

ABSTRACT

Agriculture, with different Neolithic cultures, starts in the Near East more than 10,000 years ago. This new way of life has very different archaeological manifestations than previous Mesolithic. After its Near Eastern emergence, the farming practices rapidly penetrated into southeastern Europe and the first signs of Neolithic in Central Europe are already 7,000 years old. It is being considered that the cultural innovations influenced demographic growth of the populations that have taken part in the Neolithic spread. In such situation, new mutations would have to fix and could form new specific haplogroups for Europe with ancestral ties to the Near East. Phylogeographic studies such as founder analysis of European and Near Eastern mtDNA sequences found that the European Neolithic component was enriched mainly by haplogroups J and T1, and that the genetic contribution of farming economy in European gene pool is about 10 - 20%. However, studies like these have not been yet realized in particular parts of Europe. The aim of this thesis is to disentangle the internal variability of Central European haplogroups J and T1 thought to be involved in the Neolithic demic diffusion. We classified these haplogroups from the HVS-I mtDNA sequences of 281 samples of the recent population of the Czech Republic. We used 36 sequences J and T1 mtDNA haplogroups plus 124 J and 40 T1 sequences of the six countries of Central Europe published before to calculate networks. We provide here age estimates of all revealed J and T1 Central European clades by conventional phylogenetic methods. We identified only three subclades of haplogroup J - J1b1a, J1c2, J2a1a whose coalescence age might indicate participations in the Neolithic expansion. Since their presence in our dataset is only 3.9%, we suppose that the demographic growth in the Neolithic could not be too strong in Central Europe and bearers of haplogroups with older coalescence age must have been engaged in the spread of the Neolithic technology in this region. Our results are also confronted with these obtained on ancient mtDNA isolated from the Central European Neolithic and Mesolithic remains.