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Original article

Bioactive metabolites of OMEGA-6 and OMEGA-3 fatty acids are associated with inflammatory cytokine concentrations in maternal and infant plasma at the time of delivery



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SUMMARY

Background & aims: Inflammation is necessary for a healthy pregnancy. However, unregulated or excessive inflammation during pregnancy is associated with severe maternal and infant morbidities, such as pre-eclampsia, abnormal infant neurodevelopment, or preterm birth. Inflammation is regulated in part by the bioactive metabolites of omega-6 (n-6) and omega-3 (n-3) fatty acids (FAs). N-6 FAs have been shown to promote pro-inflammatory cytokine environments in adults, while n-3 FAs have been shown to contribute to the resolution of inflammation; however, how these metabolites affect maternal and infant inflammation is still uncertain. The objective of this study was to predict the influence of n-6 and n-3 FA metabolites on inflammatory biomarkers in maternal and umbilical cord plasma at the time of delivery.

Methods: Inflammatory biomarkers (IL-1 β , IL-2, IL-6, IL-8, IL-10, and TNF α) for maternal and umbilical cord plasma samples in 39 maternal-infant dyads were analyzed via multi-analyte bead array. Metabolites of n-6 FAs (arachidonic acid and linoleic acid) and n-3 FAs (eicosapentaenoic acid and docosahexaenoic acid) were assayed via liquid chromatography-mass spectrometry. Linear regression models assessed relationships between maternal and infant inflammatory markers and metabolite plasma concentrations.

Results: Increased plasma concentrations of maternal n-6 metabolites were predictive of elevated pro-inflammatory cytokine concentrations in mothers; similarly, higher plasma concentrations of umbilical cord n-6 FA metabolites were predictive of elevated pro-inflammatory cytokine concentrations in infants. Higher plasma concentrations of maternal n-6 FA metabolites were also predictive of elevated pro-inflammatory cytokines in infants, suggesting that maternal n-6 FA status has an intergenerational impact on the inflammatory status of the infant. In contrast, maternal and cord plasma concentrations of n-3 FA metabolites had a mixed effect on inflammatory status in mothers and infants, which may be due to the inadequate maternal dietary intake of n-3 FAs in our study population.

Conclusions: Our results reveal that maternal FA status may have an intergenerational impact on the inflammatory status of the infant. Additional research is needed to identify how dietary interventions

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that modify maternal FA intake prior to or during pregnancy may impact maternal and infant inflammatory status and associated long-term health outcomes.

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Abbreviations			
AA	arachidonic acid	HETrE	hydroxy-eicosatrienoic acid
COX	cyclooxygenase	HODE	hydroxy-octadecadienoic acid
DHA	docosahexaenoic acid	HOTrE	hydroxy-octadecatrienoic acid
DiHOME	dihydroxy-octadecenoic acid	IL	interleukin
DiHDPA	dihydroxydocosapentaenoic acid	KODE	keto-octadecadienoic acid
DiHET	dihydroxy-eicosatrienoic acid	LA	linoleic acid
DiHETE	dihydroxy-eicosatetraenoic acid	LOX	lipoxygenase
EET	epoxyeicosatrienoic acid	LXA4	lipoxin A4
EPA	eicosapentaenoic acid	FA	fatty acid
EpDPA	epoxydocosapentaenoic acid	n-3 FA(s)	omega-3 fatty acid(s)
EpETE	epoxyeicosatetraenoic acid	n-6 FA(s)	omega-6 fatty acid(s)
EpOME	epoxyoctadecenoic acid	nM	nanomolar
EPOX	cytochrome-P450 epoxygenase	PGD ₂	prostaglandin D ₂
HDHA	hydroxydocosahexaenoic acid	PGE ₂	prostaglandin E ₂
HEPE	hydroxyeicosapentaenoic acid	PGF ₂ α	prostaglandin F ₂ α
HETE	hydroxyeicosatetraenoic acid	TNFα	tumor necrosis factor α
		TXB2	thromboxane B23

1. Introduction

Inflammation plays a key role during pregnancy [1], with excessive systemic inflammation potentially increasing the risk of both maternal and neonatal morbidity. In pregnant women, inflammation contributes to the development of complications, such as hypertensive disorders of pregnancy [2,3], peripartum cardiomyopathy [4,5], and gestational diabetes [3]. In infants, exposure to excessive *in utero* inflammation is associated with abnormal birth outcomes, such as preterm birth [6], altered neurodevelopment [7–9], diminished lung function [10,11], failed newborn hearing screens [12], and decreased birth weight [13,14]. Exposure to elevated inflammation *in utero* is also associated with an increased risk for developing chronic diseases such as asthma [15,16], cerebral palsy [7], or schizophrenia [17].

