

THE HISTORY OF CENTRAL AFRICAN PYGMY AND BANTU FARMER POPULATIONS

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Researchers from the CNRS and the Institut Pasteur¹, in collaboration with an international, multidisciplinary team², studied the demographic and genetic history of Pygmies and Bantu farmers of Central Africa. Their study suggests that the two groups began to diverge from a common ancestral population no more than 70,000 years ago, and then remained isolated from each other, before exchanging genes again starting 40,000 years ago, through the marriage of Pygmy women to male farmers. Once confirmed by other, independent genetic markers, these results will serve as a basis for studying the impact of the settling process on the evolution of the genome, and in particular, on vulnerability or resistance to certain pathogens.

Population geneticists, from both the CNRS and the Institut Pasteur¹, joined with other researchers in bioinformatics, ethnolinguistics, and epidemiology² to study Pygmy populations (nomadic hunter-gatherers) and Bantu villagers (settled livestock owners and farmers) who live in Central Africa. The objective: to determine to what degree social, cultural, and demographic factors have influenced these populations' genetic heritage.

They worked on mitochondrial DNA³ (mtDNA), which is only transmitted by the mother. Their population sample was composed of 1,500 individuals from 20 populations of Bantu village farmers and 9 populations of Pygmy hunter-gatherers from Gabon, Cameroon, the Central African Republic, and the Democratic Republic of the Congo.

The researchers identified an ancestral and native line of mtDNA from Central Africa once shared by the Western Pygmies and the farmers. This evolved in a single line in today's Western Pygmies and in a wide variety of lines among the farmers. Generally speaking, there is much less variability of mtDNA among the Pygmies than among the farmers: the maternal gene pool of Pygmies today derives from a small number of common ancestors.

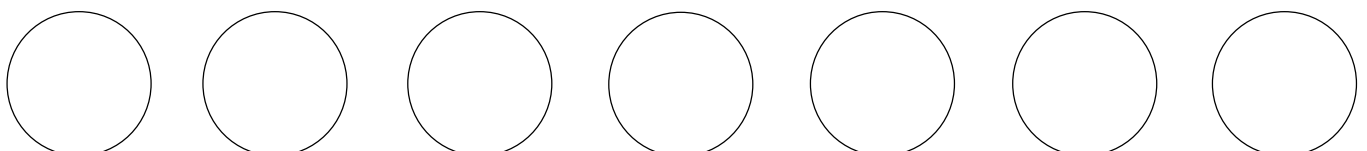
This study suggests the following scenario: the Pygmies started to diverge from the ancestral population at most 70,000 years ago. After a period of isolation, during which the current phenotypic differences between the Pygmies and farmers accumulated, Pygmy women began to marry male farmers (but not the other way around), at most 40,000 years ago; this continued until at least a few thousand years ago. Subsequently, the Pygmies' gene pool was not expanded by external contributions, contrary to that of the farmers, during the "Bantu expansions"—an event that corresponds to the technological, demographic, and linguistic changes in the later Stone Age.

The researchers are now going to study nuclear DNA, especially the Y chromosome, to verify these conclusions. They chose West Africa, because it is one of the only regions where nomadic and settled populations cohabit. Ultimately, they hope to study the relationships between the genome and the vulnerability or resistance of populations to pathogens. Transition to a settled way of life is accompanied by three factors that have a significant impact with regard to pathogens: demographic growth, which allows them to better propagate, the presence of

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²Eco-anthropology and ethnobiology laboratory (CNRS/Natural History Museum/Université Paris) and Language dynamics (CNRS/Université Lyon 2), and in collaboration with the Universities of Barcelona, Haifa, Santiago de Compostela, and Yale, the Centre for Human Polymorphism (CEPH - Fondation Jean Dausset) in Paris and the Franceville International Centre for Medical Research (CIRMF),

³Mitochondria are cellular organelles that allow cells to breathe. They possess their own DNA, called mitochondrial DNA.



waste in the living environment, which also constitutes vectors for diseases, and the presence of domestic animals, whose diseases are more likely to be passed on to humans.

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BIBLIOGRAPHY

Maternal traces of deep common ancestry and asymmetric gene flow between Pygmy hunter-gatherers and Bantu-speaking farmers. Quintana-Murci L, Quach H, Harmant C, Luca F, Massonnet B, Patin E, Sica L, Mougouma-Daouda P, Comas D, Tzur S, Balanovsky O, Kidd KK, Kidd JR, van der Veen L, Hombert JM, Gessain A, Verdu P, Froment A, Bahuchet S, Heyer E, Dausset J, Salas A, Behar, *Proc Natl Acad Sci USA* 105:1596-601 (February issue, published 4 February 2008).

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