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Predicting the spread of feral populations of the American mink in Italy: is it too late for eradication?

F. Iordan · S. P. Rushton · D. W. Macdonald · L. Bonesi

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Abstract Predicting the speed and direction of the spread of alien species is one of the ways in which models can contribute to managing invasions. In Italy, the American mink is an alien invasive living in feral populations whose distribution and impacts are little known. The aim of this study was to predict the likely distribution of the American mink across Italy and the rate of population spread. An extended spatially explicit population dynamics model (SEPM) was used to simulate mink expansion in Italy across a period of 20 years. We used the current and recent distribution of mink farms as the initial points of invasion and validated the model in two ways: (1) by comparing the predicted distribution with the distribution of known populations of mink in Italy; (2) by comparing the predicted rates of spread with those observed in real populations. The application of the model to the Italian landscape highlighted the possibility that mink are already widespread in the country even though only few reports of this species have ever been made. This is of serious conservation concern considering that mink has proven to be a damaging invasive elsewhere. However, the fact that this species should mostly be restricted to north-east Italy suggests that eradication may still be possible. This study highlights the risks posed by American mink and shows that modelling, which is generally less expensive than field studies, can be used to guide surveys and future management of alien invasives.

Keywords American mink · Eradication · Individual based models · Rate of population spread · Italy · Validation

Introduction

The invasion of non-indigenous species is one of the most serious threats facing native ecosystems (IUCN 2000). In Europe the problem is widespread, but national governments have often been slow to respond, and policies have not always been coordinated or science-based. These environmentally damaging shortcomings may be due to several concurrent causes such as unawareness of the potential consequences of an invasion, the inadequacy of a legislative

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F. Iordan · L. Bonesi (✉)
Department of Life Sciences, University of Trieste,
via Weiss 2, 34127 Trieste, Italy
e-mail: bonesi.laura@gmail.com

S. P. Rushton
School of Biology, University of Newcastle upon Tyne,
Devonshire Building, Newcastle upon Tyne NE1 7RU,
UK

D. W. Macdonald
Wildlife Conservation Research Unit, Department of
Zoology, The Recanati-Kaplan Centre, University of
Oxford, Tubney House, Tubney, Oxford OX13 5QL, UK

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context, and scarcity of resources (Genovesi 2005). Introduced species can have effects at several levels within a biological system: at the individual level by changing the behaviour or the body size of native species (Sidorovich et al. 1999); at population and community levels by changing the abundance of native populations (Lambrinos 2000), and also at the ecosystem level by altering the function of ecosystems (Kennedy et al. 1984). At least initially, the costs associated with each of these effects will grow with time as the invader occupies new areas (Neubert and Parker 2004). Control or eradication costs generally increase with the area occupied and may increase with the time since invasion (Gosling and Baker 1989). Therefore, it is important to detect new aliens early, to predict which species will become invasive, and to respond rapidly to the invasion (Genovesi and Shine 2003). Preliminary modelling exercises are intended to assist such a response, underpinning decisions about which action to undertake, where and when (Gosling and Baker 1987; Bonesi et al. 2007).

The American mink (*Neovison vison*) is a semi-aquatic mustelid, native to North America and now established as an invasive species in South America, Europe, Russia and Asia (Dunstone 1993; Bonesi and Palazon 2007). The species has been exported outside its native range for the fur farming industry since the beginning of the last century (Dunstone 1993), but it had not been imported to Italy until the 1950s, with the first feral populations being observed in the country in the 1980s (Lapini 1991). Nonetheless little is known about the distribution and the ecological impacts of mink in Italy where the fur farming industry has never been particularly important and where there are only about 30 mink farms (Bonesi and Palazon 2007), mostly located in the north-east (Fig. 1). There is no systematic study of the distribution of mink in Italy, but feral populations are known to be present in the wild mainly in central and north-east Italy (Lapini 1991; Angelici et al. 2000; Ferretto and Bonesi 2008). No effort has been made to control or eradicate these feral populations apart from attempts to re-trap individuals that escaped following intentional or accidental releases. Intentional releases occur sporadically in Italy and are enacted by animal activist groups, however most of the animals that are released are usually captured or die within a few days of the release. Intentional releases occurred in Italy since the 1980s both in the north and in central regions. Several studies across Europe have demonstrated that feral mink can have serious impacts on native species, in particular ground nesting birds, rodents and also on other mammals (reviewed in Macdonald and Harrington 2003; Bonesi and Palazon 2007). It is therefore important, as a basis for pre-emptive measures, to assess the extent, and pattern, with which the mink is likely to spread in Italy.

