



# Variants in *CPT1A*, *FADS1*, and *FADS2* are associated with higher levels of estimated plasma and erythrocyte delta-5 desaturases in Alaskan Eskimos

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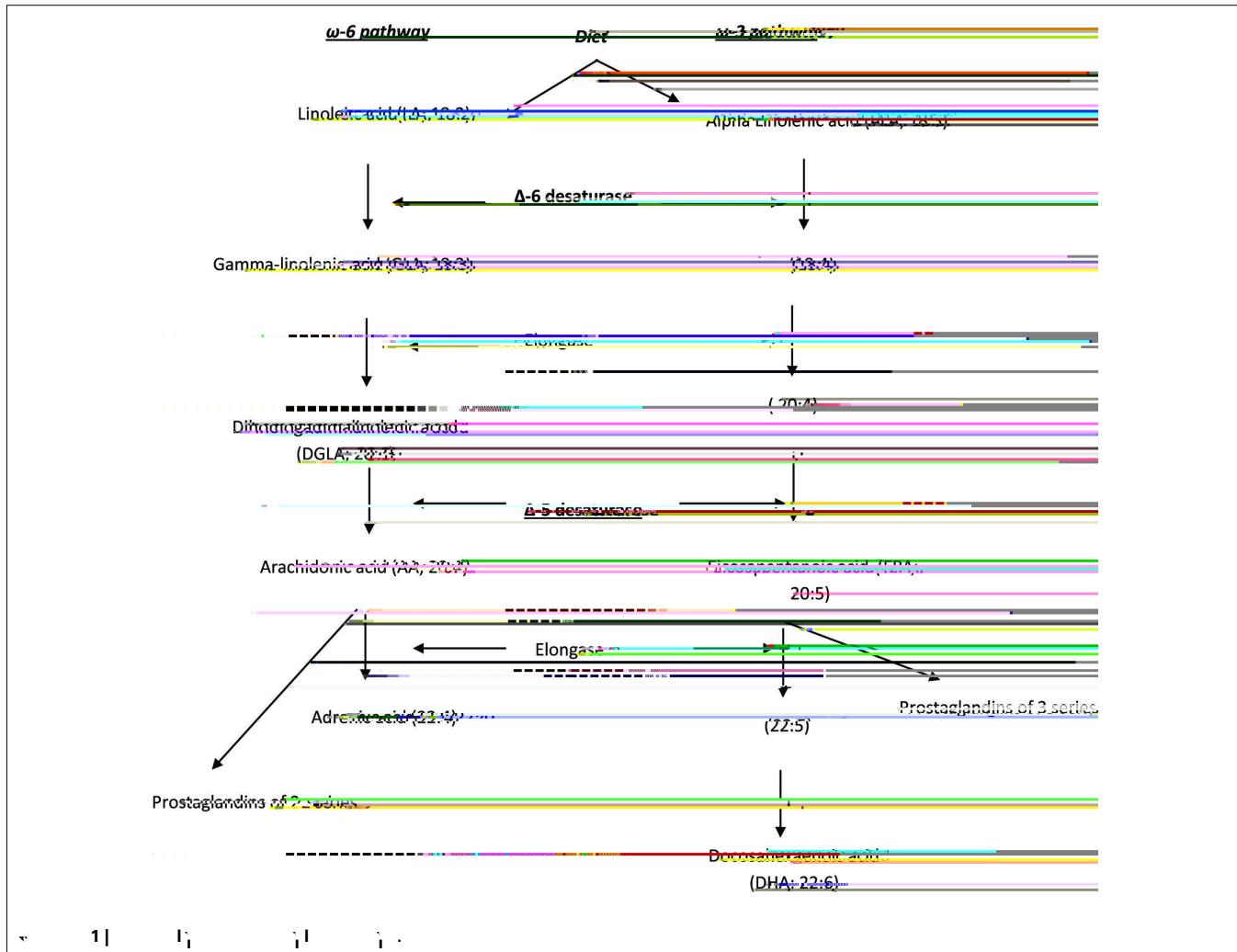
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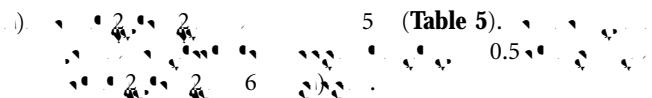
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The delta-5 and delta-6 desaturase (D5D and D6D), encoded by fatty acid desaturase 1 (*FADS1*) and 2 (*FADS2*) genes, are key enzymes in the metabolism of omega-3 and omega-6 fatty acids. The objective of this study is to identify genes influencing a variation in estimated D5D and D6D activity in plasma and erythrocytes in Alaskan Eskimos ( $n=761$ ) participating in the GOCADAN study. We found evidence of linkage for estimated D5D (eD5D) on chromosome 11q12-q13 (logarithm of odd ratio = 3.5). The confidence interval contains candidate genes *FADS1*, *FADS2*, 7-dehydrocholesterol reductase (*DHCR7*), and carnitine palmitoyl transferase 1A (CPT1A). Measured genotype analysis found a association between *CPT1A*, *FADS1*, and *FADS2* single-nucleotide polymorphisms (SNPs) and estimated eD5D activity ( $p$ -value between  $10^{-28}$  and  $10^{-5}$ ). A Bayesian analysis revealed a significant association between *CPT1A* and eD5D activity ( $p$ -value = 3019594).







