Abstract

Rare diseases are a heterogeneous group of disorders. Knowledge of their molecular basis is poor and till recently there were no appropriate methodical approaches due to a limited number of patients. Novel genomic techniques, especially the DNA array technology and the next generation sequencing emerging in last few years, enabled studies of these diseases even in small families and sporadic cases.

This PhD thesis focuses on application of novel genomic techniques in studies of rare inherited diseases. It describes a use of DNA array technology in linkage analysis, analysis of differential gene expression, analysis of copy number variations and homozygous mapping, and a use of next generation sequencing technology. Combination of these methods was used for identification of molecular basis of adult neuronal ceroid lipofuscinosis, Rotor syndrome, isolated defect of ATP synthase and mucopolysaccharidosis type IIIC.