Fig. 1 Distribution of mink farms in Italy between 1997 and 2008 and total susceptible range of expansion of mink given by suitable river cells identified with the criteria described in the text. The resolution of the river cells is 1 × 1 km

In this work, we apply an extended spatially explicit stochastic population dynamics model (SEPM) that had been previously developed and tested on the American mink in Britain (Bonesi et al. 2007), to estimate the possible distribution of the American mink across Italy and the likely rate of spread of its populations. While the model published in 2007 was developed as a planning tool for mink control and included also the population dynamics of a species hunted by mink, the present work exploits exclusively the mink population module of the 2007 model as we wanted to focus on mink expansion and also because no mink trapping is carried out in Italy. A projection of the invasion rate with which a species could expand in a newly colonised area could be crucial to preventing or controlling its spread (Neubert and Parker 2004). Similar models have been applied to predict the spread of another alien invasive in Italy, the grey squirrel (*Sciurus carolinensis*) (Lurz et al. 2001). One challenge facing the present work is that few initial data are available on the current distribution and demography of mink in Italy. However, the strength of our approach is that the model, populated with data gathered from other sources, highlights the likely risks of mink invasion. It also provides a basis for prioritising fieldwork and management interventions.

Materials and methods

Study area

The study area comprised the whole of Italy including the islands of Sicily and Sardinia (Fig. 1). Italian physical conformation is characterised by large mountain complexes and the landscape is crossed by a dense river network, seemingly highly suitable to facilitate mink dispersal and establishment. The most important Italian basin is the Po (Fig. 1).

Model structure

We applied a spatially explicit individual based model previously developed for American mink and originally applied to a case study in the UK by Bonesi et al. (2007). The model consisted of two components: (1) a GIS that stored habitat and animal population information; and (2) an individual-based population dynamics module (IBM) that simulated individual life histories and dispersal within the GIS-held landscape. The GIS stored and retrieved habitat information and we used Geographic Resources Analysis Support System (GRASS) for map output (GRASS_Development_Team 2005). The population dynamics module was written in the programming language C and integrated with the GIS component through a UNIX-shell environment. The original model by Bonesi et al. (2007) included three modules that simulated different and interacting processes: the dynamic of the mink population, trapping of mink, and the dynamics of the water vole population that was hunted by mink. In the present work, we only considered the module relating to the dynamics of the mink population.

GIS: properties of the spatial component of the model

The spatial resolution of the model was 1 km, smaller than a typical mink home range (1–6 km length of riparian habitat) (Linn and Birks 1981; Dunstone and Birks 1985) but still amenable for computation. Considering that mink have a territorial system characterised by intrasexual exclusivity and intersexual overlap (Powell 1979), the spatial distribution of females was modelled independently from males, i.e. same-sex home ranges could not overlap but those of males could overlap those of females. Home range length was considered to be fixed for females (3 km) and males (4 km) (Chanin 1976; Yamaguchi 2000) apart from the mating season when home range of males was increased (Table 1—'Mate search distance') to simulate their roaming behaviour aimed at maximising their mating opportunities (Dunstone 1993, p. 131; Yamaguchi et al. 2004).

Each 1 × 1 km cell was assigned to two possible classes: (1) habitats through which mink could move when dispersing but in which they could not settle (unsuitable cells), and (2) habitats that could be used by mink for foraging, breeding and dispersing (suitable cells).

Table 1 Ranges and average values of life-history parameters used as model inputs based on studies in Europe and North America

Life history parameter	Range	Average scenario	Source
Dispersal distance of juveniles in October (km)	10–50	30	Mitchell (1961), Gerell (1971)
Mate search distance (km)	5–20	14	Dunstone (1993)
Monthly adult mortality (proportion)	0.02–0.05	0.032	Bonesi et al. (2006a)
Monthly kits and juveniles mortality (proportion)	0.12–0.26	0.205	Gerell (1971)
Litter size	3–7	5*	Gerell (1971)

* This was increased to 6 when the model was run for the whole of Italy

To discriminate between suitable and unsuitable habitat cells we used three criteria: presence of water (Digital map of River Network), type of land uses (CORINE Land Cover 2000 map), and altitude (Digital Elevation Model map). Digital cartographic data were obtained from the Italian Agency for Environmental Protection (APAT). Regarding the presence of water, only those cells of 1 × 1 km that were covered at least by 5 % of water were considered to be suitable. Regarding type of land uses, based on studies of the American mink in Europe (Zabala et al. 2007; Melero et al. 2008) the following land use categories were considered unsuitable for mink: *continuous urban fabric*, *discontinuous urban fabric*, *industrial* or *commercial units*, *road and rail networks and associated land*, *port areas*, *airports*, *mineral extraction sites*, *dump sit*es, *construction sites*, *green urban area*s, and *sport and leisure facilities*. Although mink have been observed in urban and sub-urban areas both in their native (Mech 2003) and introduced range (Garcia et al. 2009), this habitat is not preferred by mink (Barreto et al. 1998) and therefore we have not considered it as suitable because we assumed that it would not be chosen during the expanding phase of colonisation when better habitats are available. On the same basis we have not considered coasts to be suitable because in Italy they are densely populated and patterns of colonisation in southern Spain, which hosts a similar coastal situation, show that coasts are not initially colonised (Ruiz-Olmo et al. 1997). Furthermore, studies on shoreline habitats showed that building development has a negative impact on mink prey availability which, in turn, affects the ability of those habitats to support populations of the species (Racey and Euler 1983). All areas above 1,200 m in the Digital Elevation Model were considered unsuitable for mink on the basis that, above that altitude, broad-leaved forests tend to disappear giving way to coniferous forests (Pignatti 1982) where lower small mammal richness and abundance are observed (Niedziałlkowska et al. 2010). All three maps (water, land uses, altitude) were then overlaid and suitable and unsuitable cells identified. The total susceptible range of expansion given by all suitable river cells is represented in Fig. 1.

