

Abstract

Although West Africa is region rich in its cultural and lingvistical diversity, patterns and distributions of genetic diversity are still not fully understood. Most of the studies dealing with the population genetics of mitochondrial DNA comes from the variability of its hypervariable segment (HVS-1) only. In this diploma work I have focused on whole control region aiming for determination of the contribution of HVS-2 segment to phylogenetical classification and explanation of genetic relationship in African Sahel. To investigate these two goals 1075 sequences from 24 populations have been analyzed (104 sequences comes from this study, the rest was publicated previously by other authors). The results indicated that HVS-2 has a specifying meaning in the phylogenetical classification in case of complete reference database is available. On the population level African Sahel seems to be quite homogeneous and its populations are mostly differentiated from Saharan groups. It seems that geographic factors have bigger impact on distribution of genetic diversity then the lingvistic ones. Close genetic relationships of West African populations and their difference with Saharan populations suggests a higher importance for migratory corridor along Sahel belt.