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Original investigation

SEMICE: An unbiased and powerful monitoring protocol for small mammals in the Mediterranean Region

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ABSTRACT

Schemes to monitor biodiversity change should detect properly target species without harmful effects on individuals and populations, and be powerful enough to detect expected population trends in the face of global change. Targeting is a key aspect of monitoring schemes since there is no single method able to detect unbiasedly all species of any given community, especially the rarest ones. Here we test whether SEMICE (*SEguimiento de MIcromamíferos Comunes de España*), a monitoring protocol for small mammal biodiversity in the Mediterranean Region, fulfil these requirements. The protocol aims at monitoring common species easy to catch with the two most widely used commercial live traps (18 Sherman and 18 Longworth traps alternated in position across 6 × 6 trapping grids spaced 15 m, brought into operation for three consecutive nights in spring and fall). We used pilot data from twenty-two plots distributed along wide environmental gradients in Catalonia (NE Spain), sampled from 2008 to 2015. The wood mouse (*Apodemus sylvaticus*) was dominant throughout the study period (992 individuals, 39.0%), followed by the white-toothed shrew (*Crocidura russula*, 598 individuals, 23.5%) and the Algerian mouse (*Mus spretus*, 269 individuals, 10.6%). The two most common rodent species experienced strong population declines during the eight-year period (91% for *A. sylvaticus* and 83% for *M. spretus*). Regional community data obtained from diet studies of small mammal predators showed that common keystone prey and seed dispersers were sampled properly. No differences among trap types regarding community parameters and similarity indexes, sampling efficiency, detectability, trap-induced mortality, mean size and sex-ratio were detected, confirming previous results for a smaller pilot study. The method was sensitive enough for detecting expected population changes. We recommended extending the SEMICE protocol to sample common keystone small mammals along wide Mediterranean environmental gradients, since the method was sensitive enough to detect, and even test, expected population trends associated to global change for all them.

Introduction

Changes in biodiversity due to extinctions and range shifts are the result of anthropogenic global change, such as climate change, habitat loss/fragmentation, pollution, invasive species or the interaction of these factors (Sala et al., 2000; Vitousek, 1994). Monitoring biodiversity change has been increasingly required for two main reasons: the need for systematic evaluation of the performance of conservation policies aimed at stopping biodiversity change (EEA, 2010, 2012; Díaz and Concepción, 2016), and to determine how changes in biodiversity impact ecosystem function and structure (Gilman et al., 2010).

Monitoring requires the development of standardised sampling protocols for target groups based on scientific rigor (e.g. Satterfield et al., 2017; Voříšek et al., 2010). Monitoring considerations include variation in detectability of species within sampled groups depending on the monitoring technique used (e.g. Heisler et al., 2016; Satterfield et al., 2017; van Swaay et al., 2008; Watkins et al., 2010), and the harmful effects of monitoring techniques on individuals and populations when active sampling (i.e. trapping) is needed (Spotswood et al., 2012). Usually, there is no single technique able to sample all species within a group with the same degree of accuracy and safety, so that each technique is in fact focused to a smaller group of target species (e.g. passerines and some small non-passerines when using bird point counts or line transects, or walking insects and small vertebrates when using pitfall traps; Sutherland, 2006). Monitoring protocols should ideally consider spatial and temporal variation to prevent low power to

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detect changes in relevant parameters such as population abundance or species richness (MacKenzie et al., 2005). Therefore, the use of pilot data is highly recommended to estimate detection probabilities of target species with multiple methods and use this information as a basis for selecting a primary sampling method for future studies (Otto and Roloff, 2011).

