Supplementary data 12. SNPs linked to GSS and GGT7 gene polymorphisms

The functional effects of *GSS* and *GGT7* gene polymorphisms might be explained by linkage disequilibrium to some other SNP(s) at neighboring genes. A polymorphism rs13041792 is located at 1.4kb 5' of the *GSS* gene and is in a strong linkage disequilibrium (D'≥0.91) to SNPs situated near or in neighboring genes such as *MYH7B* (rs6120772, rs6120775, rs7261969, rs6088667, rs3746446, rs7268266, rs6120788, rs3746436, and rs3746435), *MIR499A* (rs3746444) and *TRPC4AP* (rs752075). Interestingly, certain of these SNPs tightly linked to a polymorphism rs13041792 of the *GSS* gene are associated with the risk of several common diseases. In particular, an SNP rs3746446 at *MYH7B*, a myosin heavy chain 7B, showed a strong association with the risk of congenital heart defects [1]. Numerous studies have reported that SNP rs3746444 of *MIR499A*, a gene encoding microRNA 499a, is associated with the risk of biliary atresia [2], cancer [3,4,5,6], arthritis [7,8], and coronary heart disease [9] as well as diabetic neuropathy in type 2 diabetes [10,11]. Interestingly, Latini with co-workers observed a correlation of allele rs3746444-G at *MIR499A* with a decrease in the number of mtDNA copies in peripheral blood of patients with type 2 diabetes especially those who develop diabetic peripheral neuropathy [12]. A polymorphism rs3746444 in the miR-499 precursor was found to affect the maturation of miR-499-5p, thereby altering its antiapoptotic function [12]. Since polymorphisms rs13041792 of *GSS* and rs3746444 of *MIR499A* are in a strong LD (D'=0.9807) and rs13041792-A allele is correlated with rs3746444-G allele, it can be suggested that the carriage for rs13041792-A may increase susceptibility of the cell to apoptosis. This means that pancreatic β-cells may have an increased sensitivity to apoptosis in the carriers of the rs13041792-A allele of *GSS*. In addition, the DNAse and histone ChIP-Seq data from Roadmap Epigenomics Consortium showed that polymorphisms of the *GSS* gene are involved in epigenetic regulation of transcriptional activity of genes in the pancreatic islets through the changes in chromatin states at enhancer or promoter regions. In particular, a polymorphism rs13041792 at *GSS* along with closely linked SNPs such as rs6088662 (4kb 5' of *GSS*), rs6119548 (9kb 5' of *GSS*), rs6088667 (at *MYH7B*) are located at genomic region regulating gene expression in the pancreatic islets through DNase hypersensitivity site, acetylation at the 9th lysine residue of the histone H3 protein (H3K9ac), methylation at the 4th lysine residue of the histone H3 protein (H3K4me), and chromatin state, respectively.

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