

[[CV of Arnaud Estoup]]



My major scientific theme is the genetics of disequilibrium populations. These disequilibrium situations are often found in endangered and invasive/pullulating species. My research activity is both methodological (development of inferential methods, especially those based on approximate Bayesian computations - also named ABC methods) and empirical (field work and production of molecular data on species of interest). So far, my empirical studies were mainly based on the polymorphism analysis of strongly variable markers such as microsatellites and mtDNA sequences. For the last three years, we started to work with genetic markers produced by new generation sequencing (NGS) methods (i.e. SNP produced at a populational scale by RAD or shotgun sequencing approaches). We also included the study of key (quantitative) life history traits measured in the laboratory. Altogether, these studies aim at improving insights into the historical, demographical and adaptive factors underlying biological invasions and pullulations. They also participate to the design of management measures of invasive species. The main biological model that I am studying at the moment is the Harlequin ladybeetle *Harmonia axyridis*, an Asian species used as a biological control agent against aphids, which became established and invasive on four continents. We are presently using an ensemble of quantitative genetics, genomics and modelling approaches to learn about the ecological, demographical, historical and adaptive factors that were instrumental of the worldwide invasive success of this emblematic invasive insect species.

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Last update: **19/03/2015 16:08**