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Genetic variation in *FADS* genes is associated with maternal long-chain PUFA status but not with cognitive development of infants in a high fish-eating observational study

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Abstract

Long-chain n-6 and n-3 PUFA (LC-PUFA), arachidonic acid (AA) (20:4n-6) and DHA (22:6n-3), are critical for optimal brain development. These fatty acids can be consumed directly from the diet, or synthesized endogenously from precursor PUFA by Δ-5 (encoded by *FADS1*) and Δ-6 desaturases (encoded by *FADS2*). The aim of this study was to determine the potential importance of maternal genetic variability in *FADS1* and *FADS2* genes to maternal LC-PUFA status and infant neurodevelopment in populations with high fish intakes. The Nutrition Cohorts 1 (NC1) and 2 (NC2) are longitudinal observational mother-child cohorts in the Republic of Seychelles. Maternal serum LC-PUFA was measured at 28 weeks gestation and genotyping for rs174537 (*FADS1*), rs174561 (*FADS1*), rs3834458 (*FADS1-FADS2*) and rs174575 (*FADS2*) was performed in both cohorts. The children completed the Bayley Scales of Infant Development II (BSID-II) at 30 months in NC1 and at 20 months in NC2. Complete data were available for 221 and 1310 mothers from NC1 and NC2 respectively. With increasing number of rs3834458 minor alleles,

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Compliance with Ethics Guidelines

This study was conducted in accordance with the ethical standards of the Helsinki Declaration of 1975 and all study procedures involving participants were reviewed and approved by the Seychelles Ethics Board, the Research Subjects Review Board at the University of Rochester, and the Regional Ethics Committee at Lund University, Sweden. Informed consent was obtained from all participants included in the study.

Uncited references

[1,15,20,29,34,5].

maternal concentrations of AA were significantly decreased (NC1 p=0.004; NC2 p<0.001) and precursor:product ratios for linoleic acid (LA) (18:2n-6)-to-AA (NC1 p<0.001; NC2 p<0.001) and α-linolenic acid (ALA) (18:3n-3)-to-DHA were increased (NC2 p=0.028). There were no significant associations between maternal FADS genotype and BSID-II scores in either cohort. A trend for improved PDI was found among infants born to mothers with the minor rs3834458 allele. In these high fish-eating cohorts, genetic variability in FADS genes was associated with maternal AA status measured in serum and a subtle association of the FADS genotype was found with neurodevelopment.

Keywords

Δ-5 Desaturase (Δ5D); Δ-6 Desaturase (Δ6D); Maternal fish consumption; Neurodevelopment; Seychelles Child Development Study (SCDS)

1. Introduction

An adequate supply of long-chain PUFA (LC-PUFA) arachidonic acid (AA) (20:4n-6) and DHA (22:6n-3) is critical for optimal brain development [11]. The fetus relies entirely on the maternal supply of these fatty acids *in utero*. These LC-PUFA can be obtained directly from the diet, but can also be endogenously synthesized in all mammalian systems from their essential n-6 and n-3 PUFA precursors, linoleic acid (LA) (18:2n-6) and α-linolenic acid (ALA) (18:3n-3) respectively. This synthesis involves a series of elongation and desaturation steps, catalyzed by the fatty acid desaturase enzymes [39], where Δ-5 desaturase (Δ5D) and Δ-6 desaturase (Δ6D) are recognized as rate-limiting enzymes [28] (Fig. 1). However, the endogenous synthesis of LC-PUFA, particularly that of DHA from ALA, is recognized to be extremely inefficient [35]. For this reason consumption of preformed DHA from fish sources is recommended.

The *FADS1* (encoding Δ5D) and *FADS2* (encoding Δ6D) genes are located head-to-head in a cluster on chromosome 11 (11q12-q13) [10,24,36]. Carriers of certain genotypes in the FADS gene cluster have consistently been shown to have higher biological status of PUFA precursors, LA and ALA, and lower status of LC-PUFA products, AA and EPA (20:5n-3), probably as a result of having lower expression of the functional enzymes [17,19,23,30,33,47,9]. The highest and the lowest proportion of variability, with respect to the influence of FADS genes on PUFA composition, have been found for AA and for DHA respectively [44].

Among cohorts of pregnant women, maternal genetic variation in FADS has frequently been associated with lower concentrations of AA and EPA in maternal blood and breast milk, as well as infant blood [19,22,26,47]. Importantly, variation of the maternal FADS genotype resulting in lower *FADS1* and *FADS2* activity has also been associated with lower cognitive development of infants, possibly owing to lower LC-PUFA status during critical stages of fetal development [27,40,6].