This paper addresses whether the small mammal monitoring program we established recently in Spain and Andorra (SEguimiento de MIcromamíferos Comunes de España, SEMICE, Torre et al., 2011) fulfil these requirements. The program aims at monitoring common species with high detectability using commercial live traps (i.e., Longworth and Sherman). Using as small pilot study in Iberia, we have demonstrated that both trap types provided similar estimates of community parameters and similarity indexes, sampling efficiency, species detectability, trap-induced mortality, mean body size, and sex-ratio of the most abundant species when deployed simultaneously (Torre et al., 2016). First, we briefly reanalysed among-trap differences with a larger data set covering the environmental variability of the study region to confirm results obtained regarding trap bias (or lack thereoff) with data. This confirmation is essential in Mediterranean regions because diversity is mostly due to a strong spatial turnover (beta diversity) across mosaic landscapes shaped by altitudinal, climatic and land-use gradients, rather than to high local (alpha) diversity (Blondel et al., 2010; Doblas-Miranda et al., 2015). Spatial variability in small mammal communities may exacerbate detection biases associated to trapping (e.g. Heisler et al., 2016; Sibbald et al., 2006).

Diet analyses of generalist small mammal predators can be used to establish the composition of small mammal communities (Torre et al., 2004), as far as the spatial and temporal extent of diet sampling compensates for bias due to predator's variation in foraging behaviour (Embar et al., 2014). Diet of generalist owl and carnivore species have been recently used to analyse small mammal communities in our study area (Torre et al., 2013, 2015a,b). We took advantage of the availability of these data to ascertain to what extent the SEMICE protocol undersampled these communities at regional scales (Torre et al., 2004). This explicit comparison allowed us to define more precisely the list of species properly sampled by the SEMICE protocol.

Finally, we tested the power of the monitoring protocol to detect the population trends of all species properly sampled, in order to evaluate its usefulness to monitor biodiversity change and validate model predictions of how changes in climate and land use may influence biodiversity change (Doblas-Miranda et al., 2015). Range borders of many species lie through the Mediterranean region because of its transitional nature between temperate and tropical regions (Blondel et al., 2010). Population trends rather than dynamic stability, and even range shifts, are to be expected in the near future due to climate and land use changes (Araújo et al., 2011; Torre et al., 2015a).

Material and methods

Field work was carried out within six Natural Parks (Montseny, Montnegre-Corredor, Sant Llorenç del Munt i l'Obac, Serralada de Marina, Collserola, and Garraf) of Barcelona province (Catalonia, NE Spain), located on the eastern side of the Iberian Peninsula (Fig. 1). Woodlands (i.e., pinewoods, holm oak, deciduous and fir forests) represented the main habitats in the region (65%), followed by open natural habitats (shrublands and grasslands, 22%), and with

