

Using barn owl *Tyto alba* pellet analyses to monitor the distribution patterns of the yellow-necked mouse (*Apodemus flavicollis* Melchior 1834) in a transitional Mediterranean mountain

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Abstract. In this study we aimed to investigate the utility of the barn owl diet as a tool for determining the spatial distribution and abundance of the yellow-necked mouse, a forest-dwelling small mammal species, in the Montseny mountains and surrounding plains (Barcelona, NE Spain). After validating the molar shape criterion for species discrimination (t9 of second upper molar), we classified a sample of 2,684 *Apodemus* spp. identified from 8,831 small mammals of 17 species from barn owl pellets collected in 18 roosting places. Almost all individuals were determined as *A. sylvaticus* (91.8%) and the remainder were considered as *A. flavicollis* (8.2%). Frequencies of occurrence of *A. flavicollis* were related to 11 environmental descriptors by means of Redundancy Analysis and partial constrained ordination. Frequencies of occurrence changed along a strong environmental gradient (increased towards rainy localities covered by deciduous forests), and this pattern coincided with the observed for other forest predator (*Genetta genetta*). The use of non-invasive sampling methods, like the barn owl diet analysis, can be more efficient in detecting the presence of the yellow-necked mouse than other conventional sampling methods, since accurate species determination of the binomial *A. sylvaticus*/*A. flavicollis* is difficult after live-trapping in NE Spain.

Key words: *Apodemus flavicollis*, discriminant criteria, electrophoresis, environmental predictors, molar shape.

The yellow-necked mouse (*A. flavicollis*) is a forest-dwelling species with mid-European requirements that can be considered as dominant in small mammal communities of central Europe (Niedzialkowska et al. 2010; Suchomel et al. 2014). Nonetheless, this species becomes increasingly scarce as far as it reaches the limit of its distribution area in Southern Europe. In Catalonia (NE Spain), *A. flavicollis* inhabits deciduous forests but also Mediterranean humid forests (Torre et al. 2009), reaching in this area the southernmost limit of its distribution range in Spain (Arrizabalaga and Torre 2007). It has been suggested that the yellow-necked mouse will face important retractions of the potential distribution range due to climate change during this century (Araújo et al. 2011). Expected changes in the distribution ranges will affect structure of assemblages especially in transitional areas between biogeographic Regions (e.g., Mediterranean-Eurosiberian), where small mammal communities will be affected by reorganization processes caused by range

shifts and extinctions (Moritz et al. 2008). Therefore, it seems necessary obtaining accurate data on present small mammal species distribution to understand what will happen with species ranges in the near future in the face of different threats like climate change (Torre et al. 2013).

Monitoring changes in the distribution and abundance of the yellow-necked mouse can be challenging, however. Accurate separation from the sympatric and much more abundant *A. sylvaticus* from live-trapped individuals is almost impossible unless expensive molecular methods are routinely incorporated to live-trapping schemes, due to the lack of conspicuous differences in body size and fur colour in Southern Europe (Filippucci et al. 1989; Arrizabalaga and Torre 2007). Identification of prey remains in owl pellets or carnivore scats may be more promising, since specific discrimination of sibling *Apodemus* can be reached by examining teeth morphology (Libois et al. 1993; Panzironi et al. 1993). Using

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this method, Torre et al. (2013) were able to analyze the environmental factors associated to the patterns of distribution and abundance of the yellow-necked mouse in NE Spain on the basis of analyses of the scats of a generalist forest predator, the genet (*Genetta genetta*). Carnivore scats are however hard to find out, and difficult to analyze due to the highly fragmented state of skeletal remains (Torre et al. 2004, 2013). Barn owl (*Tyto alba*) pellets are much more abundant and easier to detect and analyze. Besides, fidelity to nesting and roosting sites and general knowledge on the size of foraging territories and opportunistic character of barn owl diets makes barn owl pellets an ideal method for monitoring small mammal responses to global change (Torre et al. in press). Two critical points are to be demonstrated before using this method routinely for yellow-necked mice in the study area: a) whether accurate methods of separation from sympatric *Apodemus* spp. on the basis of skeletal remains exists and b) whether the preference of barn owls for open habitats while foraging may bias estimates of abundance from forest-dwelling species such as the yellow-necked mouse (Torre et al. 2004).