These findings suggest that the FADS genotype may be an important determinant not only of LC-PUFA status, but also of the biological effects exerted by LC-PUFA. With respect to

dietary variation, it is not fully understood how dietary availability of LC-PUFA impacts on the association between FADS genotype and LC-PUFA status [14]. It has been suggested that FADS genotype may be a greater determinant of LC-PUFA status in populations where fish consumption is low and there is expected to be greater dependence on endogenous synthesis of LC-PUFA [37]. Yet there remain no data on the influence of FADS genotype, on either LC-PUFA status or neurodevelopment, in populations with high fish consumption. These data would be important for risk assessment by providing further evidence on the risks and benefits of fish consumption during pregnancy.

The objective of the current study was to characterize mothers in two high fish-eating cohorts of the Seychelles Child Development Study (SCDS) for *FADS1* and *FADS2* and to investigate associations among maternal genotype, LC-PUFA status and developmental outcomes of their infants. It was hypothesized that mothers with minor alleles of SNPs in either *FADS1* or *FADS2* would have higher blood concentrations of precursor n-6 and n-3 PUFA, LA and ALA, and lower concentrations of LC-PUFA products, AA and DHA. We further hypothesized that such variation in the maternal status of these PUFA during pregnancy could impact the cognitive development of their children.

2. Methods

2.1. Study population

The SCDS is a longitudinal observational study conducted in the Republic of Seychelles, an archipelago in the Indian Ocean. The population resides mainly on the island of Mahé and is of mixed African, European and East Asian origin. The overall aim of the SCDS is to investigate the effects of methyl mercury (MeHg) and nutrient exposure, from maternal fish consumption during pregnancy, on child developmental outcomes. The study has found no consistent pattern of adverse associations of prenatal MeHg exposure and neurodevelopment in children of mothers consuming an average of 12 fish meals per week [38,43,45].

Apparently healthy mothers were recruited to Nutrition Cohort 1 (NC1) and Nutrition Cohort 2 (NC2) during their first antenatal visit (from 14 weeks of gestation) at eight health centers across Mahé. NC1 mothers were recruited in 2001 until 300 volunteers had consented [7], and NC2 mothers were enrolled from 2008 until 2011 when the target number of 1500 mothers had consented [43]. Further information on inclusion criteria and power calculations for NC1 [41] and NC2 have previously been described [43]. In NC1, mothers completed a 4-day food diary at 28 weeks gestation to estimate their average daily consumption of fish [4]. In NC2, mothers completed a retrospective Fish Use Questionnaire, also at 28 weeks gestation, to estimate their weekly consumption of fish during pregnancy. This study was conducted according to guidelines laid down in the Declaration of Helsinki and all study procedures involving participants were reviewed and approved by the Seychelles Ethics Board, the Research Subjects Review Board at the University of Rochester, and the Regional Ethics Committee at Lund University, Sweden.

2.2. Blood sampling and analyses

At 28 weeks gestation non-fasting blood samples were collected in both cohorts and serum and whole blood were obtained after processing at the Public Health Laboratory of the

Ministry of Health. Maternal serum samples were shipped at −80 °C to the University of Ulster where they were analyzed for fatty acid concentrations. Total lipids were extracted and fatty acid methyl esters (FAME) were prepared by boron trifluroide methanol (BF_3) according to an adaptation of the Folch method [8]. FAME were detected and quantified using the gold-standard technique of Gas Chromatography–Mass Spectrometry (GC–MS) (Agilent 7890A-5975C, UK) using heptadecaenoic acid (C17:0) as the internal standard, as previously described [41]. All analytical standards were of >99% purity and purchased from Sigma-Aldrich, UK. Total serum PUFA composition is presented as mg/ml to indicate physiological quantities. In NC1, there were 11 women missing 28 week PUFA status, but values for these women were imputed from PUFA concentrations which were also measured at delivery in the NC1 cohort [7]. As described previously, the efficiency of blood processing in the Seychelles was improved in NC2 compared to NC1 [42].