IBM: dynamics of the model

Change in population size was modelled in terms of gains, due to birth and immigration, and losses, due to death and emigration. The model was stage-structured so that discrete stages were recognised in the population (Caswell 2001) and simulated on a time step of one month. The life history processes of mortality, mating, breeding, and dispersal were modelled at the level of the individual within different age classes. Three age classes of mink were considered in the model: kits, juveniles, and adults (Dunstone 1993). Kits were 1–3 months of age, during which time they were still associated with their mother. Juveniles were 4–6 months of age, during which time they were dispersing and acquiring territories. Adults were >7 months and they held territories. The ranges, mean values, and bibliographic sources of the parameters used in the model are listed in Table 1. A flow chart representing schematically the dynamics of the model can be found in Appendix S1.

Mortality

Mortality was modelled on a monthly basis and was specific to the different stages of the mink life cycle: (1) adults; (2) kits and juveniles; and (3) density-dependent mortality for dispersing juveniles. Dispersing juveniles incurred additional mortality if they could not find a territory where to settle, thereby adding a ceiling density-dependent component to mortality. Mortality of adults, kits, and juveniles was derived from estimates obtained from two feral American mink populations in Europe (Bonesi et al. 2006a). These estimates were then transformed into monthly mortality using the formula provided by Krebs whereby survival on a standardised time basis (A_s) is calculated as (Krebs 1999, p. 500):

$$A_s = O_s^{t_s/t_o}$$

where O_s is the observed survival rate, t_s is the standardised time interval, and t_o is the observed time interval. Mortality is then calculated as one minus survival. The probability of death for each individual was determined by sampling deviates from a uniform distribution in the range 0–1, with mortality occurring if the deviate was greater than the value set for that specific simulation. This way of determining mortality introduced stochasticity in the model.

Reproduction

Females could mate only if there was a male within a certain distance of their home range (Table 1). Mating was assumed to occur once a year in February and March and only for females ≥1 year (Birks 1981; Yamaguchi 2000). Kits were born in May and kits and juveniles were assumed to be associated with their mother until the end of September.

Dispersal

Dispersal was modelled so that acquisition of home ranges was considered to occur in October (pre-dispersal movements of juveniles in August and September was not relevant in this model as those movements were introduced in the first model (Bonesi et al. 2007) only to increase chances of being trapped, a feature that has not been applied here). Continuous portions of river-corridor free from other mink and hence suitable for establishing a home range were identified using a clustering algorithm (Hoshen and Kopelman 1976). This algorithm classifies each suitable cell as belonging to a given cluster according to the classification of the neighbouring cells, if the latter are suitable themselves. A detailed description of how home ranges were identified is given in Appendix S2. Dispersing mink were assigned to clusters randomly provided that these were long enough to host a mink home range and were within the dispersal distance from the mother's home range (Table 1).

Sensitivity analysis

The model has been thoroughly tested and subjected to sensitivity analyses to assess how the parameters influenced the results. The most important parameters in determining the monthly density of mink were adult mortality, kit mortality, litter size and juvenile dispersal distance. These analyses were carried out in the original work (Bonesi et al. 2007) so they were not repeated here.

Model calibration

We evaluated the suitability of using the mean life history parameters (Table 1), as identified by Bonesi et al. (2007), to model expanding mink populations. Specifically, the purpose of this analysis was to verify whether the mean life history parameters would accurately predict the presence or absence of mink after a period of time, given that we knew the distribution at the start and the end of the period considered. For this purpose we applied the model to two calibration areas, one previously used by Bonesi et al. (2007) and located in the Upper Thames catchment—Area 1 (Ordnance survey: N 222000, S 192000, E 447000, W 397000) and a new area located west of the river Cherwell near Oxford—Area 2 (Ordnance survey: N 250000, S 200000, E 450000, W 500000, square SPse) (Appendix S3). Data on mink distribution and spread in Area 1 were taken from Barreto (1998), Barreto and Macdonald (2000), and Strachan et al. (1998). Data on mink distribution in Area 2 were collected during the National Otter Survey by the Vincent Wildlife Trust (Lenton et al. 1980; Strachan et al. 1990; Jefferies 2003; Jefferies et al. 2003). We derived maps of river networks from the 1:250,000 Ordnance survey map and these were rasterised at a 1 km resolution for both areas. The land surface was partitioned into suitable and unsuitable habitat—rivers, streams and brooks and their immediate surroundings were considered suitable, and all the rest unsuitable. All the observed mink distributional data were grouped into 5×5 km squares of the National Grid. Maps at the equivalent resolution were created by scaling up the model output from 1 to 5 km resolution using the GRASS GIS. We used the larger resolution of 5×5 km squares, rather than the 1×1 km resolution used for the model, because we did not expect the model to be able to match reality at a resolution that is smaller than the size of a mink's home range. Data on mink distribution from 1975 in Area 1 and from 1978 in Area 2 were used to set the initial conditions. The model was then run for 20 and 22 years (respectively in Area 1 and Area 2) to match the length of the observed data and it was set to perform 100 simulations of mink spread in each area. Probability density maps were obtained for each calibration area by averaging 100 simulated maps. The probability density maps were then transformed into presence/absence maps by setting a 50 % threshold above which a 5×5 km square was considered to be occupied by mink. Maps of observed and predicted distributions were then compared and the output was classified in a confusion matrix that cross-tabulates the observed and predicted presence/absence patterns (Landis and Koch 1977; Fielding and Bell 1997).

