project group and/or the VKM Panel on Biological Hazards, appointed specifically for the assignment.

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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

Background. The VKM Panel on Biological Hazards has updated the Scientific Opinion regarding introduction and establishment of the parasite *Echinococcus multilocularis* (EM) in mainland Norway. The previous risk assessment was published in 2012 and is, therefore, in need of updating, as the situation may have changed, and new information has become available.

Methods. Data was collected through a literature search and examination of published surveillance reports, providing an update on existing literature on monitoring for introduction of EM into mainland Norway, the spread of EM, particularly in Sweden, and contamination of imported fresh produce with EM. The effects of different control measures, as described in the literature, were also investigated. The feasibility and advantages of adopting a more quantitative approach to assess the spread of EM in Norway were also evaluated.

Results. A decade after its first identification in Sweden in 2011, the prevalence of EM in the country is still low, with a limited distribution. This indicates a slow rate of spread, with no indications that the parasite has spread closer to the border with Norway. EM has not been detected in mainland Norway and analysis of imported fresh produce has not detected EM DNA. Control measures, such as mandatory treatment of dogs entering Norway with appropriate anthelminthics (containing praziqunantel) are in place. However, the extent to which treatment compliance is checked and enforced at land and maritime borders is not documented.

The possibility for modelling was explored and quantitative methods, like general episystems modelling (GEpMs), were identified as potentially relevant.

Conclusion. Conclusions reached in the previous Scientific Opinion were valid at that time and remain valid now for EM in Norway. Infected dogs can introduce the parasite, and even a single infected dog may result in local establishment. This depends on various factors, such as whether suitable rodent hosts, and subsequently foxes preying on those rodents, occur locally and are exposed and susceptible. Spread of EM from Sweden to Norway by foxes is likely a question of time. Estimation of introduction-time distribution is, however, currently impossible.

Increased border controls, to ensure dogs entering Norway have been suitably treated to eliminate the parasite, and, potentially, risk-dependent surveillance of foxes in areas bordering Sweden are identified as preventative measures. In addition, use of de-worming bait, rather than culling of foxes, in areas where parasite is detected, could be important aspects of EM control in wildlife should the parasite be introduced.

Uncertainties and data gaps. The main uncertainties are linked to the limited size of the Swedish outbreak and thus the data available from Sweden, the lack of information regarding the number of dogs entering Norway untreated, and the nature of sampling and surveillance in Norway. This means there is a substantial risk for

introductions of EM to Norway becoming established in wildlife before they are detected by surveillance.

Key words: VKM, risk assessment, Norwegian Scientific Committee for Food and Environment, Norwegian Food Safety Authority, Norwegian Environment Agency, *Echinococcus multilocularis*

Sammendrag på norsk

Bakgrunn: VKMs faggruppe for hygiene og smittestoffer har oppdatert den vitenskapelige uttalelsen om introduksjon og etablering av parasitten *Echinococcus multilocularis* (EM) i fastlands-Norge. Oppgaven er initiert av faggruppen selv.

EM er også kjent som revens dvergbendelorm. Parasitten lever hovedsakelig i tarmen hos rovdyr, som rødrev, ulv og mårhund. Den bruker smågnagere som mellomverter, men kan også infisere mennesker.

Den forrige risikovurderingen ble publisert i 2012. Denne oppdateringen vurderer om situasjonen har endret seg, og om ny informasjon er tilgjengelig.

Metode: Dataene ble samlet inn gjennom litteratursøk og undersøkelse av publiserte overvåkingsrapporter. Materialet oppdaterer eksisterende litteratur om:

- Overvåking av introduksjon av EM til fastlands-Norge

- Spredning av EM, spesielt i Sverige, men også andre deler av Europa og Nord-Amerika hvor EM er relativt nylig etablert

- Kontaminering av importerte ferskvarer med EM

Hvor effektive de ulike kontrolltiltakene er, slik de er beskrevet i litteraturen, ble også undersøkt. I tillegg evaluerte vi gjennomførbarhet og fordeler ved å bruke en mer kvantitativ tilnærming, ved bruk av modellering, for å vurdere spredningen av EM i Norge.

Resultater: Et drøyt tiår etter at EM ble påvist i Sverige (2011), er forekomsten fortsatt lav og begrenset i utbredelse. Dette indikerer en langsom spredningshastighet, uten tegn på at parasitten har nærmet seg grensen til Norge. EM er ikke påvist i fastlands-Norge og analyser av importerte ferskvarer har ikke påvist EM-DNA.

I dag er det krav om at hunder som krysser grensen til Norge skal være behandlet med ormemidler mot parasitter. Det er ikke dokumentert i hvilken grad dette sjekkes ved land- og sjøgrensene.

Muligheten for modellering ble undersøkt, og kvantitative metoder, som generell episystemmodellering (GEpMs), ble identifisert som relevante.

Konklusjon: Konklusjonene i den forrige vitenskapelige uttalelsen står seg fortsatt: Smittede hunder kan innføre parasitten til Norge. Selv ett smittet individ kan føre til lokal etablering av EM. Dette avhenger bl.a. av forekomst av mottagelige gnagere, og rev som spiser disse gnagerne, i området.

Smitte av EM fra Sverige til Norge via rev er også sannsynligvis et tidsspørsmål, men vi kan ikke anslå når det vil skje.

Økt grensekontroll, hvor man sjekker om hunder er behandlet, vil kunne hindre spredning av parasitten.

Andre viktige tiltak for å kontrollere EM i dyrelivet, dersom parasitten kommer til Norge, kan være å overvåke rev i områder hvor parasitten har blitt påvist. I tillegg kan vi, i områder hvor parasitten er funnet, bruke ormemiddel i stedet for å felle rev.

Usikkerhet og kunnskapsmangler: De største usikkerhetene i vurderingen skyldes det begrensede omfanget av utbruddet i Sverige, og dermed tilgjengelige data. Vi mangler også informasjon om antall ubehandlede hunder som kommer inn i Norge.

Faggruppen vurderer på bakgrunn av dette at det er betydelig risiko for at EM innføres til Norge, og etablerer seg i dyrelivet før det oppdages gjennom overvåkning.

Background as provided by the Panel on Biological Hazards

In 2012, VKM published a Scientific Opinion regarding the potential for *Echinococcus multilocularis* (EM) to spread to Norway. EM is of public health significance as people may act as accidental dead-end intermediate hosts if they ingest eggs, either via contaminated foods or water, or from contact with infected definitive hosts (e.g., dogs and foxes) or their faeces. The disease in untreated patients is usually fatal. The findings of the 2012 opinion indicated that Norway could expect the parasite to spread to Norway from southern Sweden and it may be necessary to update the work to obtain an overview of the need for risk-reducing measures. Therefore, the Panel on Biological Hazards has taken the initiative to update the Scientific Opinion regarding the probability of introduction to and establishment of EM in mainland Norway.

Terms of reference as provided by the Panel on Biological Hazards

The Panel on Biological Hazards of the Norwegian Scientific Committee for Food and Environment has decided on the following terms of reference:

1. Critical review of the previous Scientific Opinion assessing whether the assumptions and conclusions from the previous Scientific Opinion are still valid.

2. Assess the potential for spreading of EM and the likelihood of EM becoming established in mainland Norway under different scenarios for introduction via:

   2.1. Entry of infected dogs into mainland Norway

   2.2. Entry of infected foxes into mainland Norway

3. To describe control options that have been investigated elsewhere, discussing potential measures for use in different scenarios in Norway

4. If Q2 or Q3 indicate the need, and feasibility to assess the probability of detection under current monitoring conditions should EM be introduced into mainland Norway via any of the routes considered

1 Data and information gathering

Data were collected through a literature search and examination of published surveillance reports, providing an update on existing literature.

The feasibility and advantages of adopting a more quantitative approach to risk assessment compared to the previous Scientific Opinion was also evaluated.

2 Literature search and selection

2.2 Update on the situation in Norway and Sweden

For Norway, we summarised information from annual surveillance reports published by the National Veterinary Institute (NVI) in Norway (https://www.vetinst.no/sykdom-og-agens/revens-dvergbendelmark-echinococcus-multilocularis).

For Sweden, in January 2023 we performed a literature search in PubMed. The following search string was used for PubMed: Echinococc* AND Swed*. We did not restrict language. Studies published prior to the first detection of the parasite in Sweden in 2011 were not considered. In October 2024, the search was repeated. The first PubMed search identified 65 articles according to the PubMed search string, of which 10 were considered relevant to this current Scientific Opinion regarding the Swedish situation and human and animal cases. Seven studies focused exclusively on the Swedish situation, and others considered other Nordic or Scandinavian countries. Studies from around the time of the first reported observations of EM occurrence in Sweden that considered the probability of freedom from the parasite in 2009 (Wahlström et al., 2011) or willingness to pay for compulsory deworming to prevent introduction of the parasite to Sweden (Höjgård et al., 2012), were considered to add no further new information.

In addition, reports published by the Swedish Veterinary Institute (SVA) available on their homepage, along with supplementary information concerning surveillance and control for EM in Sweden and Norway, were included on a case-by-case basis. In addition, searches in Google Scholar were used to identify relevant literature on modelling, as determined by expert opinion.

2.2 Update on introduction and spread of EM in the other parts of the world

A non-systematic review of other recent literature (based on searching with "Echinococc*" AND individual country names in PubMed, with no restriction on publication date) were also conducted in January 2023 and October 2024 to investigate introduction and spread of EM in other countries, primarily North America, but also

Europe. References in the selected papers were searched for additional relevant papers.

2.3 Relevance screening

Inclusion criteria: Studies that were within the mandate (i.e., prevalence, echinococcosis, fox, rodents, spreading, detection, fresh produce (fruits and vegetables)). Information from Sweden was limited to articles published from 2011 and onwards. For other searches, there was no date restriction, but, in general, the more recent information was prioritized.