2.3. Genotyping

Maternal whole blood samples were shipped at −80 °C to the University of Lund, Sweden for genotyping. Four candidate SNPs*: FADS1* rs174537 and rs174561, *FADS1-FADS2* rs3834458 and *FADS2* rs174575; were selected based on evidence of impacting on LC-PUFA in epidemiological studies (Online Resource 1). The rs3834458 is located in the promoter of *FADS2* and 5′ of *FADS1* and is often referred as intergenic [26]. DNA was extracted from maternal blood using the Qiagen DNA Blood Mini kit (Qiagen, Hilden, Germany). SNPs were genotyped by using the iPLEX® Gold assay on the MassARRAY platform (Sequenom™, San Diego, USA) and by TaqMan allelic discrimination assay on an ABI 7900 instrument (Applied Biosystems, Foster City, CA, USA), according to the manufacturer's instructions. A random selection of the samples were re-analyzed for quality control purposes with perfect agreement between original and repeat genotyping runs for all SNPs. Mother's DNA samples missing more than two of the five SNPs recorded in each genotyping batch were considered unreliable and not included in the database, whilst those missing less than two of all SNPs were included. These differences in genotyping efficiency account for different sample sizes for each SNP measured.

2.4. Developmental assessment

When infants were aged approximately 30 months in NC1 and 20 months in NC2, they completed developmental testing with the Bayley Scales of Infant Development (BSID-II). Testing was conducted by specially trained nurses at the Child Development Centre, Mahé. All study forms were shipped to the University of Rochester, where data were double-entered and the Mental Development Index (MDI) and Psychomotor Development Index (PDI) endpoints were scaled according to the child's age at testing. Test reliabilities for the BSID-II were determined as previously described [41].

2.5. Statistical analyses

Deviations from Hardy–Weinberg equilibrium were tested using chi-square analysis. One SNP (rs174561) was in Hardy Weinberg disequilibrium in both populations (Online Resource 2). As this SNP was genotyped with two different methods (NC1 with Sequenom and NC2 with Taqman) and there was a perfect match between re-runs, we considered the

genotyping results correct. Linkage disequilibrium was evaluated using Haploview [3]. Tests for associations between outcomes and SNPs were carried out from *a priori* analysis plans and all effects were tested using two-sided tests of significance at the α =0.05 level. Unadjusted linear regression was used to estimate the effect of each of the four FADS SNPs on each of the eight individual LC-PUFA measurements and on the precursor:product ratios, LA:AA, ALA:EPA and ALA:DHA. The ratios of LA:AA and ALA:EPA are commonly used as crude indicators of desaturase activity [46]. The minor allele frequencies were sufficiently large in each of these SNPs that heterozygote and variant homozygote effects were estimated separately. In order to make the LC-PUFA results more comparable, we scaled maternal serum PUFA composition in each cohort using homozygote carriers of the common SNP as a reference and the relative differences are presented [31,32].

Multiple linear regression was used to estimate the effect of FADS SNPs on the child's neurodevelopment, measured as BSID-II scores. Adjustments were made for covariates previously chosen to cover the most important determinants of neurocognitive development in children [41]. These include child sex, maternal age at delivery, presence of two parents in the household, socioeconomic score, and birth weight (NC1) or child age at testing (NC2).

The children in the NC2 cohort were tested approximately 10 months before the age at which testing of NC1 children took place. Over the course of the SCDS, we have observed that the mean scaled score within each cohort decreased with age when followed longitudinally. To make the results more comparable between cohorts, we scaled the BSID-II scores in each cohort by using estimated mean scores in homozygote carriers of the common SNP as a reference and the relative differences are presented.

3. Results

A total of *n*=222 NC1 mothers and *n*=1400 NC2 mothers were included in the current study after exclusions owing to missing data in developmental outcomes, LC-PUFA, SNPs and covariates. Descriptive characteristics of the two cohorts, including covariate data, are presented in Table 1. The LC-PUFA values differed between the cohorts and were, apart from LA, generally higher in NC2. This finding may be as a result of potential oxidation of samples during blood processing in NC1, as previously described [42]. NC1 mothers consumed on average 9 fish meals per week [41], whereas NC2 mothers consumed an average of 8.5 estimated fish servings per week [43].

The genotype distributions in NC1 and NC2 are presented in Table 2. The allele frequencies for the FADS SNPs were similar between the Seychellois cohorts (Online Resource 2). For all SNPs, the minor allele frequencies were lower in the Seychellois populations compared to European and African populations [12]. *FADS2* rs174575 was found not to be in linkage disequilibrium (LD) with any of the other SNPs, whereas the other three SNPs (*FADS1* rs174561 and rs174537, *FADS1-FADS2* intergenic rs3834458) had pairwise LD values ranging from 0.83 to 0.93 (data not shown). Therefore, the following results are presented for rs174575 (not in strong LD with other SNPs) and rs3834458 (in strong LD with

rs174561 and rs174537). Results for the other SNPs in LD with rs3834458 are presented in Online Resources 3 and 4.