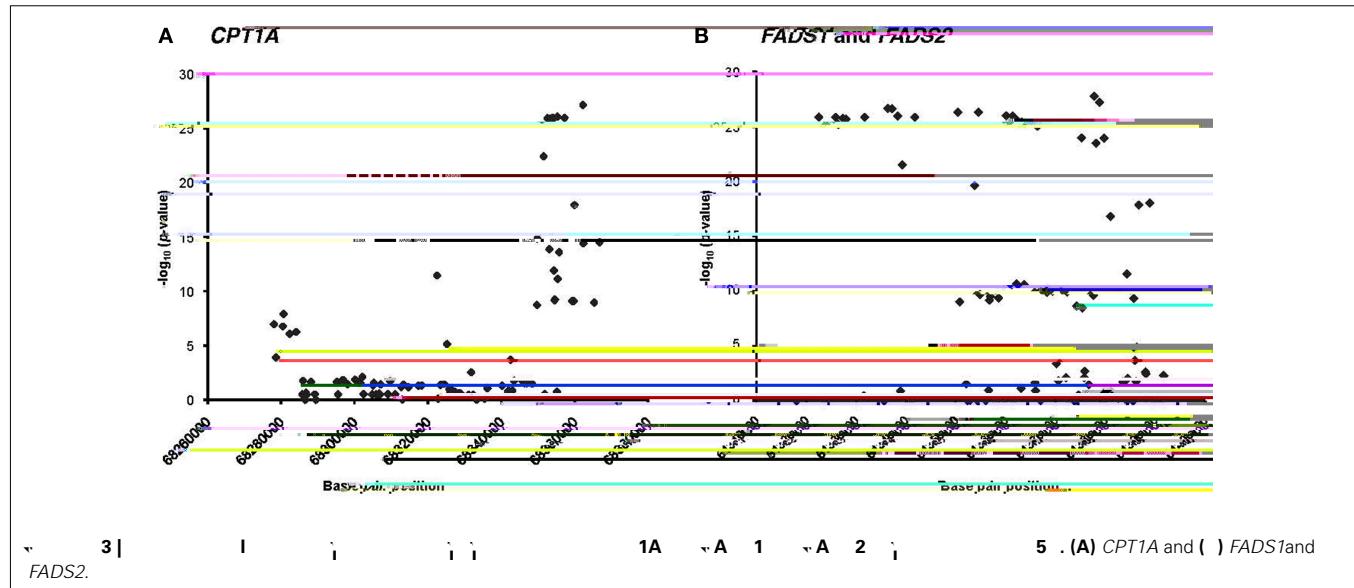
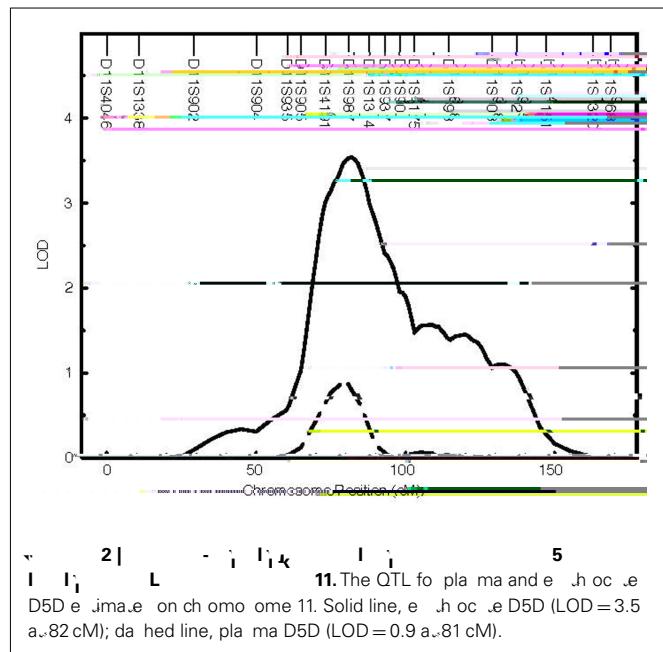


