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Where do they come from? Where do they go? Population genetics studies on *Culicoides* biting midges

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Determining and understanding the factors underlying the genetic diversity of vector species or invasion success of species allow predicting potential other biological invasion, assess vector competence of isolated taxonomic units and develop more accurate epidemiological models. Although the role of winds and local air movements have an undeniable role in the dispersal of *Culicoides*, anthropogenic factors also play a predominant role, particularly at the local level (distribution of hosts, landscape structure). The influence of these different factors will also be modulated according to the species considered, which have different host preferences and larval ecology. It is therefore crucial to understand the relative importance of the different modes of dispersal of the *Culicoides* and the influence of the biotic and abiotic factors influencing it.

Using several examples with the Afrotropical vector species *Culicoides imicola* in the Mediterranean basin and autochthonous Palearctic vector species *Culicoides obsoletus* and *C. chiopterus*, we will present studies that characterize the main factors explain the genetic diversity over the spatial range of important vector species of viruses to livestock and equines. This presentation will also highlight the need for integrative work using multi-loci approach combining population genetics analyses, ABC methods and mathematical modeling of dispersion.