

MEETING ABSTRACT

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Evaluation of potential role of Atp5g3 in modulating alcohol preference and obesity

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Background

Mitochondrial ATP synthase, subunit c, isoform 3 (*Atp5g3*), encodes subunit 9 of a multisubunit enzyme that catalyzes the synthesis of ATP during oxidative phosphorylation. Each ATP synthase complex has multiple copies of subunit 9 in its transmembrane portion (Fo). While much is known about the molecular mechanisms and function of this complex in the mitochondrial membrane, the impact of variants in this complex and its connection to other pathways and human diseases and disorders is unknown.

Materials and methods

Using extensive phenotype and gene expression data sets in GeneNetwork, we generated correlations between variation in the expression of Atp5g3 in three tissues (hippocampus, cerebellum, and liver) and traits that are related to alcoholism and metabolism/obesity.

Results

With limited numbers of strains, current data in Gene-Network suggested potential associations between expression levels of Atp5g3 and alcohol and obesity. The expression patterns of Atp5g3 and each of its 12 partner genes/transcripts varied greatly in the same tissue. The correlation in expression levels between Atp5g3 and each of these partners are different in tissues and genes. Transcriptome QTL mapping indicates that the Atp5g3 is differentially regulated in hippocampus, cerebellum, and liver. However, there is currently no reported polymorphism in Atp5g3 and its immediate up- and downstream among three inbred strains—C57BL/6J, DBA/2J, and BALB/cJ.

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Conclusions

The potential role of variants in Atp5g3 in both alcoholism and metabolism warrants further investigation. In particular, the focus should be on immediate genetic regulation of Atp5g3 expression and to adduce further evidence to support or refute potential causal links.

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