Several cytokines and chemokines have emerged as valuable markers of inflammation during pregnancy (Fig. 1) [18]. Tumor necrosis factor alpha (TNFα), interleukin 1-beta (IL-1β), and

interleukin 8 (IL-8) are considered pro-inflammatory cytokines. TNFα plays an important role in stimulating immune cells to produce reactive oxygen species [19] and promotes embryo implantation into the uterus [20]. IL-1β promotes antibody production and facilitates T cell differentiation [21]. IL-8 regulates immune cell activation [22] and promotes placental cell invasion into the maternal uterus [23]. However, excess levels of TNFα and IL-8 are associated with pregnancy loss, pre-eclampsia, and other poor pregnancy outcomes [20,23]. In contrast, interleukin 10 (IL-10) is an anti-inflammatory cytokine known for inhibiting pro-inflammatory cytokine production and immune cell proliferation [24]. Decreased maternal IL-10 levels are associated with pregnancy complications such as preterm birth, intrauterine growth restriction, and pre-eclampsia [25]. Interleukin 2 (IL-2) and interleukin 6 (IL-6) have pleiotropic inflammatory effects. IL-2 promotes inflammation by increasing effector T cell differentiation and growth; however, it also simultaneously promotes the resolution of inflammation by activating regulatory T (T_{reg}) cells [26]. Similarly, IL-6 induces synthesis of some inflammatory acute phase proteins while simultaneously inhibiting the production for other acute phase proteins [27]. IL-6 is also involved in regulating embryo implantation and placental development during pregnancy [23].

The metabolism of dietary fatty acids (FAs) – which is tightly regulated during pregnancy – plays an important role in modulating inflammation [28]. Figures 2 and 3 show the metabolism of the polyunsaturated omega (n)-6 and (n)-3 FAs via the lipoxygenase (LOX), cyclooxygenase (COX), and cytochrome-P450 epoxygenase (EPOX) enzymatic pathways into biologically active metabolites [29]. Metabolites produced from n-6 FAs such as arachidonic acid (AA) and linoleic acid (LA) generally promote inflammation by stimulating immune cell activation and migration [30,31]. However, several n-6 FA metabolites also have anti-inflammatory effects including 20-hydroxyeicosatetraenoic acid (HETE) which resolves oxidative stress [32]; prostaglandin E₂ (PGE₂) which inhibits neutrophil activation [33]; and 13-hydroxy-octadecadienoic acid (HODE) which inhibits the formation of inflammatory cytokines [30]. The effects of other n-6 FA metabolites,

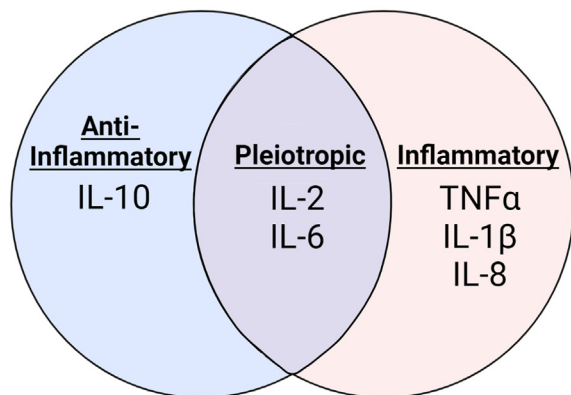


Fig. 1. Primary inflammatory properties of cytokines assessed in this study.

