

# LANDSCAPE GENETICS OF *CULICOIDES* VECTOR SPECIES

## Evaluation of cryptic diversity and gene flow in the Palearctic region

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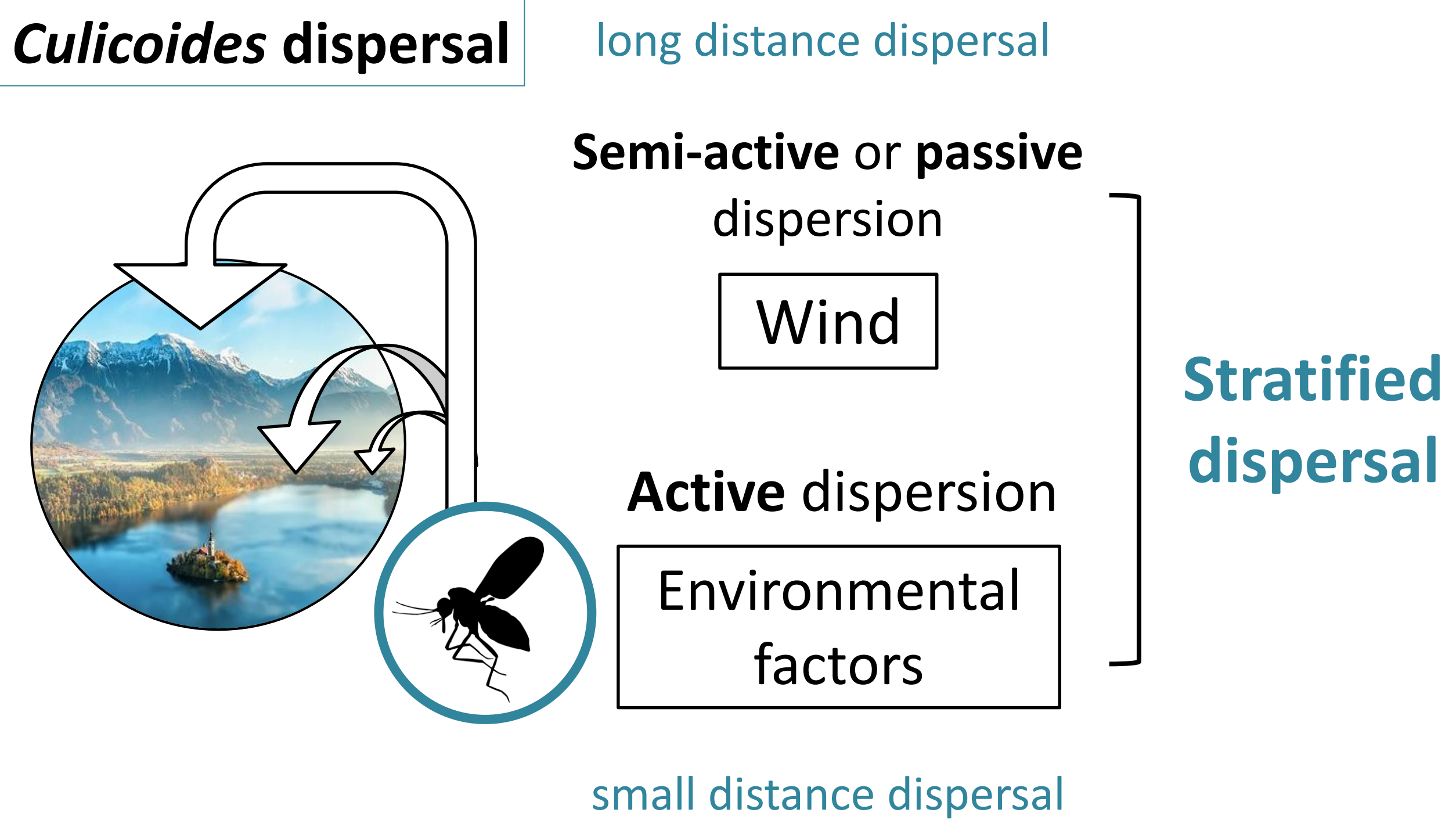
### Background

