# MOLECULAR GENETIC APPROACHES IN DIAGNOSIS OF DUSCHENNE/ BECKER MUSCULAR DYSTROPHY

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**Keywords: Duchenne /Becker muscular dystrophy, mutations, MLPA**

**Introduction**: Duchenne/Becker muscular dystrophy (DMD/BMD) is inherited X-linked disease with a frequency of 1: 3,500 newborn males. Deletions and duplications in the DMD gene are errors of reading frameshift and premature termination of translation. Structural rearrangements of BMD does not lead to reading frame rule, DNA polymerase can "skip" deleted exons , which leads to the synthesis of truncated protein, which can fulfill its functions some extent.

**Methods**: We studied the DNA of 104 patients with suspected DMD / BMD and heterozygous, as well as chorionic villi samples (CVS) obtained by prenatal diagnostics. Multiplex Ligation - dependent Probe Amplification(MLPA) (MRC Holland) was used to study of copy number variations of 79 exons of DMD gene. Validation MLPA results and whole exome sequencing (WES) of patients with MLPA negative results were performed at Centogene (Germany). Detection of nonsense mutations leading to the appearance in mRNA a premature stop codons of DMD gene are relevant to stratify patients for antisense-targeted therapy of Duchenne muscular dystrophy.

**Results**: Mutations of (36) 37 % of patients were revealed in the DMD gene. Deletions were detected in (27) 75 %, duplications in (9) 25% of cases. WES of 41patients was conducted for validation and MLPA negative results. Point mutations were identified in 30 (73%), frameshift missense mutations - in 7 (23%), nonsense mutations - in 9 (30 %) cases. Validation of MLPA results (deletions) were performed in 14 patients (46 %).

**Conclusions**: Algorithm of molecular diagnostic of DMD /BMD by MLPA is a method for the detection of large deletions and duplications 79 exons of DMD gene and WES should be to determine the missense and nonsense mutations of DMD gene. Our results formed the basis of clinical protocols of diagnostic and treatment of Duchenne/Becker muscular dystrophy in Kazakhstan.