

Estimating stone marten population size using genetic CMR

Project

The stone marten (*Martes foina*) is a meso-carnivore listed as a protected species in Appendix III of the Bern Convention on the Conservation of European Wildlife. This convention allows hunting and other types of exploitation of stone martens, as long as their populations are “kept out of danger”. In France, stone martens are legally trapped and hunted because of their predation on poultry farms. It is thus of prime importance to investigate population size to ensure the long-term viability of the population.

An efficient way to estimate population size is called capture-mark-recapture (CMR). This method involves capturing a sample group of the population, marking it, releasing it, and then do a series of recaptures to determine the ratio of marked to unmarked animals in the population that will allow estimating the entire population size. However, the stone marten low population density and its elusive behaviour make it difficult to capture and even more to recapture, and so far, no population size estimation is available.

Recently, Müller et al. 2020 developed a new CMR model called “genetic-based CMR” (*g*-CMR). This method only requires identifying parent-offspring pairs in a sample using genetic markers, thus overcoming the need of multiple recaptures to estimate population size and could be suited for species such as the stone marten.

In the Bresse region (France), the stone marten population has been intensively monitored, and 370 stone martens have been genotyped at 17 microsatellite loci. The aim of this project is thus to estimate the stone marten population size and density in Bresse. The candidate will start with parentage analyses to identify parent–offspring pairs among the 370 individuals using pedigree analysis software such as COLONY. The candidate will then apply the *g*-CMR model of Müller et al. 2020 to determine the population size in Bresse.

Candidates selection

Ideal candidate should have a strong interest in developing skills and expertise in population genetics, statistical modelling and R statistical software. Good communication skills in written and spoken English would be an asset.

Interested candidates can send me an email (sebastien.devillard@univ-lyon1.fr) with their CV and a one-page motivation letter.

Supervision

Supervisors:

- Sébastien Devillard – University of Lyon (France)

Collaborators:

- Jeremy Larroque – University of Göttingen

- Niko Balkenhol – University of Göttingen
- Sandrine Ruetten – French National Hunting and Wildlife Agency (France)

Recommended reading

Jones, A.G., Small, C.M., Paczolt, K.A. and Ratterman, N.L. 2010. A practical guide to methods of parentage analysis. *Mol Ecol Res*, 10: 6-30.

Jones, O.R., Wang, J., 2010. COLONY: a program for parentage and sibship inference from multilocus genotype data. *Molecular Ecology Resources* 10, 551-555.

Larroque, J., Ruetten, S., Vandell, J.-M., Queney, G., Devillard, S., 2016. Age and sex-dependent effects of landscape cover and trapping on the spatial genetic structure of the stone marten (*Martes foina*). *Conserv Genet* 17, 1293-1306.

Müller, B, Mercker, M, Brün, J. 2020. Population size estimates based on the frequency of genetically assigned parent–offspring pairs within a subsample. *Ecol Evol.* 1– 8.