GENETIC, LINGUISTIC AND CULTURAL DIFFERENCES IN GABON (AFRICA). NEW INSIGHTS INTO THE EARLY BANTU DISPERSAL

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Introduction.

In this work we have compared the linguistic and genetic diversity of Gabon (Africa) in order to contribute new elements to the scenarios concerning the early Bantu expansion related to the adoption of agriculture. To do so, we processed two independently collected datasets accounting for a total of 126 different linguistic varieties consisting of Swadesh word lists. The languages, belonging to the A and B zones defined by Guthrie (A75; B10-20-30-40-50-60-70), have been classified using a validated pronunciation distance measure (see below) and the results compared to the genetic diversity of 17 ethnic groups from Gabon. To further explore the cultural diversity of this region, we addressed traditional musical practices (Le Bomin *et al.* 2016).

Methods.

Linguistic data have been processed using the Levenshtein method that enables one to compare the pronunciation of the same concepts (phonemes) in a pairwise fashion, leading to the computation of differences that can be aggregated in a single general distance matrix. From published data, we have attempted to make the genetic dataset (Y-chromosome, mitochondrial DNA,) more representative of the 17 ethnic groups studied by filtering-off all the DNA donors that were born outside the areas typically inhabited by their respective ethnolinguistic communities. Autosomal data (Patin *et al.* 2017) have been considered too, but without improving their representativeness. Musical differences, coded as multistate characters, led to the computation of a phylogenetic tree. All classifications have been tested for their robustness by bootstrap resampling methods.

Results.

The two linguistic datasets lead to similar results, showing that the languages cluster into a comparable number of groups. Levenshtein linguistic distances are fully compatible with the classification of Grollemund *et al.* (2015) based on shared vocabulary, where sharing is operationalized as the percentage of words (not) having the same historical origin. This coding is unnecessary with the Levenshtein method, making it simpler to use and, for the larger amount of information it accounts for, more sensitive.

On the genetic side, the re-analyses of the 17 ethnic groups (representative of all the linguistic groups) did not show noteworthy signals of differentiation, meaning that the whole population is quite homogeneous. There are measurable, though very weak, differences concerning parental markers, the Y-chr. showing a higher level of differentiation and being pointing to the different profile of the Fang population (A75), which we assume is due to its recent immigration to Gabon from the north. A genetic diversity that is lower for the mitochondrial DNA than it is for the Y-chromosome probably corresponds to a differential migration rate related to the widespread practice of patrilocality in which women move into their husbands' residences after marriage, a behavior that happens even in matrilineal societies. Autosomal genome wide typing for all the groups confirms the specificity of the Fang

people but also shows that the linguistic group B20 is genetically more differentiated than all the other populations (B10, B30, B40, B50, B60, B70) that are close to each other.

The classification of musical diversity, as originally published, did not match the classification of the languages spoken by the same populations. Nevertheless, when re-processing the data of Le Bomin *et al.* (2016) by adopting resampling techniques, we obtain new results that are compatible with linguistic data. This outcome raises theoretical and methodological questions that are relevant to the conference as they concern inherent aspects of culture that might be part of a package transmitted as a whole (for example gastronomic traditions and language).

Conclusions.

Palaeoenvironmental and archaeological studies show that the opening of savannah plains on the costal region of Gabon started about 4000 ybp, with a Neolithization process dated at around 3500 ybp (and a detectable sedentarization starting at 2700 ybp in northern Gabon. According to linguistic cartography we suggest that B20 varieties emerged after an early migration southwards of Cameroon, through the rainforest, to the north of Gabon, a result that is compatible with genome-wide autosomal data (Patin *et al.* 2017). It is possible that a second early migration wave(s) took place by following the Atlantic coast from Cameroon to Gabon (varieties B10 and B30). Other languages probably emerged or arrived later (B40; B50; B60; B70), and the ethnic groups speaking them long remained within a defined geographic region as shown by their geographically-continuous linguistic areas.

Besides the Fang (A75) and the Kele (B20) group, the Bantu-speaking populations of Gabon are genetically homogeneous, meaning that the different migration waves concerned closely related people, therefore confirming the fast demic diffusion process of the Bantu-speaking populations. Nevertheless, 3000 years of history are enough to allow a genetic differentiation detectable on parental markers (Y-chromosome, mitochondrial DNA). The fact that we do not find evidence for it, suggests that considerable gene flow has taken place over this time and that the construction of social identity and ethnical belonging may better rely on social norms and cultural aspects than on ancestry.

To end, we would like to mention the population crises starting 1000 years ago (Oslisly *et al.* 2013) that was brutal enough to scramble pre-existing patterns of genetic and cultural diversity and which leads us suspect that the later cultural and genetic variability of Gabon has been largely shaped by population dynamics happened over the last millennium. They seem to cloud the historical signal.

References:

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