Genetic associations with maternal PUFA composition were evaluated as shown in Table 3. There was a significant association between rs3834458 and serum composition of AA and the ratio of LA:AA in both cohorts. With increasing number of variant alleles, the relative concentrations of AA were reduced in both cohorts (NC2 $p<0.001$; NC1 $p=0.004$). The magnitude of association was somewhat larger in NC2 where rs3834458 deldel carriers showed 20% lower AA than TT carriers, compared to 16.5% lower AA shown in NC1 deldel carriers (Fig. 2). The association with the LA:AA ratio was as expected, with ratios being significantly higher with increasing number of variant alleles (NC2 $p<0.001$; NC1 $p<0.001$). In the larger NC2 cohort further associations between rs3834458 and PUFA status were found with variant carriers having significantly higher LA ($p=0.002$) and ALA ($p=0.017$) concentrations and significantly different ratios of ALA:DHA ($p=0.028$, all 2 df tests). For ALA:DHA, deldel carriers had a 24.4% higher ratio compared to TT carriers. The results were very similar for the two other SNPs in LD with rs3834458 (Fig. 2).

In NC1, rs174575 appeared to modify LA:AA in that G allele carriers showed higher ratios compared to CC carriers ($p=0.002$, 2 df test). In NC2, rs174575 was associated with lower AA concentrations with increasing number of variant alleles ($p=0.025$). There were no significant associations between FADS genotype and concentrations of EPA (Fig. 3), DHA or the ratio of ALA:EPA in either cohort.

The genotype of the mothers was evaluated in relation to neurodevelopmental outcomes in the children as shown in Table 4. There were no significant genetic associations between FADS genotype and child developmental scores in either NC1 or NC2. A non-significant trend for infants of rs3834458 del carriers to score higher on the Psychomotor Developmental Index (PDI) was found in both NC1 and NC2 ($p=0.07$ and 0.07 respectively).

4. Discussion

We found in two high fish-eating observational mother-child cohorts from the Republic of Seychelles that maternal FADS genotype rs3834458 was significantly associated with LC-PUFA status. The strongest associations were observed for AA and the LA:AA ratio, with variant homozygotes in the much larger cohort (NC2) showing 20% lower AA and 42% higher LA:AA than those with the homozygous reference genotype. These findings support prior studies reporting that carriers of the minor alleles of FADS SNPs, including rs3834458, tend to have a lower blood composition of LC-PUFA, particularly of AA but also of EPA [19,33,47]. However, in our study there was no association of rs3834458, or any other FADS genotype, with either serum EPA or DHA composition. This finding agrees with the majority of studies which have shown DHA status to be less influenced by genetic variation in FADS genes [13,19]. One plausible reason for this finding is that whilst the LC-PUFA desaturation pathway mainly takes place within the endoplasmic reticulum, the final conversion step from docosapentaenoic acid (DPA; C22:5n-3) to DHA (partial β-oxidation) requires a translocation to the peroxisomes [39]. This peroxisomal conversion accounts for

DHA being the least efficiently synthesized n-3 LC-PUFA in the body and as a result, the impact of genetic variation may be 'diluted' and less likely to influence DHA status [21]. It could also be hypothesized that the reason for a lack of genetic influence on DHA status shown in the current study may be related to high fish consumption and subsequently higher levels of preformed DHA in the population, which may mean lower dependence on the endogenous synthesis pathway. This hypothesis is supported by the recent study by Scholtz et al where the influence of FADS genotype on DHA status became non-significant following fish oil supplementation among a group who had lower DHA status at baseline [37]. However, despite high fish intake in our cohorts, some endogenous activity for production of n-3 LC-PUFA might exist and thereby account for the higher LA:AA found in both cohorts and higher ALA:DHA found in NC2. A recent randomized controlled trial of fish oil supplementation reported that increased dietary intakes of EPA and DHA were associated with higher activity of Δ5D and lower activity of Δ6D [2]. These findings may suggest that the endogenous LC-PUFA synthesis pathway remains active, and perhaps enhanced, despite abundant preformed LC-PUFA in the diet. However we must acknowledge that the ALA:DHA ratio is limited as an indicator of FADS enzyme activity given the notably low conversion of DHA which occurs from ALA endogenously. We also cannot clearly differentiate which of the SNPs is related to the LC-PUFA phenotype, as there is strong linkage for the *FADS1* SNPs and the *FADS1-FADS2* intergenic rs3834458. However, a less pronounced association was found for *FADS2* rs174575 compared to the *FADS1* SNPs, which could suggest that the functional association is related to differences in Δ5D rather than Δ6D activities, but we cannot exclude the potential influence of other genes in the LC-PUFA pathway.