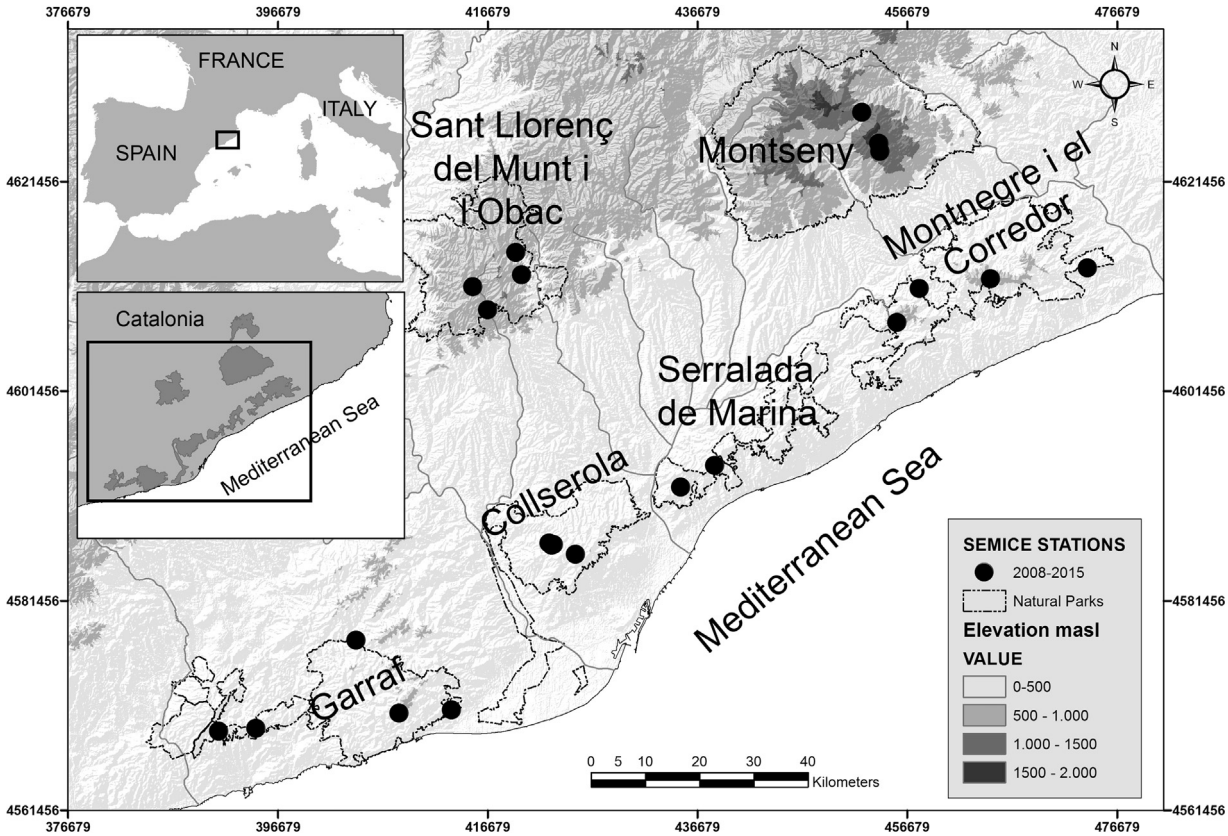

Fig. 1. Map showing the location of the study area and the sampling plots according to elevation. The habitats sampled in every Natural Park were: P.N. Garraf (3 post-fire shrublands-Quercus coccifera, and 2 pinewoods-Pinus halepensis), P.N. Collersola (4 holm-oak/pine mixed woodlands- Quercus ilex/Pinus pinea), P.N. Serralada de Marina (1 holm oak/pine mixed woodland Quercus ilex/Pinus pinea, 1 post-fire shrubland), P.N. Montnegre-Corredor (1 riverbed, 2 holm oak-Quercus ilex, 1 canary oak woodland-Quercus canariensis/Q.ilex), P.N. Montseny (1 shrubland-Juniperus communis, 1 fir forest-Abies alba, 1 poplar with meadows), P.N. Sant Llorenç del Munt i l'Obac (3 holm oak/pine mixed woodland, 1 post-fire shrubland).

Table 1
Number of individuals of small mammal species found in diet analyses of common genets (after Torre et al., 2013) and barn owls (after Torre et al., 1996, 2015b) in the study area, compared with those captured with the SEMICE scheme (this study).

	Common genet scats		Barn owl pellets		SEMICE	
Species	N	%	N	%	N	%
Sorex minutus	22	0.35	43	0,26	–	0.00
Sorex araneus	8	0.13	4	0,02	12	0.47
Neomys anomalus	1	0.02	9	0,05	–	0.00
Crocidura russula	169	2.66	5242	31,44	598	23.31
Suncus etruscus	58	0.91	383	2,30	–	0.00
Talpa europaea	18	0.28	5	0,03	–	0.00
Sciurus vulgaris	50	0.79	–	0,00	–	0.00
Glis glis	24	0.38	–	0,00	–	0.00
Eliomys quercinus	23	0.36	6	0,04	–	0.00
Myodes glareolus	355	5.59	264	1,58	86	3.35
Microtus duodecimcostatus	9	0.14	2145	12,87	–	0.00
Microtus agrestis	24	0.38	87	0,52	–	0.00
Arvicola sapidus	4	0.06	16	0,10	–	0.00
Apodemus flavicollis	1385	21.81	102	0,61	–	0.00
Apodemus sylvaticus	4008	63.12	682	4,09	992	39.02
Apodemus spp.	5393	84.93	4855	29,12	1577	62.04
Rattus rattus	51	0.80	94	0,56	–	0.00
Rattus norvegicus	–	0.00	111	0,67	–	0.00
Mus musculus	15	0.24	230	1,38	–	0.00
Mus spretus	126	1.98	2393	14,35	269	10.49
TOTAL	6350		16671		2542	