Since 2006, Europe has faced recurrent outbreaks of bluetongue and Schmallenberg diseases, both transmitted by native haematophagous midges, *Culicoides* (Diptera : Ceratopogonidae) (1). The main objective of this work is to **determine how vector's dispersion is influenced by landscape and habitat characteristics**. We study *C. obsoletus* and *C. chiopterus*, two Palearctic vector species showing different host-vector behavior using genetic pattern.

Moreover *C. obsoletus* is sympatric with a morphologically indistinguishable species, *C. scoticus*. In addition, several authors have recently reported existence of cryptic diversity (2, 3, 4). We need to ensure the taxonomic status of individuals included in our study.

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### *Culicoides* dispersal



### Results

#### 1 Cryptic diversity within *C. obsoletus/C. scoticus*

Identification of 1,978 individuals *C. obsoletus sensu stricto* used in study of population genetics

#### Methods

Sequencing Cox1 mitochondrial gene of **3,200** *C. obsoletus/C. scoticus* from **17 European countries**.

Confirmed results with rDNA 16S mitochondrial gene and RNA 28S gene encoding ribosomal sequences over the entire haplotypic diversity resulting from Cox1 barcoding.

Presence of at least **four undescribed clades** within *C. obsoletus s.s.* (*C. obsoletus* #O2, *C. obsoletus* #O3, *C. obsoletus* #Dark and one not yet described)