In this study we aimed to address both points. First, we determined the simplest and reliable method for species

separation in our study area. In order to do so, a sample of *Apodemus* spp. was submitted to protein electrophoresis; once individuals were assigned specifically to both sibling species, tooth morphology was examined to validate the molar shape criteria (Filippucci et al. 1989; Libois et al. 1993). Second, we ascertained whether the distribution pattern derived from analyses of barn owl pellets were correlated with patterns resulting from analyses of genet scats (Torre et al. 2013; Torre et al. in press). Close associations will indicate that barn owl diets will sample the distribution of forest-dwelling mice as accurately as generalist forest predators, hence supporting the utility of barn owl pellets for monitoring distribution changes of this interesting species at the trailing edge of its distribution range.

Materials and methods

Study area

The study area is about 700 km² in size and is situated between the provinces of Barcelona and Girona (Catalonia, NE Spain; Fig. 1), being almost delimited by the Montseny Natural Park and Biosfere Reserve, and its surrounding plains. The area shows strong spatial

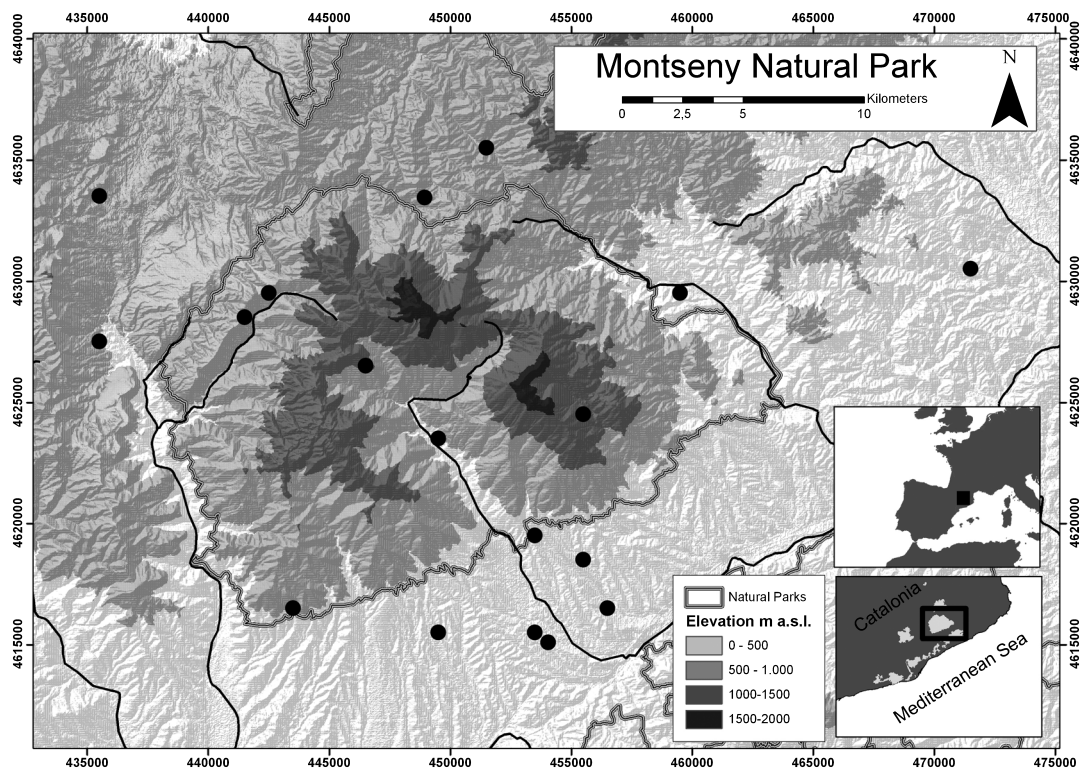


Fig. 1. Spatial distribution of the 18 barn owl roosts (black dots) sampled to determine the frequency of occurrence of *A. flavicollis* along a strong environmental gradient in the Montseny mountains and surrounding plains (Catalonia, NE Spain).

variation in climate, elevation, and landscape composition. Coastal mountain ranges influence rainfall and temperature patterns at close spatial scales, and the Montseny mountain range (1,714 m a.s.l.) allows the presence of well-established Mid-European plant (de Bolòs 1983) and animal (Terradas and Miralles 1986) communities within Mediterranean areas. Lowlands are mainly occupied by crops and villages, whereas the mountains are covered by forests (both deciduous and evergreen). The Montseny area has experienced a strong process of climate and landscape change during the last 50 years (increased temperatures, Peñuelas and Boada 2003), with an increase of the forest cover (from 76.5% to 85.3%) and urban areas, and a decrease of crops and shrublands (Vicente et al. 2014).

