

« Étude génétique des populations de langue Austro-Asiatique : de la famille linguistique au groupe de parenté ».

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November 22th, 2018 at 2pm - Auditorium de la Grande Galerie de l'Evolution, Muséum National d'Histoire Naturelle, Paris

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Abstract

The genetic diversity of a population carries with it traces of cultural practices and is a testimony of certain past events. Thus, language, which can be a cultural barrier to reproduction, and the kinship system, which will determine when, where and with whom individuals reproduce, will influence genetic diversity. The aim of this PhD thesis is to try to retrace the demographic histories of populations of South and Southeast Asia, at several cultural scales, from the Austroasiatic language family to descent groups using the genetic data.

Firstly, we studied in the Austroasiatic language family. Languages belonging to the same linguistic family come from the same "mother" language and we wanted to know whether, in addition to this linguistic kinship, the speakers of these languages shared a genetic kinship. We have studied the autosomal genetic diversity of Austroasiatic speaking populations and compared them to neighboring populations belonging to other linguistic families. We could not highlight any particular genetic kinship between populations speaking Austroasiatic languages. These results exclude the hypothesis of a common origin of populations speaking Austroasiatic languages and favor the hypothesis of a cultural diffusion of Austroasiatic languages.

Then, we investigated genetic kinship in descent groups in eight Southeast Asian populations. Individuals belonging to the same descent group claim to descend from a common paternal ancestor, in patrilineal populations, or from a common maternal ancestor, in matrilineal populations. We wanted to know if the common ancestor of these populations is mythical or biological. We investigated the genetic diversities of the Y chromosome and mitochondrial DNA of eight populations in Southeast Asia: four matrilineal populations and four patrilineal populations. Our data showed that individuals belonging to the same matrilineal clan are closely genetically related to their maternal line, visible in their mitochondrial DNA. Conversely, individuals belonging to the same patrilineal clan are no more genetically related to each other than two individuals randomly selected from the population in their paternal line, visible on the Y chromosome. These results reflect different realities between the patrilineal and matrilineal populations of Southeast Asia with a real common ancestor in matrilineal populations and a mythical common ancestor in the patrilineal clans.

Together, these results showed how different cultural processes have left genetic signatures on uniparental and autosomal genetic diversities and illustrated how the population geneticist can use these genetic diversities to trace the populations' demographic history.