The maternal FADS genotype was not significantly associated with infant development in either cohort. However, we did find a trend for improved psychomotor development among infants of mothers with the variant allele for rs3834458 in both NC1 (p=0.07) and NC2 (p=0.07). This suggests a subtle association of the FADS genotype with neurodevelopment, even at high fish intake. We suspect, from the lack of associations between rs3834458 and EPA or DHA, that this trend might be related to lower production of AA, which is a precursor for pro-inflammatory eicosanoids [18]. Data from the English mother–child ALSPAC cohort, also found children of mothers with the rs3834458 minor allele performed better in tests of intelligence quotient at 8 years [40]. In our recent analysis of the associations between maternal PUFA status and neurodevelopment in NC2, we found no direct associations of maternal AA status with cognitive outcomes. However, we did find significant adverse associations between higher maternal n-6/n-3 ratios and both infant psychomotor development and communicative ability at 20 months of age. This suggests that the balance between AA and DHA may be important for neurodevelopment and a possible mechanism would be through influencing the inflammatory milieu [43].

Recent studies suggest that the interaction between PUFA and genetic variability is complex. One recent study suggests that n-3 LC-PUFA supplementation can induce epigenetic regulation of FADS genes and genes encoding the elongase enzymes, *ELOVL5* and *ELOVL2*, in a sex-specific manner [16]. If true, this regulation may explain why different populations, with similar allelic frequencies of FADS SNPs but with distinct diets,

may present health disparities [25]. Future studies may need to consider genetic variation in genes controlling eicosanoid synthesis from LC-PUFA, such as 5-lipoxygenase (*ALOX5*) [25]. Taken together, these data provide a firm basis for considering each population group separately in studies of FADS and PUFA status.

There are some methodological issues to consider with the current study. The processing time of the blood collected was different between the two cohorts, and may partially explain the different serum concentrations of LC-PUFA reported [42]. However, to compensate for this and make the cohorts more comparable, we scaled PUFA values in each cohort to the estimated mean concentration in homozygote carriers of the reference genotype, as described [31,32]. We included developmental testing points in the two cohorts that were reasonably close in age (30 months in NC1 and 20 months in NC2) to enhance comparability. Average MDI scores across the cohorts were similar whereas PDI scores were greater in the NC2 cohort, possibly owing to the younger age at examination. We further included similar *a priori* covariates in the regression analysis to increase comparability of associations across cohorts. We observed relatively consistent genetic associations in the two cohorts, but fewer were statistically significant in the NC1 cohort, perhaps owing to the smaller sample size. We acknowledge that the precursor:product PUFA ratios are limited as markers of enzyme activity. However, these ratios have been used frequently for this purpose and we believe that our use of serum absolute PUFA concentrations in denoting these ratios is a strength of the current study.

In conclusion, we found that the maternal FADS genotype is an important predictor of maternal AA, but not of EPA and DHA status. To our knowledge this is the first time that such associations have been described within a high fish-eating cohort. These results highlight the importance of considering FADS genotype, even at high fish intake, to aid understanding associations between maternal LC-PUFA status, fish consumption and child development.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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The authors' responsibilities were as follows: KB conceived, designed and conducted the research; GJM, PWD, EvW, GEW, CFS and JJS conceived and designed the SCDS and conducted the research; AJY, MSM, EMM, AA, KW and KB conducted the research; TML, SWT, KG and KE performed the statistical analyses; AJY and KB interpreted the data, drafted the manuscript and KB has primary responsibility for final content. All authors have read and approved the final version to be published.

Abbreviations

AA	Arachidonic acid
ALA	Alpha-linolenic acid
BSID-II	Bayley's Scales of Infant Development II
Δ5D	Δ5-desaturase
Δ6D	Δ6-desaturase
LA	Linoleic acid
LC-PUFA	Long-chain polyunsaturated fatty acids
MDI	Mental Developmental Index
NC1	Nutrition Cohort 1
NC2	Nutrition Cohort 2
PDI	Psychomotor Developmental Index
SCDS	Seychelles Child Development Study

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Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.plefa.2015.08.004.

