Mental retardation (MR) is a very heterogeneous common neurodevelopmental disorder with a population prevalence of 2.5-3 %. The importance of genetic factors in the development of MR is high but in a significant number of cases the etiology remains unexplained. Recent studies using array methods pointed to frequent occurrence of copy number variants (CNVs) in patients with MR. Pathogenic CNVs were identified in 10-15 % patients with idiopathic MR and normal karyotype.

The aim of our work was the analysis of genome-wide gains and losses of genetic material in a group of Czech patients with MR and a thorough bioinformatic analysis of the genetic changes identified aiming at the assessment of their clinical significance.

We performed whole genome analysis using the HumanCytoSNP-12 BeadChips (Illumina) in 183 patients with idiopathic MR, normal karyotype and no FMR1 gene expansion. Data analysis was carried out using two independent programmes, GenomeStudio and QuantiSNP. The findings were subjected to two rounds of thorough bioinformatic analysis. Based on this analysis we classified the CNVs into 4 categories: pathogenic CNVs, probably pathogenic CNVs, CNVs with uncertain clinical significance and benign CNVs. With the exception of the benign variants, all CNVs were confirmed using an independent laboratory method such as FISH, MLPA, QFPCR, etc.

A total of 1207 findings were assessed with an average number of findings per patient of 6.6. In the first round of analysis 1080 findings were classified as probably not significant, and the remaining 127 findings were independently verified. After the verification and the second round of bioinformatic analysis, 21 CNVs were classified as pathogenic because they have been associated with MR previously, and 19 CNVs were included in the group of probably pathogenic CNVs. Together these aberrations were identified in 13.1 % of cases, in agreement with published studies.