3 Hazard identification and characterization

EM is a small tapeworm (just a few mm in length) residing in the intestine of canids (e.g., foxes and dogs) that function as definitive hosts for the parasite. Felids may also be infected, but to a considerably lesser extent, and experimental infections indicate that the worms cannot not usually reach maturity and/or patency (when the worms produce eggs that are shed in the host faeces)(Kapel et al., 2006). Infection in definitive hosts gives few or no apparent symptoms (symptom-free carriers). Adult tapeworms produce hundreds of eggs that are released in the faeces of infected canids. These eggs are extremely robust and can survive in the environment for prolonged periods; they have been reported to survive heating to + 65°C for 120 min and freezing at -18°C for several months (EFSA, 2018). The eggs may be ingested by mammals that act as intermediate hosts, usually rodents (predominantly voles) or lagomorphs (e.g., hares and rabbits). In intermediate hosts, the larval form of the tapeworm produces cysts, mostly in the liver, where they proliferate (asexual reproduction) and may invade the surrounding tissues. If the infected intermediate host, alive or dead, is eaten by a susceptible definitive host, the adult tapeworm develops in the intestines of that definitive host and its lifecycle is completed (Figure 1).
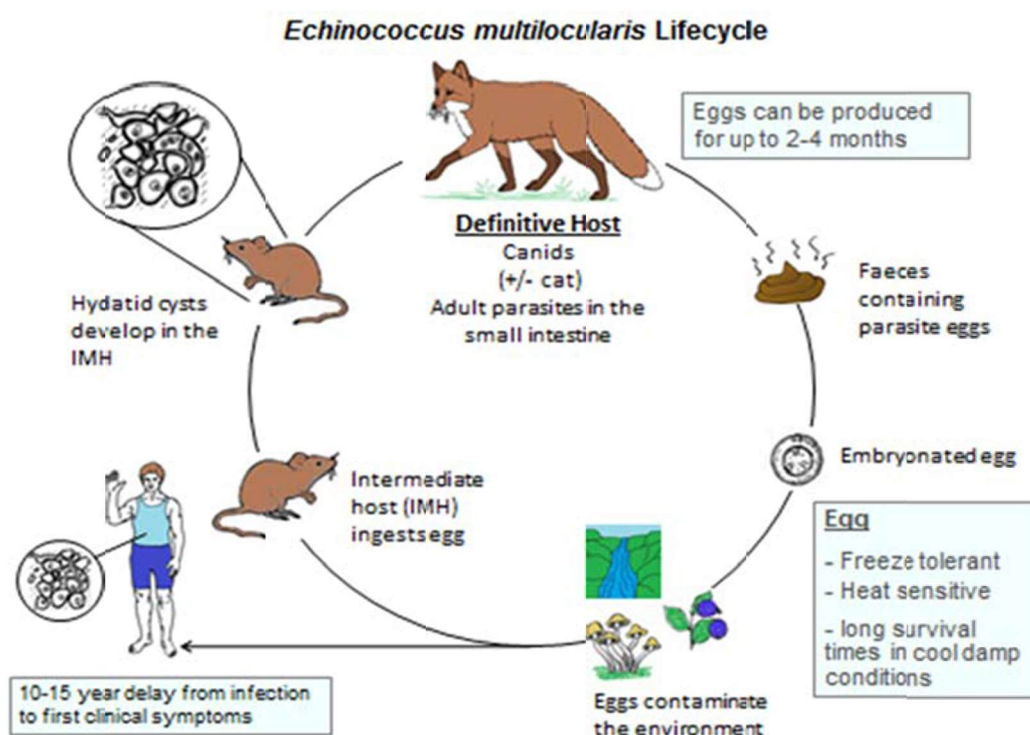

Figure 1. *Echinococcus multilocularis* lifecycle (Inger Hamnes, Norwegian Veterinary Institute).

EM is of public health significance as humans may act as accidental intermediate hosts (i.e., dead-end hosts, as it is extremely unlikely that they will be ingested by an appropriate definitive host) should they ingest eggs, either through contaminated foods or water, or from contact with infected definitive hosts (dogs, foxes) or their faeces. In untreated patients, the disease, alveolar echinococcosis (AE) is often fatal. The 10-year survival rate for AE is under 25% for untreated cases and over 80% for patients that have received treatment (Kern et al., 2017). Anthelmintic treatment lasts for several years (possibly life-long). It is expensive, and a liver transplant may be required.

4 Conclusions of the previous Scientific Opinion

In the light of the findings of EM in four red foxes from three different locations in Sweden in 2011, the Norwegian Scientific Committee for Food Safety (now the Norwegian Scientific Committee for Food and Environment, VKM), Panel on Biological Hazards took the initiative to undertake a risk assessment regarding the probability of EM being introduced to mainland Norway and thus becoming a threat to public health in the country. In the Scientific Opinion from 2012, VKM concluded:

1. Based on the fact that EM is endemic in many European countries, that the incidence of EM in foxes in endemic countries is increasing, and that the areas of endemicity are expanding, it seems likely that EM will be imported into Norway at some point, perhaps within the next 10 years.

2. Given the high number of pets crossing the border between Sweden and Norway and the paucity of checks of treatment legislation compliance, this seems to be a likely route of entry of EM to Norway, should this occur. Introduction of checks may reduce this likelihood.

3. Under the monitoring conditions of 2011, VKM find it unlikely that EM will be detected upon the first introduction to Norway. EM will probably only be detected once the prevalence in foxes is greater than 1%. The red fox population size is estimated to be between 70,000 to 120,000 animals. This means that between 700 and 1,200 red foxes would need to be infected before EM infection is likely to be detected under the current monitoring programme. If EM is identified early enough after introduction, then it might be possible to avoid the establishment of EM in Norway and/or to limit the region of endemicity. This is dependent on optimal detection techniques and sufficient monitoring.

4. VKM considers that it is unlikely that EM will be imported to Norway via contaminated produce (berries, fruits and mushrooms).

5. Norway's strong 'outdoor' culture, in which hunting, camping, berry-picking and other outdoor activities play a significant role, may place the Norwegian population at greater likelihood of contracting EM than populations in other European countries. However, it should be noted that even in countries with endemic EM, human echinococcosis is, apparently, relatively rare.

5. Updated information

5.1 Information from surveillance in Norway

Surveillance for EM in Norway is in accordance with the Annex to Commission Implementing Regulation (EU) 2018/722, in which it is stipulated that there must be compliance with the rules laid down in Article 2 of Commission Delegated Regulation (EU) 2018/772 on "rules for categorisation of Member States in view of their eligibility for preventive health measures for the control of EM infection in dogs entering their territory." The surveillance involves analysis of faecal samples from red foxes (*Vulpes vulpes*) hunted during the licensed fox-hunting season and, since 2015, grey wolves (*Canis lupus*) killed in the same period (Table 1). None of the samples tested have been positive for EM to date, indicating that the occurrence in carnivore hosts (foxes and wolves) during these sampling years was below 1%, at a confidence level of at least 95% according to (Hamnes et al., 2024). It should be noted that sampling was not randomised, as it was largely based on samples sent by hunters. However, if we assume the situation to be stable, a total sample size over 11 years (Table 1) of 5915 foxes and 143 wolves would seem satisfactory as long as it did not systematically bias against high-risk areas. Sample analysis was based on the PCR-fishing technique with PCR-based detection (Isaksson et al., 2014).

If screening remains at the current intensity, but targets areas where infection via wildlife from Sweden is most likely to occur first and then spread, the likelihood of missing all positive cases is low even at low levels of EM prevalence. As an example, for 500 annual tests to be all negative at 1% prevalence, the probability is below 1%. Even with the error rate of 50% (i.e., when 1 out of 2 positive samples yields a false negative), the probability of no detection is below 10%. However, if screening remains at the current intensity, but covers all areas of mainland Norway, the likelihood of missing all positive cases could be much higher, as the prevalence is expected to be far below 1%, at the national level, for some years after the first EM introduction.

Table 1. Number of samples analysed in surveillance programmes 2012-2023. No samples were positive. (https://www.vetinst.no/sykdom-og-agens/revens-dvergbendelmark-echinococcus-multilocularis)

Year	Red foxes	Grey Wolves
2012	614	0
2013	625	0
2014	523	0
2015	523	4
2016	No sampling	No sampling
2017	495	11
2018	536	34
2019	541	18
2020	532	20
2021	511	20
2022	503	24
2023	512	12
Total	**5915**	**143**

5.2 Information from Sweden

5.2.1 Surveillance for EM in foxes

After the first detection of EM in red foxes in Sweden in 2011, a national surveillance programme was initiated in Sweden that continued until 2014. This surveillance was based on samples from intestines collected from red foxes shot within 20 km from locations where the parasite had originally been found. The material consisted of 30 foxes each from Uddevalla, Katrineholm, Borlänge, and Växjö, and 15 foxes from Gnesta. During this surveillance, EM was found in 2 foxes from Uddevalla, 2 from Katrineholm, and 1 from Gnesta.

Swedish surveillance studies from 2013-2015 (Miller, Olsson, Sollenberg, et al., 2016; Miller et al., 2017; Miller, Olsson, Walburg, et al., 2016) reported on cestode parasites in both intermediate (voles) and definitive hosts (foxes) of EM. One collection site (Gnesta/Nyköping) had a much higher proportion of EM-positive fox faecal samples (13/25; 52%) than the others. This site also had 6/79 positive rodent samples, i.e., EM-positive liver lesions. None of the 655 *Myodes glareoulus* (bank vole; klatremus) or

the 285 *Apodemus* spp. (wood mouse, skogmus) had such lesions. However, 1.8% of the *Arvicola amphibius* (European water vole, vånd, n=439) and 0.5% of the *Microtus agrestis* (short-tailed field vole, markmus, n=187) had liver lesions, suggesting that these two species play a role in the epidemiology of EM in Sweden (Miller, Olsson, Walburg, et al., 2016). The rodents found to be parasitised with EM were captured exclusively in open field habitats, indicating to the authors that the distribution of the parasite in the environment is highly aggregated and future monitoring efforts for EM in Sweden should focus on habitats (e.g., fields) where *M. agrestis* and *A. amphibius* occur in abundance. The authors also note that their finding of infected foxes indicated a higher occurrence than previous monitoring, also including surveys using fox scats from the environment. However, it is unclear how many fox scats may have been collected from the same fox, which could skew the data in either direction. This may reflect that the studies of Miller et al were targeted, whereas the national screening studies aimed at collecting representative samples from the whole country (Miller, Olsson, Sollenberg, et al., 2016).

Between 2015 and 2019, there were no official investigations for EM in Sweden. Targeted surveillance in 2020 detected EM in 7 of 12 (58%) fox scat samples from Gnesta and in 12 of 109 (11%) of scat samples from Uddevalla. As several scat samples from the same individual fox may have been collected, the numbers may not reflect the prevalence in the fox population. From 2021, samples have been collected through a national surveillance programme as well as through targeted sampling of fox scats from in or around locations where the parasite had previously been found. During 2021-2024, 23 positive samples have been found, 16 detected in 2021, 2 in 2022, 3 in 2023 and 2 in 2024 (as per Nov. 1st). Fifteen of these 22 positive samples were detected in or around locations where the parasite had previously been found (targeted surveillance, 147 samples analysed), whereas 8 positive samples were detected in other regions through the national surveillance programme (2015 samples analysed, 665 samples collected but yet to be analysed) (SVA, 2024)).