Small mammal sampling

During September of 1996 we sampled three different localities situated at 1,100 m a.s.l. within the Montseny Natural Park by means of standard live-trapping procedures. We placed three lines of 50 Sherman traps—that were exposed for a single night—in deciduous forests within beech (*Fagus sylvatica*) and broad-leafed oaks (*Quercus petraea*) forest communities. Other species but wood mice (*Apodemus* spp.) were immediately released at the point of capture, while the target individuals were transported to the laboratory to undertake an electrophoresis analysis of proteins (Filippucci et al. 1989).

We used the diet of the barn owl as a general source of small mammal distribution in the study area, provided that previous studies performed in that area using the same method confirmed its efficiency (Torre et al. 1996, 2004). The pellets produced by barn owls accurately reflect changes in its diet and, at the same time, they would reflect changes in prey availability, owing to the generalist predator behaviour of the owl (Tores et al. 2005; Meek et al. 2012). The diet of the barn owl can be applied to the study of the small mammal's distribution and abundance due to the widely accepted generalist-opportunistic hunting behaviour of this raptor. Evidence of this has been recorded based on functional responses of the barn owl against changes in small mammalian prey along the distribution range of the predator (e.g., dietary shifts, breeding performance, Tores et al. 2005; Bernard et al. 2010). However, this is the first time in which the spatial distribution of the yellow-necked mouse is analysed using barn owl dietary studies in the area. Arrizabalaga et al. (1999) were the first authors to identify and quantify the presence of the yellow-necked

mouse in natural communities of the Montseny Natural Park. In all studies undertaken previously to that date the presence of *A. flavicollis* was overlooked, since there was the belief that only *A. sylvaticus* was present in Catalonia (Gosàlbez 1987).

We analysed 8,831 small mammals of 17 species from pellets collected in 18 roosting places between years 1978 and 2012. We collected large and heterogeneous samples (490 small mammals on average) in order to compensate for the effects of temporal variations in small mammal abundance and, consequently, on local owl diets (Torre et al. 1996, 2004). The roosts were located along a strong environmental gradient in a transitional area between Mediterranean and Eurosiberian communities, with an average elevation of 529 m a.s.l. (range 180–1,140 m).

In order to compare frequencies of occurrence of *A. flavicollis* in the barn owl's diet and in the diet of the genet we reviewed the literature about the diet of the genet in the study area, selecting a total of 26 latrines analysed within the Montseny Natural Park (Arrizabalaga et al. 2002; Torre et al. 2004, 2013). We used a conservative approach, only selecting latrines with more than 30 small mammal individuals (Torre et al. 2013).

Apodemus species determination

Wood mice individuals were taken to the laboratory after live-trapped and were sacrificed by using standard euthanasia procedures (Sikes et al. 2011). Tissues of each specimen were preserved in the laboratory at -80°C until processed. Homogenates for electrophoresis were obtained from portions of kidney tissue crushed in distilled water. Genic variation of structural genes encoding for enzymatic proteins was assessed using standard horizontal gel electrophoresis (Filippucci et al. 1989), following the procedures described by Pasteur et al. (1987). Homogenates obtained from kidney were processed for the following enzymatic proteins: isocitrate dehydrogenase (IDH), malic enzyme (ME), 6-phosphogluconate dehydrogenase (6-PGDH1 and PGDH2), α -glycerophosphate dehydrogenase (α -GPDH), lactate dehydrogenase (LDH1 and LDH2), and phosphoglucomutase (PGM). Only eight loci were analysed according to previous experience on *Apodemus* species discrimination by our team (F. Catzefflis, F. Renaud, and F. Santalla, personal communication).

Since some barn owl roosts were collected and analysed previously to the date in which *A. flavicollis* was first identified (see above), we reviewed 2,684 cranial remains of *Apodemus* spp. held in the Granollers Museum

of Natural sciences for correct species identification. The upper mandibles were set on a plasticine support and observed under the microscope. Identification was performed after the morphological differences in the shape of molar tubercles (t) between both congeneric species: in particular, the presence of a well developed t7- clearly differentiated from the t4 on the first molar (*A. flavicollis*), or both tubercles joined (*A. sylvaticus*), and the presence (*A. sylvaticus*) or absence (*A. flavicollis*) of the t9 in the second upper molar (Filippucci et al. 1989; Libois et al. 1993; Panzironi et al. 1993; Marchand and Denys 2003).

In order to test for the reliability of the molar shape identification criteria, results from the unequivocal electrophoretic analysis were crossed to the results obtained with cranial inspection using a blind trial (e.g., without knowing the specific identity of individuals analysed). Chi² tests with randomization (Gotelli and Entsminger 2001) were used to compare frequencies of occurrence of molar characters (presence/absence of t9; presence/absence of t7) and allelic frequencies.