a lower proportion of habitats occupied by urban areas (8%) and croplands (4%). Sampling stations were distributed along a wide elevation gradient (95–1502 m a.s.l.) within the two of the three vegetation/climatic domains found in the study area: Mediterranean, Eurosiberian, and Boreo-subalpine (de Bolòs, 1983). Most of the plots were situated on the Mediterranean domain (19/22, 81.8%), and the remaining three on the Eurosiberian domain (Fig. 1).

Sampling was performed from spring 2008 to fall 2015. We surveyed plots (N = 22) during 16 trapping sessions (two sessions per year) following the SEMICE monitoring scheme (Torre et al., 2011, 2016), which was partially inspired in UK monitoring programs (Mallorie and Flowerdew, 1994; Flowerdew et al., 2004). At each site, we used 36 traps arranged in a 6 × 6 trapping grid, consisting of 18 Sherman traps (Sherman folding small animal trap; 23 × 7.5 × 9 cm; Sherman Co., USA) and 18 Longworth traps (Penlon Ltd., Oxford, UK), alternated in position and deployed simultaneously (Cáceres et al., 2011; Nicolas and Colyn, 2006). Traps were placed on the ground spaced 15 m, and were baited with a piece of apple and a mixture of tuna, flour and oil, and insulated by including hydrophobic cotton for bedding (Sikes et al., 2011). Traps were operated during three consecutive nights and revised during the early morning of the first, second and third day. The small mammals caught were identified to species, sexed, marked (rodents with ear tags –National Band Co.USA- and shrews with fur clips, Sikes et al., 2011), and released at the point of capture (Gurnell and Flowerdew, 2006). Research on live animals followed America Society of Mammalogists guidelines (Sikes et al., 2011).

Data analysis

Comparison among trap types.- We compared community parameters (species diversity and similarity), species' abundances and biomass, species' occupancy, detectability, mortality, and sex-related within-species differences between trap type. We used captures/unit effort to estimate population size in each study plot (Hopkins and Kennedy, 2004; Slade and Blair, 2000). Species accumulation curves (Gotelli and Colwell, 2001) were analysed with the EstimateS software (version 9.1.0., Colwell, 2013), and rarefied community parameters (species richness, Shannon diversity, PIE Hulbert's index, and dominance) were obtained with the Ecosim software (Gotelli and Entsminger, 2001). We considered 50 captures as the minimum number to include sampling plots in the analyses, and all community parameters were rarefied to the minimum number of individuals trapped (n = 53). Presence software (Mackenzie, 2012) was used to determine whether estimated occupancy (Ψ) and detection probabilities (p) changed between species and sampling methods. We fitted the same model for all the species with high capture rates: occupancy was left invariable between sampling periods, but with variable probability of detection (Otto and Roloff, 2011; Watkins et al., 2010).

Comparison with community data based on predator diets.- Indirect sampling techniques based on carnivore and raptor diet analyses usually yielded more exhaustive samples of small mammal communities for biodiversity assessments (de la Peña et al., 2003; Heisler et al., 2016). We used for comparison common genet *Genetta genetta* (Torre et al., 2013) and barn owl *Tyto alba* (Torre et al., 1996, 2015b) diet data gathered in more than 90 sites scattered along an altitudinal gradient from 108 to 1166 m a.s.l. (392 ± 265 (SE) m). The final database contained over 23,000 small mammals of 19 species (Table 1). Sampling sites were visited several times during the last decades, and material for each site (pellets or scats) was pooled. We discarded samples were remains of less than 30 individual small mammals were found. Identification of species and estimates of the number of individuals were based on skeletal remains. For detailed information on methods and location of sampling sites see Torre et al. (1996, 2013, 2015b).

