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Sequencing complete mitochondrial genomes to solve *Culicoides* biting midge (Diptera: Ceratopogonidae) phylogeny

Inhalt

Accurate species identification of biting midges (Diptera: Ceratopogonidae) is essential for understanding pathogen transmission dynamics and developing effective vector control strategies. Traditional morphological identification is challenging and in many cases impossible due to the occurrence of cryptic species. Although sequencing of the mitochondrial cytochrome c oxidase subunit I (COI) gene is widely used for molecular species identification, this marker frequently lacks sufficient resolution within the genus *Culicoides*. To overcome these limitations, we used sequence comparison of complete mitochondrial genomes (mitogenomes). Compared to single-locus markers, mitogenomes provide substantially greater phylogenetic signal. This approach is valuable for taxonomically challenging groups such as the subgenera *Avaritia* and *Culicoides*, in which morphological similarity and low COI divergence complicate species discrimination. In this study, we generated 32 complete mitogenomes representing 17 *Culicoides* species. Specimens were collected from multiple locations across Germany during various monitoring programmes, pre-identified morphologically and, if possible, by COI barcoding. Complete mitogenomes were assembled from high-throughput sequencing data. Results indicate the presence of two distinct mitochondrial structures in the two subgenera. These, for example, confirm that *Culicoides dewulfi* does neither belong to the *Obsoletus* Group nor to the subgenus *Avaritia*.

Keywords

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Professional Status of the Speaker

Postdoc

Junior Scientist Status

No, I am not a Junior Scientist.

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