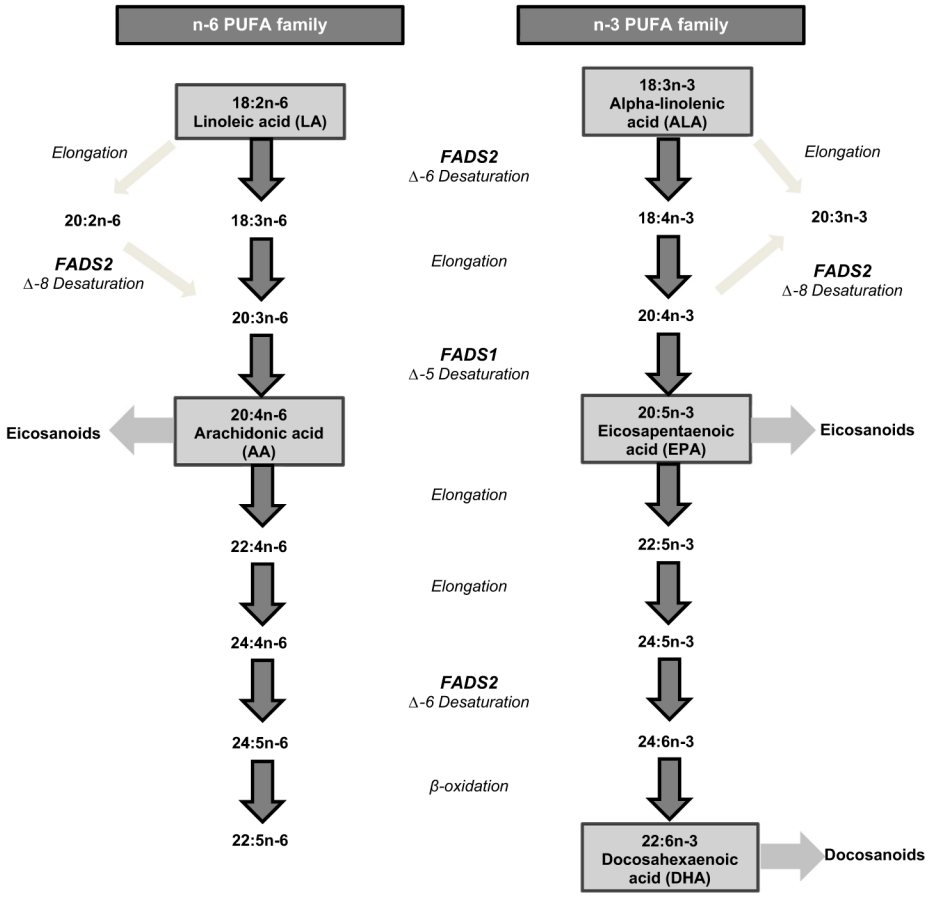

Fig. 1.

Pathways for endogenous n-6 and n-3 PUFA elongation and desaturation showing the activity of *FADS1* and *FADS2* and corresponding desaturation steps.

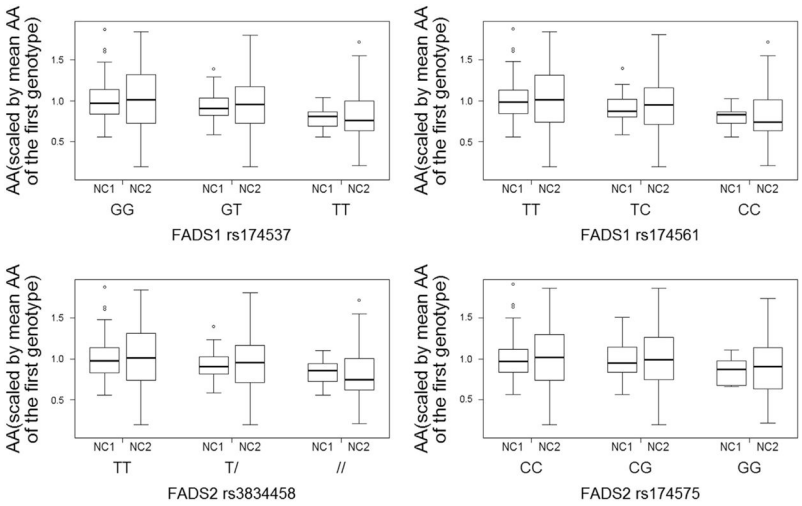

Fig. 2.

Prenatal arachidonic acid (AA; to compare the two cohorts we report the relative difference compared to the mean AA in carriers of the reference genotype). Boxplots are shown for each genotype in both the NC1 and NC2 cohorts. Differences between the genotypes are significant for all four SNPs in both cohorts except rs174575 in the NC1 cohort (see Table 3 and S3).

