

Genetic variants of the fatty acid desaturase gene cluster predict amounts of red blood cell docosahexaenoic and other polyunsaturated fatty acids in pregnant women: findings from the Avon Longitudinal Study of Parents and Children

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Background: Blood and tissue long-chain polyunsaturated fatty acid (LC-PUFA) amounts, which have been associated with early development and lifelong health, depend on dietary intake and endogenous conversion of precursor fatty acids (FAs) by the enzymes D5-desaturase and D6-desaturase. Polymorphisms in the desaturase encoding genes FADS1 and FADS2 have been associated with several n26 (omega-6) and n23 (omega-3) FAs and especially with arachidonic acid (AA) amounts. Associations with docosahexaenoic acid (DHA), which is considered particularly important for brain and retina development, are hardly existent.

Objective: We explored the relation between FADS gene cluster polymorphisms and red blood cell (RBC) FA amounts in 4000 pregnant women participating in the Avon Longitudinal Study of Parents and Children.

Design: Linear regression analysis of 17 single nucleotide polymorphisms (SNPs) in the FADS gene cluster was conducted with RBC phospholipid FAs from 6711 samples from 4457 women obtained throughout pregnancy (mean 6 SD gestational age: 26.8 6 8.2 wk).

Results: Independent of dietary effects, the minor alleles were consistently positively associated with precursor FAs and negatively associated with LC-PUFAs and product:substrate ratios of the n26 (AA:linoleic acid ratio) and n23 (eicosapentaenoic acid:alpha-linolenic acid ratio) pathways. In contrast to previous studies, we also showed significant inverse associations with DHA. Similar but weaker associations were shown for the FADS3 SNP rs174455.

Conclusions: FADS genotypes influence DHA amounts in maternal RBC phospholipids and might affect the child's DHA supply during pregnancy. It is highly likely that a gene product of FADS3 has a desaturating activity.

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