We used two measures of classification accuracy:

1. Correct classification rate $= (a + d)/N$
2. Kappa coefficient $= \frac{[(a+d)-(((a+c)(a+b)+(b+d)(c+d))/N)]}{[N-(((a+c)(a+b)+(b+d)(c+d))/N)]}$

where N is the total number of 5 × 5 km squares; a is the total number of 5 × 5 km squares observed and predicted to be occupied; b is the total number of squares observed to be empty but predicted to be occupied; c is the total number of squares observed to be occupied but predicted to be empty: d is the number of squares observed and predicted to be empty. Correct classification rate (CC) and Kappa coefficient (K) measure the proportion of squares where there is '*spatial*' agreement between the observed and the predicted distribution of mink (K giving better information by making full use of the confusion matrix values). Low values in these indices could arise insofar as not all of the ecologically-relevant processes have been specified in the model (Fielding and Bell 1997). Landis and Koch (1977) classify the Kappa statistic results as: Poor <0.0; Slight 0.0–0.2; Fair 0.2–0.4; Moderate 0.4–0.6; Substantial 0.6–0.8; Almost perfect 0.8–1.0. We then ran the model using the mean life history parameters (Table 1) and calculated the Correct classification rate and the Kappa coefficient for each area.

Model validation

We used two approaches to validate the model. First, we verified whether the model predicted the locations of mink populations in Italy. These locations were gathered from published studies (Lapini 1991; Bon and Mezzavilla 1995; Angelici et al. 2000; Spagnesi et al. 2002; Mortelliti et al. 2008), from personal communication with Italian researchers working on mink (Piero Genovesi, Luca Lapini, Dino Scaravelli) and from studies in north-east Italy by our research group (Ferretto and Bonesi 2008). However, because of the paucity of mink records in Italy, the species' distribution is likely to be greatly underestimated. We therefore developed an alternative approach for validation that rested upon verification of whether the rate of population spread predicted by the model was comparable to that observed in real populations in other parts of Europe. For this second approach to validation, we used data on the rate of population spread of mink from the UK and published data from Spain (Ruiz-Olmo et al. 1997). For the UK, raw data on mink populations were derived from the National Otter Surveys of the 1970s, 1980s, and 1990s (Lenton et al. 1980; Strachan et al. 1990; Strachan and Jefferies 1996) and rates of population spread for the UK were calculated for intervals of 7 years (from 1978 to 1985 and from 1985 to 1992). Of the 32 squares of 50 × 50 km of the National Otter Survey, we selected four squares where mink numbers progressively increased from 1978 to 1992 (Squares SPnw, SEse, SEnw and TLnw—Appendix S3). These four areas were different from the two areas used for the calibration. We did not use the latest National Otter Survey because in that case the surveyors stopped as soon as they found the first otter sign rather than walking the full 600 m section.

In all these areas otters were absent or present in small numbers hence mink population dynamics were not likely to be influenced by the presence of this competitor (Bonesi et al. 2006b). As an index of the area progressively invaded by the species we considered increments of 5 × 5 km squares at each time interval. Like for the calibration, we used the larger resolution of 5 × 5 km squares, rather than the 1 × 1 km resolution used for the model, because we did not expect the model to be able to match reality at a resolution that is smaller than the size of a mink's home range. We divided each square of 50 × 50 km into squares of 5 × 5 km and calculated an estimate of the rate of spread in each of the four selected squares. To estimate the rate of spread (TE) we used the formula proposed by Hengeveld (1989):

$$TE = \frac{\sqrt{S}}{t}$$

where S is the area of new 5 × 5 km squares occupied by the population group in time t (expressed in years). The rate of spread of mink populations in Spain was available from the work of Ruiz-Olmo et al. (1997) and calculations followed the same formula, but in this case the original authors had used squares of 10 × 10 km and reported values of rate of spread for several different time intervals (2, 8, 9 and 30 years).

The rates of spread of real populations of mink were compared to those calculated by the model for the Italian landscape. Rates of spread in the model were calculated in ten randomly selected squares of 50 × 50 km (Appendix S4). We set the initial population of mink at 10 females and 10 males in each square and ran the SEPM model for 14 years. We considered the number of 5 × 5 km squares occupied by mink in years 7 and 14. We performed 200 simulations for each area and obtained the maximum, minimum and mean predicted rate of spread of mink for each interval of 7 years.