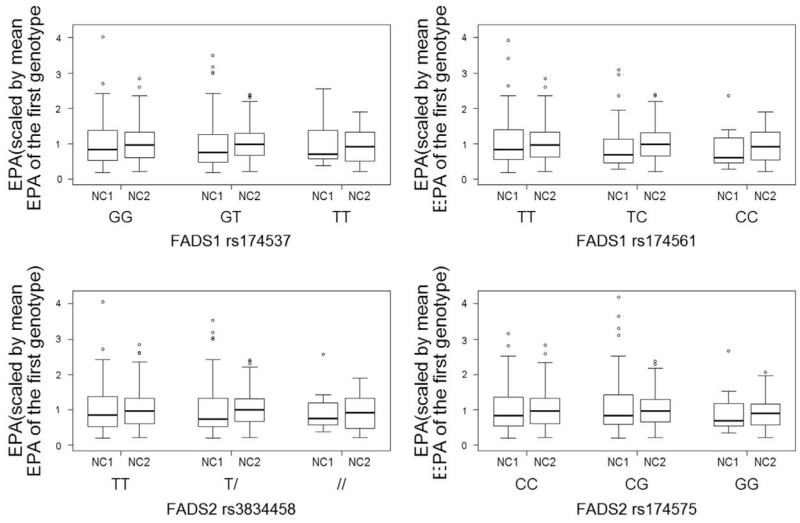

Fig. 3.

Prenatal Eicosapentaenoic acid (EPA; to compare the two cohorts we report the relative difference compared to the mean EPA in carriers of the reference genotype). Boxplots are shown for each genotype in both the NC1 and NC2 cohorts. Differences between the genotypes are not significant for either cohort or any SNP (see Table 3 and S3).

Table 1

Summary statistics for the NC1 and NC2 cohorts[a,b,c].

Maternal Serum PUFA composition (mg/ml)	NC1			NC2		
	n	Mean	SD	*n*	Mean	SD
LA	222	1.170	0.219	1399	0.898	0.252
AA	222	0.101	0.022	1399	0.202	0.081
ALA	222	0.002	0.001	1399	0.037	0.006
EPA	222	0.031	0.009	1399	0.183	0.084
DHA	222	0.003	0.002	1399	0.052	0.008
BSID-II						
MDI	221	84.97	9.59	1358	87.71	10.69
PDI	218	89.80	13.78	1356	96.78	10.58
Demographics						
Maternal age (yr)	222	27.7	6.0	1400	27.0	6.3
Maternal BMI (kg/m^2)	221	25.8	6.4	1291	26.9	6.5
Hollingshead SES	222	33.9	11.1	1353	32.0	10.3
Girls (% in cohort)	222	51.4	–	1401	48.0	–
Parents at home (% in cohort)	221	42.1	–	1353	72.5	–
Child birth weight (g)	222	3232.2	470.4	1393	3178.8	498.3
Maternal fish consumption (meals/week)	221	9.1	4.1	1321	8.5	4.6

[a] NC1, Nutrition Cohort 1; NC2, Nutrition Cohort 2; LA, linoleic acid; AA, arachidonic acid; ALA, α-linolenic acid; BSID-II, Bayley Scales of Infant Development II; MDI, Mental Developmental Index; PDI, Psychomotor Developmental Index; Hollingshead SES, socioeconomic status.

[b] Data shown are for all models.

[c] BSID-II scores are from 30 mo assessment in NC1 and 20 mo assessment in NC2.

Table 2

Genotype distribution in NC1 and NC2 mothers[a,b,c].

NC1	*N* genotyped	Reference homozygote	Heterozygote	Minor allele homozygote
		(%)		
FADS1 rs174537	180	63.3 GG	31.1 GT	5.6 TT
FADS1 rs174561	193	77.2 TT	16.1 TC	6.7 CC
FADS1-FADS2 rs3834458	220	65.9 TT	28.2 Tdel	5.9 deldel
FADS2 rs174575	214	59.8 CC	35.0 CG	5.1 GG
NC2				
FADS1 rs174537	1413	67.9 GG	28.5 GT	3.6 TT
FADS1 rs174561	1413	72.1 TT	24.8 TC	3.1 CC
FADS1-FADS2 rs3834458	1414	70.4 TT	26.4 Tdel	3.2 deldel
FADS2 rs174575	1413	61.2 CC	33.3 CG	5.5 GG

[a] NC1, Nutrition Cohort 1; NC2, Nutrition Cohort 2; del=one base-pair deletion.

[b] *n*=180–220 in NC1 and *n*=1413–1414 in NC2 depending on genotyping efficiency for the different SNPs.

[c] rs3834458 is FADS1-FADS2 intergenic (NCBI).

