Genome-wide association study of the plasma triglyceride response to an n-3 polyunsaturated fatty acid supplementation

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Funding: Studies have shown a large interindividual variability in plasma TG response to long-chain n-3 PUFA supplementation, which may likely be attributable to genetic variability within the populations studied. The objective is to compare the frequency of SNPs in a genome-wide association study between responders (reduction in plasma TG levels ≥0.01 mM) and nonresponders (increase in plasma TG of ≥0.01 mM) to supplementation. Genomic DNA from 141 subjects who completed a 2-week run-in period followed by 6-week supplementation with 5 g of fish oil daily (1.9-2.2 g EPA and 1.1 g DHA daily) were genotyped on Illumina HumanOmni-5-QuadBeadChip. Thirteen loci had frequency differences between responders and nonresponders (P < 1 x 10(-5)), including SNPs in or near IQCJ-SCHIP1, MYB, NELL1, NXPH1, PHF17, and SLIT2 genes. A genetic risk score (GRS) was constructed by summing the number of risk alleles. This GRS explained 21.53% of the variation in TG response to n-3 PUFA supplementation when adjusted for age, sex, and BMI (P = 0.0002). Using Fish Oil Intervention and Genotype as a replication cohort, the GRS was able to explain 2% of variation in TG response when adjusted. In conclusion, subjects who decrease their plasma TG levels following n-3 PUFA supplementation may have a different genetic profile than individuals who do not respond.

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