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PRESENTATION

3166: *Culicoides imicola*: Phylogeography, population genetics, and invasive status in the Mediterranean basin

Thursday, September 29, 2016 02:15 PM - 02:30 PM

Convention Center - Room W330 A

Introduction: Biological invasions are of major concern because of their environmental, economic, and health consequences. Determining and understanding the factors underlying invasion success of species allows predicting potential other biological invasions and developing vector control strategies. *Culicoides imicola* is a major vector species of *Orbivirus*, including the bluetongue virus (BTV) which affects domestic ruminants. Following BT emergence in the Mediterranean basin, *C. imicola* populations were recorded in territories where the species was considered to be absent, and consequently was described as expanding its distribution range on a short period. This work aimed at understanding the colonization history of the Mediterranean basin by *C. imicola* and determining the factors underlying the current distribution of the species.

Methods: We used a multi-loci approach and combined population genetics analyses, *Approximate Bayesian Computation* (ABC) methods and mathematical simulations of the atmospheric dispersion of the species.

Results/Conclusion: This approach enabled us to (i) demonstrate that *C. imicola* Mediterranean populations originated from the northern region of sub-Saharan Africa and are established in the Mediterranean basin since the Pleistocene/Holocene period, (ii) confirm a North African origin of southwestern European populations and reveal two routes of colonization: starting from Morocco to the Iberian Peninsula and from Algeria to France and Italy, and (iii) highlight the major role of wind-mediated dispersal and population abundances in the range expansion success of the species. Altogether, our study shed a new light on the evolutionary and demographic history of *C. imicola*.

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