Environmental data and statistical analyses

The home range of the barn owl varies from 2 to 7 km² and it is frequently assumed that a radius of 3 km around resting/breeding sites is sufficient to characterize barn owl's habitat (Martínez and Zuberogoitia 2004; Bond et al. 2005; Szpunar et al. 2008). This area represents the hunting territory of the raptor, where the great majority of nesting and roosting activity takes place (Szpunar et al. 2008). A similar approach was used for genet latrines, but considering an area of 9 km² around every latrine (Torre et al. 2013). Environmental information of every locality was taken from land use information after the "Land use classification of Catalonia 2002" (Generalitat de Catalunya, Departament de Territori i Sostenibilitat: (<http://www20.gencat.cat/portal/site/territori>), and averaged from 5 × 5 km square UTM units centred in that locality (Requejo 2011).

A species accumulation curve was used to estimate actual species richness of the small mammal species detected by barn owls (Gotelli and Colwell 2001). The expected richness function was calculated with EstimateS (Colwell 2013), after 50 randomizations (default option) of the observed number of species as far as samples accumulated. To ascertain the completeness of the inventory we used the Clench equation, fitting the function provided by EstimateS using the non-linear estimation module of Statistica v7.0 (Stat Soft Inc.), following the procedure outlined by Jiménez-Valverde and Hortal (2003).

A species matrix was constructed with relative species abundances for every barn owl roost. A Detrended Correspondence Analysis (DCA) was performed with the species abundance matrix in order to test for the heterogeneity of small mammal communities found in its diet. Short gradient lengths, as was the case, indicated a low degree of species turnover (low beta diversity) in community composition, so linear ordination techniques were applied in the following step (Leps and Smilauer 2003). We used Redundancy analysis (RDA) with constrained ordination to assess whether changes in the frequency of occurrence of *A. flavicollis* among barn owl roosts were explained by a matrix of environmental variables. We included a set of representative environmental variables related to topography and climate (five descriptors), and land-use (six descriptors). We followed the approach outlined by Borcard et al. (1992), using partial constrained ordination (Leps and Smilauer 2003) in order to have an estimate of the variance explained by the geo-climatic and the land use descriptors, and the variance shared by both, on the yellow-necked mouse frequencies. Two partial constrained ordinations were performed (1) to remove the influence of the land use effects on the geo-climatic effects on the species abundance, and (2) conversely, to remove the influence of geo-climatic variables on land use on the species abundance. Both analyses yielded the pure geo-climatic and land use effects on the species abundance matrix.

Analysis of covariance (ANCOVA) with the separate slopes model was used in order to compare the regression slopes of the frequencies of occurrence of *A. flavicollis* along elevation by both predators.

Results

Discriminant criteria for A. sylvaticus/A. flavicollis

Twenty-nine wood mice (*Apodemus* spp.) were live-captured and were conducted to the laboratory for the genetic analysis. Five out of eight loci (IDH, ME1, 6-PDG1, 6-PDG2 and LDH2) were genetically interpretable after the electrophoresis analysis. These five loci showed alleles of different electrophoretic mobility (named as "a" and "b") for both of the studied taxa (*A. sylvaticus* and *A. flavicollis*, Table 1). According to this analysis, 23 individuals were assigned to *A. sylvaticus*, and the remainder six to *A. flavicollis*. The shape of the tubercles of first and second upper molars of the 29 individuals were examined under the microscope, confirming that 23 showed a developed t9 in M2 and six did not show

Table 1. Alleles showing different electrophoretic mobility (named as “a” and “b”) in five discriminant loci from 29 *Apodemus* spp. submitted to protein electrophoresis analysis, and classification of the same individuals according to the molar shape criteria (tubercles t7 of molar 1 and t9 of molar 2)

CRITERIA	Protein electrophoresis analysis					Molar morphology	
	IDH (allele a/b)	ME1 (allele a/b)	6-PDG1 (allele a/b)	6-PDG2 (allele a/b)	LDH2 (allele a/b)	t7 (M1) (yes/no)	t9 (M2) (yes/no)
<i>A. sylvaticus</i>	22/0	23/0	23/0	23/0	23/0	1/22	23/0
<i>A. flavicollis</i>	0/6	0/6	0/6	0/6	0/6	4/2	0/6

it, whereas only four individuals showed an isolated t7 in M1 (Table 1). After tooth examination, data were crossed with electrophoretic results, and the t9 criterion completely coincided (100% of individuals compared) with the enzymatic protein analysis. A Chi² test with randomization confirmed that frequencies of occurrence of *Apodemus* individuals among the two discriminant methods were identical (*Observed index* = 0, $P = 1$, $n = 1000$ randomizations). Nonetheless, the t7 criterion was not so discriminant, since 96.7% of *A. sylvaticus* and 72.3% of *A. flavicollis* matched with the electrophoretic analysis.

