



Short Note

A gap analysis for threatened bat populations on Sardinia

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Abstract

Sardinia is home to three bat species of chief conservation importance, the endemic *Plecotus sardus* as well as *Myotis punicus* and *Rhinolophus mehelyi*, for which the island constitutes the Italian stronghold. We carried out two gap analyses by overlapping the network of protected areas present on Sardinia respectively with 1) the occurrence records of all species and 2) the binarized maps obtained from maximum entropy models. Unlike the other two species, *P. sardus* known records are confined to the central sector of the island and its suitable habitat partly overlaps with that of *M. punicus* but not with *R. mehelyi*. Due to its uniqueness and restricted range *P. sardus* requires a very specific management strategy for its protection to be successful. Both analyses led to the conclusion that all species considered require more extensive protection than is currently granted so that urgent measures should be taken to improve the current situation.

Understanding the effectiveness of a reserve system in protecting rare species is a fundamental step towards effective conservation. Within this context, gap analysis is a powerful approach to identify interruptions (“gaps”) or areas underrepresented in a reserve network, based on the comparison between the distribution and extent of reserves with those of the geographic occurrence of a given species (Jennings, 2000).

When the real distribution of a species is not well known, for example when rare or elusive species are considered, gap analysis may be applied to potential distribution, or habitat suitability maps generated by species distribution models instead of restricting it to observed distributions (Bosso et al., 2013). Moreover, because for such species “absence” data may in fact merely represent overlooked occurrence, presence-only models are commonly used to overcome this limitation (e.g. Phillips et al., 2006).

Islands are geographic sets where conservation actions are most needed, as species occurring there exhibit intrinsic vulnerability due to their endemic status, small population size or low genetic diversity and are subjected to especially strong human pressures (Kier et al., 2009). Sardinia is an island of great biogeographic value due to the significant presence of endemic taxa or populations that are scarcely represented on the neighbouring mainland (Grill et al., 2007). Bats make no exception to this rule: three species occurring on the island have special conservation importance. The Sardinian long-eared bat *Plecotus sardus* (Mucedda et al., 2002), roosting in caves and buildings and associated with forest (Mucedda and Pidinchèdda, 2003), is endemic to the island and classified as endangered or vulnerable respectively in the Italian and global Red Lists due to its small population size and the threats posed by human action to key habitat (Hutson et al., 2008; Rondinini et al., 2013). The Maghrebian mouse-eared bat *Myotis punicus* (near threatened on a global scale but vulnerable in Italy), a strictly

cave-dweller native to North-west Africa, Corsica, Malta, Gozo and Sardinia and recently recorded for Sicily (Bogdanowicz et al., 2015) but absent from the rest of Europe, appears at risk on such Mediterranean islands where population declines were recorded (Rondinini et al., 2013). Finally, the Mehely’s horseshoe bat *Rhinolophus mehelyi*, globally listed as vulnerable (Hutson et al., 2008) is mostly confined to the Mediterranean and shows a progressively shrinking range. Its presence on mainland Italy is limited to a cave in Apulia, where a single bat was observed after many years (Dondini et al., 2014), whereas in Sicily only two small colonies are present. Noticeably, Sardinia appears to be the Italian stronghold for this bat, occurring there with large colonies (Mucedda et al., 2009; Russo et al., 2014): yet, these are also on the decline, as much as the species is listed as vulnerable in the Italian Red List (Rondinini et al., 2013). The absence of this bat species from most mainland Italy is not the result of past extinction but likely the outcome of a peculiar biogeographic history (Russo et al., 2014).

Overall, the biogeographic importance of the three taxa on the island and their threatened status make the planning of effective conservation especially urgent. To help reach this goal, in this study we carried out a gap analysis for *P. sardus*, *R. mehelyi* and *M. punicus*. Our aims were to assess the effectiveness of the current reserve network, identify major interruptions in the protection of the three bat species and inform management decisions. Because several studies have evaluated the degree of protection granted by nature reserves based on species’ occurrences (Maiorano et al., 2007; Parra-Quijano et al., 2012), here we also compared the performance of this approach with that based on maximum entropy modelling (Bosso et al., 2013).

For this study we considered the entire territory of Sardinia corresponding to an area of ca. 24100 km² with an elevation range of 0–1834 m a.s.l.