Most of the surveillance in Sweden has focused on geographical regions where the parasite has already been found. The parasite is now detected in five different municipalities, with positive fox scats repeatedly found in two of these, showing that the parasite is still present in these locations. No positive samples have so far been identified north of the county Dalarna. An updated map of the results of ongoing surveillance can be found at SVA, Sweden (Karta över rävens dvärgbandmask - SVA).

Figure 2. Occurrence of EM in Sweden on 4.12.2021. (left) and 22.11.2022 (middle) and 24.11.2024..
(Karta över rävens dvärgbandmask - SVA)

The surveillance data from SVA indicate that EM occurrence is low in foxes in Sweden at the national level, and that it primarily has a local, clustered occurrence, albeit at several locations (Figure 2). This, together with possible reintroductions to the country, makes eradication difficult. Treatment of foxes with praziquantel distributed in baits has been discussed as a control measure, and experimental studies have shown that this may be effective (see section 0), especially when the infection is less widespread (EFSA Koutsoumanis et al., 2018), but this has not been implemented in Sweden.

5.2.2 Information on other canid hosts in Sweden

EM can also infect other canids, such as wolves, raccoon dogs (*Nyctereutes procyonoides*), and golden jackals (*Canis aureus*) (see Section 0), but EM has not been detected in other canids in Sweden than the red fox. A total of 70 wolves were investigated in 2015 and 22 wolves in 2019. In contrast, *E. granulosus*, a close relative to EM, was detected in 2 wolves in Sweden in 2021, in samples originating from 2012 (Wahlström et al., 2011).

5.2.3 Human cases of EM infection in Sweden

Although very few human cases of AE have been diagnosed in Sweden (only 9 cases since 2012), the authors of a particularly relevant study (Bläckberg et al., 2020) reported 6 cases in the previous two years (presumably 2018-2020). Five women (mean age at diagnosis of 61 years) who were diagnosed with AE had a Swedish background, and the other patient had lived in Sweden for 30 years without returning to their former homeland. The authors are clear that the location and route of infection cannot be determined, as all patients had made short-term trips to EM-endemic areas (e.g., Central Europe) within a timeframe concomitant with the incubation period of the disease. The authors do not imply that the humans were infected in Sweden, but rather point to the diagnostic difficulty, even in endemic countries. Nevertheless, they do cite a press release (ref 11 in article) from the Swedish public health authorities stating that domestic infection can no longer be ruled out (Bläckberg et al., 2020).

An earlier paper (Wahlström et al., 2015), reported two human cases of AE diagnosed in Sweden in 2012. Based on epidemiological information, both individuals were believed to have acquired the infection abroad. The same article specifies that the screening method used by the Norwegian Veterinary Institute (NVI) for analysis of material from foxes until and including 2012, was not as sensitive as had previously been estimated. Therefore, from 2012 NVI adopted the method used in the Swedish surveillance (magnetic capture PCR) (Isaksson et al., 2014).

5.3 Update on the introduction and spread of EM in other parts of the world

Although the situation in northern Europe is of immediate importance to Norway, the introduction and spread of EM in other parts of the world can also be of relevance. Different countries can have different ecologies and climates, but Sweden is considered to be very similar to Norway.

An overview of Europe-wide surveillance of foodborne parasitic diseases from a One Health perspective (van der Giessen et al., 2021), reported that in many countries in Europe, including all countries in Northern Europe except for Sweden, there is active surveillance of wildlife for EM (mainly red foxes). Given that this parasite was identified as being in the top ten priority causes of communicable diseases in Sweden, this may seem surprising (Dahl et al., 2015). Molecular analysis of EM worms, isolated from 7 Swedish foxes between 2011 and 2013, as well as from 38 worms from 9 Danish foxes, showed relatively low genetic diversity. The analysis, which utilized the EmsB-satellite marker, showed only 4 distinct profiles in worms retrieved from Swedish foxes. All of these corresponded to previously identified European EM genetic profiles (Knapp et al., 2019). Although the authors seem surprised by the finding, it presumably reflects the low numbers of worms analysed, and the relatively recent introduction of EM to Sweden, perhaps by only a single (or a couple of) introduction event(s).

A systematic review and meta-analysis of geographical distribution and prevalence of EM in animals in the European Union and adjacent countries (Oksanen et al, 2016) noted that pooled prevalence was higher in raccoon dogs (2.2 %), golden jackals (4.7 %), and wolves (1.4 %) than in dogs (0.3 %) and cats (0.5 %), and that the high pooled prevalence of EM in raccoon dogs and golden jackals correlated with that in foxes. Although the authors comment that dogs could be important for parasite introduction into non-endemic areas, they suggest that they could be less relevant in the lifecycle of the parasite in Europe. As previously commented, studies on the occurrence of EM are typically not based upon random sampling, and there are no prevalence estimates available.

Of these other potentially important definitive hosts of EM, a survey in southwestern Hungary from 2016 until 2020 of *Echinococcus* species infecting golden jackals demonstrated a high prevalence of almost 16% of EM infection, with 27 of 173 animals infected, and a lower level (<2%) of *E. granulosus* s.l. (Balog et al, 2021). The authors suggest that invasion with this host species around Europe may increase the spread of EM. It is worth noting that in February 2021, the golden jackal was officially reported

to have been observed in Norway for the first time (Bogdanowicz et al., 2024), with observations reported from Porsanger in 2019 and 2020 (Sørensen and Lindsø, 2021; this article was not retrieved as part of the search described in section 2.1).

Regarding racoon dogs, a survey from Poland of gastrointestinal parasites in 96 individuals found more than 10% infected with EM, with all infected animals being adults (Pilarczyk et al., 2022); the distribution of raccoon dogs in Norway as of today is unclear, as they have been observed in low numbers, mostly in northern Norway, but are expected to be found dispersed over larger parts of southern and central Scandinavia too.

Of particular interest are reports of EM emerging in new regions or countries previously considered non-endemic for EM. In Western Canada, clusters of EM infection have been reported since 2012. These have been found in a range of hosts. Firstly 5 dogs, 3 lemurs, 1 chipmunk in southern Ontario were found infected; thereafter, following targeted surveillance between 2015 and 2017, among 24% of wild coyotes (around 400 sampled) and 21% of wild red foxes (around 40 sampled) were found infected; Kotwa et al. (2019). A retrospective survey of dog samples submitted to a specific lab during 2022-2024 from US and Canadian veterinary clinics found 26 cases by qPCR among over 2,300,000 samples (Evason et al., 2024).

Although it is not possible to determine definitively how the parasite was introduced into these new areas of North America, introduction with dogs is suspected as a likely route (Massolo et al., 2014).

Another study (Santa et al., 2023) reported on human infection. The incidence of human AE has generally been low in continental North America, with only two locally acquired cases ever reported prior to 2013 (in 1923 and 1977). However, since 2013, there have been at least 17 human cases reported in Alberta (Houston et al., 2021; Santa et al., 2023), one of whom died. An additional case was reported in 2021 in the neighbouring province Saskatchewan (Houston et al., 2021), and two more cases were reported in Vermont, USA, in 2020 and 2022 (Santa et al., 2023). A more recent study, based on data from administrative hospital and ambulatory visits to determine the incidence of human cases of echinococcosis in Canada between 2000–2020, reported a small absolute increase in the mean annual cumulative incidence of cases between 2011–2020 compared to 2000–2010, and hypothesise that the new European-type EM strain maybe of relevance, in addition to other factors such as climate change and urbanization (Khalid et al., 2024).

Interestingly, molecular characterisation of EM from some cases (Santa et al., 2023) indicated the presence of European haplotypes (although these haplotypes are not always considered identical, more recent work on the mitogenome has indicated that they may be very closely related; (Lallemand et al., 2024)). It has been suggested that the low genetic diversity indicates relatively recent introductions (Santa et al., 2023). Of particular interest is the relatively rapid spread of this parasite into the human population. Santa et al. (2023) pointed out that the number of introduction events, along with the number of infective stages released, which are often important for

establishment of an invasive species, may be less important for this hermaphrodite parasite. This trait enables self- and cross-fertilization in the definitive host, along with the asexual reproduction in intermediate hosts. The same authors also speculate that the "mainland-island" transmission system proposed for the historical dispersal of this parasite in Europe (in which an ancestral focus serves as a 'mainland' supplying the peripheral 'island' areas) likely follows the expansion of fox populations. The situation may be different in North America, where not only foxes contribute to the spread of the parasite, but also the more abundant coyotes, which have larger territories, and thus greater dispersal distances. In addition, previous research indicates that coyotes may harbour a greater worm burden, possibly related to the absence of co-evolution of this host and this parasite strain (Santa, Rezansoff, et al., 2021). It is thus important to recognise that data on EM from North America may not be directly applicable to the Norwegian situation, where the host situation is different.

Closer to Norway, seven European countries (Belgium, the Netherlands, Slovakia, Hungary, Lithuania, Latvia, and Slovenia), reported their first autochthonous human cases of AE between 2001 and 2018, i.e., cases originated in the area rather than being imported (Baumann et al., 2019). In addition, data from Germany indicate a rise in the incidence of AE, with an increase in the number of cases diagnosed in Hessen, Rheinland-Pfalz and Nordrhein-Westfalen – that is, beyond the known endemic areas for this parasite of Baden-Württemberg and Bavaria (Kwiedor et al., 2023). Another focus of apparent emergence of AE in Europe is in Bjelovar-Bilogora County of central Croatia (Balen Topić et al., 2023): a single case was identified in 2017, but from 2019-2022 five further autochthonous cases were diagnosed. Yet another focus is Slovakia, where the average annual incidence increased about six times in the last decade, rising from 0.031 per 100,000 inhabitants between 2000 and 2011, to an average of 0.187 since 2012 (Antolová et al., 2024). Baumann et al. (2019) emphasise that there appears to be an increasing spread of reported cases and elevated cases numbers reported in the twenty-first century, especially in western, northern and eastern Europe. It remains uncertain whether these trends could partially reflect increased focus on AE in health services in these countries. In addition, in 2024 the first case of autochthonous human AE was registered in Italy (Tamarozzi et al., 2024).

The route of introduction to different countries is not always known. As well as the introduction via movement of dogs (e.g., to North America), other hosts may also be involved. For example, in France, introduction of EM was associated with the transport of infected foxes for sport (cited in Santa et al., 2021), and in Svalbard, either movement of Arctic foxes over the ice or import of infected rodents with straw for horses from St. Petersburg have been proposed (Davidson et al., 2012). It is interesting to note that in all three of these examples, the movement of animals in association with people seems to play a possible role, rather than independent movement of wildlife.