Barn owl diet analysis and determination of A. flavicollis from cranial remains

According to the coincidence between genetic and morphologic discriminant criteria, we used the t9 criterion to analyse a sample of 2,684 *Apodemus* spp. identified in the 18 barn owl roosts. The t4–t7 criterion was also used to give support, especially when t9 criterion failed due to molar erosion. Almost all (91.8%) individuals were determined as *A. sylvaticus* and the remainder 8.2% were considered as *A. flavicollis*.

Considering the whole sample analysed ($n = 8,831$ small mammals), the most commonly preyed species was the Algerian mouse (*Mus spretus*, 27.9%), closely followed by the wood mouse (27.9%), and the white-toothed shrew (*Crocidura russula*, 25.9%). On the other hand, when considering the average frequency of occurrence per locality, the most preyed species was *A. sylvaticus* (37.4%), followed by *C. russula* (20.5%) and *M. spretus* (18.9%). *Apodemus flavicollis* represented only the 2.5% of all the small mammals identified, being the sixth species more preyed by barn owls, in order of importance. The yellow-necked mouse was present in the 61.0% of the localities sampled in the Montseny and surrounding plains (11 out of 18 localities), with a mean frequency of occurrence per locality of $5.3\% \pm 8.8$ SD (range 0–34.0%).

The species accumulation curve showed an asymptotic

pattern, suggesting that barn owls preyed on almost all the small mammals' species available. The Clench equation fitted very well to the species accumulation curve ($r^2 = 0.986$), and the expected asymptotic species richness was 17.82, so the 95.4% of the species actually present were detected by the barn owls.

Environmental analysis

The localities studied were mainly covered by forests (mean = $75.5 \pm 19.7\%$ SD, range 28.5–92.2%), with a reduced fraction devoted to crops (mean = $13.4 \pm 14.6\%$ SD, range 0.9–57.3%), and urban habitats (mean = $3.6 \pm 3.4\%$ SD, range 0.0–7.2%). As a whole, natural environments (forests and shrublands) accounted for more than 80% of the mean area covered in the 18 localities (mean = $83.0 \pm 17.2\%$ SD, range 33.0–99.1%).

The first redundancy analysis (RDA) with the frequency of occurrence of *A. flavicollis* constrained by the matrix of five geo-climatic descriptors achieved a significant level after the Monte Carlo permutations test (F -ratio = 6.82, $P = 0.02$ for the first and all other axes extracted; variance explained: 87.2%, Table 2). The only variable significantly affecting its frequency of occurrence was rainfall (77.0% of variance, $P = 0.002$). The first axis extracted was positively related to rainfall, elevation, and latitude, and inversely related to temperature. The second axis was negatively related to longitude. The frequency of occurrence of *A. flavicollis* increased along axis 1 and decreased along axis 2 (Fig. 2a). The second redundancy analysis (RDA) with the frequency of occurrence of *A. flavicollis* constrained by the matrix of six land-use descriptors achieved a significant level after the Monte Carlo permutations test (F -ratio = 12.26, $P = 0.01$ for the first and all other axes extracted; variance explained: 94.8%). Two variables significantly affected its frequency of occurrence: crops (82.0% of variance, $P = 0.002$), and esclerophyllous forests (11.0% of variance, $P = 0.04$). The first axis extracted was positively related to deciduous forests, and inversely related to crops and

Table 2. Results of the two RDA performed with the frequencies of occurrence of *A. flavicollis* constrained by the geo-climatic (5) and land-use (6) predictors

Redundancy Analyses (RDA)	Predictors	Code	F-ratio	P-level	Variance (%)
Constrained Ordination with geoclimatic predictors	Rainfall	RAIN	29.78	0.002	77
	Temperature	TEM	2.36	0.17	6
	Longitude	LON	1.11	0.32	3
	Latitude	LAT	0.42	0.51	1
	Altitude	ALT	0.14	0.73	0
	TOTAL		6.82	0.02	87.2
Constrained Ordination with land-use predictors	Crops	CROP	21.12	0.006	70
	Esclerophyllous forests	ESCF	7.07	0.04	11
	Deciduous forests	DECF	2.91	0.1	8
	Urban	URB	2.79	0.13	3
	Shrublands	SHRUB	2.01	0.18	2
	Coniferous forests	CONF	0.12	0.78	0
	TOTAL		12.26	0.01	94.8

