

The diet of the genet (*Genetta genetta* Linnaeus, 1758) as a source of information on local small mammal communities

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Small mammals are the most diverse group of species within mammals. However, sampling the small mammal communities living in a defined area (with a degree of completeness) can be complex, due to the fact that species showed different niche use, behavior, and body size. Traditionally, sampling with traps is one of the most commonly used techniques to investigate the composition of small mammal communities (Fonturbel 2010). Nonetheless, traps are passive devices (see however Nicolas & Colyn 2006), so small mammals need to be attracted to them, and some species cannot be captured due to the factors formerly explained (ie. different size, behavior, and niche). Trapping is a selective technique, and the use of different traps, baits, and even trap situation (within the ground, on the ground, on the trees), may affect the number of species captured (O'Farrell *et al.* 1994, Lambert *et al.* 2005, Fonturbel 2010). Indirect sampling techniques, like the analysis of the diet of bird raptors, can be used to investigate the composition of small mammal communities. These methods can be more comprehensive than trapping when analyzing species distribution data since raptors are active hunters that can capture trap-elusive species. Despite the diet of the barn owl (*Tyto alba* Scopoli, 1769) has been used for this purpose (Love *et al.* 2000), the interpretation of composition of communities can be affected due to the fact that aerial raptors are showing strong habitat selection, and some small mammal preys can be over or underrepresented in their diets (Torre *et al.* 2004). The diet of some terrestrial and generalist predators can also be used to study the small mammal communities' composition. The common genet (*Genetta genetta*) is a forest-dwelling generalist carnivore showing an eclectic diet (Virgós *et al.* 1999). In

northern Spain and France the diet of the genet is mostly based on small mammals (Virgós *et al.* 1999, Torre *et al.* 2003), and frequencies of occurrence of the species in the diet are valuable for understanding their distribution patterns along environmental gradients (Torre *et al.* 2013). This method was considered by the latter authors as an exhaustive source of small mammal information (ie. distribution and relative abundance) when different latrines from a large area were analyzed altogether. Nonetheless, this method has not been yet validated for the inventory completeness in the case of local small mammal assemblages (i.e., within the spatial range of a single latrine).

So, our goal in this short communication was evaluating the efficiency of diet of the genet as an indirect method to sample thoroughly (with a high degree of completeness) the small mammal community within the spatial range of a single latrine.

Study area and methods

The latrine analysed was situated in Sant Sadurní d'Osormort (Barcelona, UTM 31TDG4741), within the Guillerics-Savassona Natural Reserve, at a mean elevation of 687 masl, being collected in 1983. The content of the latrine was oven-dried at 60 °C for a day, and the dry content was then separated by decantation under a jet of water and filtered with a sieve. In order to characterise the diet of the genet, we counted the minimum number of prey items present in the whole sample. Since only small vertebrates were found, we relied on skeletal remains to determine the number of individuals (ie. number of teeth; Rosalino & Santos-Reis 2002, Klare *et al.* 2011). All skeletal remains were dried

and were put on a plasticine support to be identified under the microscope. Species were identified following conventional keys based on morphological discriminant criteria (Gosàlbez 1987, Torre *et al.* 2015). The habitat around the latrine was described from the environmental information available nearer to the sampling data (Land-use classification of Catalonia 1987, Torre *et al.* in press). We used the UTM squares of 1x1 km centred on the latrine, plus the information of the eight UTM squares surrounding it, thus considering an area of 9 km² (Torre *et al.* 2013). The mean climatic variables for the area surrounding the latrine were 11.7°C (mean annual temperature), and 903 mm (mean annual rainfall), thus considered as a Mediterranean humid climate. The 87% of the area surrounding the latrine was covered by forests (evergreen 50%; coniferous 21%; deciduous 16%), with a small fraction of the area covered by open habitats (12% crops and meadows). No urban infrastructures were found within the study area. Frequencies of occurrence of the main habitats (i.e., forest, open-land) were compared with small mammal guilds following

their habitat preferences described by Torre *et al.* in press (Table 1).

A species accumulation curve (individual-based rarefaction of abundance data) was used to estimate actual species richness of the small mammal species consumed by genets (Gotelli & Colwell 2001). The expected richness function was calculated with EstimateS (Colwell 2013), after 100 randomizations (default option) of the observed number of species as far as individuals 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 & Hortal (2003).