Application of the model to the Italian landscape

To place the initial populations of mink in the landscape we considered the distributions of both current and former (up to 10 years ago) mink farms. As mink were observed in Italy only after mink farming started and as they could not immigrate from nearby countries because there are no populations close to the border (Bonesi and Palazon 2007), we think that the assumption that mink in Italy originated mostly from mink farms is reasonable. We derived information on the distribution of mink farms from various sources and verified it with A.I.A.V., the Italian Association of Mink Farmers. A total of 30 mink farms was identified and mink were placed in the immediate surrounding of each farm, for a total starting mink population of 665 animals (Fig. 1). The assumption that the number of mink escaped from farms is proportional to the number of farms in an area is supported by the work of Hammershøj et al. (2005) who found this to be true in their study areas in Denmark. The model was run for 20 years using mean values for the life history parameters of mink (cfr Bonesi et al. 2007; Table 1). We performed 30 simulations considering as model output for each simulation the total number of mink present each year. We calculated the mean growth rate of the Italian population of mink predicted by the model, as the geometric mean of the ratio between the mean number of animals in the year $N + 1$ and the mean number of animals in the in year N. To produce a probability density map of the predicted distribution of mink in year 20 we added all the simulated maps of year 20 together ($n = 30$) and then selected only those 1 km squares that were positive for mink in at least 50 % of the simulations.

Results

Evaluation of mean life history parameters

The use of mean life history parameters (Table 1) in the Upper Thames region (Area 1) provided a relatively good correspondence between the observed and the predicted distribution of mink (Correct classification rate = 0.76; Kappa coefficient = 0.50—moderate; Fig. 2), confirming the results of Bonesi et al. (2007). The slight differences in the values of the Correct classification rate (0.76 vs. 0.73) and the Kappa coefficient (0.50 vs. 0.46) between our results and those by Bonesi et al. (2007) were due to the stochastic nature of the model. Using the mean life history parameters in Area 2, located west of the river Cherwell, led to frequent extinctions and the Correct classification rate was low (0.56) and Kappa coefficient was very low (0.0). As it is known that expanding populations, when at low densities, tend to increase their litter size (Sidorovich 1993), we decided to increase this parameter and to run the model with a litter size of six instead of five. With this change we obtained an acceptable correspondence between the observed and predicted values also in Area 2 (Correct classification rate = 0.66; Kappa coefficient = 0.12—slight; Fig. 3).

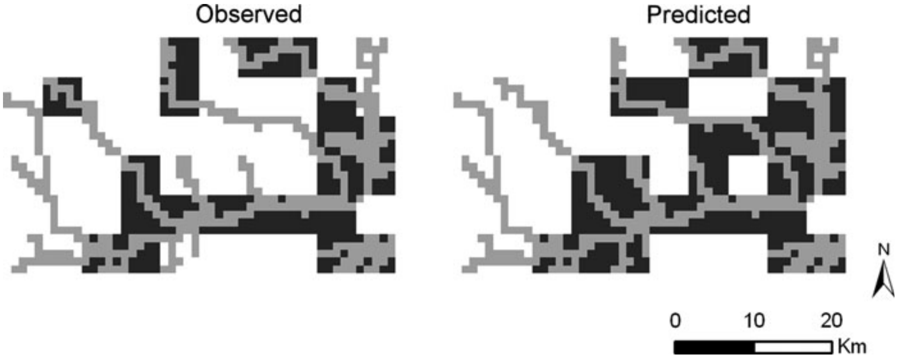

Fig. 2 Map of the observed and predicted distribution of mink in the first calibration area (Area 1). The *black squares* represent the observed distribution of mink in 1995 in the Upper Thames (*left*) and the predicted one after running the model for 20 years (*right*). The distribution of mink is reported at a 5 × 5 km resolution while the river sections in *grey* are reported at a 1 × 1 km resolution

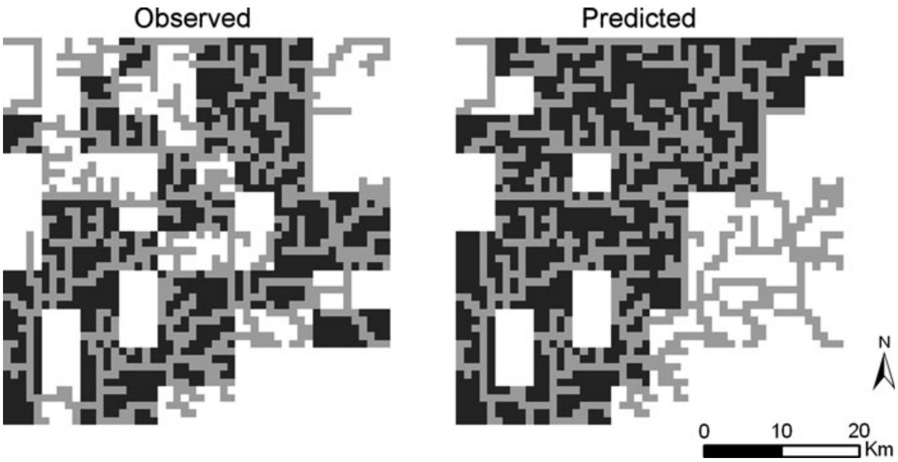

Fig. 3 Map of the observed and predicted distribution of mink in the second calibration area (Area 2). The *black squares* represent the observed distribution of mink in 2000 in an area west of the river Cherwell (*left*) and the predicted one after running the model for 22 years (*right*). The distribution of mink is reported at a 5 × 5 km resolution while the river sections in *grey* are reported at a 1 × 1 km resolution

