

biodiversity, mainly on the native species, through the measure of predation and competition relations. We used trapping (capture/mark/recapture) and survey methods to determine the abundance of different competitors (carnivores) and preys in three study areas: one where the invader was absent, another where the invader was present and we removed it, and the third where it was present but we didn't remove. The aim was to compare native species abundances, between areas with presence and absence of the alien species, and in the same area before and after mink removal. We also defined reproductive, dispersal and population parameters, which improve our current control methods. Preliminary results indicated that, competing species were less abundant in areas of American mink presence as expected, (taking into account the only exception of the European otter *Lutra lutra*). However this pattern was not so evident in preys, which can vary significantly between species. At last, our main objective is to acquire the basis for a better management of the increasing future mink populations.

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### **An improved non-invasive genetic sampling protocol for otters: first insights into a peripheral Italian population**

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Successful conservation and management of threatened wild species requires accurate information on population status and structure. However this kind of data are difficult to obtain when dealing with rare and elusive species. Advances in molecular ecology permit to monitor wildlife in a non-invasive way. The main challenges concern the low quality and quantity of target DNA. The Eurasian otter (*Lutra lutra*) is a suitable species for applying non-invasive genetic sampling (NGS), due to the typical marking behaviour used for intra-specific communication. Nevertheless *L. lutra* is one of the most problematic species presenting very low DNA amplification success rates. We collected 225 samples along the river Sangro basin (central Italy), recently re-colonized by otters and strategic for the future expansion of the species northward. We compared two different microsatellite sets, buffer solutions and extraction kits in order to better characterize our small population and obtain reliable results for population analyses. We obtained a mean amplification success rate of 78.0% and a genotyping success rate of 33.3%. The critical values of theoretical probability of identity among unrelated (PID) and sibling individuals (PIDsibs) were 0.001 (six loci) and 0.002 (13 loci) respectively. The 17 individual genotypes sampled highlighted the presence of at least two familiar clusters living in 60 km of river stretches.

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### **Diet changes in American mink population in Iceland**

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The American mink *Neovison vison* is fully established in the low biodiversity environment of Iceland. The mink population peaked in 2003, followed by a continuous decline. The Icelandic marine environment has experienced various changes during these years, including rising sea temperature and sand-eel collapse followed by seabird recruitment failure and population declines. Furthermore the arctic fox population has increased six-fold in the last three decades. In an effort to reveal the causes of the population decline we analysed the stomach contents of 662 mink obtained from hunters in 2001-2009 in the Snæfellsnes Peninsula, West Iceland. Three, nonexclusive, explanations for mink population decrease were considered; decrease in prey availability, less access to prey and reduced capability of mink to hunt. The most marked shift in diet composition was a decrease in consumption of birds. Our findings indicate that climate change events on top of terrestrial diet constraints, caused by increasing numbers of arctic foxes, contributed to the sharp reduction in the mink population from 2004 and onwards. Despite their generalist behaviour, mink have apparently failed to adapt fully to these environmental changes. Furthermore, these results may prove to be valuable in the context of climate change and various invasive carnivores elsewhere.

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