The influence of predictors was tested by a forward stepwise selection procedure after Montecarlo permutation tests ($n = 499$). Significant values ($P < 0.05$) were marked in bold.

urban areas. The second axis was negatively related to esclerophyllous forests, and inversely related to crops and deciduous forests. The frequency of occurrence of *A. flavicollis* increased along both environmental axes (Fig. 2b). The two partial constrained ordinations performed allowed to determine the pure geo-climatic (28.0%) and the pure land-use (22.7%) effects on the yellow-necked mouse abundance. The shared variance between both environmental matrices was very high (59.2%), without unexplained variance. As a whole, the geo-climatic and land-use variables explained 100% of the variance on the species abundance along the strong environmental gradient analyzed.

The ANCOVA showed that elevation was a highly significant predictor for *A. flavicollis* considering both predators altogether ($r^2 = 0.75$, $F_{3,35} = 39.3$, $P < 0.0001$), and the lack of interaction suggested that frequencies of occurrence along elevation showed a similar pattern for both predators (interaction elevation \times predator: $F_{1,35} = 0.02$, $P = 0.88$; Fig. 3). This analysis also evidenced that frequencies of occurrence were higher in genets than in barn owls for the same elevation.

Discussion

In this study we validated the molar tubercle 9 (t9) criterion (with a secondary support of the t4–t7 criterion) for specific discrimination of the pair of sibling species *A. sylvaticus*/*A. flavicollis* in the Montseny mountains and surrounding plains (see also Filippucci et al. 1989; Libois

et al. 1993; Panzironi et al. 1993; Marchand and Denys 2003). This criterion can be considered useful when spatial distribution of both species is analysed by means of indirect sampling methods (e.g., diet of predators). Despite the reduced sample size, the 29 *Apodemus* spp. analysed by protein electrophoresis completely coincided with the discriminant criterion based on the shape of the t9 of the second upper molar. In our case, five loci were enough to differentiate the two species, and similar results were obtained by Panzironi et al. (1993). However, Libois et al. (1993) suggested that some *A. sylvaticus* populations can have the t9 reduced in size, so using only this criterion can be inconclusive for correct species determination. In fact, a well developed t9 was present in the 12% of *A. flavicollis* and in the 91% of *A. sylvaticus* from Italian populations (Filippucci et al. 1989). In our case, the complete coincidence of both criteria (electrophoresis and t9) in all the individuals compared allowed using this discriminant method, at least in our study area. In cases of t9 erosion, we used the t4–t7 criterion that was highly confident for *A. sylvaticus* (96.7% of individuals correctly identified).

We have shown that the frequency of occurrence of a scarce forest-dwelling species (*A. flavicollis*) in the diet of the barn owl responded to a strong environmental gradient in a transitional area between the Mediterranean and the Eurosiberian regions. Dietary studies about the barn owl have been performed around the globe from the early 20th century (Errington 1930) to our days, most of them dealing about the utility of the diet as a source of informa-