Results and discussion

The analysis of a single latrine reported a total of 697 small vertebrates, without presence of invertebrates and fruits. Considering only mammals, 692 individuals of 17 species were identified: two species were not considered as small mammals (1

Table 1. Number of individuals and frequency of occurrence of small mammals (O. Soricomopha, O. Rodentia) from a single genet latrine in Barcelona (NE Spain). In brackets, the main habitat preference of the species following Torre *et al.* in press (F: Forests; O: Open-land; X: other habitats)

Species	Number of small mammals	Frequency of occurrence (%)
<i>Sorex minutus</i> (X)	9	1.31
<i>Neomys anomalus</i> (X)	1	0.15
<i>Crocidura russula</i> (O)	48	6.97
<i>Suncus etruscus</i> (O)	5	0.73
<i>Talpa europaea</i> (X)	4	0.58
<i>S. vulgaris</i> (F)	6	0.87
<i>M. glareolus</i> (F)	45	6.53
<i>A. sapidus</i> (X)	3	0.44
<i>M. duodecimcostatus</i> (O)	3	0.44
<i>M. agrestis</i> (O)	4	0.58
<i>A. flavicollis</i> (F)	95	13.79
<i>A. sylvaticus</i> (F)	444	64.44
<i>R. rattus</i> (X)	1	0.15
<i>M. spretus</i> (O)	15	2.18
<i>E. quercinus</i> (X)	6	0.87
TOTAL	689	100

weasel *Mustela nivalis*, and two rabbits *Oryctolagus cuniculus*), so they were not included in further analyses. Small mammals represented the 98.8% of all vertebrates consumed by genets (Table 1). The proportion of small mammals in the diet was higher than in any other published information in nearby areas (Ruiz-Olmo & López-Martín 1993, Virgós *et al.* 1999, Torre *et al.* 2003), confirming that the genet increases the stenophagy (specialization) in the northern part of its distribution range (Virgós *et al.* 1999). The small mammal species accumulation curve showed an approach to its asymptote, and the Clench equation adjusted to the species accumulation curve fitted very well ($r^2= 0.986$). Estimated species richness was 15 ± 0.97 (SD) species at the end of the species accumulation curve, and 16 species were expected after fitting richness asymptotic estimators (Chao1, Fig. 1). The Clench equation was fitted to the species accumulation curve to ascertain the inventory completeness after reaching the asymptote. The asymptotic species richness was 16.25, so 92.3% of the small mammal species were recorded during the present inventory. The local species list obtained from the analysis of genet scats can be considered as almost complete (> 90%; Moreno & Halffter 2000). Only one species was missed from the inventory: the edible dormouse (*Glis glis*), a species that was known to be present in nearby areas and that was also preyed by genets (Torre *et al.* 2013). However, this species depends on deciduous forests, and in the study area the availability of this habitat was reduced (16%

of all habitats available). Synanthropic species, like the house mouse (*Mus musculus*) and the brown rat (*Rattus norvegicus*), were seemingly absent from the diet due to the lack of urban areas in the environment surrounding the latrine.

Woodland rodents represented the 85.6% of small mammal preys, whereas open-habitat species only accounted for the 10.9%. Genets preyed almost on forest-dwelling species; the wood mouse (*Apodemus sylvaticus*) was the dominant species (64%, Table 1), followed by the yellow-necked mouse (*Apodemus flavicollis*, 14%), and the bank vole (*Myodes glareolus*, 6.5%). These results were in agreement with the frequencies observed in the diet of the genet in larger areas in which woodland rodents are dominant (Torre *et al.* 2013). Frequencies of occurrence of woodland/open habitat small mammals (86% *vs* 11%) were closer to the frequencies of forest/open habitats available (87% *vs* 12%) around the latrine (Yates corrected $\chi^2= 0.00$; $df= 1$; Fisher exact $p= 1$, two-tailed), suggesting that genets preyed on small mammals according to their accessibility on the habitats available. This result is in accordance with the generalist feeding behaviour reported (Virgós *et al.* 1999), and highlights the utility of the diet of the genet for determining the small mammal species composition, at least in forest environments (Torre *et al.* 2013). Since genets are considered as strict forest-dwellers (< 1% of open habitats used, Ruiz-Olmo & López-Martín 2001), further investigations need to be performed in order to