We used presence records (Fig. 1) for *M. punicus* (n=111), *P. sardus* (n=20) and *R. mehelyi* (n=60) from published work (Mucedda et al., 2002; Russo et al., 2014) or unpublished data collected by two of

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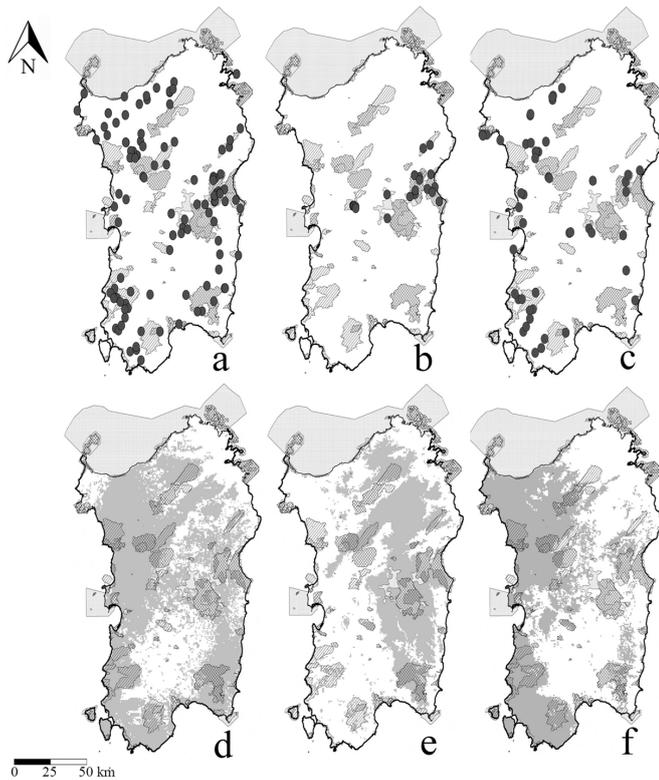


Figure 1 – Overlay between boundaries of SACs (simple hatch), SPAs (crosshatch) and PAs (ordered stipple) and respectively presence records (black points) and Maxent binary maps (light grey) of *M. punicus* (a and d), *P. sardus* (b and e) and *R. mehelyi* (c and f) in Sardinia.

us (MM and GF). Occurrences refer to variable numbers of roosting bats (*M. punicus*, 108.5 ± 256.8 bats/occurrence record, range=1–1500; *P. sardus*, 9.1 ± 18.1 bats/ occurrence record range=1–60; *R. mehelyi*, 47.5 ± 95.5 bats/occurrence record, range=1–500). Records were screened in ArcGIS (version 9.2) for spatial autocorrelation using average nearest neighbour analyses to remove spatially correlated data points (e.g. Russo et al., 2015; Bosso et al., 2016). After this selection, 60, 13 and 40 independent presence records for *M. punicus*, *P. sardus* and *R. mehelyi* respectively were used to generate species distribution models.

To predict habitat suitability for the three species, we used a set of 21 ecogeographical variables (EGVs) These included altitude, 19 bioclimatic variables and land cover. Altitude and the bioclimatic variables were obtained from the WorldClim database (www.worldclim.org/current) (Hijmans et al., 2001). Land cover was obtained from the Corine Land Cover IV level for the year 2012 (available at <http://www.sinanet.isprambiente.it/it/sia-ispra/download-mais/corine-land-cover/corine-land-cover-2012/view>). All variable formats were raster files (grid) with a 30-arc second resolution ($0.93 \times 0.93 \text{ km} = 0.86 \text{ km}^2$ at the equator). To select the number of variables for the final distribution models, we first eliminated the highly correlated predictors by retaining those with a Pearson's $|r| \leq 0.80$.

From this first set of predictors, we considered those most relevant to the ecological requirements for the three species in Sardinia according to expert opinion and current knowledge (Mucedda et al., 2002, 2009; Russo et al., 2014). This led to the following final set of 12 vari-

ables used for model training: altitude (m), land cover, mean diurnal range ($^{\circ}\text{C}$), isothermality (%), temperature seasonality ($^{\circ}\text{C}$), temperature annual range ($^{\circ}\text{C}$), mean temperature of wettest quarter ($^{\circ}\text{C}$), mean temperature of driest quarter ($^{\circ}\text{C}$), precipitation seasonality (%), precipitation of wettest quarter (mm), max temperature of warmest month ($^{\circ}\text{C}$) and precipitation of coldest quarter (mm).