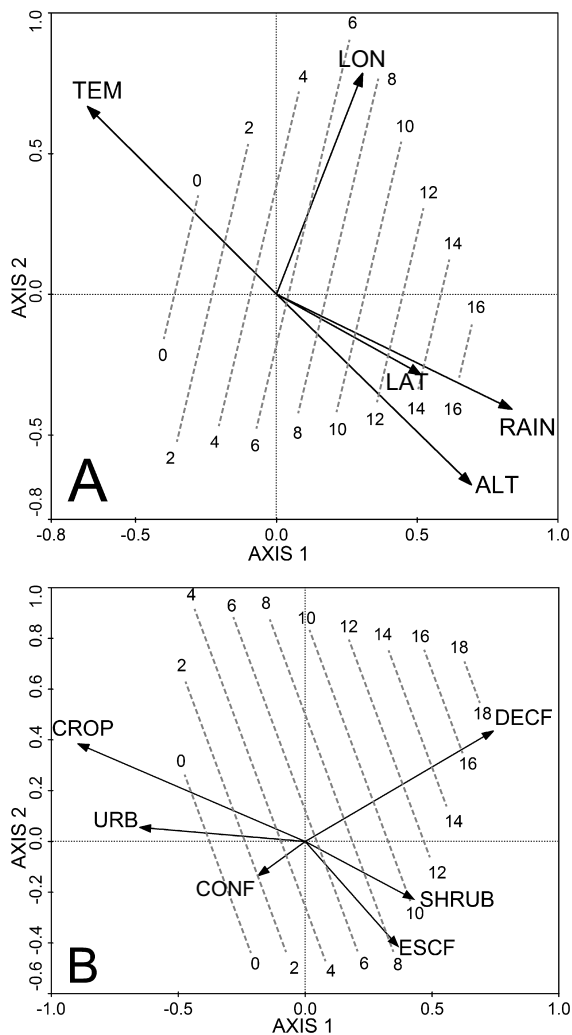


Fig. 2. Responses of the frequency of occurrence (%) per locality of *A. flavicollis* in the barn owl diet to environmental variables in the Montseny mountains. Frequency isoclines were fitted with Generalized Linear Models using the first two axes extracted in RDA as predictors. (A, geoclimatic predictors: $F = 6.08$, $df = 15$, $P = 0.011$; B, land-use predictors: $F = 5.38$, $df = 15$, $P = 0.017$). Predictor codes as in Table 2.

tion on the distribution of the small mammals in agricultural environments related to different farming practices (de la Peña et al. 2003; Gonzalez Fischer et al. 2012). However, misinterpretation of patterns (e.g., distribution and occurrence) for forest-dwelling small mammals in the owl's diet can be expected due to the opposite habitat preferences of both predator and preys. Barn owls are mainly open habitat predators in Western Europe (Love et al. 2000), and their diet is mostly based on open habitat species like the field vole and the common vole (Love et al. 2000; Rodríguez and Peris 2007; Bernard et al. 2010; Meek et al. 2012). So, diet analyses may well underestimate the occurrence of the small mammal fauna from

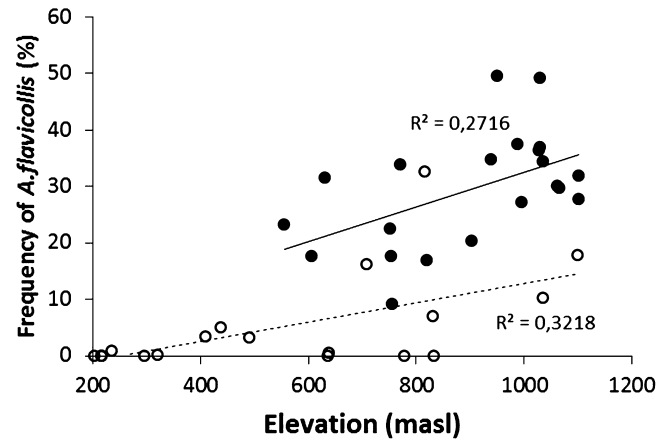


Fig. 3. Frequency of occurrence of *A. flavicollis* in the barn owl (open circles, dashed line) and genet (black dots, solid line) diets along an elevation gradient in the Montseny mountains. Both regression lines are significant (both $P < 0.05$), and the slopes are not significantly different (ANCOVA: interaction Predator \times Elevation, $F_{1,35} = 0.02$, $P = 0.88$).

forest habitats and overestimate the fauna living in open habitats (Torre et al. 2004). Nonetheless, the barn owl preys on a regular basis on forest-dwelling species, like the bank vole (*Myodes glareolus*) and the yellow-necked mouse, but the frequencies of occurrence of these species in the diet are relatively small (Alegre et al. 1989; Love et al. 2000; Bernard et al. 2010). Some authors have claimed about the inconvenience of inferring the spatial distribution of rare species after barn owl dietary studies (Rodríguez and Peris 2007), and this can be especially challenging for forest-dwelling species in transitional areas between biogeographic regions. First, frequencies of occurrence of rare species are more subject to stochastic variations due to sampling biases and detectability. Second, low frequencies of occurrence in the owl's diet can be expected due both to reduced densities in the field (intrinsic to marginal populations), and to opposite habitat requirements of both predator and prey which rarely share the same environment. The distribution breadth of *A. flavicollis* (number of localities present/total localities $\times 100$) was lower in the diet of the barn owl (11 out of 18 roosts, 61%) than in the diet of the genet in the Montseny mountains (26 out of 29 latrines, 90%, Arrizabalaga et al. 2002). Besides, the yellow-necked mouse was the sixth species preyed by owls (2.5% of all the small mammals identified), but was the second most frequently small mammal species preyed by genets (28%), after the more ubiquitous wood mouse (*A. sylvaticus*, 56.5%, Arrizabalaga et al. 2002). So, our results were in close agreement with expected findings about the fre-

quency underestimation of forest-dwelling species using the barn owl diet (Torre et al. 2004). Nonetheless, frequencies of occurrence can be interpreted according to specific responses to environmental gradients. In our case, *A. flavicollis* response to a gradient of elevation exactly coincided with the species response observed using the diet of a generalist forest-dwelling carnivore (*G. genetta*) in the same study area. As a whole, almost all the variance of the frequency of occurrence of *A. flavicollis* in the barn owl diet was explained by the 11 descriptors used. The two RDA performed evidenced that frequencies of occurrence increased towards rainy localities covered by deciduous forests. On the other hand, patterns of spatial covariation of environmental predictors precluded sound interpretations of abundance patterns of the yellow-necked mouse in the study area. Most of the variance explained by the statistical model was shared by both sets of predictors (59.2% explained by geoclimatic and land use variables), and reduced variance was explained by geoclimatic (28%) and land-use variables (22.7%).