Power of trend analyses.– We used TRIM (Trends & Indices for Monitoring data, Pannekoek and van Strien, 2005) for the analysis of time series of counts with missing observations. TRIM uses statistical procedures for estimation and testing that consider serial correlations and overdispersion of count data following a Poisson distribution. Since TRIM uses linear models for the logarithm of expected counts in contingency tables, indices of abundance of the species were Log (X + 1) transformed to avoid error in calculations. Indices with and without transformation showed strong correlations for the three species allowing calculations (r = 0.978–0.999, n = 16, p < 0.001 all). Furthermore, we also assessed the power of pattern detection of the monitoring scheme by means of Monitor software (v. 11.0.0, Gibbs and Ene, 2010). Power was defined as the probability that the monitoring program will detect a trend in sample measurements if a trend is occurring. We used the mean ± SD of the abundance indices obtained in every plot as a starting point to calculate power on an eight years period series conducted in plots with more than one year of monitoring data.

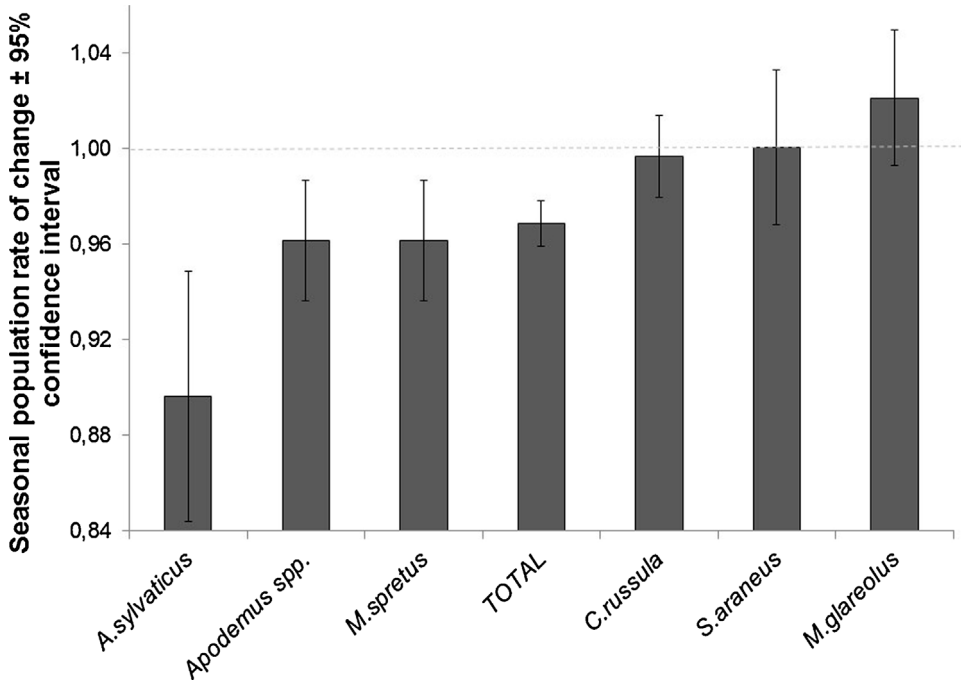

Fig. 2. Seasonal population rate of change (± 95% CI) of the small mammal species trapped (and total) in the study period [2008–2015].

The SEMICE monitoring scheme is based on volunteer collaboration, so that plots varied in sampling duration (mean duration was 10.58 sampling sessions/plot, or five years and a half, with a range of 2–16 sampling sessions/plot, which represented from one to eight years). For some calculations, we only used data on the 17 plots with continuous records.