Revealed **two clades** within *C. scoticus*

Questioning on the taxonomic status of *C. montanus*

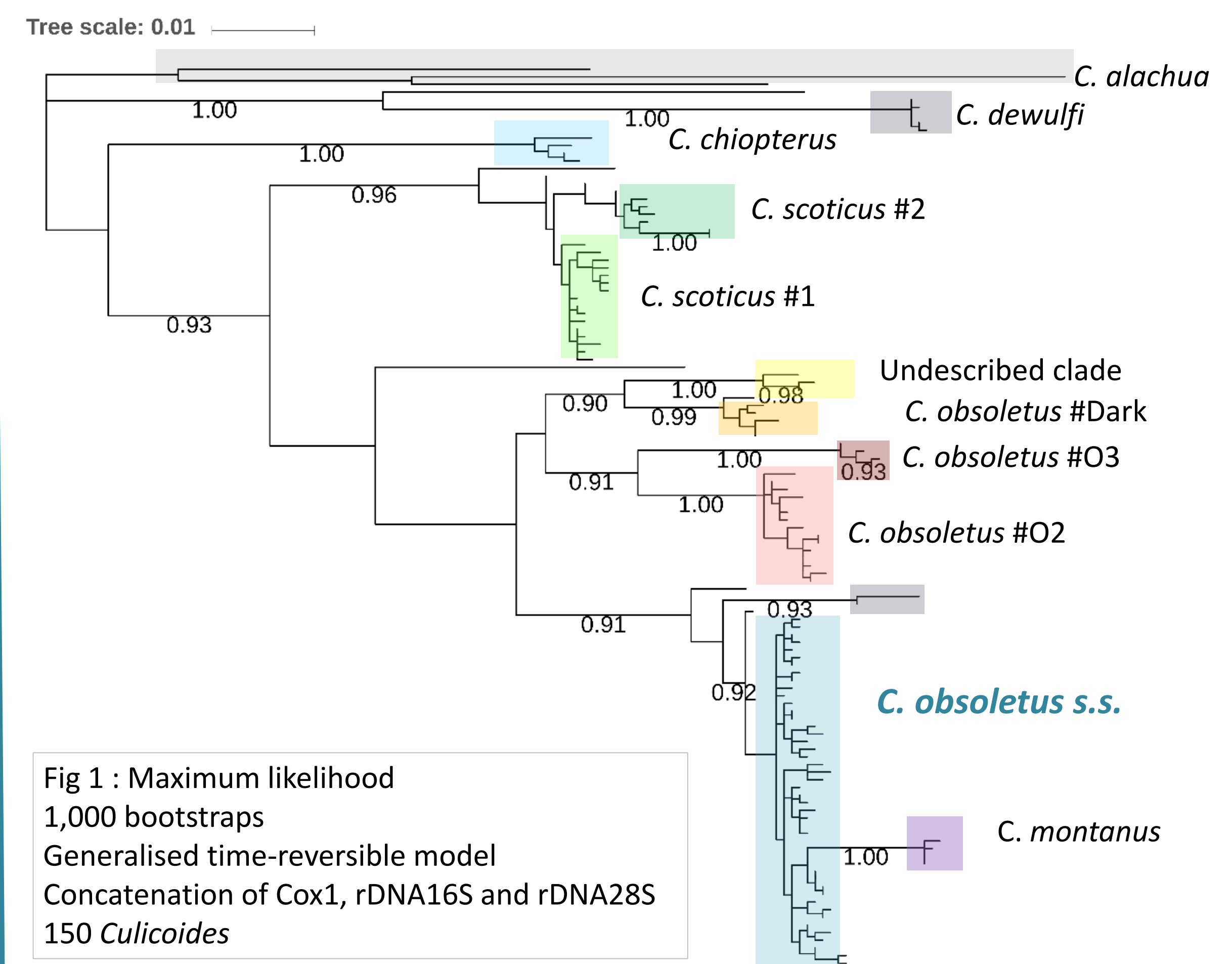


Fig 1 : Maximum likelihood 1,000 bootstraps Generalised time-reversible model Concatenation of Cox1, rDNA16S and rDNA28S 150 *Culicoides*

#### 2 Diversity and genetic structure of populations of *C. obsoletus s.s.*

North/South genetic structure of *C. obsoletus s.s.*

Significative isolation by distance

#### Methods

To understand diversity and genetic structure of *C. obsoletus s.s.* in Europe, a first classical population genetic analysis was carried out on **729 individuals** from **17 countries** (1-2 sites per country), using **13 microsatellite markers**.

