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ORIGINAL ARTICLE

Combining genetic non-invasive sampling with spatially explicit capture-recapture models for density estimation of a patchily distributed small mammal

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Abstract

Estimating the size of animal populations is essential for understanding the demography and conservation status of species. Genetic Non-Invasive Sampling (gNIS) combined with Spatially Explicit Capture-Recapture (SECR) modelling may provide a practical tool to obtain such estimates. Here, we evaluate for the first time the potential and limitations of this approach to estimate population densities for small mammals inhabiting patchily distributed habitats, focusing on the endemic Iberian Cabrera vole (*Microtus cabrerae*). Using 11 highly polymorphic microsatellites and two sex-linked introns, we compared population estimates in November/December 2011 based on live-trapping and gNIS and assessed the impact of distinct consensus criteria to differentiate unique genotypes. Live-trapping over 21 days captured 31 individuals, while gNIS over 5 days recorded 65–69 individuals. SECR models indicated that individual detectability was positively affected by live-trapping capture success on the previous occasion, while for gNIS, it was mainly affected by genotyping success rates and patch size. Live-trapping produced the lowest density estimates (mean ± SE) of 16.6 ± 3.2 individuals per hectare of suitable habitat (ind/ha). Estimates based on gNIS were higher and varied slightly between 25.2 ± 4.0 and 28.8 ± 4.5 ind/ha depending on assuming one or two genotyping errors, respectively, when differentiating individual genetic profiles. Results suggest that live-trapping underestimated the vole population, while the larger number of individuals detected through gNIS allowed better estimates with lower field effort. Overall, we suggest that gNIS combined with SECR models provides an effective tool to estimate small mammal population densities in fragmented habitats.

Keywords Cabrera vole · SECR model · Population biology · Population size estimates · Fragmented habitats · Faecal DNA

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