Accurate separation of *A. flavicollis* from the sympatric and much more abundant *A. sylvaticus* is difficult for live-trapped individuals due to the lack of conspicuous differences in body size and fur colour in Southern European populations (Torre et al., 2015b). Despite a combination of external characters can help to differentiate them in the laboratory (Capdevila, 2013), none of them can be used with total confidence in the field (authors' unpub.data). Both species were found sharing the same habitats in five out of 22 plots (after DNA analyses from a sample of 104 individuals, authors' unpub.data). We considered as *A. sylvaticus* the individuals trapped in the 17 plots were no *A. flavicollis* was detected. Individuals caught in the 5 plots with *A. flavicollis*, as well as the whole sample, were labelled as *Apodemus* spp. for comparative analyses.

Results

We captured a total of 2542 small mammals (3756 including recaptures) of six species (Table 1, Appendix S1 in Supplementary material) in the sixteen sampling occasions corresponding to 18,252 trap-nights (13.92% total trapping success, range per sampling session 7.96-36.40%). Total estimated species richness (Chao1 estimator) was 6.0 ± 0.0 (SD) species, and observed and estimated species curves converged. The Clench equation adjusted to the species accumulation curve fitted well ($r^2 = 0.89$), and the slope of 0.003 showed the proximity to an asymptote. Asymptotic species richness was 6.08, so 98.7% of the small mammal species would have been recorded during the present inventory. There were no differences among trap types regarding community parameters and similarity indexes, sampling efficiency, detectability, trap-induced mortality, mean weight or sex-ratio (Appendix S1 in Supplementary material).

Wood mice (*Apodemus* spp.) were dominant throughout the study period, most of them being *A. sylvaticus*, followed by the white-toothed shrew and the Algerian mouse (Table 1). The remaining species (*Sorex araneus* and *Myodes glareolus*) were trapped at frequencies lower than 10%. The number of individuals belonging to the species captured in the present study represented 95% of those found in common genet *Genetta genetta* scats (Torre et al., 2013) and 76% of those found in barn owl *Tyto alba* pellets (Torre et al., 1996, 2015b) in the same study area.

Site Occupancy Analysis (SOA) was performed with the four species more frequent and widely distributed (*S. araneus* was not analysed because of restricted range, see below). *M. spretus* showed the highest mean detectability (0.88 ± 0.03 SE, range 0.67–1, median = 1), followed by *C. russula* (0.77 ± 0.03, range 0.55–1, median = 0.79), *A. sylvaticus* (0.70 ± 0.07, range 0.31–1, median = 0.69), and *M. glareolus* (0.54 ± 0.08, range 0–1, median = 0.50). Overall, wood mice (*Apodemus* spp.) also showed high detectability (0.84 ± 0.08, range 0.38–1, median = 0.91). Nonetheless, differences in detectability did not affect occupancy estimates (Ψ), that were the same than the observed (naïve) values for all the species. Mean density indexes of abundance were correlated with detectability through the sampling sessions in the most abundant species: *A. sylvaticus* ($r = 0.65$, $P = 0.01$, n = 16 for all comparisons) and *C. russula* ($r = 0.64$, $P = 0.007$), except for *M. glareolus* ($r = 0.42$, $P = 0.10$) and *M. spretus* ($r = 0.03$, $P = 0.86$).

The analyses of population trends showed that *A. sylvaticus* experienced a steep decline during the study period (-10.36% seasonal rate of change, $P < 0.05$), followed by *M. spretus*, −3.82%, $P < 0.01$, Fig. 2), two species showed stable trends (*S. araneus*, and *C. russula*), and one species showed an uncertain trend (*M. glareolus*). As a whole, total small mammal abundance also showed a significant decline (-3.13%, $P < 0.01$), as well as wood mice (*Apodemus* spp., −3.84%, $P < 0.01$). Population declines during the eight-year period represented a 91% population loss for *A. sylvaticus*, 83% for *M. spretus*, and 31% for total small mammals. Power analyses evidenced that the temporal series analysed would yield power for detecting trends of ± 2% rate of change during a ten years' period in *Apodemus* spp., but was only powerful for detecting increase patterns (+4%) in *M. spretus* populations. Small mammal captures were positively associated among sampling periods in the habitats sampled for the most common species: *A. sylvaticus* (mean $r = 0.99$, $P < 0.001$,