More recently, (Lallemand et al., 2024), focuses on the phylogeny of EM globally. It described, amongst other things, that by sequencing the entire mitochondrial genome, it could be demonstrated that whereas EM in Svalbard (from voles in 2004 - 2006) clustered with EM from Russia (haplotype HG1), in Sweden the haplotype (from a human patient) was HG3, as was reported from elsewhere in Europe. This information,

particularly at the sub-haplotype level, could be of value for discerning potential routes of entry into Norway.

5.4 Update on the detection of EM in fresh produce in Europe

Since the publication of the previous VKM Opinion, various surveys have been undertaken in Europe regarding contamination of fresh produce with EM eggs. A 2015 study of contamination of fresh produce in Poland (Lass et al., 2016), reported that over 23% of fresh produce samples were contaminated with EM DNA. However, these findings were challenged by Robertson et al. (2016), who questioned several aspects of the study including the authors' interpretations of findings. In Italy, a survey of mixed-salads and berries (324 samples of each) in 2021 (Barlaam et al., 2021) found EM DNA on one RTE-salad sample grown in Italy; this finding was backed up by microscopy, in which a taeniid egg was reported in the same sample by another laboratory. EM is known to be established in both Poland and Italy. It is worth noting that detection of DNA does not necessarily indicate that one or more infectious EM eggs are present on the fresh produce, nor that the fresh produce represents a risk of infection with EM.

In addition, a European survey was conducted as part of the European Joint Project "MeMe" and results indicate some contamination with EM DNA in samples from Denmark, Estonia, France, Latvia, Netherlands, and Switzerland – all countries known to be endemic for EM. Although Norway participated in the MeMe project, apparently, it did not participate in the survey as no results are presented. Unlike in the Italian survey mentioned above (Barlaam et al., 2021), no effort was made to support positive qPCR results with microscopy in the MeMe project.

Of potential relevance to Norway, is the apparently high occurrence of EM DNA on berries in Estonia and Latvia, with 4 of 30 strawberry samples found to be positive in Latvia and 5 of 30 strawberry samples found to be positive in Estonia (Barosi & Umhang, 2024), reflecting a relatively high prevalence of infected canids in these countries. Given the regular car-ferry services between Sweden and Estonia, this should not be overlooked as a potential transport route of infected animals.

In Norway itself, a survey of berry samples (N=820), both imported and locally grown, sold on the open market in Norway between August 2019 until November 2020 were analysed by the same method as used for the Italian survey (Barlaam et al., 2021), and EM DNA was not detected (Temesgen et al., 2022). Further samples of fresh produce have been analysed more recently at the Norwegian reference laboratory for parasites in fresh produce at Norwegian University of Life Sciences; with 15 samples analysed in 2023 and 15 samples analysed in 2024. All were negative for EM DNA,

5.5 Introduction to Norway

The prevalence of EM is challenging to obtain, as targeted sampling might miss parasites in areas not sampled, while randomised sampling will be extensive and would

therefore be very expensive. Non-randomised sampling can be useful; however, it cannot be translated into statistical measurements when a positive result occurs. Moreover, identification of a single introduction does not preclude further introduction events occurring possibly at a considerable distance from the first event. It is, therefore, more interesting to consider what happens after introduction. There is a difference between introduction in wildlife and introduction via dogs. Any finding of the parasite in a wildlife host like a fox or wolf, will likely indicate an endemic situation, in which the parasite has already established itself in small mammal and the fox populations. When introduced via dogs, it is possible to find the parasite in the dog(s) before establishment of the parasite is likely to have occurred.

5.5.1 Introduction via dogs

Based on our knowledge from previous introductions of this parasite into new areas or countries, it seems likely that the first introduction of EM into Norway will be into one, or possibly a small number of areas (as seen in Sweden).

Other hosts may also bring in the parasite (see section 0). The optimal strategy for detecting introduction of EM depends on the introduction route for the parasite. We cannot predict this route, but introductions into other countries previously considered to be EM-free, or free of a particular EM-strain, have been associated with movement of dogs (e.g., Canada) (Kolapo et al., 2023; Santa, Musiani, et al., 2021).

If the parasite is most likely to be introduced to Norway through the movement of domestic dogs (as has been suspected to have occurred elsewhere, e.g. North America; (Massolo et al., 2014)), then it may be useful to target sampling in areas with more dogs, or with more dogs that travel to and from endemic areas (e.g., potentially hunting dogs or sled dogs). Of even greater value to control the parasite would be to strengthen enforcement of the mandatory treatment nationwide, for dogs entering Norway. Today we do not know the extent to which these regulations are followed.

5.5.2 Introduction via wildlife

A total of 21 new cases in foxes have been identified in Sweden between 2021-2024, and there are indications of a development of some hot spots in areas as close as 70 km from the border with Norway. This does not necessarily indicate expansion towards Norway, as one of the first findings in 2011 in Sweden was in Uddevalla, approximately 60 km from the Norwegian border.

In the potential scenario where the parasite is introduced by infected foxes crossing the border with Sweden, surveillance in the border region would be an appropriate method for early detection.

Introduction of EM to Norway may also take place via small rodents (Miller, Olsson, Sollenberg, et al., 2016; Miller et al., 2017; Miller, Olsson, Walburg, et al., 2016). Rodents normally do not migrate long distances, but may be transported long

distances through import of fodder such as dried hay, which has been hypothesized as one of the possible ways EM was introduced to the Svalbard archipelago (Davidson et al., 2012).

5.5.3 Introduction via fresh produce

Although no quantitative estimates of risk have been undertaken due to a paucity of the relevant data, an extensive survey of fresh produce (including imported berries) on the market in Norway has been conducted (see 0). The series of events required for fresh produce to be contaminated, imported, and reach the consumer is complex and appears as unlikely. Although this scenario could have a direct effect on human health, and thus may be of concern to consumers, it is nevertheless extremely unlikely to result in the establishment of EM in Norway as the contaminated berries would have to be consumed by an appropriate intermediate host, which, in turn, would need to be consumed by an appropriate definitive host, which would then spread the parasite further.

4.1 Human exposure

A source attribution study (Torgerson et al., 2020) suggested that possibly 32.5% (CI 10.0%-53.2%) could be transmitted by food, but it has also been shown that gathering the evidence for this estimate can be difficult (Torgerson and Robertson, 2021). More frequent infections have been linked to dog ownership, farming and kitchen-garden owners, going to forests, chewing grass, and hunting/handling foxes (Conraths et al., 2017). These activities also take place in other European countries that are endemic for EM, and thus people with these activities in known areas of EM establishment are more likely to encounter infective EM eggs than people doing these activities in Norway. A recent investigation in Canada also supports dog ownership as an important risk factor for human infection (Toews et al., 2024).

5.7 Update on methodology

5.7.1   Lack of quantitative modelling

The assessments and estimates made in the previous VKM Scientific Opinion were largely qualitative in nature due to the paucity of quantitative data. The qualitative assessments addressed the probability of various events related to introduction of EM to mainland Norway. Three types of probability/likelihood were assessed: (i) introduction of EM to mainland Norway via movements of pets (cat and dogs) and (ii) wildlife and (iii) probability of detection of EM once introduced. Two risks were assessed: (i) risk of EM reaching endemic level in mainland Norway and (ii) risk to human health. Finally, effectiveness and efficiency of applicable disease control options were assessed.

Different ecological modelling approaches to EM are possible. The final choice depends on available resources for data acquisition, time, and priorities for model output (see

Appendix: Ecological disease models). A set of ecological models similar to that of Hassell et al. (2021), termed "General Episystem Models" (GEpMs, see chapter 6) by Hassell and co-authors was introduced to the project group for assessment of how they can be adapted to available resources and needs. A description of such a model type that is expected to inform surveillance and control of EM and similar wildlife and zoonotic diseases under increasing human influence and climate change is presented in the chapter 6 (Appendix).

5.7.2   Qualitative presentation of likelihood and risk

In the previous VKM opinion, likelihood and risk were each split into four classes by level, all of which had qualitative definitions ranging from highly likely to highly unlikely for likelihood and from high to negligible for risk. These definitions were based on the Biosafety Resource Book, published by the Food and Agriculture Organization of the United Nations (Sensi et al., 2011), where "highly likely" is defined as "expected to occur in most circumstances" and "high risk" is defined as "risk is unacceptable unless actions for mitigation are highly feasible and effective", and "highly unlikely (negligible or effectively zero)" is defined as "may occur only in very rare circumstances" and "negligible risk" is defined as "risk is insubstantial and there is no present need to invoke actions for mitigation".

Since the previous Scientific Opinion was written, EFSA has developed a table for description of probability terms (see Table 2), and we have used this in the current opinion.

Table 2. Mapping between qualitative and quantitative probability assessment (reproduced from Table 4 in Guidance on Communication of Uncertainty in Scientific Assessments (EFSA Koutsoumanis et al., 2019)

Probability term	Subjective probability range	Additional options	
Almost certain	99–100%	More likely than not: > 50%	Unable to give any probability: range is 0–100%
Extremely likely	95–99%		
Very likely	90–95%		Report as 'inconclusive', 'cannot conclude', or 'unknown'
Likely	66–90%		
About as likely as not	33–66%		
Unlikely	10–33%		
Very unlikely	5–10%		
Extremely unlikely	1–5%		
Almost impossible	0–1%		

6. Measures

6.1 Measures before introduction

Discussions of potential control measures before introduction of EM need to focus on possible scenarios for introduction. Establishing control measures based upon hypothetical scenarios is always challenging, but some approaches could be considered. We distinguish between geography-independent approaches (introduction via dogs) and geography-dependent approaches (introduction via foxes).

Treatment of dogs before transport into Norway. The number of dogs crossing the border into Norway is not known, nor is the proportion of these dogs that receive treatment for EM before entry into Norway. A limited survey of dogs and cats entering Norway from Sweden at one border crossing point, demonstrated that of 97 animals checked, 13 did not have appropriate, legislated treatment against EM (NFSA, 2011). In addition, a survey conducted in 2011 found that pet owners from different European countries may struggle to obtain the correct information regarding treatment of dogs before entry into Norway (Davidson & Robertson, 2012). Furthermore, a survey conducted in 2012 of imported street dogs from Eastern European countries (Høgåsen et al., 2012), indicated that fewer than 30% had been adequately treated against EM.

