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Using population genetics to assess tick dispersal, from the mainland to the landscape scale : a review of current knowledge and its utility to design tick-control methods

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Assessment of tick dispersal is a central issue for the understanding of the eco-epidemiology of tick-borne diseases and the development of effective control methods. Tick dispersal is assumed to be due to host movements. However, because (1) Ixodes ricinus -the most common European tick vector- uses a high diversity of hosts, (2) these hosts show a wide range of dispersal distances (ranging from a few hundred meters for rodents to hundreds of kilometers for birds) and (3) the relative contribution of the different host species to tick feeding is unknown, estimating tick dispersal is a challenging task. Population genetics have been used to assess gene flow and thus dispersal at different scales, from the whole distributional range of I. ricinus, to local areas, using a variety of genetic markers. The sequencing of mitochondrial and nuclear genes has revealed that the Eurasiatic populations do not group according to their geographical origin, suggesting a high level of gene flow, probably due to migrating birds or to the movement of large mammals, including domestic livestock, between countries. Only the North African populations are genetically highly divergent from the other populations, suggesting inefficient geneflow between these two groups. At a smaller scale, the analysis of microsatellite loci among populations along 60 km long-transects located on both sides of wide rivers have revealed that there are no barriers to geneflow, highlighting the role of birds or large mammals in the dispersal of ticks. Genome wide SNP (Single Nucleotide Polymorphism) identification using Restriction-site Associated DNA Sequencing (RAD-Seq) was performed on a regional scale, where mountain groups and rivers have already been shown to be barriers to movement for many species; however, even here, extensive geneflow was observed for ticks. Finally, another set of SNPs based on the sequencing of Restricted Representative Libraries (RRL) were also used to investigate geneflow at the landscape scale (from tens of meters to a few kilometers). No isolation by distance has been detected at this scale either, also suggesting high levels of geneflow between populations. The contribution of those results for the design of control methods against ticks will be discussed.