



Combining distribution modelling and non-invasive genetics to improve range shift forecasting



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ABSTRACT

Forecasting species range shifts under climate change is critical to adapt conservation strategies to future environmental conditions. Ecological niche models (ENMs) are often used to achieve this goal, but their accuracy is limited when species niches are inadequately sampled. This problem may be tackled by combining ENM with field validation to fine-tune current species distribution, though the traditional methods are often time-consuming and the species ID inaccurate. Here we combine ENM with novel field validation methods based on non-invasive genetic sampling to forecast range shifts in the globally near-threatened Cabrera vole (*Microtus cabreræ*). Using occurrence records mapped at 10 km × 10 km resolution, we built the first ENM (ENM1) to estimate the current species distribution. We then selected 40 grid squares with no previous data along the predicted range margins, and surveyed suitable habitats through presence-sign searches. Faecal samples visually assigned to the species were collected for genetic identification based on the mitochondrial *cytochrome-b* gene, which resulted in 19 new grid squares with confirmed presence records. The second model (ENM2) was built by adding the new data, and species distribution maps predicted by each model under current and future climate change scenarios were compared. Both models had high predictive ability, with strong influence of temperature and precipitation. Although current distribution ranges predicted by each model were quite similar, the range shifts predicted under climate change differed greatly when using additional field data. In particular, ENM1 overlooked areas identified as important by ENM2 for species conservation in the future. Overall, results suggest that combining ENM with non-invasive genetics may provide a cost-effective approach in studies regarding species conservation under environmental change.

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1. Introduction

There is growing evidence that many species will change their current ranges in response to climate change. These range shifts, may have multiple conservation implications on, for instance, the design of reserve networks (Hannah, 2008; Hannah et al., 2002), assisted colonization approaches (Hoegh-Guldberg et al., 2008), and habitat restoration priorities (Mawdsley et al., 2009).

Species range shifts are caused by the expansion or contraction of favourable climatic conditions, and typically emerge from extinction–colonization processes mostly driven by the species physiological tolerances, dispersal abilities, and habitat availability along their distribution limits (Anderson et al., 2009; Thomas, 2010; Walther et al., 2002). Generally, species tend to occupy newly available patches at their expanding margins, being more likely to become locally extinct at the retracting margin (Anderson et al., 2009). Support for such climate-induced range dynamics in many plants and animals has led to the recognition that effective conservation planning should move from a static to a dynamic approach. Accurate projections on potential species distribution

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ranges, should allow the conservation of both present-day and future biodiversity (Fuller et al., 2011; Hannah et al., 2002; Peterson et al., 2011).

Ecological niche models (ENMs) are commonly used to assess the relation between the species and the environment (Guisan and Zimmermann, 2000), evaluating the existing fundamental niche of the species (Peterson et al., 2011). While these models provide a valuable tool for designing policies to lessen the effects of climate change on biodiversity (e.g. Peterson et al., 2011), they are not impervious to some potential biases and uncertainties (Beale and Lennon, 2012; Hanspach et al., 2011; Rocchini et al., 2011). A primary source of uncertainty underlying ENM is related to the quality and quantity of species occurrence data. Small sample sizes or inadequate spatial coverage decreases the statistical confidence of correlations underlying niche models (Wiens et al., 2009, and references therein). Uncertainties in occurrence information may be particularly common along range margins, where the species might occur at lower densities (Hengeveld and Haeck, 1982), increasing the risk of erroneous results and predictions (Hanspach et al., 2011). These uncertainties may have important implications for the evaluation of the ecological niche, and for the computation of accurate projections of current and future distributions, particularly in rare or elusive species which are difficult to sample.

Although interactive modelling and ground validation sampling can provide a useful method to fine-tune current species distribution ranges, its implications in forecasting species range shifts are still largely unexplored, often because field surveys are logistically difficult, inaccurate, and time-consuming. In this context, novel non-invasive genetic techniques may provide a fast and effective solution to assess the impact of combining ENM and post-modelling sampling on species range shift forecasting. The combination of non-invasive genetic sampling with DNA-based tests for species identification, highly improved the efficiency of using field signs (faeces, hair, feathers, etc.) for determining species presence and distribution (see e.g. Beja-Pereira et al., 2009; Waits, 2004). In what concerns small mammals, for instance, reliable occurrence data typically require relatively demanding field sampling efforts, often involving intensive capture campaigns, or owl pellet dissection (e.g. Landete-Castillejos et al., 2000; Mira et al., 2008; Pita et al., 2006, 2007, 2011). Recently, it has been shown that non-invasive genetic sampling of small mammals (e.g. using faecal samples) may provide a promising alternative to monitor populations, by allowing the indirect identification of species (Alasaad et al., 2011; Barbosa et al., 2013). However, to the best of our knowledge, no study has yet combined ENM and non-invasive genetics to refine range shifts estimates, and so the potential value of this approach remains untested.

