

Phylogeography of *Curruca melanocephala*: an enigmatic genetic arrangement along the Mediterranean distribution range

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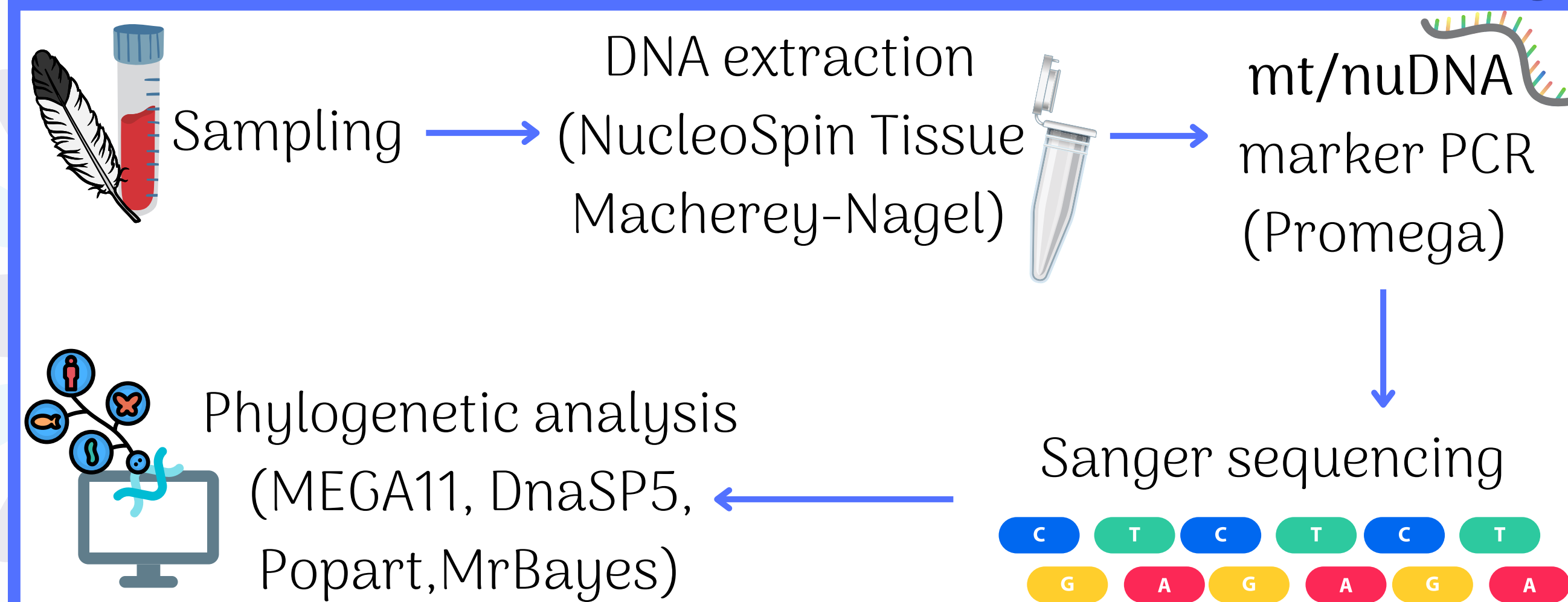
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Introduction

- Although the avian phylogeography in the Western Palearctic has been profoundly investigated, the genetic history of the species that persist in the Mediterranean basin needs to be deepened;
- The Sardinian Warbler (*Curruca melanocephala*) is a largely-sedentary passerine belonging to the *Curruca* clade, a genus among the Sylviidae family, recently split from the *Sylvia* group. Currently, 4 subspecies are recognized, based on distribution and morphological characteristics [1]: i) *C. m. melanocephala*; ii) *C. m. leucogastra* (Canary islands); iii) *C. m. momus* (Levant); iv) *C. m. valverdei* (Western Sahara);

