

## **The genetic history of Poland**

After discovery of the DNA structure by Watson and Crick (double helix) and deciphering of the genetic code, we are now at the stage of learning full sequences of genomes of many organisms, including humans. On the January 26<sup>th</sup>, 2002, the President Bill Clinton and the Prime Minister Tony Blair, announced at the press conference that the sequence of the first human genome, i.e. of all genes, was described. They claimed this as a very important achievement. Since then, we observe an enormous progress in techniques of DNA sequencing and each person can obtain his own DNA sequence at the cost of 1 000 \$.

What are the reasons for genome sequencing? First of all, it is very important for medical genetics. It allows to learn whether in our genomes the genes responsible for predisposition towards heritable diseases and cancer are present. It allows also to learn the degree of our kinship with other people and to reconstruct history of our species starting from times when our ancestors left Africa, or even from earlier. We have learned how big at the DNA level is a difference between us and our closest cousins, The chimpanzees (ca. 1,5 %) and that we have ca. 2% of Neanderthal genes, what means that the two species, *Homo sapiens* and *Homo neandertalensis*, hybridized with each other.

The main goal of this project is to reconstruct the genetic history of Poles. We will analyze the contemporary and ancient genomes to find answer to several important questions: (1) What was the genetic structure and polymorphism of human population inhabiting the area of the present-day Poland and how it was changing during the last thousands of years? (2) Were the changes in population structure connected with major events in our history, as shift from the hunting – gathering culture to agriculture? (3) Is there (and how big it is) in our genomes an admixture of genes inherited after Vandals, Goths and other tribes, who invaded Eastern and Central Europe in the period of Great Migrations? (4) How big are genetic differences between various Polish sub-populations and populations of neighboring countries?

Studies of similar character are carried on in many countries; special consortia are created to analyze sequences of numerous genomes. For example, the inhabitants of British Isles want to learn, how many genes in their genomes is of “German”, “Roman” or Norman origin. Archeologists had discovered many commentaries of people who inhabited Poland in past centuries. Material (bones) are available for DNA isolation and sequencing to identify the ethnical affiliation of buried people. The project will be carried on in close cooperation with archeologists and with research groups who have gathered data on genomes of the contemporary Polish population. We are sure that thanks to this cooperation, the project has good chances for success.