

STANDARDIZATION OF DNA BARCODING TECHNIQUES TO IDENTIFY *CULICOIDES* SPECIES IN EUROPE

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The design of efficient control strategies for *Culicoides* midges lies in correct species identification. From the approximately 1340 described *Culicoides* species, only 30 have been incriminated as vectors of bluetongue disease virus. However, the actual number of vector species could be different considering that relatively few species have been studied. In Europe, the most important vector was assumed to be *Culicoides imicola*, an Afro-Asian vector. However, during the last two years other species such as *C. pulicaris* (Pulicaris complex), *C. dewulfi*, *C. chiopterus* and species of the *Obsoletus* complex have increased in importance, as their populations have been found abundant in outbreak areas, outside the geographical range of *C. imicola*. Whereas *C. imicola* is the

most easily identified, *C. obsoletus sensu stricto* and *C. scoticus*, from the *Obsoletus* complex, are extremely difficult to identify by using traditional methods such as morphological examination. The deoxyribonucleic acid (DNA)-barcoding regions is located in the cytochrome oxidase 1 gene (CO1). Recent studies have shown that this region is valuable in the identification of *Culicoides* species; however, the CO1 fragment to be used must be selected with great care. We propose to standardize the methodology and the selection of the fragment to be amplified to homogenize results obtained by different groups.

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