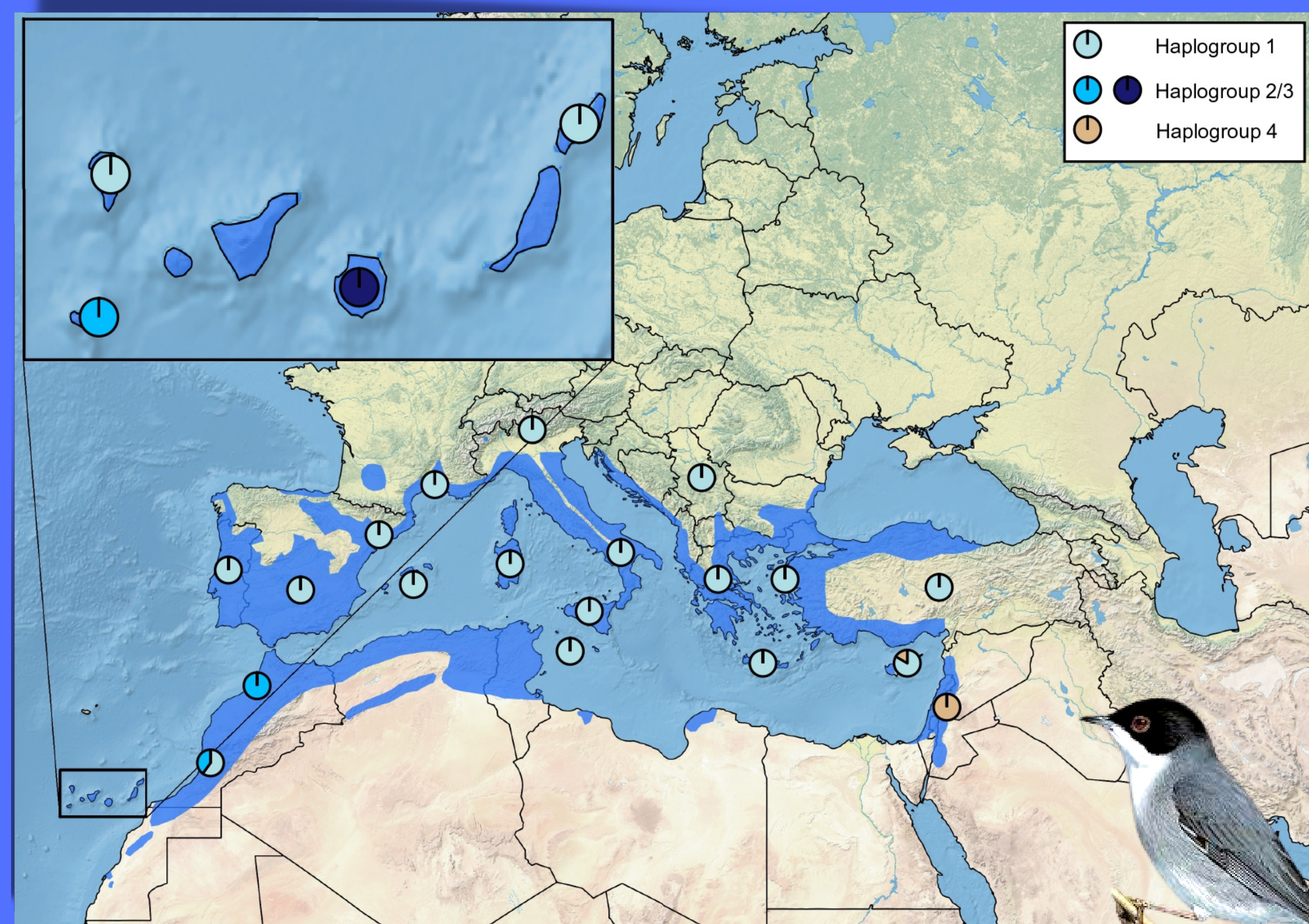
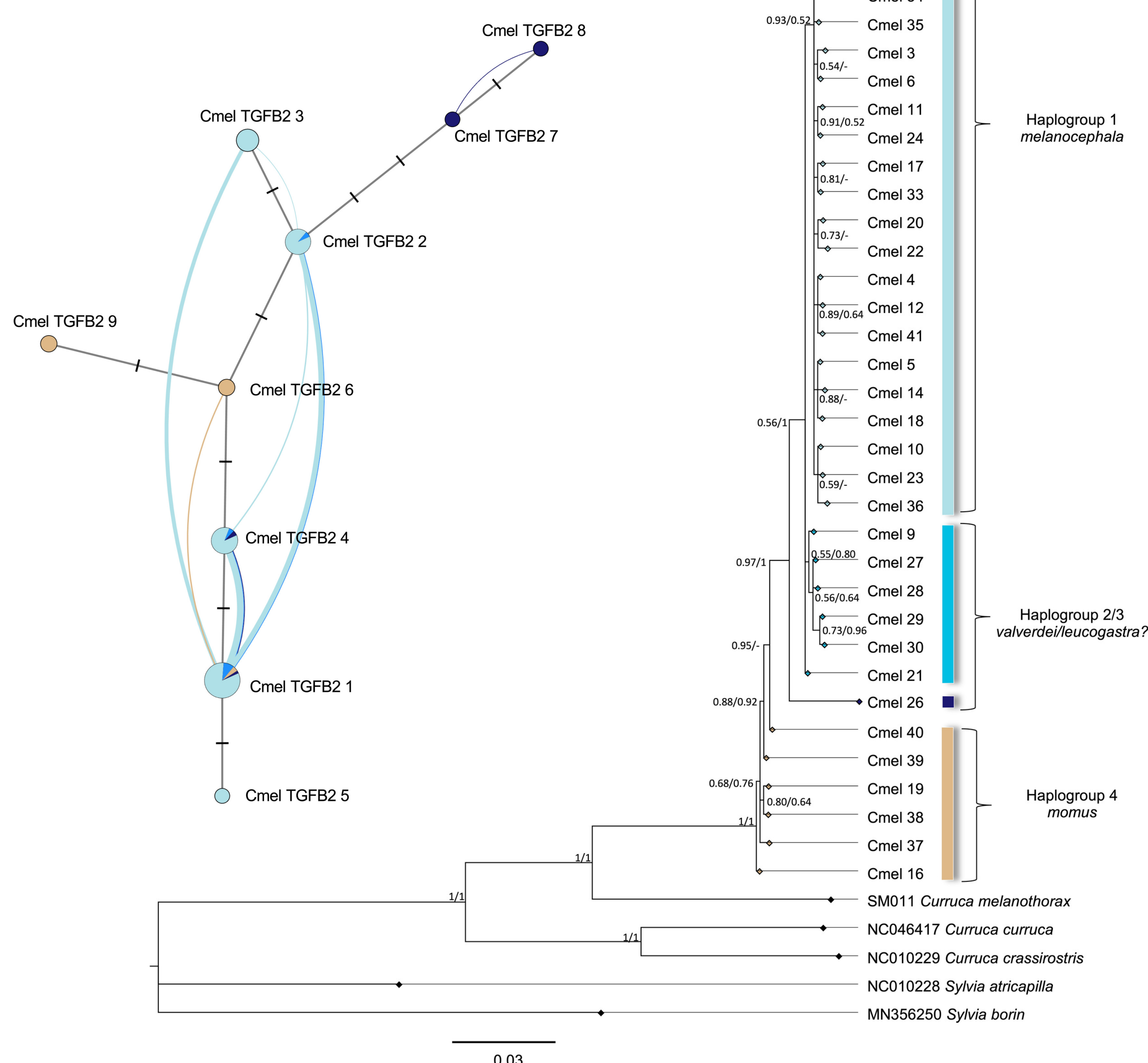
This study aims to increase the phylogeographical knowledge of the species and to infer whether there is a correlation between the subspecies ranges and their genetics.

