

ABSTRACT

Y chromosome is due to its special characteristics the ideal tool of archaeogenetic studies. Its diversity is influenced by several factors and I analysed two of them (geographical location and subsistence). I generated SNPs and STRs data from several loci of samples from Slovakia (156 samples, 5 regions) and sub-Saharan Africa, where I analysed samples of sedentary farmers (481 samples, 18 regions) and nomadic pastorals (405 samples, 16 regions).

Slovakia is situated at the meeting point of two migration ways. First of them was spread from the east to the west and is associated with enlargement of haplogroup R1a in Europe. The second came from the Iberian Peninsula eastward and is associated with enlargement of haplogroup R1b. Results of MDS graphs replicate the geographical map of Europe. Slovakia is situated in the middle of Russian, Balkanian and Iberian samples. Correlation between genetics and geographic distances is indicated by hierarchical AMOVA analysis and Mantel tests.

Populations in sub-Saharan Africa differ from each other by the subsistence pattern. Different life style influence the diversity of the Y chromosome. Nomadic pastoralists and sedentary farmers share different haplogroups, for example, while haplogroup R1b was detected only in nomadic pastoral groups, sedentary farmers are characterized by the high presence of E1a-M33. Median networks indicated that different sources contributed to the current male-specific gene pool of the nomadic pastoral and sedentary farmer populations.

Pastoral population Rashaayda is statistically and significantly different from other African populations due to their recent arrival to Africa from the Arabian Peninsula. Rashayda also shows reduced diversity of Y chromosome that indicate of small founder population that came into Africa.

Key word: Y Chromosome, SNPs, STRs, Slovakia, Africa, nomadic pastoral populations, sedentary farmer populations