E-P06.14 - High genetic heterogeneity of lysosomal storage diseases in Ukraine

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Disclosures

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Abstract

Introduction: Lysosomal storage diseases (LSD) are inherited metabolic diseases that are caused by genetic alterations in lysosomal enzymes genes. Most of the human disease is characterized by marked genetic heterogeneity, far greater than previously appreciated. This degree of allelic, locus, and phenotypic heterogeneity has important implications for gene discovery and has important implications for development of molecular treatments for individual patients.Aim: Analysis of genetic heterogeneity of the most common lysosomal storage diseases in patients from Ukraine.Materials and methods: The frequencies and spectrum of causes mutations in patients with Gaucher (n=62), Niemann-Peak A/B (n=16), metachromatic leukodystrophy (MLD) (n=28), mucopolysaccharidosis type I (MPS I) (n=17), mucopolysaccharidosis type IIIA (MPS III A) (n=21), GM1-gangliosidosis (n=32) were analyzed. Mutation analysis was performed using classical PCR analysis and Sanger sequencing. Comparative analysis of the common mutations in different populations was performed according to the published data.Results: Our research has shown that the frequencies of common mutations in patients with Niemann-Peak A/B, MLD and GM1-gangliosidosis in Ukraine is significantly different from other European. Frequencies of common mutations in patients with Gaucher, MPS I and MPS IIIA is close to that in the nearest neighbors -

Poland, Hungary and Slovakia, but are lower than European average, and the genetic heterogeneity of these diseases in Ukraine is pronounced. Conclusions: Existence of high genetic heterogeneity of LSD in Ukraine creates significant problems during medical genetic counseling for families and requires the development of specific diagnostic algorithm that regulates the stages of diagnostic search using DNA analysis.