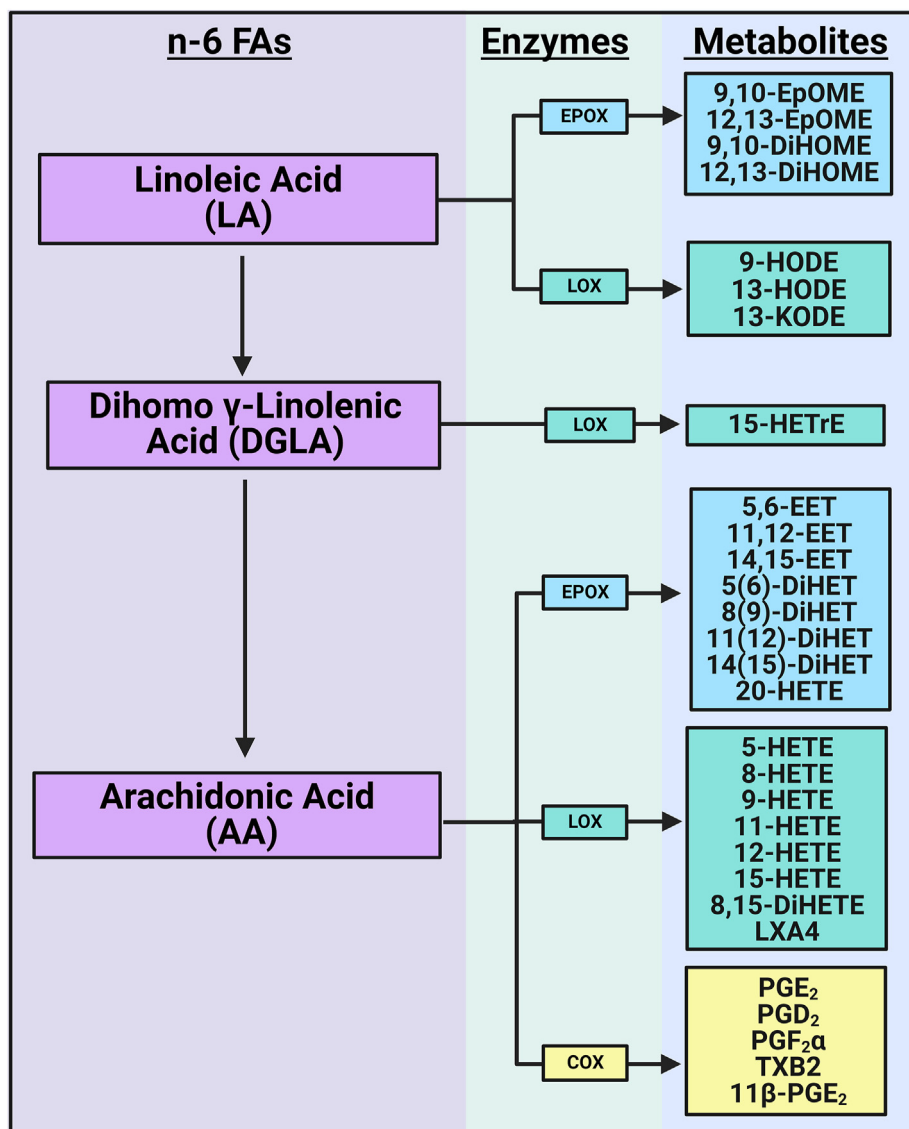


Fig. 2. Biological pathway of n-6 FA metabolites assessed in this study. Metabolites produced via the EPOX pathway are shown in blue, via the LOX pathway in green, and via the COX pathway in yellow [82]. Intermediate compounds in the enzymatic pathway are not shown. Created with BioRender.com. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

such as dihydroxy-eicosatrienoic acid (DiHET), on inflammation are unknown. In contrast, metabolites produced from the n-3 FAs eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), including 19,20-dihydroxydocosapentaenoic acid (DiHDPA), 15-hydroxyeicosapentaenoic acid (HEPE), and 7-hydroxydocosahexaenoic acid (HDHA), generally have an anti-inflammatory effect by inhibiting the recruitment of immune cells, inhibiting inflammatory cytokine production, or inducing T_{reg} cell differentiation [34–37].

