

Polymorphism of the mitochondrial DNA control region among residents of the West Pomeranian Voivodeship in the context of its post-war history

Summary

The population of West Pomerania is distinctive due to the almost complete replacement of the German population in the area after World War II by migrants from different parts of Poland and Europe. Therefore, it was hypothesized that the genetic variation of the population of the West Pomeranian Voivodeship is likely to be higher than that of populations with a distinct demographic history from Poland and Europe. This research aims to estimate the variation in the mitochondrial genome of the inhabitants of West Pomeranian Voivodeship, thereby enabling inferences regarding the impact of post-war migrations on the observed variation. In this study, the sequences of the entire control region in Poland were analysed for the first time and compared with available data for other European populations.

The material for the study, in the form of oral swabs, was collected from 300 unrelated residents of 101 urban and rural municipalities and 3 cities with district rights in the West Pomeranian Voivodeship. The analysis was conducted on the most variable region of mtDNA, namely the control region, which serves as a universal tool for reconstructing population, demographic and migration patterns. The following parameters were used to estimate the level of variation within the study population, as well as to compare it with other populations: number of polymorphic sites and haplotypes, nucleotide and haplotype diversity, neutrality coefficients, random match probability (RMP), genetic distance (pairwise F_{ST}) and molecular variance AMOVA. The given parameters were analysed independently at the level of the entire control region and the HVSI and HVSII areas, due to the available literature data for Polish and European population comparative analyses.

The mtDNA analyses revealed a high level of genetic diversity within the mtDNA control region of the residents of the West Pomeranian Voivodeship. The number of identified haplogroups and sub-haplogroups in the above study proves, in accordance with the research hypothesis, that the West Pomeranian Voivodeship is one of the most diverse populations compared to other Polish and European populations. The uniqueness of the population of the West Pomeranian Voivodeship is evident both in the data for the whole mtDNA control region and its HVI and HVII fragments. The negative values of the neutrality

tests, indicating numerous migrations from Poland and Europe, confirmed the turbulent demographic history of the West Pomeranian Voivodeship following World War II. In the region, no genetic differences between urban and rural residents were observed. The haplotype and nucleotide variations indicate distinct genetic characteristics of the West Pomeranian Voivodeship.

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