Model validation

The model predicted well the location of all the currently known Italian populations of mink, as all the 25 validation points, apart from two that were just outside, fell within the area of predicted mink expansion (Fig. 4). Regarding the second validation approach, all the 13 observed rates of spread fell within the predicted ones apart for one case in Spain, where the rate of spread was unusually high (Fig. 5). The relatively wide range of predicted rates was due to the stochasticity of the model. The mean annual rate of spread estimated for mink by the model in the first time interval ranged between 0.714 and 5.200 km/year with a mean of 2.036 (±0.081) km/year and between 0.714 and 5.249 km/year with a mean of

Fig. 4 Map illustrating the distribution of American mink after 20 years as predicted by the model. *Points* represent the locations where mink have actually been observed to be present. Italian administrative regions are also represented

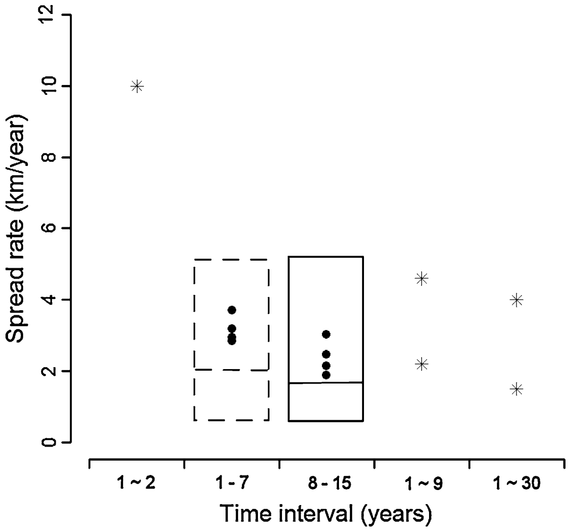

Fig. 5 Comparison between the American mink observed rates of spread in the UK (*points*) (data from National Otter Surveys) and Spain (*asterisks*) (Ruiz-Olmo et al. 1997) and rates of spread predicted by the model in Italy (*boxes*). The *upper* and the *lower* side of the boxes represent respectively the maximum and the minimum values obtained by the model in the ten randomly selected Italian squares; *lines* within the boxes represent the mean value for the simulated rate of spread

1.715 (±0.181) km/year in the second time interval. The values of the rates of spread in the first 7 years interval were positively correlated with the values of the spread rate in the second 7 years interval, but the correlations were not significant both for the observed values of the rates in the UK (Pearson's correlation, $r = 0.693$, $p = 0.307$, $df = 2$) and for the predicted values in Italy (Pearson's correlation, $r = 0.478$, $p = 0.162$, $df = 8$). Both the values of the rate of spread in the UK (Fig. 5) and in the ten areas of Italy (Table 2), showed a significant slowing down between the two 7 years intervals (Paired Student's t test: $t = 4.435$, $df = 3$, $p < 0.05$ and $t = 6.381$, $df = 9$, $p < 0.01$ respectively for the UK observed rates and the ones predicted in Italy). It was not possible to carry out similar comparisons between time intervals with the data on mink spread rates from Spain because the rates there were calculated over single periods.

Application of the model to the Italian landscape

The starting points from which mink could potentially colonise the Italian river network, corresponding to the locations of the mink farms, were concentrated in the north-east of the country, although farms were present also in central Italy and in the island of Sardinia (Fig. 1). To apply the model to the Italian landscape, we ran it assuming a litter size of six rather than five (often considered to be average) because the initial distribution of mink in Italy was more similar to that in calibration Area 2 than that of calibration Area 1 (see above).

The mean number of animals in Italy after 20 years, as estimated by averaging data obtained from the 30 simulations, was 4,026 (±311 SD), of which 2,035 (±289 SD) were females and 1,991 (±245 SD) were males. The model predicted that there was an exponential increase in the mean number of animals with an annual mean population growth rate of 1.094. The probability density map located the majority of animals in the north-east part of the country, while the population in the central and southern regions did not expand much (Fig. 4). A population of considerable size developed instead in Sardinia.

Relationship between density of river network and spread rate

Density of water in the ten 50 × 50 km squares selected to validate the model was higher in the northern and central regions of Italy than in the southern ones (Table 2) and we expect that that the higher the density of water in each area, the faster mink can colonise the river network. Indeed, the rate of spread predicted by the model in each of the ten squares in Italy was significantly correlated with the density of 1 × 1 km water cells in the area, both in the first (Pearson's correlation, $r = 0.689$, $p < 0.05$, $df = 8$) and in the second 7 years interval (Pearson's correlation, $r = 0.778$, $p < 0.01$, $df = 8$).