A significant number of dogs are transported from or through Sweden, with these animals potentially originating from countries where EM is endemic. This includes significant illegal trafficking of live dogs across European Union borders (Davidson & Robertson, 2012) and legal routes (Sandvik, 2023). Information campaigns from the Norwegian Food Safety Authority (NFSA) aimed at dog owners could have an impact. However, the main challenges for dog owners will be the practical considerations and costs associated with frequent treatments of their dogs at veterinary clinics. NFSA investigating this issue in collaboration with relevant organizations such as the Kennel Club, dog racing clubs, and veterinarians may alleviate the issue.

Anthelmintic treatment with praziquantel has a curative effect, but if compliance is low, then this treatment requirement will not reduce the probability of EM introduction via an untreated infected dog crossing the land border with Sweden. However, if introduction by migrating infected foxes or other wildlife is highly probable within a certain time horizon, then even stringent compliance with the dog treatment requirement will not prevent the introduction of EM. Thus, while compliance can be improved by more rigorous enforcement of the existing regulations, the magnitude of its effect on the overall probability of EM introduction remains uncertain. Nevertheless, it is clearly best to ensure that all potential routes of introduction are kept as strong as possible.

Active sampling of dogs. Dogs could be sampled at various locations such as dog shows, dog races, parks with a high dog population, as part of a more proactive surveillance. However, the anticipated probability of discovering infected animals is currently extremely low. This also holds true for sampling dogs at veterinary clinics. In

practice, active sampling of dogs would only become a consideration once an introduction has been confirmed.

Better surveillance for EM in wildlife. Foxes are currently surveyed for infection with EM in mainland Norway in order to maintain the evidence for the European Commission that Norway remains free of this parasite (EU, 2024).

While it may seem attractive to utilise voles or other rodents as target species for surveillance, the labour involved would be immense, and the likelihood of success would be low due to the recognised low prevalence in intermediate hosts (Giraudoux et al., 2006). A top predator like the fox is likely to harbour significantly more EM than rodents. Although analysis of samples collected during rodent control programmes has been conducted in France (Umhang et al., 2021), the lack of positive samples in a known endemic region indicates that the prevalence must be of a certain magnitude before detection in rodents (Umhang et al., 2021). However, in higher prevalence areas analysis of such samples may provide useful information.

Increasing the number of faecal samples analysed from foxes in Southeast Norway, areas neighbouring Sweden, is feasible through collaboration with hunters and offering greater compensation for submitted samples for analysis. Current sampling of foxes for analysis for EM to maintain inclusion on the Annex mentioned in the previous paragraph is described as "simple random sampling" (EFSA et al., 2023). However, it is not clear from the text how the randomisation is conducted; rather it seems that the samples are analysed based on hunters sending in suitable samples.

The main challenge for estimating spread, and thus the per-annum risk of introduction through wildlife, as noted in ecological models and Swedish experiences, lies in the long horizon (decades) of the disease's spread through the natural migration of foxes. Following a potential introduction to wildlife, the initial occurrence will be extremely low and restricted to a limited geographical distribution, i.e., present only in local ecosystems. Consequently, in practical terms, the current level of fox surveillance would only be capable of detecting EM several years post-introduction.

As the surveillance and control efforts needed to detect and eradicate EM in Norway depend heavily upon the introduction and establishment scenario in question, such quantitative advice is pending ongoing research using ecological disease modelling described earlier.

Environmental surveillance. In theory, EM DNA can be detected in environmental samples. There are indeed instances where pathogenic bacteria and coronaviruses have been identified in water sources to demonstrate infection in the catchment (Lu et al., 2024; Mihajlovski et al., 2022). However, EM eggs are extraordinarily robust and do not easily release DNA (Saelens & Gabriel, 2020). Moreover, EM eggs will sediment relatively rapidly according to Stokes' law and may not be present in water samples. Coupled with the current low occurrence, this approach is unlikely to provide much useful data at present nor assistance in detecting introduction. A DNA survey in water samples from an EM endemic of Japan (Mori et al., 2023), detected only one EM-

positive sample among 128, and the authors comment that detectability of the parasite using eDNA is rather low. Indeed, even for the one positive sample the DNA concentration was very low (CT value of 39.93 indicating that the DNA of the parasite in the sample was at a concentration below 0.01 pg/reaction) and was not detected in repeats of the same samples, in the samples taken from the same stream, or in the samples taken from the same location at different times.

6.2 Control measures after introduction

6.2.1 Tracing of contact patterns and treatment of dogs and foxes

A dog diagnosed with EM. The most straightforward scenario is that in which EM is detected in one or more dogs. This will either be on suspicion of a dog known to be transported from endemic areas or an incidental finding in a dog faecal sample at a veterinary clinic. This would be considered as an outbreak by the NFSA, and outbreak investigation (including contact tracing of dogs and mapping of where the dog has been in Norway) should be implemented. Owners of the dog might be interviewed about whether and how they dispose of the dogs' faeces, and could, potentially, be offered investigation for potential infection.

The tracking should also consider the potential for relevant wildlife (rodents, foxes) to have become infected, by investigation of populations where the infected dog has been; here, using a more specific ecological model to try to optimize resources for further surveillance in foxes, would be of value. Dogs that have been in the same area may be investigated or treated for infection, and it should also be determined whether treatment of foxes should be implemented.

Ecological spread of EM in foxes. A finding indicating ecological spread into Norway (detection in fox(es) and/or rodent(s)) will most likely be associated with an introduction some years previously. In this situation, the ecological model or similar models presented in the chapter 6 of this document could provide a basis for focusing on specific areas for more extensive surveillance, and, potentially, for treating local fox populations.

Model-driven surveillance in wildlife. Once available, the fox model will be able to predict the likely trajectories and speed of EM spread among foxes following detection in foxes or rodents. This can inform proactive surveillance strategies, such as targeted sampling of foxes in high-risk areas, and inform mitigation measures to control the spread of EM. Spread of EM in foxes/wildlife more likely than not has a long-time horizon, while spread via infected untreated dogs may be fast when linked to transportation over long distances.

Controlling or treating the relevant population of definitive hosts (foxes and dogs). Culling the fox population in a region will most likely be counter-productive, as will probably result in more foxes entering the area (Comte et al., 2017). Treatment of foxes with anthelminthic bait has been demonstrated to have an impact.

Various studies have been conducted in Europe and Japan regarding the effect on infection with EM in foxes by distributing baits containing praziquantel (König et al., 2019; Romig et al., 2007; Tackmann et al., 2001; Takahashi et al., 2013; Tsukada et al., 2002; Uraguchi et al., 2022). In general, these studies have documented a substantial decrease in infection rate in foxes (and also in rodents, when investigated), but elimination (infection rate below the level of detection in a particular targeted area) has only been reported in one of these studies (König et al., 2019); most studies report that elimination of the parasite has not been achieved.

A systematic review of anthelminthic control programmes for EM in definitive hosts concluded that, overall, the studies included demonstrated that such treatments result in a sharp and statistically significant drop in parasite prevalence in foxes, with no overlap in CI between pooled risk differences for control and treated areas (Umhang et al., 2019). In addition, even in highly endemic areas, monthly baiting decreased the prevalence in foxes in a short period of time. However, it was also noted that there was a strong capacity for the parasite to return to its initial prevalence if deworming did not reach all infected hosts (some infected animals remained), and thus a cost-benefit analysis would likely be required by stakeholders. In addition, it should be noted that some bait is likely to be consumed by non-target species.

One study (Uraguchi et al., 2022) claimed not to be attempting to achieve elimination, or even to reduce infection in foxes (although it did achieve the latter, and almost the former), but to reduce the number of egg-positive faeces within the limited target area (an urban university campus, with an area of 1.8 km^2) in order to reduce the likelihood of human infection. This intention may be of relevance in Norway, particularly if it is indicated that the area where the infection occurs, regardless of introduction route, is commonly used by the public for recreational activities.

Due to the closeness between dogs and people, treatment of infected dogs, education of dog owners, and checking potentially infected dogs for infection will be important.

7 Conclusions (with answers to the terms of reference)

1. **Critical review of the previous report**

   1.1. Assess whether the assumptions and conclusions from the previous Scientific Opinion are still valid

Below, we summarise our assessment regarding the validity of the five conclusions given in the 2012 report, and whether they remain valid today.

Conclusion 1: *"Based on the fact that EM is endemic in many European countries, that the incidence in endemic countries is increasing, and that the areas of endemicity are expanding, it seems likely that EM will be imported into Norway at some point, perhaps within the next 10 years."*

Although EM has not been detected in mainland Norway to date, the situation described is still considered valid and it seems likely (66%-90% probability range) that EM will be detected in Norway in the next ten years.

A total of 23 new cases in foxes were found in Sweden between 2021-2024, and there are indications of a development of some hot spots in areas as close as 70 km from the border with Norway. This does not necessarily indicate expansion towards Norway.

Conclusion 2: *"Given the high number of pets crossing the border between Sweden and Norway and the paucity of checks of treatment legislation compliance, this seems to be a likely route of entry of EM to Norway, should this occur. Introduction of checks may reduce this likelihood."*

The statement is still considered valid. For more details see conclusion 3 below.

Conclusion 3: *"Under the monitoring conditions of 2011, VKM find it unlikely that EM will be detected upon the first introduction to Norway. EM will probably only be detected once the prevalence in foxes is greater than 1%. The red fox population size is estimated to be between 70 000 to 120 000 animals. This means that between 700 and 1200 red foxes would need to be infected before EM infection is likely to be detected under the current monitoring programme. If EM is identified early enough after introduction, then it might be possible to avoid the establishment of EM in Norway and/or to limit the region of endemicity. This is dependent on optimal detection techniques and sufficient monitoring."*

The statement is considered valid, but only as a qualitative statement and not in pinpointing the occurrence levels necessary for first detection.

Based on our knowledge from previous introductions of this parasite into new areas or countries, it seems likely (66%-90% probability range) that the first introduction of EM into Norway will be into one, or possibly a few of areas (as in Sweden).

If the parasite is likely (66%-90% probability range) to be introduced to Norway through the movement of domestic dogs (as has occurred elsewhere), then it may be useful to target sampling in areas with a high density of dogs, or to target dogs that travel to and from endemic areas (e.g., potentially hunting dogs or sled dogs). Of even greater value to control the parasite, would be to strengthen enforcement of treatment for dogs entering Norway.

In the scenario where the parasite is likely (66%-90% probability range) to be introduced by infected foxes crossing the border with Sweden, the surveillance in the border region would be an appropriate method for early detection.