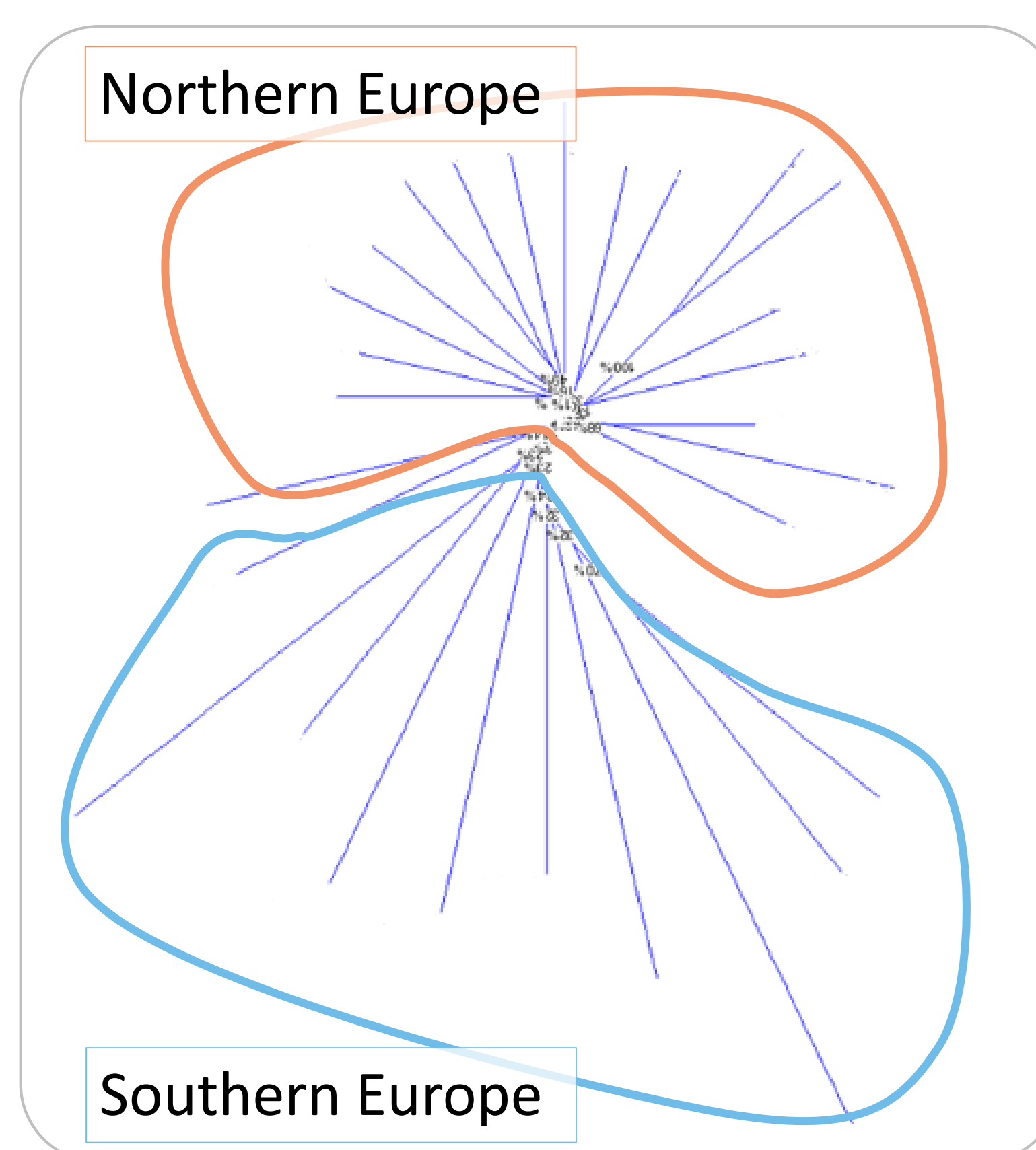


Fig 2 : Phylogenetic neighbor-joining tree (NJ) based on Cavalli-Sforza Edwards genetic distances

