



CICLO DE CONFERÊNCIAS ISPA-IU

Centro de Investigação e Intervenção

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POPULATION GENETICS IN SPACE AND TIME: CAN WE RECONSTRUCT THE DEMOGRAPHIC HISTORY OF (ENDANGERED) POPULATIONS?

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Molecular data contain information on the recent evolutionary history of populations and much of the work carried out today owes to the work of the theoreticians who demonstrated that it was possible to use genetic data to detect departures from equilibrium conditions (e.g. panmitic population/mutation-drift equilibrium) and interpret them in terms of deviations from neutrality or stationarity. The detection of population size changes has usually been carried out under the assumption that samples were obtained from populations that can be approximated by a Wright-Fisher model (i.e. assuming panmixia, demographic stationarity, etc.). However, natural populations are usually part of spatial networks and are interconnected through gene flow. In the case of endangered species, the situation is thus particularly complex because tehy are facing at the same time a significant decrease in population size though habitat loss and an abrupt change in the patterns of gene flow because of habitat fragmentation.

Recent years have seen the development of landscape genetics, whereby environmental variables and landscape features (roads, agricultural land, elevation) can be analysed jointly with population genetics data, to identify potential barriers to gene flow. While such studies are very interesting they tend to ignore the temporal dimension (i.e. the fact that habitats have significantly changed in the last millenia).

In the last years our group has been increasingly involved in Madagascar, one of the hottest Biodiversity hotspots and a place undergoing major environmental changes. I will present some research carried out in Madagascar and Borneo and hopefully show that both the spatial and temporal scales must be taken into account.

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