Regardless of being considered a generalist open habitat hunter worldwide, the barn owl has been exceptionally found behaving as a forest hunter using ambush techniques similar to typical forest-dwelling raptors (Trejo and Ojeda 2004). Nonetheless, in the study area mainly covered by forests (Vicente et al. 2014), barn owls behaved mostly as open habitat predators according to the ratio open/forest habitat small mammal species in the diet (60%/30%, respectively). Forest-dwelling small mammals use forest edges on a regular basis (Bernard et al. 2010; Hille and Mortelliti 2010), and this habitat can be used by barn owls for hunting in forest matrices.

The yellow-necked mouse is a recently discovered species in the fauna of Catalonia (Arrizabalaga et al. 1999), since its presence was overlooked by previous investigations. So, we are still in an inventory phase since the actual spatial distribution has been underestimated by identification problems with its sibling species, the wood mouse (Arrizabalaga and Torre 2007). Some of this new information on the distribution of the yellow-necked mouse was not yet incorporated to the European mammal atlas (<http://www.european-mammals.org>). As previously stated, accurate species determination of the binomial *A. sylvaticus/A. flavicollis* is difficult after live-trapping due to the lack of conspicuous differences between species in body size and fur colour in Southern Europe (Filippucci et al. 1989; Arrizabalaga and Torre 2007). For that reason, accurate separation from the sympatric and much more

abundant *A. sylvaticus* from live-trapped individuals is almost impossible unless expensive molecular methods are routinely incorporated to live-trapping schemes. Nonetheless, the analyses of skeletal remains can be readily used for species discrimination. Some authors suggested using discriminant function analyses on several skull/jaw measures to separate sibling *Apodemus* species (Barciová and Macholán 2009). However, discriminant functions based on size differences can be only valid for small geographic areas, and individuals found outside these areas can be misclassified since both sibling species change their size with age as well as along latitudinal and longitudinal gradients (Alcántara 1991). Furthermore, this technique cannot be applied to cranial remains found in carnivore scats (e.g., genet) because the material is highly fragmented (Torre et al. 2004, 2013). More application can have those methods relying only on molar shape differences analysed by means of geometric morphometry (e.g., Jangjoo 2010), and this method has been considered to be valid at least in our study area. In this vein, the use of non-invasive sampling methods, like the barn owl diet analysis, can be more efficient in detecting the presence of the yellow-necked mouse. In fact, most of the recent citations of the species in Barcelona province have been obtained using non-invasive sampling methods (Torre et al. 2009). Besides, the barn owl diet has been proved to be more efficient in determining the small mammal community composition when compared to other more labour-intensive and invasive sampling methods (i.e., live-trapping: Millán de la Peña et al. 2003; Torre et al. 2004; Avenant 2005; Bernard et al. 2010).

Future scenarios of climate change in Spain suggested that the yellow-necked mouse will face important retractions of the potential distribution range during this century (Araújo et al. 2011). Climate has changed in the Montseny mountains since the middle of the past century producing significant shifts of vegetal communities (Peñuelas and Boada 2003). Deciduous forests have shifted towards higher altitudes, and these were replaced by Mediterranean forests in the south. Owing that *A. flavicollis* showed a strong increase of abundance towards rainy localities covered by deciduous forests, our results can give support to a potential shift in the spatial distribution of the yellow-necked mouse following its habitat retreat (deciduous forests, Arrizabalaga and Torre 2007). Nonetheless, human induced land-use changes in this area produced a significant expansion of the forest cover (from 76.5% to 85.3% in the last 50 years, Vicente et al. 2014), and *A. flavicollis*, as a forest-dwelling species, can

be benefitted by these changes. Following the spatial responses of mesic species facing environmental change in other mountain areas (Rowe 2007), we hypothesised that, in the Montseny mountains, range contractions of *A. flavicollis* related to climate warming can be compensated by range expansions due to increased forest cover caused by human induced land-use changes (Torre et al. in press).

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