### CONDITIONAL LINKAGE

Figure 4 shows the LOD score plot for conditional linkage analysis. The y-axis represents LOD (0 to 5) and the x-axis represents Chromosome Position (cM) (0 to 150). A solid black line represents the LOD score for the entire genome scan, showing a primary peak at approximately 82 cM (LOD = 3.5) and a secondary, smaller peak at approximately 81 cM (LOD = 0.9). A dashed line represents the LOD score for the FADS1 and FADS2 genes, showing a peak at approximately 81 cM (LOD = 0.9). Horizontal lines indicate LOD thresholds of 2.0 and 3.5.

### EXAMINATION OF CIS-REGULATED FADS1, FADS2, AND CPT1A TRANSCRIPTS IN MEXICAN AMERICANS

Figure 5 shows the results of the examination of cis-regulated FADS1, FADS2, and CPT1A transcripts in Mexican Americans. The y-axis is LOD (0 to 5) and the x-axis is Chromosome Position (cM) (0 to 150).

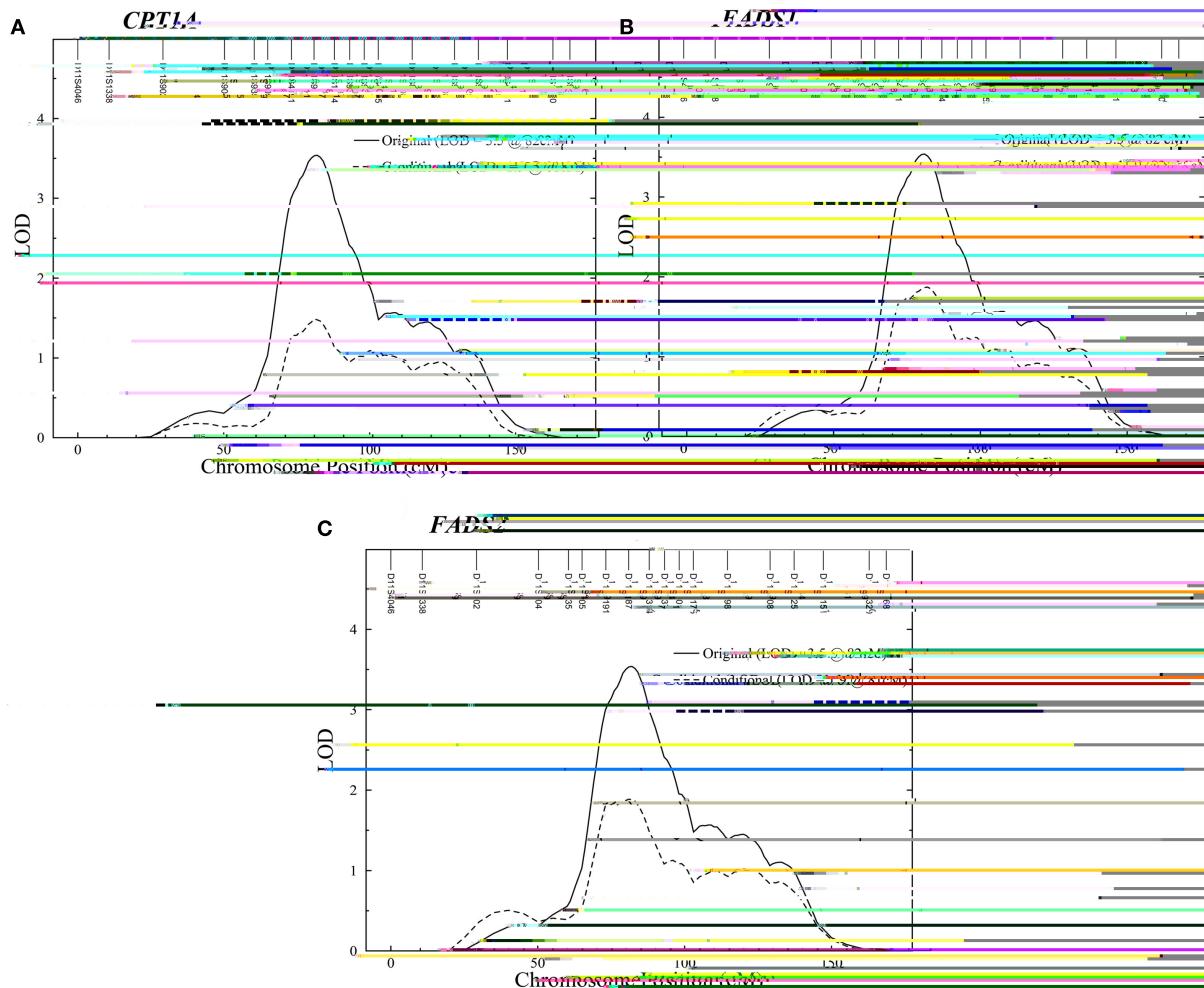


### DISCUSSION

The results of this study provide evidence for a QTL for plasma and ex-heme D5D esterification on chromosome 11. The LOD score plot for the entire genome scan shows a primary peak at approximately 82 cM (LOD = 3.5) and a secondary, smaller peak at approximately 81 cM (LOD = 0.9). The LOD score plot for the FADS1 and FADS2 genes shows a peak at approximately 81 cM (LOD = 0.9). These findings suggest that the QTL for plasma and ex-heme D5D esterification is located near the FADS1 and FADS2 genes on chromosome 11. The results also indicate that the FADS1 and FADS2 genes are cis-regulated by the same QTL. The examination of cis-regulated transcripts in Mexican Americans further supports this finding, as it shows a similar pattern of association with the QTL on chromosome 11.

**| 2 |****| 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 |**





4 | 11 | 1 | 5  
 11. Linkage analysis conditional on the model is significant.

a ocia ed SNP in (**A**) *CPT1A*, ( ) *FADS1*, and ( ) *FADS2*. Solid line, e hoc e D5D; dashed line, e hoc e D5D conditional on SNP .

| 6 |

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