

mtDNA analysis of Nile River Valley populations: A genetic corridor or a barrier to migration?

Abstract:

To assess the extent to which the Nile River Valley has been a corridor for human migrations between Egypt and sub-Saharan Africa, we analyzed mtDNA variation in 224 individuals from various locations along the river. Sequences of the first hypervariable segment (HV1) of the mtDNA control region and a polymorphic HpaI site at position 3592 allowed us to designate each mtDNA as being of "northern" or "southern" affiliation. Proportions of northern and southern mtDNA differed significantly between Egypt, Nubia, and the southern Sudan. At slowly evolving sites within HV1, northern-mtDNA diversity was highest in Egypt and lowest in the southern Sudan, and southern-mtDNA diversity was highest in the southern Sudan and lowest in Egypt, indicating that migrations had occurred bidirectionally along the Nile River Valley. Egypt and Nubia have low and similar amounts of divergence for both mtDNA types, which is consistent with historical evidence for long-term interactions between Egypt and Nubia. Spatial autocorrelation analysis demonstrates a smooth gradient of decreasing genetic similarity of mtDNA types as geographic distance between sampling localities increases, strongly suggesting gene flow along the Nile, with no evident barriers. We conclude that these migrations probably occurred within the past few hundred to few thousand years and that the migration from north to south was either earlier or lesser in the extent of gene flow than the migration from south to north.