Although increased dietary intake of n-3 FAs is associated with increased maternal erythrocyte concentrations of n-3 FAs [38,39] and reduced maternal inflammation markers [40,41], diets with a high intake of n-3 FAs have shown mixed results in preventing inflammation-driven pregnancy complications [40–44]. Investigating FA metabolites could provide mechanistic insight into the relationship between dietary intake of FAs and pregnancy outcomes, but few studies have evaluated how the bioactive metabolites of n-6 and n-3 FA impact inflammation in pregnant women and their infants. This study aims to fill this gap in the scientific literature and predict the influence of n-6 and n-3 FA metabolites

on inflammatory biomarkers in maternal and umbilical cord plasma at the time of delivery.

2. Materials and methods

2.1. Participant enrollment

The University of Nebraska Medical Center Institutional Review Board provided ethical approval for this study (#112-15-EP). Maternal-infant dyads were enrolled upon admission to the Labor and Delivery Unit at Nebraska Medicine from June 2017 through August 2017. Written consent from the mother was obtained prior to participation. Inclusion criteria included maternal age ≥19 years and delivery of a single live-born infant. Exclusion criteria included infants deemed wards of the state and maternal or infant conditions which could affect normal nutrient metabolism such as gastrointestinal disease, kidney disease, liver disease, inborn errors of metabolism, or certain congenital abnormalities.

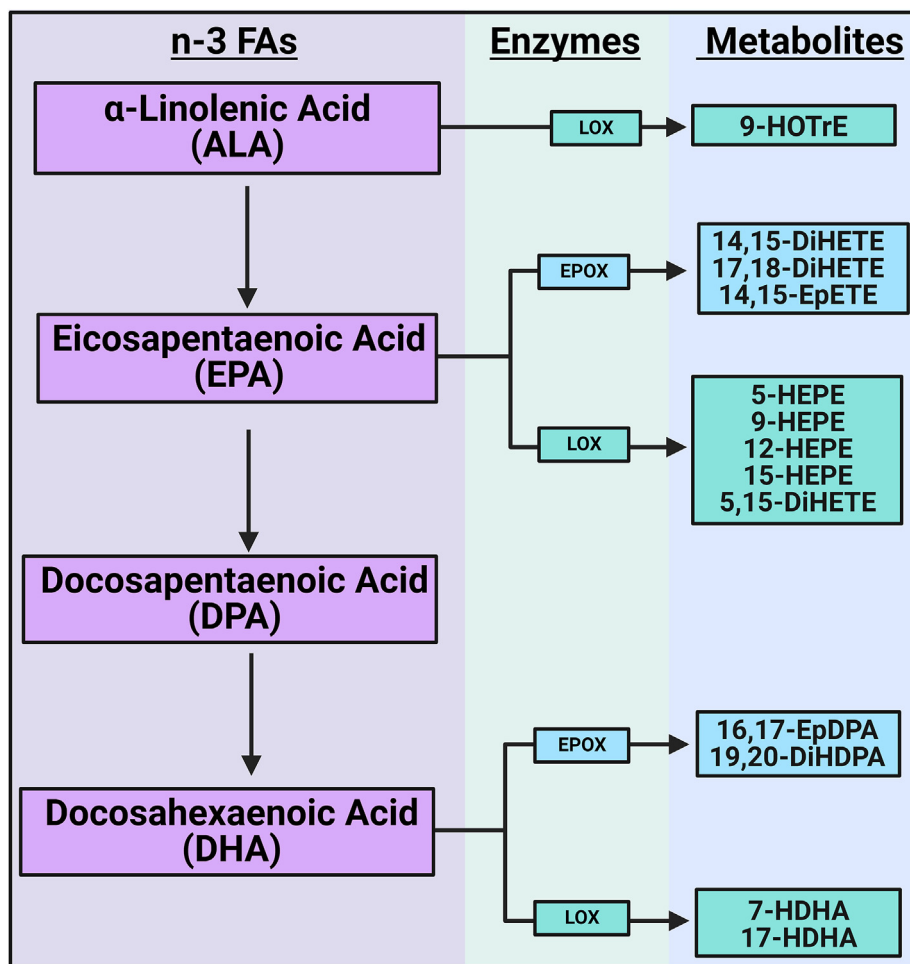


Fig. 3. Biological pathway of n-3 FA metabolites assessed in this study. Metabolites produced via the EPOX pathway are shown in blue and via the LOX pathway in green [82]. Intermediate compounds in the enzymatic pathway are not shown. Created with BioRender.com. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

2.2. Plasma sample collection and analysis

Maternal and infant umbilical cord whole blood samples were collected in K2 EDTA tubes during routine clinical blood draws at the time of delivery. Samples were protected from heat and light, separated into plasma and red blood cell components via centrifugation, and frozen within 12 h of collection.

