Abstract

This doctoral thesis is submitted in the form of science publications with impact factor and presents human biological variation in two different ways.

The first part is the study of phenotype variation focused on the degree of limb bones bilateral asymmetry. Besides genetic and hormonal factors asymmetry may develop as a response to biomechanical and to environmental factors influencing the individual/population. Therefore this trait can be considered as a measure of person’s living conditions, health or environmental stress of different origin or examine the effects of behavioral distinctions as sexual division of labor and differences in subsistence strategy. The submitted publication (Kujanová et al., 2008) is based on samples of two diachronic populations (medieval and recent) from Bohemia with different expected levels of health/environmental stress. The study is focused especially on these aspects that may be indicative of various stresses, such as malnutrition or other nonspecific factors influencing health of persons living in the studied populations. According to the results we propose that bilateral asymmetry observed in the diachronic populations showed some differences supporting the theory that the medieval population was not subjected to as highly stressful conditions as the recent population. These results provide important information about different variation of postcranial skeleton and contribute to knowledge of human growth, adaptation, and development in both living and past populations.

The second part of the thesis presents human biological variation in the light of population genetics. To understand biological history of chosen regions the submitted studies were based on the analyses of neutral polymorphisms that are uniparentally inherited, the mitochondrial DNA and the nonrecombining portion of the Y-chromosome. Over the last twenty years these polymorphisms have played a crucial role in population genetics as they enable connection between the observed variability and evolutionary events we are trying to detect. The submitted studies were focused on genetically unknown regions/populations of Africa, namely the Egyptian Western Desert (Kujanová et al., 2009), the Chad Basin (Černý et al., 2007) and the populations of the Tuareg (Pereira et al., 2010). The results, that enabled to reveal the local ancient demographic events, have considerably contributed to clarifying the colonization of Africa. The other study (Černý et al., 2008) shed light on some ancient migration events of Yemen representing the key location for population movements out of and back into Africa. Finally, the study Černý et al. (2009) provides the first genetically based information about the colonization of the Soqotra archipelago that is situated near the proposed southern migration route of anatomically modern humans out of Africa ∼ 60,000 years ago (kyr).