Methods



Results

- High genetic admixture was revealed both in the concatenated mtDNA tree (*cox1* and *cytb*) and in the nuDNA TGFB2 network;
- An exception is represented by the well-defined haplogroup 4 (*momus*). The haplogroup belonging to the supposed *valverdei/leucogastra* subspecies shows an enigmatic arrangement;



Between groups genetic distances - Concatenated Dataset	Other <i>Sylvia/Curruca</i> spp.	Haplogroup 1	Haplogroup 2/3	Haplogroup 4
Other <i>Sylvia/Curruca</i> spp.	-	± 0,0056	± 0,0057	± 0,0054
Haplogroup 1	0,1062	-	± 0,0016	± 0,0024
Haplogroup 2/3	0,1075	0,0078	-	± 0,0023
Haplogroup 4	0,1049	0,0116	0,0136	-

Between groups genetic distances - <i>cytb</i> dataset	All <i>C. melanocephala</i>	Gran Canaria
All <i>C. melanocephala</i>	-	± 0,0048
Gran Canaria	0,0252	-

Taking into consideration the *cytb* dataset only (including GenBank records), an haplogroup of sequences from Gran Canaria is found.

Conclusions and perspectives

- Considering the low genetic differentiation between haplogroups, it is possible to assume a high degree of gene flow between populations across the entire distributional range. Recent and spaced expansions of this species are already described in the literature;
- Complex scenarios regarding the subspecies *valverdei/leucogastra* are found; no clear geographic lineages can be confirmed, except for unique haplotypes from Gran Canaria island, while for the Western Sahara subspecies a strongly supported clade was identified, including haplotypes from Morocco but also from El Hierro island;
- A well-supported clade is found for *C. m. momus*, thus validating the allopatric Levant subspecies, but still with genetic distance values included in the intra-specific range.

Further investigations could include a wider sampling, whole-genome approaches and spatial analysis that might be helpful to shed light on the movements of individuals and genes across populations.