

## *Insights into the Y Chromosome variation in central-west Africa*

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Around 5,000 years ago, Bantu farmers left their Bantu homeland, situated near the border between Cameroon and Nigeria, to initiate one of the most dramatic migrations in pre-modern times; the Bantu expansion. Although much is known about this vast population movement in terms of linguistics and archaeology, little is known from a genetic point of view. In order to unravel the origin of male lineages associated to this Bantu expansion, we have typed 18 Y-STRs and 36 Y-SNPs in over 750 samples from the African locations of Gabon and Cameroon, comprising 22 Bantu groups and 3 Pygmy groups. Our results, like those obtained from mitochondrial DNA typing, show not only that Bantu populations are very homogenous, but also, that they are significantly different from Pygmy populations. This is not only visible at the Y-STR level, where genetic distance computations and Analysis of Molecular Variance (AMOVA) show Pygmies to be statistically different to Bantu populations, but also, at the Y-SNP level, where haplogroup B2b\* is the most predominant haplogroup in Pygmy populations (reaching 67% in some populations) in contrast to haplogroup E (including haplogroups E\*, E3\*, E3a) being the most predominant haplogroup in Bantu populations (reaching up to 90% in some populations). An interesting finding is the presence of the non-African haplogroup R (including haplogroups R1b and R1\*) in the Bantu population of the Fang. What can this unexpected haplogroup, present at a frequency of 18%, learn us about the origin of the (male) Fang population? Fang, as well as some other Bantu-speaking west-central African populations, claim a Semitic origin. Although this theory has become very popular in some circles over the last decades, it remains highly controversial. From a maternal point of view (cf. the analysis of mtDNA data by Llu s Quintana-Murci and his colleagues), the Fang do not show any genetic affinities with north African/Middle Eastern populations, clustering nicely with its Bantu-speaking neighbours from west-central Africa. Further refinement of the composition of the male R lineage, therefore, needs to be performed in order to provide insights into its origin.