ポスターセッション 17
Molecular Biology

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日本語

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Molecular and Functional Characterization of Primary Severe Hypertriglyceridemia using Whole Exome Sequencing

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Background: Few data exist regarding clinical application of whole exome sequencing (WES) for the molecular diagnosis of severe hypertriglyceridemia (HTG).

Methods: WES was performed on 28 individuals exhibiting severe HTG (> 1,000 mg/dl) without any transient causes (median TG 1,756 mg/dl [IQR 1,288-2,443]) followed by recessive and dominant inheritance modeling in known monogenic HTG genes and disease-network candidate analysis gene ranking to identify a causative mutation(s).

Results: We determined possible causative mutation(s) in 14 individuals (50%). Among them, we identified 2 individuals with LPL deficiency with double mutations in LPL gene, and 2 individuals with a heterozygous mutation carrier in LPL gene, one individual harboring a double mutations in LPL gene and APOA5 gene, one individual with a heterozygous mutation in LMF1 gene, and 2 individuals with type 3 hyperlipidemia harboring mutations in APOE gene, including novel ones. Interestingly, we also identified 6 other individuals harboring a deleterious mutation either in CREB3L3, MLXIPL, SLC25A40, or GCKR gene.

Conclusion: We identified potential causative mutations in 14 among 28 individuals (50%) with severe HTG. Clinical WES is now feasible where molecular diagnoses could be made in such extreme cases, which could potentially provide appropriate therapies.