Abstract

Metabolic syndrome (MetS) is a complex condition with a number of interacting genes, epigenetic and environmental factors underlying its pathogenesis. The analysis of genetic component of MetS showed that number of defining parameters of the syndrome is linked to regions of rat chromosome 4. In order to verify these quantitative trait loci (QTL), a double congenic strain was derived with parts of chromosome 4 of spontaneously hypertensive rat (SHR, an inbred MetS model) origin introgressed onto genomic background of congenic Brown Norway strain (BN-*Lx*). The aim of the proposed thesis is comprise detail genetic mapping of differential segments of the above mentioned double congenic strain BN-*Lx*.SHR4 and comparison of its metabolic profile under different dietary conditions with varying carbohydrate and fat content. Utilizing DNA sequence and gene expression comparisons, candidate genes or polymorphisms for the MetS aspects and potential nutrigenetic interactions will be identified.

Key words:

nutrigenetics, experimental models, metabolic syndrome, congenic strain,
genotyping, rat