We used Maxent ver. 3.3.3k (<http://www.cs.princeton.edu/~schapire/maxent>) (Phillips et al., 2006) to model the potential distribution of the three species in Sardinia. This approach relied on presence-only datasets and is especially useful when presence data are scarce. This algorithm usually results in good predictive models compared with other presence-only models (e.g. Elith et al., 2006). To build the models, we used the occurrences of *M. punicus*, *P. sardus* and *R. mehelyi* and the EGVs selected as described above. In the setting panel, we selected the following options: random seed; write plot data; regularisation multiplier (fixed at 1); 10000 maximum number of background points; random test percentage 20% (percentage of records to be randomly set aside as test points); 1000 maximum iterations; and, finally 20 replicate effects with bootstrap replicated run type. This replicated run type makes it possible to replicate sample sets selected by sampling with replacement. The average final maps obtained had a logistic output format with suitability values from 0 (unsuitable habitat) to 1 (suitable habitat). We selected the 10th percentile (the value above which the model classifies correctly 90% of the training locations) as the threshold value to define the presence of the three species (e.g.: Bosso et al., 2013; Russo et al., 2015; Bosso et al., 2016).

To assess the degree of protection granted to *M. punicus*, *P. sardus* and *R. mehelyi* by the reserve network of Sardinia, we carried out two conservation gap analyses, one based on the actual occurrence maps, the other based on the binarized potential distribution maps (e.g. Bosso et al., 2013). We overlaid such maps with the shape files containing the boundaries of the Sardinian (1) special areas of conservation (SACs), special protection areas (SPAs) and Natura 2000 network (SACs + SPAs), (2) protected areas (PAs) i.e. national parks; regional parks and state reserves and (3) protection network (PN) (SACs + SPAs + PAs).

We tested the predictive performance of the models with different methods: the receiver operating characteristics, analyzing the area under curve (AUC) (Fielding and Bell, 1997); the true skill statistic (TSS) (Allouche et al., 2006); and the minimum difference between training and testing AUC data (AUC_{diff}) (Warren and Seifert, 2011).

Maxent models showed high levels of predictive performance as can be seen from AUC, TSS and AUC_{diff} values (Table 1). The EGVs that were most important to explain the potential distribution of *M. punicus*, *P. sardus* and *R. mehelyi* in Sardinia were as follows. *M. punicus* occurs more likely in areas of holm and cork oak woodland, low scrubland and agroforestry (18% of contribution to model) at an altitude of ca. $450 \pm 231 \text{ m a.s.l}$ (8% of contribution to model). Highly suitable areas are characterized by mean temperature of wettest quarter of $11 \pm 3 \text{ }^{\circ}\text{C}$ (24% of contribution to model), max temperature of warmest month of $28 \pm 1 \text{ }^{\circ}\text{C}$ (14% of contribution to model) and precipitation seasonality of $54 \pm 4 \%$ (11% of contribution to model). *P. sardus* is more likely to occur in areas with the same land cover (38% of contribution to model) characteristics of those suitable to *M. punicus* but at an altitude of ca. $492 \pm 264 \text{ m a.s.l}$. (10% of contribution to model) with temperature seasonality of $56 \pm 2 \%$ (38% of contribution to model) and an isothermality of $51 \pm 2 \%$ (15% of contribution to model). Finally, *R. mehelyi* is more likely to occur in areas of holm and cork woodland and agricultural land (27% of contribution to model) at an altitude of ca. $308 \pm 198 \text{ m a.s.l}$. (8% of contribution to model). Moreover the areas where this species is likely to occur have precipitation seasonality of $57 \pm 3 \%$ (49% of contribution to model), max temperature of warmest month of $28 \pm 1 \text{ }^{\circ}\text{C}$ (10% of contribution to model) and annual mean diurnal range of $8 \pm 1 \text{ }^{\circ}\text{C}$ (9% of contribution to model). We found that over 65% of *M. punicus* and *R. mehelyi* presence records, and ca. 40% of *P. sardus* presence records fall outside the PN (Fig. 1 and Tab. 2). The overall PN protects ca. 30%, 40% and 17% of the colonies (hibernal and reproductive) of *M. punicus*, *P. sardus* and

Table 1 – Performance of Maxent Species Distribution Models for *M. punicus*, *P. sardus* and *R. mehelyi* in Sardinia assessed with different validation methods: Area Under Curve ($\text{AUC} \pm \text{SD}$); the True Skill Statistic ($\text{TSS} \pm \text{SD}$); and the minimum difference between training and testing AUC data ($\text{AUC}_{\text{diff}} \pm \text{SD}$).