n = 3 possible pair-wise correlations of habitats where the species was exclusively present (without *A. flavicollis*, 3 habitats), *M. spretus* (mean $r = 0.76$, $P < 0.01$, n = 6 possible pair-wise correlations of habitats where the species was present, 4 habitats), but not for *C. russula* (mean $r = 0.25$, $P > 0.05$, n = 10 possible pair-wise correlations of habitats where the species was present). In the latter case, *C. russula* populations were positively associated among sampling periods in xerophilous habitats (holm oak, shrublands, pinewoods: mean $r = 0.75$, n = 3) and deciduous forests (oak forest and riverbed: $r = 0.41$), but showed negative or no association in the remainder habitat combinations.

Discussion

Results of the SEMICE monitoring program for small mammals (Torre et al., 2011, 2016) were not biased by trap methods (Appendix S1 in Supplementary material), that were in fact a combination of the two trap types most commonly used to sample small mammals (Torre et al., 2016). It detected accurately the five species comprising the bulk of small mammal communities present in the study area and, despite the short time-series analysed [2008–2015], it was sensitive enough for detecting small mammal population changes. Hence, the protocol can be extended to monitor small mammal populations and communities at larger spatial and temporal scales (Doblas-Miranda et al., 2015).

There is still little information available on how detection probabilities of common European small mammal species can be affected by using different sampling methods (i.e. Torre et al., 2016; van Strien et al., 2015). All species analysed (common species widely distributed in the area) showed mean values of detectability well above the threshold potentially affecting occupancy assessments (observed values of p ranging from 0.54 to 0.88, higher than $p = 0.3$; Mackenzie et al., 2002). So, differences in detectability hardly affected estimates of occupancy for the common small mammal species analysed.

Two small mammal species were not analysed due to difficulties in species determination (*A. flavicollis*) or to rarity (*S. araneus*). Both *Apodemus* species were found sharing the same habitats in five out of 22 plots, and it seems probable that inaccurate species identification resulted in underestimation of the distribution and abundance of *A. flavicollis* in these plots. Conversely, an overestimation of *A. sylvaticus* would have arisen in the same shared plots. *A. flavicollis* represented 26% of *Apodemus* spp. in woodland small mammal communities of the study area based on genet scat analyses (Torre et al., 2013), but this proportion was undetermined in the present study. Molecular methods (although still expensive) could be routinely incorporated to confirm species identities, or other identification techniques could be developed if feasible, like samples of hair for microscopic examination and/or records of calls (Ancillotto et al., 2016). Regarding *S. araneus*, a species of conservation concern (Harris and Yalden, 2004), it showed lower capture rates in Sherman (25%) than in Longworth traps (75%), suggesting a lower detectability when using Sherman traps (Torre et al., 2016). Nonetheless, results did not extend to other shrews, so that claims by other authors on the highest efficiency of Longworth traps for caching shrews (Anthony et al., 2005; Jung, 2016) were not supported.

