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# Combining a molecular diet analysis (NGS) and biotraits of prey community to refine the habitat selection of a predator. The case of the endangered Pyrenean desman (*Galemys pyrenaicus*)

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## Abstract

Indirect presence signs are a wealth of information about species ecology and trophic interactions. Recent advances in molecular techniques have made it possible to identify prey species from DNA fragments contained in faeces. Also, trait-based approaches are increasingly used in community ecology as species traits may explain the local distribution of organisms assuming environmental filtering and can be considered as environmental indicators. By combining Next-Generation Sequencing diet analysis and biological and ecological traits profile of eaten vs. prey present in the rivers (i.e. macro-invertebrates), our aim was to identify the characteristics of the foraging habitat of the endangered and semi-aquatic Pyrenean desman (*Galemys pyrenaicus*). We found that the majority of its prey showed several life stages with at least one in freshwaters, supporting that the diet of this species is mainly based on aquatic food. Overall, prey species were found to be typical of the upstream part of catchments, in rivers with medium to fast flowing waters and high water quality (many species sensitive to pollution). The less frequent terrestrial prey were mobile invertebrates commonly found on riverbanks and should probably be considered as opportunistic prey. This study suggests that biological and ecological traits may be useful to

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investigate predator-prey interactions and predator foraging behaviour. In particular, using trait-based approaches on prey assemblages from faeces may be an effective tool for species conservation as it provides a non-invasive method to refine the habitat use of elusive and endangered species such as the Pyrenean desman.

**Keywords:** next generation sequencing (NGS), diet, *Galemys pyrenaicus*, biotraits, macroinvertebrates, habitat selection, predator, prey interaction, conservation