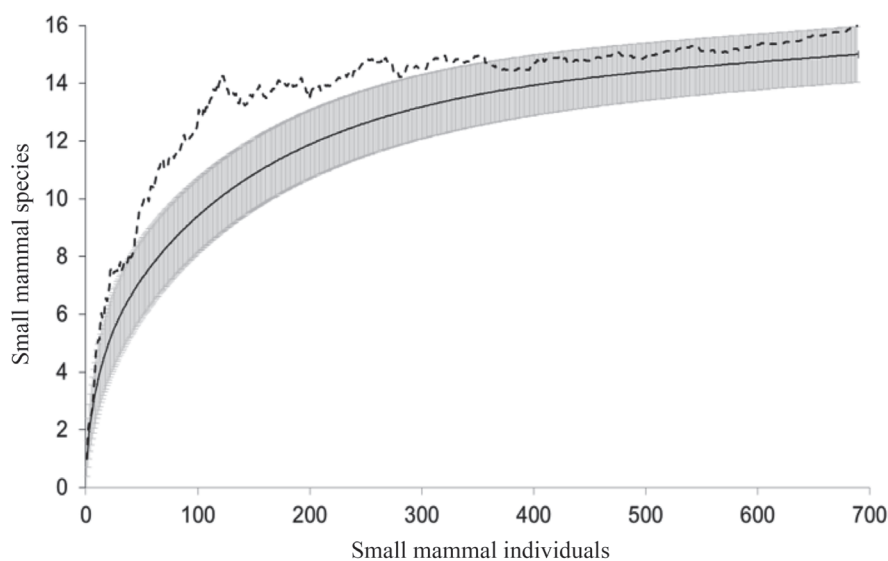


Figure 1. Small mammal's species accumulation curve (solid line) after individual-based rarefaction of abundance data (\pm SD, grey shadow). Estimated species richness was calculated after asymptotic estimators (Chao1, dashed line).

find out whether the diet of the genet represents the composition of the small mammal fauna in less forest environments.

Interestingly, the use of a single non-invasive sampling method on a discrete sampling place (latrine) has brought information on the presence and relative abundance of 15 different small mammal species. Latrines can be used by up to six different genets (Pla *et al.* 2000), since they are considered centers for exchanging information between individuals (i.e. sexual status, territoriality). Scats, even for a single latrine, may come from different individuals (and territories), allowing the representativeness of a single sample to characterize the diet. So, the sample of small mammals provided by genets can be considered as a real (and almost exhaustive) picture of the composition and relative abundance of species in the environment around the latrine (within 9 km²). A single latrine provided accurate information on the small mammal species present in a reduced area (15 species detected out of 16.25 expected; 92.5% of the species present), and this figure was similar to the one obtained after combining the information on 51 latrines from an extensive area of 800 km² (18 species detected out of 18.82 expected: 95.6% of species present, Torre *et al.* 2013). Several authors have suggested that no single method itself can sample a small mammal community thoroughly, and combinations of direct (Nicolas & Colyn 2006) and indirect sampling methods are recommended (Torre *et al.* 2004). In this case, the use of a single indirect method (diet of the genet) may suffice to have a relatively comprehensive list of species present within a studied area. However, the high number of individuals identified in the sample analyzed (689 small mammals) may well be the cause of the inventory completeness of the small mammal fauna present within the spatial boundaries of the latrine. Nine species (60% of the total species) were detected with 100 prey-items (14.5% of total preys), 12 species (80%) with 200 prey-items (29%), 13 species (86.6%) with 300 prey-items (43.5%), 14 species (93.3%) with 400 prey-items (58%), and 15 species (100%) with 500 prey-items (72.5%). Further investigations are needed on the mean sample of individuals necessary to reach the inventory completeness in other latrines with lower number of small mammals identified. So, we must be aware about that our results, coming from a single latrine, cannot be generalised to other latrines or other areas.

Nevertheless, the sample analyzed represents a picture frame of the small mammal community that was present in the area 30 years ago. Significant changes in landscape composition and climate have been detected in Catalonia during the last 50 years (Peñuelas & Boada 2003, Llebot 2012), and some of the species consumed by genets might be actually absent from the area. Some of the species found in the diet of the genet are considered today as rare in the study area, since they have experienced important population declines during the last decades (ie, *Arvicola sapidus*, Palomo *et al.* 2007). There is increasing evidence that range boundaries of small mammals are suffering significant displacements tracking changes in temperature (Rowe *et al.* 2010), and future scenarios of climate change in Spain suggested that several small mammal species will face important retractions of their potential distribution ranges during this century (Araújo *et al.* 2011). In this vein, the use of old data records can be valuable to ascertain recent changes in the small mammal communities according to landscape or climate change, both considered as relevant drivers of biodiversity. Comparative analyses of old and recent barn owl (*Tyto alba*) records have been proved to be efficient in detecting the influence of climate and/or landscape change in the composition of small mammal communities in the Mediterranean basin (Szpunar *et al.* 2008, Torre *et al.* in press). This approach, however, has not yet been applied to the diet of the genet.

Acknowledgements

Diputació de Barcelona provided financial support. We are grateful to Ferran Pàramo for obtaining the environmental information to characterise the latrine, and to Mario Díaz (CSIC) for the comments on an earlier draft.

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Associate editor was Javier Calzada