Fourteen species that were present in the study areas according to data on generalist predator's diets were not trapped at all (Table 1). Two species not detected during the present study were captured on the two mountain-top plots (1480–1502 m a.s.l.) in the period 1995–1997 (unpub. data). The absence of these species can be mostly due to stochastic processes associated to low abundance and/or detectability by the sampling methods, but also the effects of environmental change cannot be completely ruled out (both are predicted to retreat due to its climatic associations; Torre et al., 2015a). The remaining 12 species were also rare in predator's diets (frequencies <1%). In addition, some were also unlikely to be trapped because of specialist microhabitat selection. Commensal species such as *Mus musculus* or *Rattus* spp., fossorial species such as *Talpa europea* or *Microtus doudecimcostatus*, arboreal mammals such as *Sciurus vulgaris* or *Glis glis*, or aquatic species such as *Neomys anomalus* or *Arvicola sapidus* are seldom trapped unless traps are set in specific locations, whereas predators may detect and consume them thanks to their larger home ranges and generalist foraging behaviour (Heisler et al., 2016; Torre et al., 2004). Anyway, any monitoring scheme for small mammals is biased by several methodological factors. It has been proposed that schemes based on keystone and/or target species easy to monitor can be used as surrogates for ecosystem functioning (Solari et al., 2002), and population changes of common species can be measured with greater precision than those of rare species (Battersby and Greenwood, 2004). Regardless of sampling a reduced number of species, we were confident that the species monitored in this study were amongst the most relevant small mammals actors in Mediterranean ecosystems functioning as both keystone prey and seed dispersers (e.g. Carvalho and Gomes, 2004; Morán-López et al., 2016a,b; Torre et al., 2013, 2015a,b). Whether changes in the abundances of these species would be good surrogates of the changes in the abundances of the other rarer small mammals present in the area cannot be tested properly with the data available. Nevertheless, this was not the goal of the study nor the goal of the SEMICE protocol. In fact, absence of most species in SEMICE plots might be due to specialist microhabitat selection of restricted habitats that should be monitored specifically.

Seasonal trapping success was on average lower than 15% (range 8–36%), suggesting that no competition for traps was present, even in periods of higher small mammal abundance. These results justified the use of low-density (one trap per point) small grids (36 traps) operative for short surveys (three days) as a simple way of monitoring small mammal populations in the Mediterranean area. Some authors recommended higher trap densities and/or longer surveys (Conard et al., 2008; Sibbald et al., 2006) to improve precision and stability of the estimates. In our case, the lower sampling effort performed within surveys could be compensated with increased precision and stability as far as surveys are repeated in time (i.e. for eight consecutive years). Further, this sampling design was powerful enough to detect significant abundance trends of two out of the six species detected even with a still short (8 years) monitoring period. Finally, mortality at traps was lower than the average reported (Shonfield et al., 2013) even for shrews. Low overall mortality rates (6%) during this study evidenced that night revisions of traps could be avoided in mild climates without resulting in high mortality when compared to harsher climates (6.2% in Andorra, Pyrenees, with night revisions, Torre et al., 2016; 10.8% in Yukon, without night revisions, Jung, 2016). This will help establishing methodologies for monitoring schemes aimed at reducing economic costs, but also at reducing risky situations when volunteers are involved. Overall, these results validated the method proposed for small mammal monitoring in Spain and Andorra (SEMICE, Torre et al., 2011, 2016).

A. sylvaticus and *M. spretus* showed strong population declines during the study period, larger than the amber and red levels of decline established for birds and small mammals (Harris and Yalden, 2004; Sibbald et al., 2006). Calculating power detection of population trends can be considered as a priority when establishing monitoring protocols for small mammals (Flowerdew, 2004; Sibbald et al., 2006). Simulations of power detection showed symmetrical responses in *A. sylvaticus* (±2% power within an eight years' period), but asymmetrical responses in *M. spretus*, this latter situation resulting in high power to detect increasing patterns

(+4%), but no power at all to detect decreasing patterns (Gibbs and Ene, 2010). Despite some decreasing patterns could be undetected due to low power, monitoring with low power is often better than no monitoring at all (Harris and Yalden, 2004).

Summarizing, our results suggested that a combination of commercial live-traps in small grid arrays (36 sampling stations) was enough for detecting common small mammal species and their population trends. In the study area, some monitoring schemes were established long time ago (i.e., in the 90 s of the past century, Stefanescu et al., 2011) for a number of focal groups (i.e. birds, butterflies, and wild boar), and potential synergies will surely emerge when combining different bioindicators groups (Doblas-Miranda et al., 2015; Herrando et al., 2016).

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at https://doi.org/10.1016/j.mambio.2017.10.009.

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