Early human dispersal from Africa: A model-based test of two hypotheses

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INTRODUCTION
Did early modern humans leave Africa through a major migration process, dispersing simultaneously over Asia and Europe, or in two main waves, first through the Arab peninsula into Southern Asia through a Southern route (SR), and later crossing Palestine into Western Asia and Europe?

To shed light on these questions, we studied single nucleotide polymorphism from 20 worldwide populations and we developed explicit geographic models of the demographic expansions. We combined different approach including the analysis of the population structure and analysis of the LD pattern to reconstruct two key parameters of human evolution (the effective population size and the population divergence time) to identify a model describing the emergence and dispersal of our species “Out of Africa”.

Population structure analysis
We ran the ADMIXTURE analysis for increasing values of k, up to 12, performing 5 independent runs for each value (the different runs gave consistent results).

The model’s predictions appear most accurate when the genotypes fall into 6 genetic clusters.

DISCUSSION
The earlier separation from Africa estimated for Asians than for Europeans, and the correlation between levels of linkage disequilibrium and distance travelled under a Multiple Dispersal model, support the hypothesis that, before the Northward expansion from Africa through Palestine and then Eurasia, another human group left Africa through a Southern route leading to Asia.

These results might call into question the genetic relationships among and East Asian genotypes.

The split between Europeans and Africans seems to have happened some 15,000 years later than that between Asians and Africans.

Inferring changes in population size and population divergence times
Under neutrality, genetic differences between populations, measured by Fst, are inversely proportional to the effective population sizes (Ne) and directly proportional to the time since their separation (T).

We estimated Ne independently in each population using all polymorphic markers available for that population.

African populations have higher Ne over time respect to non-Africans. Europeans and Northern Central Asians started to expand around 15,000 years ago. Southern Asians generally exhibit a demographic decline.

Comparing alternative hypotheses on human dispersal

Single-Dispersal model (SD)
Anatomically modern humans left Africa through Palestine and dispersed into all of Eurasia.

Prior to the dispersal across Palestine, another exit from Africa through the Arab Peninsula and the Indian Subcontinent, all the way to Melanesia and Australia.

To obtain a realistic representation of migrational distances between populations, we modeled resistance to gene flow, based on the landscape features known to influence human dispersal. In addition, under the SD model we hampered movement from Arabia to India under the MD models, we created a buffer of low resistance value along the SR.

Genetic distances were calculated as a matrix of Wright’s Fst statistics between pairs of populations, each value being the average of the pairwise Fst estimates for each SNP, over the 3,418 SNPs in the reduced dataset.

Correlations between genetic and geographic distance matrices were calculated according to the Mantel test.

Multiple-Dispersal model (MD)

Models plausibly describe the observed patterns of genome diversity. The highest correlation was observed for the SD model, but levels of significance are the same in all cases, reflecting the fact that, in all the, the predictions of the SD and MD models have much in common.

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