Model	AUC Training	AUC Test	AUC_{diff}	TSS
<i>M. punicus</i>	0.79 ± 0.01	0.75 ± 0.01	0.03 ± 0.01	0.61 ± 0.10
<i>P. sardus</i>	0.82 ± 0.01	0.80 ± 0.01	0.02 ± 0.01	0.70 ± 0.17
<i>R. mehelyi</i>	0.79 ± 0.01	0.75 ± 0.01	0.04 ± 0.01	0.55 ± 0.12

R. mehelyi, respectively. The analysis based on Maxent binary maps offers a less optimistic picture, with ca. 26%, 25% and 22% of potential habitat protected for *M. punicus*, *P. sardus* and *R. mehelyi* (Fig. 1 and Tab. 2). Finally, the PN protects ca. 21% of the binary areas where *M. punicus*, *P. sardus* and *R. mehelyi* co-occur (Tab. 2).

Maxent models show that areas of high habitat suitability for *M. punicus* and *R. mehelyi* are largely present in the west portion of Sardinia, so that large-scale protection of these species could focus on that sector. Besides, both species are cave dwellers, so strict protection of caves would also obviously favour them. However, small-scale habitat requirements, such as e.g. differences in foraging habitat, may represent important factors implying the development of management strategies tailored on a species-specific basis (Russo et al., 2005, 2015).

P. sardus has a markedly different distribution, being confined to the central sector of the island. Suitable habitat partly overlaps with that of *M. punicus* but not with *R. mehelyi*. Besides, unlike the other species we examined, buildings are important roosts for *P. sardus* (Mucedda and Pidinchedda, 2003). Overall, *P. sardus* requires a very specific management strategy.

As for other management-dependent taxa (e.g. Bosso et al., 2013) both gap analyses, i.e. that based on occurrence records and that derived from models, show that the network's coverage of the areas important for these bats is insufficient. According to the occurrence record analysis, the situation is somewhat less critical than that depicted by the model-based gap analysis, at least for *P. sardus*, for which ca. half of records fall within PN. The fraction of suitable habitat protected by the PN system shows alarmingly low values.

Overall, our work demonstrates that even the mere legal protection of the three species considered needs substantial improvement, which might be granted by expanding the currently insufficient reserve network of Sardinia. We also highlight that bat conservation goes well beyond large-scale preservation but needs local intervention such as strict protection of roosting sites in order to secure a long-term persistence of important colonies. Finally, although bats on the island are well studied, the discrepancy between observed and potential distribution suggest that the former is an underestimate of the actual situation, so research efforts should be increased to detect any further important roost or foraging site and consider it for appropriate protection. ☞

Table 2 – Degree of protection granted to *M. punicus*, *P. sardus* and *R. mehelyi*, or to areas of co-occurrence of such species, by the reserve network of Sardinia based on the actual occurrence records and on the SDM's binarized maps. Abbreviations as follows: SACs, special areas of conservation; SPAs, special protection areas; PAs, protected areas; Natura 2000, SACs+SPAs; PN, Sardinian protection network (SACs+SPAs+PAs).

Occurrence records	% records/surface area within site				
	SACs	SPAs	Natura 2000	PAs	PNs
<i>M. punicus</i>	31.15	18.02	31.15	10.81	31.15
<i>P. sardus</i>	60.00	50.00	60.00	50.00	60.00
<i>R. mehelyi</i>	34.00	14.00	34.00	12.00	34.00
<i>M. punicus</i> + <i>P. sardus</i>	25.62	21.49	32.23	17.36	32.23
<i>M. punicus</i> + <i>R. mehelyi</i>	21.09	12.58	22.39	9.93	22.39
<i>R. mehelyi</i> + <i>P. sardus</i>	11.43	11.43	11.43	17.14	17.14
<i>M. punicus</i> + <i>P. sardus</i> + <i>R. mehelyi</i>	12.28	12.28	12.28	14.04	14.04
Species Distribution Models					
<i>M. punicus</i>	20.22	12.78	24.14	4.89	25.85
<i>P. sardus</i>	18.31	15.51	22.81	7.93	25.38
<i>R. mehelyi</i>	19.21	8.71	22.32	1.24	22.32
<i>M. punicus</i> + <i>P. sardus</i>	17.80	12.40	22.10	6.10	22.40
<i>M. punicus</i> + <i>R. mehelyi</i>	19.45	11.20	25.52	3.30	25.52
<i>R. mehelyi</i> + <i>P. sardus</i>	15.60	10.10	19.70	4.10	21.20
<i>M. punicus</i> + <i>P. sardus</i> + <i>R. mehelyi</i>	16.30	10.20	20.30	4.40	20.50

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