Table 2 List of the ten randomly selected 50 × 50 km Italian squares used for the validation analysis

UTM33 N coordinates	Region	Water density	% Extinctions	Mean TE year 1–7 (km/year)	Mean TE year 8–15 (km/year)
N 4689183 E 419847	Abruzzo	0.214	0.150	1.954 ± 0.966	1.538 ± 1.216
N 4680797 E 349606	Lazio	0.224	0.135	1.926 ± 0.808	1.405 ± 0.968
N 4548452 E 525595	Campania	0.248	0.180	2.097 ± 1.036	1.503 ± 1.146
N 4953274 E 113020	Liguria	0.249	0.210	2.002 ± 1.208	1.787 ± 1.516
N 5105932 E 285351	Veneto	0.267	0.130	1.961 ± 1.078	1.798 ± 1.480
N 5123087 E 369934	Friuli Venezia Giulia	0.281	0.170	2.128 ± 0.931	1.880 ± 1.289
N 5000964 E 277196	Emilia Romagna	0.285	0.140	2.032 ± 0.927	1.709 ± 1.218
N 4889945 E 210737	Tuscany	0.295	0.135	1.993 ± 1.109	1.883 ± 1.538
N 5060378 E 095536	Lombardy (1)	0.306	0.175	2.101 ± 0.979	1.704 ± 1.289
N 5081761 E 100735	Lombardy (2)	0.317	0.180	2.161 ± 1.153	1.946 ± 1.485

UTM 33 N northern and eastern coordinates, name of the region, density of water (1 × 1 km cells/total cells in the area), and percentage of simulations that resulted in mink extinctions. The mean predicted values and standard deviations of the rates of expansion (TE) of mink in the two time intervals are reported

Discussion

The application of the model to the Italian landscape highlighted the possibility that mink are already widespread in the country even though only few reports of the species have ever been made. Under-reporting of mink is due to the fact that they are an elusive species being small, nocturnal, and living at relatively low densities. Moreover their field signs can be easily confused with those of other species like, for examples, polecats (*Mustela putorius*) and stone martens (*Martes foina*) (Sidorovich 1999; Harrington et al. 2008). Analogous under-reporting has been observed in wild European foxes (*Vulpes vulpes*) dying from rabies for which the first reported case could represent a fairly late stage in a rapidly developing epizootic (Bacon 1981).

The model placed the bulk of the feral mink populations in the north–east of the country (Friuli Venezia Giulia and Veneto regions) and across the Padana plain (Emilia Romagna region), while the central regions had fewer mink (Fig. 4). Fur farms were more abundant in the north with a total of 20 out of 30 farms being found in the three regions of Friuli Venezia Giulia, Veneto, and Emilia Romagna (Fig. 1). The higher propagule pressure in these regions may explain why more mink were predicted to establish there (Jeschke and Strayer 2005; Lockwood et al. 2005), a phenomenon also observed in other species of plants and animals (Beirne 1975; Mack 1981; Russell 2007).

Another factor that is likely to explain the possible greater spread of mink in the northern regions is the presence of a denser river network compared to the central and southern regions (Table 2). A positive relationship between the speed of expansion and the density of water bodies has actually been observed in feral mink populations of Spain (Ruiz-Olmo et al. 1997) and in feral muskrat (*Ondatra zibethicus*) populations in the Czech Republic (Andow et al. 1990). The high density of rivers may be of particular concern on the island of Sardinia where the model predicted that mink would colonise 30 % of the water bodies within 20 years. Sardinia hosts important endemic species of freshwater amphibians like the mountain newt (*Euproctus platycephalus)* that could suffer from mink predation (Lecis and Norris 2004) and it is known that mammal invasions can be particularly dangerous on islands, because the indigenous species have often evolved in the absence of strong competition, parasitism or predation (Courchamp et al. 2003).

The average predicted rates of spread were lower than the observed ones (Fig. 5). This has at least two possible explanations. First, real populations can adapt to changes in population density by varying their life-history parameters (e.g. litter size) and hence increase their rate of spread during colonisation, while in the model these adaptations were not possible. Second, water density may explain why rates of spread were lower in the model than in the observed UK populations as the density of water in the Italian validation squares was lower (0.269 1 × 1 km cells/total cells in the area, SD = 0.034) than that of the UK squares (0.535, SD = 0.083). As stated above, water density can be an important factor in affecting rates of spread in aquatic mammals (Andow et al. 1990; Ruiz-Olmo et al. 1997).

The rates of spread observed in the four UK squares that were used to validate the model (Fig. 5) and the ones predicted by the model in the ten Italian squares (Table 2), decreased significantly between the two time intervals considered, apparently contradicting simple models that predict that populations of invasive species will enlarge at a constant rate (Williamson 1996). This observed decrease in the rate of spread was probably affected by the fact that both in the real and in the simulated populations the analyses were performed over a spatially limited area of 50 × 50 km while the constant spread hypothesis assumes that the area available for a new colonisation is unlimited. Indeed, when larger areas are considered over the same time interval mink populations grow exponentially, both in the model and in reality (Jefferies 2003: p. 150). The decrease in the simulated rate of spread between the first and the second time periods was particularly marked in the squares located in the central and southern regions of Abruzzo, Lazio and Campania, where the river network was less dense. In these areas, there was less suitable habitat and therefore mink populations were likely to fill the available river cells faster and hence the rate of spread to decelerate sooner (Table 2) even though initial populations were all set equal.

