poster 2.25

The *Culicoides* species (Diptera : Ceratopogonidae) of Senegal: towards identifying the vectors of African horse sickness virus, 40 years after the first studies

> M. Fall [1], T. Bakhoum [1], C. Garros [2], N. Diouf [3], M.T. Seck [1], J. Bouyer [2,1], M. Ndao [1], A.M. Dusom [1], X. Allène [2], I. Rakotoarivony [2], M. Diarra [1], T. Baldet [2], T. Balenghien [2], J-C. Delécolle [4], **A.G. Fall** [1]

[1] Institut Sénégalais de Recherches Agricoles (ISRA), Dakar, Senegal

[2] Cirad, Contrôle des maladies animales exotiques et émergentes, (UMR Cirad - Inra), Montpellier, France

[3] Ministère de l'Elevage, Cimel de Makhana, Saint-Louis, Senegal

[4] IPPTS, Université de Strasbourg, Strasbourg, France

African Horse Sickness (AHS) has been described for the first time in Senegal in the 1880s. Since then, it is an endemic disease, with occasional epizootic outbreaks, which caused significant economic losses. The last outbreak occurred in 2007 and caused the death of 1,169 horses in several regions, with a total cost estimated at 900 million CFA, of which the half was due to mortality and morbidity. Today, the unique available control strategy for AHS virus is mass vaccination. The vector species responsible for AHS virus transmission belong to the genus *Culicoides*. In Senegal, studies on the fauna of *Culicoides* have been conducted four decades ago and failed to highlight the species of veterinary interest involved in the virus transmission. If *Culicoides imicola* is historically recognized as the main Afrotropical vector species, its role in the transmission has never been established in Senegal.

Under the framework of the EDENext project (European FP7 project), several studies were initiated in 2011 to update the *Culicoides* diversity of Senegal and to allow a better understanding of the species role in the transmission of AHS virus. The *Culicoides* population dynamics was followed up monthly for one year, using OVI traps and horse-baited traps in five sites along a transect Dakar-Thies, in western Senegal. Captured individuals were identified morphologically at the species level, or with molecular identification tools for the *C. schultzei* group. The data obtained in this survey were then confronted with the reported incidences of the 2007 AHS outbreaks.

This preliminary work allows updating the list of *Culicoides* of Senegal, helps clarifying the species delimitation for the *C. schultzei* group and contributes to identify potential vector species of African horse sickness virus in Senegal. It also allows choosing the candidate vectors to rear in the insectarium to unable vector competence studies.