ABSTRACT

This Master's thesis analyzes and compares the allele distribution of some polymorphisms within nutrigenetics-active genes in the Czech and Vietnamese population.

The theoretic part of this thesis describes the genes along with their polymorphisms that can contribute to the metabolism of some nutrients or which are long known for their association with the onset and manifestation of some metabolic diseases and other pathologic processes. It also discusses the possible causes of positive selection and its impact on the allele and genotype frequenccy of said polymorphisms.

The own research is composed of the processes of DNA obtaining and extraction, genetic analysis' methods including PCR-RFLP and Realtime PCR along with the food frequency questionnaire (FFQ) method. Results of the analyses and questionnaire are statistically evaluated and presented with the aid of tables and graphs. The discussion brings some possible causes for said outcomes.

The results show that the distribution of the risk alleles of observed polymorphisms are usually lower in the Vietnamese community than it is in the Czech population especially within: the FTO gene which can predict the development of obesity, the CTF7L2 gene which is associated with type 2 diabetes, in ADH1B which can regulate alcohol consumption and lastly within the MCM6 gene responsible for lactase persistence. Comparable allele distributions can be found in polymorphisms of the MC4R gene, the HFE gene a the ApoE gene. Presented results also corelate with the findings in the FFQ, where it is noticeable that the Vietnamese community consumes less alcohol and milk products than the major population of Czech.

This thesis could be the first one in its focus and theme and could benefit especially the Vietnamese community living in Czech republic. The results of this thesis could serve as a tool for food recommendations and guidelines making which are targeted specifically for Vietnamese not only in disease prevention but also in the therapy of already developed pathological states especially according to the genetic predispositions found in this study.

Keywords: SNPs, polymorphisms, nutrigenetics, genetic analysis, nutrition