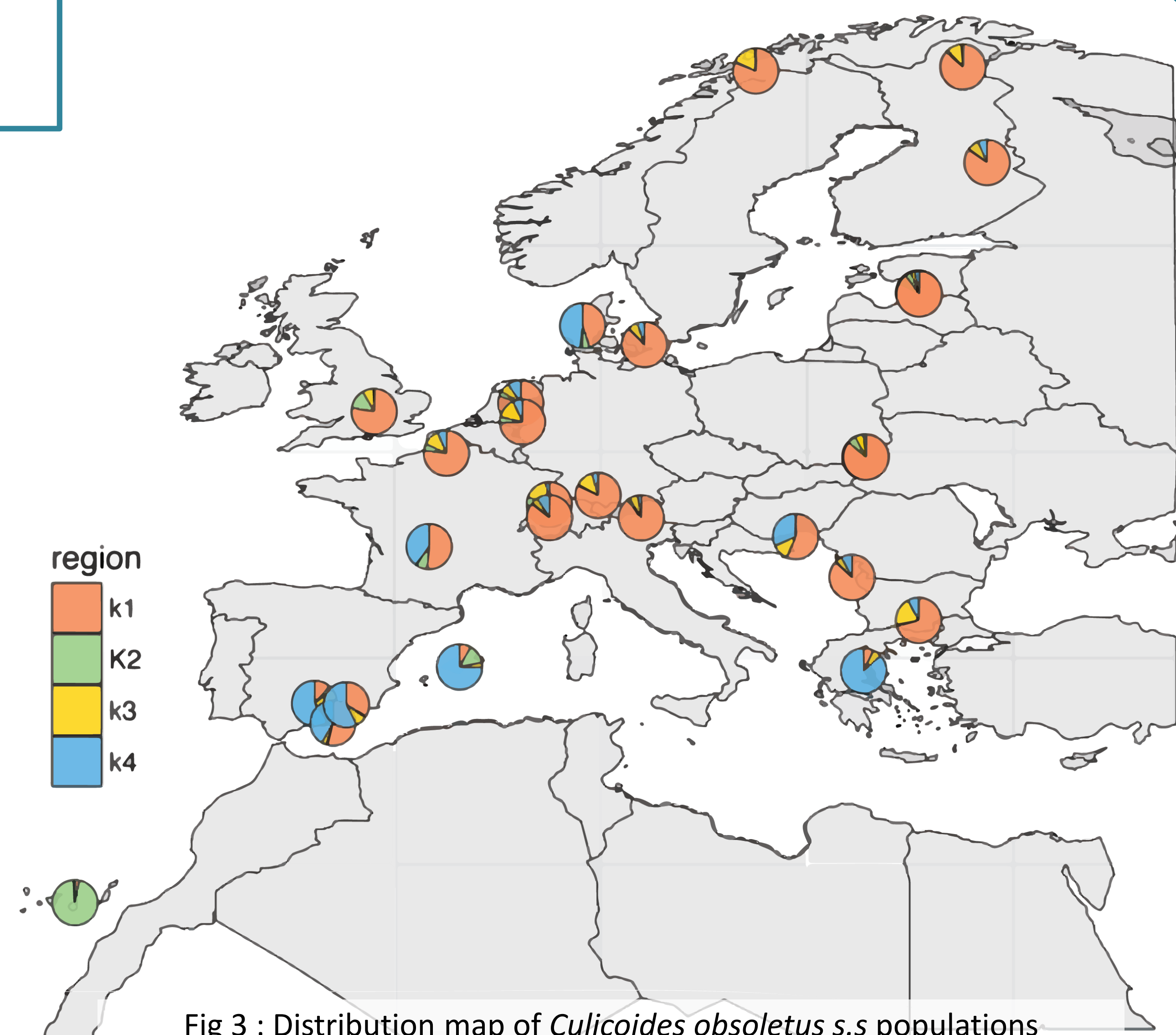


Fig 3 : Distribution map of *Culicoides obsoletus s.s.* populations represented by their percentages of assignment to a genetic cluster

### Conclusion

- 1 Significant cryptic diversity within *C. obsoletus s.s.*
- 2 Characterization of North/South genetic structure of *C. obsoletus s.s.*

### Perspectives

- To determine genetic structure of *C. chiopterus* in Europe
- To Characterize influence of landscape heterogeneity on genetic structure of *Culicoides*

(1) Carpenter, S., Wilson, A., & Mellor, P. S. (2009). *Culicoides* and the emergence of bluetongue virus in northern Europe. *Trends in Microbiology*, 17(4), 172–178. <https://doi.org/10.1016/j.tim.2009.01.001>. (2) Ander, M., Troell, K., Chirico, J., 2013. Barcoding of biting midges in the genus *Culicoides*: a tool for species determination. *Med. Vet. Entomol.* 27, 323-331. (3) Mathieu, B., 2011. Thèse : Les espèces de *Culicoides* du sous-genre *Avaritia* (Diptera : Ceratopogonidae) dans le monde : Révision systématique et taxonomique des espèces d'intérêt dans la transmission d'Orbivirus. (4) Meiswinkel, R., de Bree, F., Bossers-De Vries, R., & Elbers, A. R. W. (2015). An unrecognized species of the *Culicoides obsoletus* complex feeding on livestock in the Netherlands. *Veterinary Parasitology*, 207(3–4), 324–328. <https://doi.org/10.1016/j.vetpar.2014.12.032>