

# GENETICS SOCIETY NEWS

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## The role of habitat selection and local adaptation in the population structure of an apex predator

October - November 2020

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Understanding the microevolutionary processes that generate genetic population structure among demes within a species is essential in order to understand diversification processes and to address specific conservation issues.

Population structure depends on the extent of gene flow, which in turn is related to dispersal capabilities of a species. Large mammalian carnivores are animals with high mobility, able to overcome topographic barriers and long geographical distances. The grey wolf (*Canis lupus*) is one of the most mobile large carnivores, and may disperse over distances up to 900 km. In addition, wolves can occupy very diverse habitats, from the Arabian desert to the frozen Arctic, taiga forests or Mediterranean scrublands. However, despite this amazing dispersal capability and generalist behaviour, previous studies have reported genetic differentiation among wolf populations at a continental scale, probably associated with differences in habitat characteristics. However, it is still not clear whether ecological processes affect wolf population structure at a finer scale. If dispersing wolves favour habitat types similar to those where they were born, dispersal and population dynamics would be biased and fine population genetic structure could emerge, as suggested by the “Matching Habitat Choice” hypothesis.



Isabel Salado taking a picture of a wolf scat in the middle of a trail

In Europe, wolf population numbers have recovered in the last decades.

However, the Iberian wolf population, in the southern limit of its distribution, is not expanding and remains isolated from other European wolf populations since the mid-19th century or earlier. Iberian wolves are distributed through a diverse range of habitats, from well preserved mountain habitats with

abundant wild ungulates, to highly humanized agricultural areas with very limited forest cover. We aim to understand the ecological processes that are limiting dispersal of Iberian wolves through assessing their current genetic population structure.

To achieve this, we are performing a non-invasive genetic monitoring. We have been collecting fresh faeces from

*Large mammalian carnivores are animals with high mobility, able to overcome topographic barriers and long geographical distances.*





*Wolf scat on top of a broom (Cytisus sp.) at 1650 m above sea level in Avila (Central Spain)*



*Fieldwork team during the Coronavirus pandemic: from left to right – Carles Vilà, Alberto Fernández, Laurentino García and Isabel Salado*

different wolf packs (family groups) across most of the distribution area of the species in Iberia. Wolves use paths and trails to move through the territory and tend to leave scats at intersections as marking behaviour. We have been surveying these places in different areas in Spain and collected just a small portion of the excrement to avoid interfering with the marking behaviour of the species.

In October and November 2020 thanks to funds from the Heredity Fieldwork Grant I was able to visit two additional field areas along the edge of the main wolf distribution range in the Iberian Peninsula, the Central System Mountains. In this region, habitat is very patchy; wild mountain areas are interspersed with areas heavily used by livestock. Also, wolf packs are scattered and fluctuating in numbers every year due mainly

to anthropogenic disturbances and persecution. To collect the samples, we needed to drive long distances to check several areas with and without recent evidences of wolf presence. Fortunately, we successfully sampled at least 12 potential wolf packs, collecting a total of 25 wolf-like faeces.

Back in my institution, I have already started to extract the DNA from some faecal samples. To genotype these faeces, I will use a multilocus genotyping protocol based on next generation sequencing approaches that I have been optimizing as part of my thesis. A better understanding of the mechanisms controlling gene flow between wolf populations will shed light on possible dispersal and colonization patterns, which can help understand what are the limitations for the expansion of the Iberian wolf population at a time when wolves

are expanding across Europe. This knowledge can be of great importance in the design of landscape genetics models that might be applied in the development of conservation actions for this apex predator.

I would like to thank the Genetics Society for the funding which made this fieldwork campaign possible. I would like to thank my supervisors, Dr Carles Vilà and Dr Jennifer A. Leonard, for their guidance and for convincing me I was capable of leading this work. I also express my immense gratitude to my fieldwork colleagues, particularly Dr Alberto Fernández, Laurentino García and Marta Portolà, who helped me to collect the samples and shared together fascinating discussions which will be very useful to interpret the final results of this work.