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Table 3

Relative differences in PUFA concentrations (mg/ml) by FADS genotypes compared to the reference genotype in NC1 and NC2[a,b,c].

SNP	Cohort	Genotype	LA	AA	LA:AA	ALA	DHA	EPA	ALA:DHA	ALA:EPA
FADS1-FADS2 rs3834458	NC1	TT[d]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		Tdel	1.054	0.922	1.142	1.243	1.019	1.004	1.259	1.122
		Deldel	1.041	0.835	1.253	1.213	0.934	0.982	1.282	1.359
		P-value	0.154	**0.004**	<**0.001**	0.133	0.915	0.970	0.165	0.256
	NC2	TT[d]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		Tdel	1.044	0.933	1.106	1.011	1.019	1.014	0.987	1.000
		Deldel	1.120	0.799	1.426	1.064	0.940	1.023	1.244	1.036
		P-value	**0.002**	<**0.001**	<**0.001**	**0.017**	0.517	0.206	**0.028**	0.358
FADS2 rs174575	NC1	CC[d]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		CG	1.019	0.982	1.055	1.153	1.081	1.046	1.106	0.914
		GG	1.075	0.858	1.260	0.931	0.949	0.979	0.941	0.961
		P-value	0.399	0.118	**0.002**	0.393	0.664	0.538	0.694	0.743
	NC2	CC[d]	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		CG	1.024	0.988	1.036	1.002	1.000	1.001	1.002	1.001
		GG	0.991	0.872	1.122	0.991	0.924	0.985	1.088	1.005
		P-value	0.288	**0.025**	0.342	0.842	0.371	0.680	0.483	0.966

[a] NC1, Nutrition Cohort 1; NC2, Nutrition Cohort 2; LA, linoleic acid; AA, arachidonic acid; ALA, α-linolenic acid; del=one base-pair deletion.

[b] We present relative difference in PUFA concentrations by genotype compared to the mean concentration in homozygote carriers of the reference genotype. Therefore values greater than one show an average increase compared to the reference SNP and values less than one show an average decrease compared to the reference SNP. Bolded *P*-values, derived from unadjusted ANOVA, identify groups that differ significantly by genotype.

[c] rs3834458 is FADS1-FADS2 intergenic (NCBI).

[d] Reference genotype.

Table 4

Relative differences in child developmental scores by mother's genotype compared to the reference genotype from linear regression models[a,b,c].

BSID-II Outcome/SNP	Genotype	NC1 BSID-II scores				NC2 BSID-II scores			
		n	Relative mean	95% CI	*P*	*n*	Relative mean	95% CI	*P*
MDI	TT[d]	145	1.00	(0.982,1.018)	0.06	924	1.00	(0.992,1.008)	0.18
FADS1-FADS2 rs3834458	Tdel	61	1.02	(0.996,1.051)		343	1.01	(1.000,1.025)	
	Deldel	13	1.01	(0.951,1.069)		39	1.01	(0.972,1.046)	
MDI	CC[d]	127	1.00	(0.981,1.019)	0.88	800	1.00	(0.992,1.008)	0.50
FADS2 rs174575	CG	75	1.01	(0.982,1.030)		437	1.01	(0.996,1.018)	
	GG	11	1.01	(0.944,1.071)		68	1.01	(0.984,1.040)	
PDI	TT[d]	143	1.00	(0.975,1.025)	0.07	923	1.00	(0.993,1.007)	0.06
FADS1-FADS2 rs3834458	Tdel	60	1.04	(1.001,1.078)		342	1.02	(1.004,1.027)	
	Deldel	13	1.04	(0.961,1.124)		39	1.02	(0.985,1.053)	
PDI	CC[d]	126	1.00	(0.974,1.026)	0.91	798	1.00	(0.992,1.008)	0.69
FADS2 rs174575	CG	74	1.01	(0.972,1.039)		435	1.01	(0.996,1.017)	
	GG	11	1.00	(0.916,1.091)		70	1.00	(0.973,1.024)	

[a] NC1, Nutrition Cohort 1; NC2, Nutrition Cohort 2; del=one base-pair deletion; BSID-II, Bayley Scales of Infant Development II; MDI, Mental Developmental Index; PDI, psychomotor developmental index.

[b] β Coefficients, 95% CI and *P* values presented are from linear regression models adjusted for child sex, maternal age at delivery, presence of two parents in the household, socioeconomic status, and birth weight (for NC1) or child age at testing (NC2). *P*-values are from the 2 df tests comparing the 3 levels of each genotype.

[c] rs3834458 is FADS1-FADS2 intergenic (NCBI).

[d] Reference genotype.