Conclusion 4: *"VKM considers that it is unlikely that EM will be imported to Norway via contaminated produce (berries, fruits and mushrooms)."*

This statement appears to be still valid. Although no numerical estimates of probability have been undertaken due to a paucity of the relevant data, an extensive survey of berries (including imported berries) on the market in Norway has been conducted (see section 0). It is clear that for commercially grown fresh produce to be contaminated with EM eggs, and then imported, still contaminated, into Norway, a series of events must occur, which, cumulatively, appear unlikely (10%-33% probability range). Although this scenario could have a direct effect on human health, and thus may be of concern to consumers, it is nevertheless almost impossible (0%-1% probability range) to result in the establishment of EM in Norway as the contaminated berries would have to be consumed by an appropriate intermediate host, which, in turn, would need to be consumed by an appropriate definitive host, which would then spread the parasite further.

Conclusion 5: *"Norway's strong 'outdoor' culture, in which hunting, camping, berry-picking and other outdoor activities play a significant role, may place the Norwegian population at greater likelihood of contracting EM than populations in other European countries. However, it should be noted that even in countries with endemic EM, human echinococcosis is, apparently, relatively rare."*

Although the Norwegian population has pride in its outdoor culture, there is no strong evidence that, should EM be introduced to Norway, the human population of Norway is at any greater risk than the population of any other country. Risk factors for infection with EM investigated, and a systematic review and meta-analysis, have indicated risks associated with dog ownership, farming and kitchen-garden owners, going to forests, chewing grass, and hunting/handling foxes. These activities also take place in other European countries that are endemic for EM, and thus people with these activities in known areas of EM establishment are more likely to encounter infective EM eggs than people doing these activities in Norway.

2. **To assess the potential for spreading of EM and the likelihood of becoming established within mainland Norway under different scenarios for introduction via:**

   2.1. Entry of infected dogs into mainland Norway

Infected, untreated dogs can spread the parasite to rodents, and thereafter to foxes, via the parasite eggs shed in their faeces. The time frame for expected EM introduction depends on how often infected dogs enter Norway. Even a single incoming infected dog is likely (66%-90% probability range) to result in local domestic establishment.

Establishment might be preventable, depending on various factors. These include infected foxes being detected, the infected dog(s) being de-wormed and therefore unable to spread the parasite on multiple occasions in multiple places (which may be very unlikely (5-10% probability range), given that the infection is asymptomatic), and that fox de-worming is implemented by using appropriate anthelminthics in bait. Considerable surveillance efforts and information gathering would be needed to map the distribution of the parasite and thereby minimise the likelihood of its establishment.

2.2. Entry of infected foxes into mainland Norway

The surveillance data from SVA indicate that EM occurrence is low on a national level in foxes in Sweden, and that it primarily has a local, clustered occurrence, albeit at several locations. There are indications of a recent development of some hot spots in areas as close as 70 km from the border with Norway. Nevertheless, this does not necessarily indicate expansion towards Norway, as one of the first findings in 2011 in Sweden was approximately 60 km from the Norwegian border. Given ecological similarities and the long common border (over 1600 km), it is relevant to consider spreading from Sweden to Norway by foxes. It is, however, impossible to set any timeframe for introduction at present.

3. To describe control options that have been investigated elsewhere, discussing potential measures for use in different scenarios in Norway

Applicable control options can be divided into options appropriate **before introduction** and **after introduction** of the parasite to mainland Norway (to reduce the spread or, if possible, eradicate the introduced parasite). An ongoing surveillance programme for wildlife (see 0) is necessary in order to identify the parasite as soon as possible after introduction, as early detection and control seem crucial to hinder establishment.

Before introduction, the applicable control options to reduce the likelihood of introduction include treatment of dogs before transport into mainland Norway. However, this control option must be accompanied by appropriate control of compliance to have an effect.

After introduction culling of foxes may only hinder establishment of the parasite if it achieves a near total eradication of foxes in the relevant area and this is maintained for the survival period of the parasite eggs in the environment. Hence, appropriate anthelminthic treatment of local foxes seems to be the most realistic intervention to control spread of the parasite, and studies conducted in endemic areas indicate that it can be of good effect if introduced before distribution of the parasite is widespread. Once the area of introduction is identified, an ecological model (see chapter 6) relevant for this situation could be used to suggest the most likely areas for secondary spread, as well as which areas in the vicinity may result in fastest secondary spread. This will allow targeted distribution of bait treatments and testing efforts.

4. **If Q2 or Q3 indicate the need, to assess the probability of detection under current monitoring conditions should EM be introduced into mainland Norway via any of the routes considered**

Determining the probability of detection under current monitoring conditions is not a trivial endeavour. While the probability of timely detection in untreated infected dogs is extremely unlikely, unless monitoring is instigated, the probability of timely detection in foxes depends on geographic distribution of screening. If screening remains at the current intensity, but targets areas where infection via wildlife from Sweden is most likely to occur first and then spread to, the likelihood of missing all positive cases is low even at low levels of EM prevalence. The probability of detection can be extremely low, if no testing is done in the relevant areas in a given year.

8 Uncertainties and data gaps

8.1 Spread of EM via wildlife infections

The size of relevant wildlife populations and their geographical distribution over time are not known precisely, although the estimates are based upon empirical observations. This applies to both rodents and foxes. It is uncertain whether this results in over- or underestimation of the risks associated with EM.

8.2 Spreading of EM via infected dogs

The risk of EM entering Norway with infected untreated dogs crossing the land-border (or, potentially, by boat) depends on the number of dogs entering Norway, the extent of treatment compliance, and the rate of infection occurrence in untreated dogs entering Norway. This, in turn, may depend upon the infection status in the countries where the dog has been prior to entry to Norway.

Data for these factors are generally lacking, although there are some data on infection occurrence in some countries. Filling some of these data gaps could be achieved by implementing compliance and enforcement checks at borders, gathering data on travel patterns of arriving dogs (including those whose owners comply with EM treatments). Identifying both travel and compliance patterns, as well as potential correlations between the two, might provide important data for assessing the probability of EM introduction to mainland Norway with infected untreated dogs.

While most dog walks are short, both in duration and distance, some dog owners routinely go on longer hikes/bike rides with their dogs, and take their dogs away from where they live to hike with them, especially to mountain cabins, etc. In addition, dogs may be used in hunting or for, for example, sled racing. Such activities will often overlap with areas that are wildlife habitats (e.g., forested areas). At the same time,

owners may be less likely to dispose of their dogs' faeces in the same way as is customary in more urban areas (that is, bagged and disposed of in municipal waste). Data describing the patterns and incidence of such longer trips are lacking. It is also unknown whether dog owners that engage in these activities are also more likely to travel with their dogs abroad by car and/or violate the de-worming treatment requirement prior to their return, although there is no reason to believe that the latter is the case.

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6 Appendix: Ecological disease models

The extremely rapidly increasing impact human society has had on the natural environment in the recent years also means that practically any ecological model has a socio-economic component to its long-term predictions. There are essentially no natural systems left not influenced by human activity, from plastic accumulating on the deep-sea floor to climate change influencing the dynamics and distribution of species from the equator to the poles (Díaz et al., 2019). This fundamentally influences ecological models and makes predictions harder, by introducing non-stationary processes like underlying and unobserved trends in climate, community interactions, nutrients or pollution stress that can change the statistical relationship between known factors, necessitating a wider, more ecological perspective allowing one to account for things like climate-driven community shifts (Koons et al., 2016; Wolkovich & Donahue, 2021).This increasing human impact on, and associated rate of change in, ecosystems have coincided with greater computational power and emerging data sources. These include advances in genetic barcoding, metagenomics and environmental DNA (eDNA) analysis, and improved methods for spatial tracking of wild animals, sensor and logging technology, and particularly remote-sensing data. Integrating these different data sources in ecological models is of potentially great benefit in many application areas, (Ceaușu et al., 2021; Crandall et al., 2020; Pilliod et al., 2022; Raffini et al., 2020; Tobin & Robinet, 2022) but is methodologically complex, computationally intensive and dependent on sufficient empirical data. However, the potential for using numerical, computationally heavy methods, including AI, to address complexity in ecology and epidemiology has developed considerably from when the previous VKM opinion was written.

An ecological modelling approach may now be of value for exploring the likely spread of EM, should it be introduced to Norway under different scenarios. Such an ecological model is a mathematical representation of populations in a context of a community of species and their environment. The goal of such modelling is to represent the relationship between different processes in a way that increases our understanding of the system. In practice they are a way to combine different sets of assumptions and disparate parts of knowledge to see if our sets of assumption (1) are consistent with observation; (2) are sufficient to recreate the observations; and (3) imply emergent properties not visible when partial knowledge is examined separately.

Greater computational power and other methodological advances are increasing our potential for understanding ecological systems on every scale. Likewise, our understanding of infectious disease transmission has come a long way in the past 20-30 years, but still being rooted within concepts of single-agent, single-host systems that rely on measures like the basic reproductive number, R0, and is less suited for environmentally-borne and/or multi-host pathogens with more complex life cycles (Ceaușu et al., 2021; Crandall et al., 2020; Pilliod et al., 2022; Raffini et al., 2020; Tobin & Robinet, 2022). Most existing epidemiological models cannot explore interactions and feedback loops between multiple pathogens, hosts and their environments.

Statistical and machine learning methods adapted from ecology have made significant contributions by mapping infectious disease risk The methods are capable of identifying relationships between pathogen communities, macro fauna and ecosystem structure. However, using these top-down approaches to extrapolate beyond existing conditions is problematic, as they lack a mechanistic framework with which to test the impact of changes (Harfoot et al., 2014; J. M. Hassell et al., 2021; Tobin & Robinet, 2022).

An ecological model, on the other hand, is a mathematical mechanistic representation of populations in a context of a community of species and their environment. The scale may vary from individuals or a single population to a community or metapopulation, or even an entire biome. The behaviour of relatively simple systems may be accurately described analytically, whereas simulation models use numerical techniques to assess more complex situations. The goal of such modelling is to represent the relationship between different processes in a way that increases our understanding of the system. In practice, they are a way to combine different sets of assumptions and disparate parts of knowledge to see if our sets of assumptions (1) are consistent with observation; (2) are sufficient to recreate the observations; and (3) imply emergent properties not apparent when partial knowledge is examined separately.

This allows us to perform digital experiments to further test our assumptions and, when satisfied, perform virtual experiments to assess effects and efficacy of interventions and surveillance. There is increasing urgency for doing so brought on by human impacts on ecosystems. Integrating different data sources in ecological models is of potentially great benefit in many application areas (Ceaușu et al., 2021; Crandall et al., 2020; Pilliod et al., 2022; Raffini et al., 2020; Tobin & Robinet, 2022), but is often methodologically complex, computationally intensive and dependent on sufficient data.

