MULTIPLEX LIGATION-DEPENDENT PROBE AMPLIFICATION OF MICRODELETION SYNDROMS

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Introduction: Microdeletion syndromes are an extensive group of diseases affecting various organs and systems. These diseases are caused by deletions of small sections of chromosomes. Previously, most microdeletion syndromes were described as pathologies of unknown origin and were not even associated with "chromosomal breakdowns", since it was not possible to conduct subtle and accurate genetic diagnostics. Microdeletion and microduplication syndromes are defined as a group of clinically recognisable disorders characterised by a small (< 5 Mb) deletion or duplication of a chromosomal segment spanning multiple disease genes. Clinically well described syndromes, for which the involvement of multiple disease genes has been established or is strongly suspected, such as: 1p36 deletion syndrome, Wolf-Hirschhorn syndrome, Cri-du-Chat syndrome, Sotos syndrome, Saethre-Chotzen syndrome, Williams-Beuren syndrome, Williams-Beuren duplication syndrome, Langer-Giedion syndrome, WAGR syndrome, Prader-Willi syndrome, Angelman syndrome, Rubinstein-Taybi syndrome, Miller-Dieker syndrome, Lissencephaly-1, Smith-Magenis syndrome, Potocki-Lupski syndrome, Alagille syndrome, DiGeorge syndrome, 22q11.2microduplication syndrome, Phelan-McDermid syndrome.

Methods: MLPA (Multiplex Ligation-dependent Probe Amplification) is the go-to technique for studying gene copy number variations (CNVs) associated with disease. The power of the technique lies in its versatility: MLPA can be used to detect copy number changes in anything from complete chromosomes to single exons. This SALSA MLPA probemix for detection microdeletion syndromes contains 52MLPA probes with amplification products between 130 and 483 nucleotides (nt). The probes detect sequences involved in a distinct subset of microdeletion and microduplication disorders.

Results: At the clinical diagnostic laboratory, examined 57 children with suspected microdeletion syndrome. Among them, a heterozygous deletion was found of SNRPN-u5, SNRPN-CpGisl, UBE3A-10, UBE3A-1genes that corresponds to Prader-Willi/Angelman syndrome, heterozygous deletion (DQ=0.5) CLTCL1-3, CDC45-1, GNB1L-8, DGCR8-2, ZNF74-2, MED15-10, SNAP29-3 genes (Di Georgia syndrome) and ELN-4, ELN-6, ELN-27 heterozygous deletion of Williams-Beuren syndrome.

Conclusion: This diagnostic method allows you to detect microdeletions and microduplications, which are often not noticeable with standard cytogenetic analysis.