

Molecular phylogeny of the subgenus *Culicoides* Latreille, 1809 and related species in Italy inferred from ITS-2 sequences

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Biting midges of the genus *Culicoides* (Diptera: Ceratopogonidae) include vectors for the economically important animal diseases, bluetongue (BT) and African horse sickness (AHS). In the Mediterranean Basin these diseases are transmitted by four species of *Culicoides*: the first three belong in the subgenus *Avaritia* Fox, 1955, and are *C. imicola* Kieffer, 1913, *C. obsoletus* (Meigen), 1818 and *C. scoticus* Downes and Kettle, 1952; the fourth is *C. pulicaris* (Linnaeus), 1758 in the subgenus *Culicoides* Latreille, 1809. In the Palaearctic Region this subgenus (usually referred to as the *C. pulicaris* group) now includes a loose miscellany of some 50 taxa. The lack of clarity surrounding its taxonomy stimulated the morphological and molecular study of 11 species collected in Italy. Phylogenetic analysis of nuclear ribosomal DNA ITS2 sequence variation demonstrated a high degree of divergence. These results, combined with those from a parallel morphological study, disclosed: 1. that some previously described taxa should be resurrected from synonymy; 2. that there are new species to be described, and 3. that the subgenus *Culicoides* (as currently employed) is a polyphyletic assemblage of four lineages - the subgenus *Culicoides sensu stricto*, the subgenus *Silvicola* Mirzaeva and Isaev, 1990, the subgenus *Hoffmania* Fox, 1948 and the hitherto unrecognised Fagineus species complex. Each is discussed briefly (but not defined) and its constituent Palaearctic taxa listed. Strong congruence between morphological and molecular data holds promise for resolving many of the difficult taxonomic issues plaguing the accurate identification of vector *Culicoides* around the world.

Keywords: *Culicoides pulicaris*, Pulicaris Complex, rDNA, ITS2, Phylogenetics, Bluetongue, Italy