Thus, the feasibility has increased considerably from when the previous VKM opinion was written; the computational resources both with regards to hardware and software have experienced an explosive growth over the last decade, with certain processing elements progressing faster than Moore's law for the development of computationally intensive methods such as AI (Mehonic & Kenyon, 2022). Thus, the potential for using numerical, computationally-heavy methods to address complexity in ecology and epidemiology are today fundamentally different from what they were decades or even just a few years ago. The questions are whether methodology has been developed to take advantage of this fact, and whether such methods are being used.

6.1 Ecological models and EM

Different ecological modelling approaches to EM are possible. Applying new integrated ecological modelling methods naturally tends to lag behind development of the technologies that make them possible. Hence, the methodology and tradition for doing so seems to still be in its relative infancy with much untapped potential. In particular, while predictive systems ecology models are becoming powerful tools for the reconstruction of ecosystem functions, they are arguably as yet underutilized for

modelling infectious disease (J. M. Hassell et al., 2021). So, while the final choice depends on available resources for data acquisition, time, and priorities for model output, a set of ecological models similar to that of Hassell et al., (2021) (termed "General Episystem Models", GEpMs, by Hassell and co-authors) have been introduced to the project group for assessment of how they can be adapted to available resources and needs. The models are being developed as part of ongoing research at the Norwegian Veterinary Institute and elsewhere to be published in the scientific literature. These models will include aspects relevant for risk assessment that were brought to light through the preparation of this scientific opinion.

GEpMs (J. M. Hassell et al., 2021) incorporates an iterative process, in which systems' models are constrained and tested through field and laboratory experiments conducted over varying spatial and temporal scales. This way, statistical models that explain complex, but important, relationships can be incorporated into a mechanistic modelling framework, as a means of decreasing complexity while maintaining predictive power. Another sometimes effective way of model simplification is grouping organisms that share life-history traits to overcome data paucity and the logistical challenges of trying to model all individuals in a large and complex system. When simplified in this way with respect to pathogens, GEpMs would not be able to make predictions about the behaviour of specific pathogens but how the relative abundance of functionally related groups of pathogens changes across space and time. However, even if a focal pathogen is kept separate and specific for predictive purposes, the rest of the complex microbial community dynamics can be potentially predicted by a relatively simple set of functional traits and metabolic properties of the environment (Blackburn et al., 2019; J. M. Hassell et al., 2021; Turner et al., 2021).

Ecological models like GEpMs have multiple inputs and outputs evolving over time in accordance with different statistical properties, that depend on linked sub-models representing different biological processes. Additionally, GEpMs often have an integrated observational model. The observational model takes observable variables as inputs. The latter are not necessarily direct components of the biological mechanisms represented by the GEpMs model, but observable outcomes that depend on it. For instance, one may model the fox population dynamics using the number of observed tracks each winter as the model input, even though the number of tracks does not impact the number of foxes. The discrepancies between model output and observations may be also valuable, as they point to inaccuracies or knowledge gaps in our understanding of the system and thus generate hypotheses about ecological processes not yet known or understood. When a model is validated and found to give unbiased and sufficiently accurate predictions, it can be used for simulations of experiments impossible to perform on real ecosystems, including effectiveness and side effects of interventions such as hunting quota changes, climate change, conservation efforts, disease outbreaks and mitigation efforts.

As explicit likelihood functions are not available, model training is done by an algorithm like BayesFlow (Radev et al. 2020) or simpler learning algorithms to learn estimators' mapping from observed data to underlying model parameters by simulation, within predetermined boundaries set from literature and system knowledge. Coarse-grained statistical laws such as allometric scaling rules linking body mass, metabolism,

abundance, growth and mortality in eukaryotes and "dominance" (numeric abundance distributions between species) can be used to resolve the underlying interactions between parasite, host and vector communities at a computationally feasible resolution (Hatton et al., 2019).

Model ensembles are used to compare simulations in the context of multiple scenarios. Scenarios are defined by different hypothetical sets of events, such as for example, paths of parasite introduction (imported dog vs. cross-border fox migration), climate trajectories impacting rodent host dynamics, as well as impact of fox hunting and control strategies. Inference is inherently Bayesian: the process identifies the best-fitting distributions of uncertain events rather than a likelihood of one particular outcome. The output from the trained models is classified according to scenario and model ensemble, before being compared to validation data. The validated models then
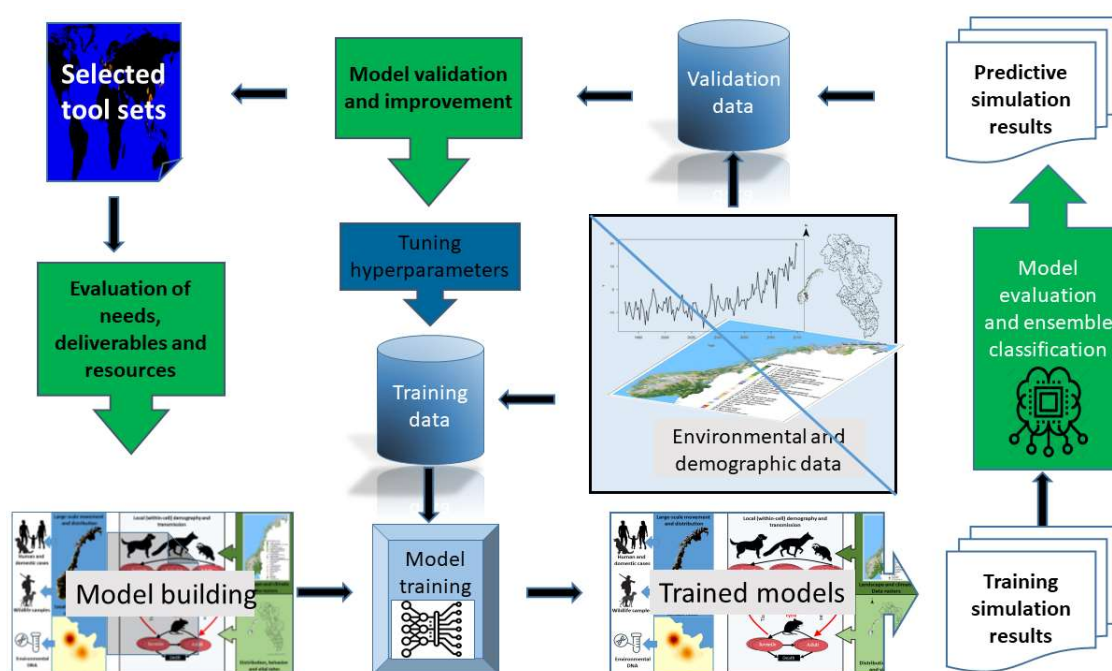

Figure 3. Diagram showing the development and flow structure of an ecological model outlined here for EM.

form the set of models and other qualitative and quantitative "tool sets" available to understand and predict the system. They are subsequently improved by tuning hyperparameters or further model training, when more data becomes available and/or tested against competing models (Figure 3).

This means that such GEpMs models can make use of many different data types to train the model. As long as those inputs can be connected to the proposed underlying mechanisms, they can inform the model. This ability to make use of existing data from different sources is a considerable strength in real-world cases where systematically collected data are not available, or model validation is needed on independent data. While this approach in no way makes systematic surveillance or experimental data any less useful (quite the opposite), it allows to extract useful insight from what is

available. For instance, when public interest arises years or decades after systematic surveillance should have been in place to generate data for a traditional population model, GEpMs allow to make use of available data in one coherent framework.

An important aspect of GEpMs approach is its iterative and evolving nature. Models are built, tuned, and iteratively updated and tested against improved versions of themselves, both through automated training algorithms and conceptually. As shown in Appendix: Ecological disease models, modelling effort begins with identifying the existing tools, needs and data, in the form of ecological system information and then building a conceptual model that represents the variables of interest as functions of the hypothesized main driving processes.

The most promising models enter the tool set available for system understanding and potentially further improvement. Often, different versions of the model are included for consideration, with different degrees of complexity or structure. They are evaluated as a group, often referred to as a model ensemble, to select robust and simplified model structures in addition to model-parameter values. Whenever data size and structure allow it, the model is preferably trained (i.e., the model parameters are estimated) using only a part of the available data, training data. The remaining data can be used for model validation based on the output of the trained model. A description of such a model type that is expected to inform surveillance and control of EM and similar wildlife and zoonotic diseases under increasing human influence and climate change is presented in the chapter 10.

For such efforts to be practical and cost effective, model design and assessment need to be an iterative process, in which the model is used to highlight data gaps and develop hypotheses, which in turn inform study design, targeted sampling and validation (preferably also including eDNA for detecting the presence of environmentally-borne parasites) and generate results, which are utilized to further simplify and constrain the GEpM or similar approach. Nevertheless, the development of ecological system models seems a logical next step for leveraging the emerging opportunities to understand our changing ecology.

6.2 Explorative modelling

A pilot study of a GEpM approach is being conducted by the Norwegian Veterinary Institute (NVI) in collaboration with the EUPAWH project (EUPAHW, 2024) and the project has been synergistically included in the preparation of this opinion. It aims, among other things, to explore and map the state of the art for modelling disease distribution in European wildlife. The study is to be regarded as preliminary as publication of EUPAHW results in the peer-reviewed literature proceeds on a longer time frame than the development period of this scientific opinion. However, the study is motivated and informed by this VKM assessment and has an ambition to contribute to the VKM assessment focus on some of the key knowledge gaps identified here. Thus, relevant methodological experiences, identified knowledge gaps and preliminary insights from the approach are fed back into this scientific opinion.

The chosen GEpM approach treats space and time as discrete variables. The time precision is limited to 1-month time steps, while event geography is defined on a grid of 1km^2. However, these choices can be easily adjusted and are subject to future sensitivity analysis.

The GEpM connects population models for red foxes and host rodents (simplified to one population defined by host capacity rather than species) and a life-cycle model of EM, as present in varying numbers in hosts and as eggs in the environment. Dogs are included as sentinels and potential hosts capable of introducing and amplifying EM risk in the environment.

The distribution of foxes is based on landscape features defined by the CORINE land cover/land use database (see below) and elevation. Early attempts at including a climate-based MAXENT model approach were discontinued, as the extremely wide distribution of red foxes in Scandinavia made this approach less informative and more prone to observation bias in the data than simply informing it by what can be inferred about landscape use on finer scale from general fox biology. Options for refining the fox-habitat-quality model are nevertheless being explored.