Increasing the litter size in the second calibration area (Area 2) improved the fit between the observed and predicted distributions of mink. This concurred with the generality that litter sizes tend to increase when an animal species colonises an area (e.g. King

1983; King 2002; Sundell 2003). Indeed, in Belarus and Germany newly introduced mink, at low population densities, tend to have an increased number of embryos, perhaps due to the higher availability of resources (Sidorovich 1993; Zschille et al. 2004) and parallel density dependence in reproductive output has been demonstrated for other invasive species (Gosling et al. 1981). In this context, it may be noteworthy that in Area 1, where a mean litter size of five provided simulations that matched reality, the number of starting mink populations was higher than in Area 2, where a litter size of six produced more plausible simulations and reduced the number of extinctions. In the real world smaller populations tend to go extinct more often due to demographic stocasticity (Caughley 1994) and in the model this phenomenon is reproduced by having modelled mortality stochastically.

There are always potential sources of error in ecological models (Corsi et al. 2000). In this case, an obvious source of error may derive from our assumption that initially populations were made up by relatively few mink, i.e. we assumed propagule pressure was low, that they all started expanding at once, and that all farms acted as propagule sources. In reality, some intentional releases have involved large numbers of mink, releases have doubtless occurred at different times, and some farms may not have experienced any escape or release at all. For example, in Friuli Venezia Giulia in 2003 animal rights groups released 3,500 mink of which only 1,500–1,800 have been recaptured (Luca Lapini, personal communication). However, Hammershøj et al. (2005) have found that in Denmark the number of feral mink escaped from farms is proportional to the number of farms in an area raising the possibility that massive releases may have a relatively small impact. Another source of error could be the impossibility to discriminate habitats based on their different carrying capacity for mink (Macdonald and Rushton 2003). The mink's considerable dietary opportunism makes habitat an unreliable proxy for food availability and hence mink numbers (Dunstone and Birks 1985). Further, some rivers may experience marked seasonal variation in water level, especially in southern Italy. Nonetheless, validation results supported the pattern of spread predicted by the model.

The application of the model developed by Bonesi et al. (2007) to the case of mink expansion in Italy, provided further insights by highlighting how sensitive simulated mink populations are to at least two conditions: the size of starting populations and the density of the river network. These two factors are known to be important in determining the establishment real populations as well as simulated ones (Caughley 1994; Ruiz-Olmo et al. 1997).

Management actions

We hope that the results of our model, showing that the American mink is potentially quite widespread in Italy, will have the effect of stimulating research and management actions to reduce the impact of this species. Our study highlights areas within Italy where management actions of the invasive American mink should be focused. The model indicates that mink have probably already colonised most of the North-Eastern regions. Further expansion is likely to be into especially sensitive areas with respect to biodiversity conservation (Fig. 6), as mink may well be approaching important wetlands, such as the Marano, Grado,

Fig. 6 Map of the sensitive areas that are likely to be invaded by mink in the near future and that host species which are impacted upon by mink. The Italian river network is also shown, with only the major tributaries

and Venice lagoons, and important deltas, such as the river Po, of international importance for gulls (*Larus melanocephalus* and *Larus genei*) and for Common and Little Terns (*Sterna hirundo* and *Sterna albifrons*) (Fasola and Canova 1996). These bird species are potential prey of American mink (Craik 1995, 1997). Furthermore, some rivers in the Friuli Venezia Giulia region, such as the Isonzo or the Natisone, could provide mink dispersal routes into nearby Slovenia, which is currently mink-free (Bonesi and Palazon 2007). A survey of the actual presence and range of the North-Eastern population would be important in order to start to sensitise the local authorities to the problem and evaluate the costs of eradicating this larger population. One of the smaller populations, that of Lazio is currently being considered for culling following a survey that was carried out in 2008 (Scalera 2008). Finally, the population of Sardinia should be eradicated as a priority, as the island hosts species that may be particularly vulnerable to mink predation and the model highlights the risk that mink will spread there quickly due to the dense river network.

Conclusions

There are several examples in the literature where introduced species are initially undetected or underestimated before their impacts on species, habitats or human activities are recognised (Mota et al. 1999). Introduced species often show a lag-phase after introduction, when the species remains localised and difficult to detect (Crooks and Soulé 1999). In this phase, when the eradication or the containment of the populations could both be possible, it is often difficult to get support for management actions. Our model indicates that the invasion by American mink in Italy could possibly be at this initial stage and therefore management actions are likely to be possible and should be sought out. Zabala et al. (2010) estimated the cost of American mink control and eradication and concluded that in continental areas mink management should move toward eradication when feasible, regarding control only as a second option. The relatively small and isolated populations of Italy constitute possibly a suitable case for this argument, so that it may not be too late for eradicating the American mink from Italy.

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