Here, we evaluate the impact of combining ENMs with non-invasive genetic sampling at the range margins in forecasting range shifts of a rodent species, for which range margins are poorly defined. Specifically, we focus on the Cabrera vole *Microtus cabrerae*, a near threatened species endemic to the Iberian Peninsula (Fernandes et al., 2008), which is restricted to wet herbaceous habitats (Luque-Larena and López, 2007; Pita et al., 2006, 2011; Santos et al., 2005, 2006). This species typically occurs at very low densities (Fernández-Salvador et al., 2005), and often persists as metapopulations in highly fragmented agricultural and pastoral landscapes, where patch-level extinction–colonization events are relatively common (Pita et al., 2007). Recent studies suggested that the Cabrera vole is a climate-sensitive species (Araújo et al., 2011, 2012; Laplana and Sevilla, 2013), implying that its conservation should consider the dynamic and uncertain effects of climate change. Identification of effective conservation actions for the Cabrera vole is hindered by difficulties to survey the species using traditional sampling approaches such as live-trapping (e.g. Fernández-Salvador et al., 2005; Pita et al., 2007). Although presence signs (e.g.

runways on grasses, faeces) have been successfully used to survey this vole (e.g. Garrido-García et al., 2009; Pita et al., 2006, 2007), the approach may be limited in situations of sympatry with other vole species producing similar signs (e.g., the field vole, *Microtus agrestis*, in Northern Iberia). Here we combine ecological niche modelling and recent DNA-based tests for species ID using faecal samples to forecast range shifts of rare and elusive species. In particular we aimed to (i) fine-tune the distribution limits of the Cabrera vole in Iberia, using non-invasive genetic sampling at the range margins; (ii) predict the species range shifts under future climate conditions, and evaluate the effect of the new occurrence records on such forecasts; (iii) assess the impacts of climate change on the conservation of the Cabrera vole, in the light of the new distribution model predictions. Results of the study were then used to discuss the potential of non-invasive genetics to improve the value of ENM in guiding conservation action.

2. Materials and methods

2.1. Study design

We followed an approach similar to Guisan et al. (2006), using spatial predictions from ecological niche models (henceforth ENM1) to guide new surveys of the Cabrera vole, and then using the data from these surveys to improve the initial models (ENM2). In contrast to Guisan et al. (2006), however, we have concentrated surveys at the range margins rather than throughout the species range (Fig. 1), aiming to gain a better representation of the extremes of the climatic niche. Sampling was conducted in Portugal, which includes a large proportion of the overall species range, and where previous surveys have been mostly based in owl pellet analysis (Mira et al., 2008), and far less intensive than those carried out in Spain (e.g. Fernández-Salvador, 2007; Garrido-García et al., 2013). Therefore, it was possible that range margins for the species were particularly ill-defined in Portugal, which could have serious consequences on the prediction errors of distribution models (Hanspach et al., 2011). Surveys were based on the detection of the characteristic faeces of the species, which were collected and identified unequivocally using molecular techniques (see below). The distribution models produced with the baseline data (ENM1) and the new dataset (ENM2) were then compared in terms of influential variables, and spatial forecasts under current and predicted future climatic scenarios.

2.2. Data sources

Presence data of Cabrera vole across its entire current range (the Iberian Peninsula) were obtained from all available literature sources documenting the occurrence of the species between 1970 and 2011 (see Fig. 1a; Table A1 in Appendix A) and recorded in a 10 km × 10 km UTM grid (Universal Transverse Mercator). Of the 6153 available squares, the species occurred in 391. We used data collected over a relatively large time span, because we wanted to maximize the size and spatial representativity of the occurrences dataset, which is essential for accurate species distribution modelling (Feeley and Silman, 2011). Although this procedure caused a mismatch between the species distribution data (1970–2011) and the climate data (1950–2000), the overlap between the two time periods was very large (30 years), and the mismatch was sufficiently small (11 years) to make it unlikely to affect significantly the modelling results (Roubicek et al., 2010).

Variables of current climatic conditions were obtained from the WorldClim website (<http://www.worldclim.org/> and Hijmans et al., 2005) and consisted of interpolations of observed data for the time period between 1950 and 2000. Variables of future

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