The distribution of dogs is assumed to be mostly proportional to the density of humans, with a slightly higher proportion of dog ownership in rural areas and a cap of dog density representing fewer dogs (at least of the types walking outside and exchanging parasites with rodents and the environment) per capita in the most densely populated urban areas. Feral dogs are not included as they seem to exist in negligible numbers in Norway and Sweden.

Wolves have been considered for inclusion as a mechanism for occasional longer-distance transport of parasites than what is commonly assumed to be the case for foxes, and into more sparsely populated areas than what is normally done by dogs. However, the sparsity of wolves in current Scandinavia has made this a secondary priority not yet implemented at the time of writing but to be considered for inclusion at a later point.

The habitat distribution of rodents is a more generic version of the fox habitat model, as capable rodent hosts are assumed to be found in most habitats, with some overrepresentation in food-rich human-dominated landscapes (i.e., lower density at high altitudes and higher density in agricultural landscapes). Fox densities in Scandinavia are assumed to be consistent with the findings of Jahren et al. (2020), and the potential for long-range spread by foxes−with Hagenlund et al. (2019).

Egg decay rate depends on environmental factors (Veit et al., 1995). However, the model currently implemented assumes a constant rate of egg decay (constant both across locations with different climates and in the course of a calendar year). This potential for both over and underestimation of decay introduces an error, but the sign of error effect on the overall EM spread dynamics is not possible to determine with the available data.

Fox and rodent dynamics are linked, i.e., foxes have higher reproductive and survival rates when plentiful rodent prey is available, while rodents have lower survival rates when many foxes are present. As foxes are generalists, they are assumed to have some alternate food sources and, thus, some reproductive capacity and survival not linked to rodent populations. Rodent dynamics are volatile due to high mortality rates and high potential reproduction rates.

Both rodent and fox survival and reproduction responds to seasonal changes in local environments. Rodents are assumed to disperse only locally (i.e., < 1km) within each time step. Foxes disperse further, covering an area of up to 5x5 km per time step, and with more long-distance movement when local fox density outstrip rodent prey availability (the exact distance and relationship to local fox density and habitat quality being a matter for sensitivity analysis and scenario exploration).

Domestic dogs are not represented by a population model as their reproduction, distribution and mortality are overwhelmingly dominated by human activity. They are assumed to exchange parasites with their local environment within 1-3 km of their home. The frequency at which infected dogs are introduced from outside of Scandinavia or are moved around longer distances (for instance, for hunting and vacation) within Scandinavia, is a result of human choices, not ecological processes. Thus, the model does not address this possibility for spread of EM.

Humans are not competent hosts for EM and are thus not represented in the model except as human population density, a data input. The relative probability of human infection can, however, be assessed based on the spatial distribution of eggs in the environment, outdoor activities like berry picking, and the occurrence of infected dogs.

The EM parasite itself is represented by the fox, rodent, and dog populations being layered into S (susceptible, i.e., uninfected), E (exposed, i.e., infected but not yet infective) and I (infected individuals capable of transmitting the parasite through faeces for foxes, or by being eaten for rodents). As long-term immunity to infection has not been assumed to play any significant role, individuals that clear the infection simply transition back into the pool of susceptible. Infection rates for rodents are a function of egg density in their local environment (i.e., within their geographic grid cell). For dogs and foxes, infection rates are proportional to the prevalence of infected rodents locally. Infected dogs and foxes then spread parasite eggs over their range (the size of which is a parameter for sensitivity analysis), and the released eggs accumulating in the environment decay at a fixed rate which is a function of environmental variables: temperature, humidity and UV exposure This rate and how it varies across environments is also a parameter to be refined.

Environmental (climate) conditions are represented as an aggregated abstract that combines the effects of weather and seasonality on rodents and foxes. Dogs are assumed to be exempt from climate effects due to being sheltered by humans, and as the EM eggs are highly resistant, no climate effects have been implemented on their environmental decay rate. However, seasonal and stochastic differences in survival and reproduction have been included in rodent and fox population models. The emergent

effects of varying the scale of spatial correlation and temporal magnitude of environmental perturbations are a major avenue of investigation for the EUPAHW part of the project.

Model training is obviously constrained by the fact that EM is not established at endemic levels in Scandinavia. The modelled area can, in principle, encompass the whole EU area, which would allow training it on areas where EM is endemic and has established dynamics, which would allow to validate and significantly improve precision and reliability. An avenue for further research thus includes training the model on European countries where EM is prevalent, but the scope of this assessment necessitates that only preliminary versions have been developed, trained and run on areas covering various parts of the Scandinavian peninsula. The results should therefore be regarded as preliminary and as illustrative of the type of results generated by the approach.

The relevant parameterisations have so far been restricted to those producing plausible distributions and densities for foxes and rodents and reproducing the rate of EM spread consistent with observations from Sweden (see section 0) when assuming a single point of introduction infecting local foxes.

6.3 Results of preliminary modelling

Running the model over a range of parameters suggests some general tentative results:

1. **An effect of climate change**. Whereas the general mechanisms behind the Fennoscandian rodent cycles are still a subject of debate, they are typified by most species in the local rodent community having population fluctuations with peaks every 3-5 years synchronized over fairly large areas. The fluctuations have been observed to become rarer, smaller, and less spatially synchronous over the last decades. This has been suggested to be caused by climate change, in particular, more frequent rain-on-snow events, together with other human-induced impacts, in particular, habitat fragmentation, and mediated partially through a shift from specialist to generalist predators (Kausrud et al., 2008; Soininen & Neby, 2024; Ylönen et al., 2019). Mimicking the observed change in rodent dynamics by adjusting the spatial scale and external impact on rodent dynamics suggests that replacing the cyclical, high-amplitude, high-synchrony population dynamics with more local rodent fluctuations of smaller amplitude tends to make establishment of the EM infection easier.

2. **Potential for control.** The speed of egg spread tends to increase with time, particularly after the first 0-3 years, so early detection and control seem crucial to hinder establishment. As foxes migrate into depopulated habitats, shooting out foxes may only hinder establishment of the parasite if it achieves a near total eradication of foxes in the infected area and keeps it up for the lifetime of the parasite eggs in the environment. Hence, anthelmintic treatment (i.e., via

baits) of local foxes seems to be the most realistic intervention to control spread of the parasite.

3. **The importance of dogs**. If infected dogs are introduced rarely but randomly in proportion to where domestic dogs are kept and spread eggs that may infect local rodents in the same fashion as foxes, effective and intensive fox surveillance is needed to detect an introduction in time to avoid establishment of the parasite (see above). Thus, if infected and untreated dogs enter the country and spread their faeces where they are in contact with rodents, great surveillance efforts are needed to avoid establishment of the parasite. The time frame depends on how often infected dogs are brought across the border, but even one untreated infected dog per year suggests local domestic establishment within two decades unless infected foxes are detected within the first two years of the parasite being spread by the infected dog(s) and de-worming is implemented by bait in foxes with overlapping ranges with dog infections of at least approximately 5 km, assuming the dog is also de-wormed.

4. **Surveillance prioritisation**. Dogs infected in areas where EM is present is one potential way of bringing EM to Norway, while the other main route is infected foxes wandering in from Sweden (or Russia). As both dogs and foxes tend to be most often found near human habitation, we get a risk map for where EM in wildlife is most likely to occur, which may be useful for prioritizing risk-based surveillance efforts (**Figure** 4).
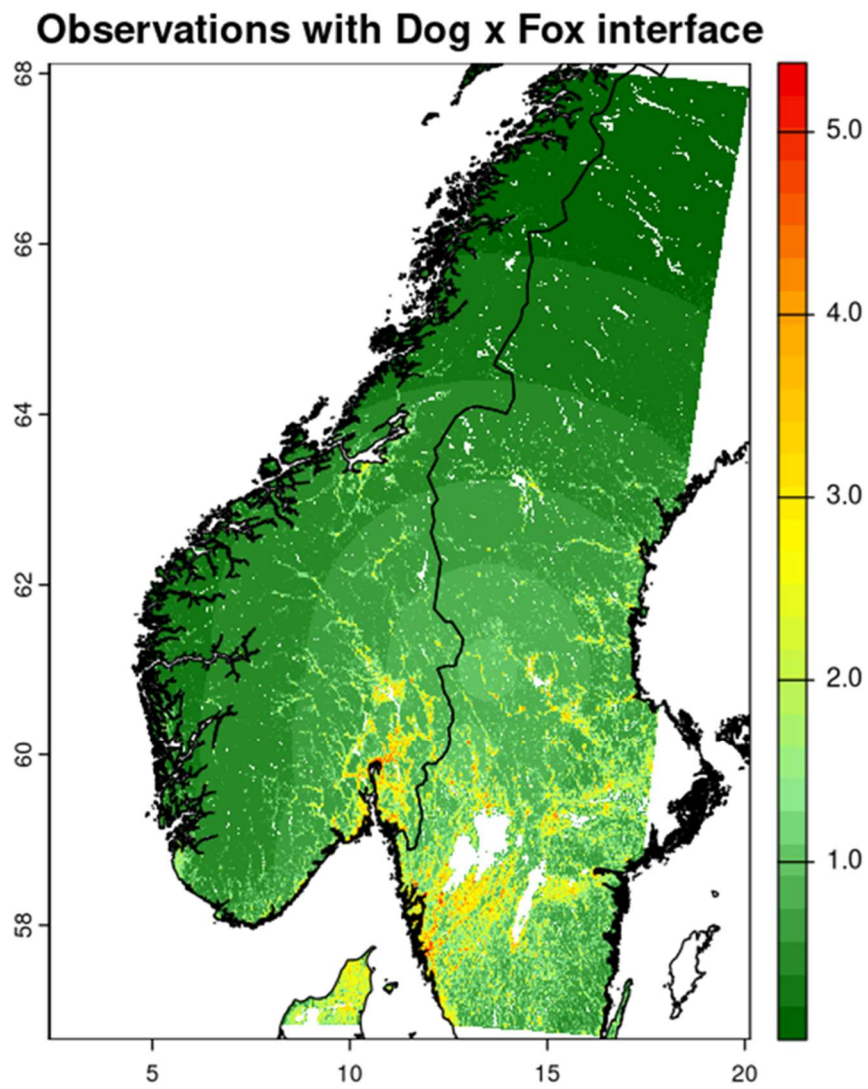
Figure 4. Overlap in dog and fox populations, combined with distances from the nearest known occurrences of EM in Sweden in 2023