Metabolite concentrations were then analyzed by high performance liquid chromatography-mass spectrometry. Chromatographic separation was achieved on an Ascentis Express column (2.1 × 150 mm, 2.7 μm particles; Sigma-Aldrich Supelco, Darmstadt, Germany) using a gradient of 90:10 volume/volume acetonitrile-isopropanol with 0.1% acetic acid at a flow rate of 0.35 mL/min at 40 °C. Standard preparations were used to build a 12-point calibration curve. Data was processed using Skyline software and Microsoft Excel. Metabolites assessed in this study are shown in Figs. 2 and 3.

Plasma concentrations of TNF α , IL-1 β , IL-2, IL-6, IL-8, and IL-10 were quantified per manufacturer's instructions using a commercially available multi-analyte bead array (Millipore; Burlington, MA). Briefly, plasma samples or control samples were incubated with Assay Buffer, Matrix Solution, and magnetic beads for 2 h at room temperature with shaking. Samples were then washed twice with Wash Buffer and incubated at room temperature for 1 h with Detection Antibodies. Samples were incubated with Streptavidin-Phycoerythrin for 30 min at room temperature prior to adding Sheath Fluid and reading sample fluorescence.

2.3. Demographic and clinical data collection

Annual household income and number of people in the household were self-reported in participant surveys. The income:poverty ratio was calculated by dividing the annual household income by the federal poverty level for the appropriate household size. Average daily maternal intake of n-6 and n-3 FA over the past year was collected using the Harvard Food Frequency Questionnaire administered at the time of delivery [45]. All other demographic and clinical variables reported in this study, including maternal smoking status, were collected from the maternal electronic health record. Maternal smoking status was categorized as never versus current/former smoker. Participants without pre-pregnancy BMI recorded in their electronic health record provided self-reported pre-pregnancy BMI.

2.4. Statistical analysis

Medians and interquartile ranges (IQR) were calculated for continuous variables and frequencies and percentages were calculated for categorical variables. Spearman's correlation coefficients were used to assess relationships between n-6 and n-3 FA metabolite plasma concentrations and inflammatory marker plasma concentrations. Linear regression modeling was performed on metabolites that correlated with inflammatory marker concentrations at a significance level of $p \leq 0.05$ in univariate analysis.

Directed acyclic graphing was utilized to identify maternal smoking status as the primary confounder, since smoking is associated with both inflammation during pregnancy and alterations in n-6 FA metabolism [46]. Metabolites and inflammatory biomarkers concentrations were log-transformed to satisfy model assumptions. To prevent model bias towards participants with high expression of metabolites or inflammatory markers, samples with non-detectable metabolite or inflammatory plasma concentration were assigned a value of 0.001 nM (nM).

3. Results

3.1. Demographic characteristics

Thirty-nine maternal-infant dyads were included in this study. Table 1 summarizes the demographic characteristics of the sample population. The median maternal age was 29.0 years (IQR 24.0–33.0) and the median gestational age was 39.4 weeks (IQR 39.0–40.3). Twenty-three percent of mothers were current or former smokers, 26.3% had an obese pre-pregnancy BMI, 25.6% had hypertension, and 5.0% had diabetes.

The median maternal intake of total n-6 FA was 16.38 g/day, including 0.17 g/day of arachidonic acid (AA) and 14.98 g/day of linoleic acid (LA; Table 1). The median maternal intake of total n-3 FA was 1.90 g/day, including 0.02 g/day of EPA, 0.09 g/day of DHA, and 1.75 g/day of α -linolenic acid (ALA). Median maternal and infant plasma concentrations of n-6 and n-3 FA metabolites analyzed in this study are shown in Table 2. The median plasma concentrations of AA metabolites were higher in cord plasma for some metabolites, but higher in maternal plasma for others. All LA metabolites assessed had a higher median concentration in maternal plasma compared to cord

Table 1
Baseline characteristics of maternal and infant participants.

	Median (IQR)
Maternal Age (years)	29.0 (24.0–35.0)
Infant Gestational Age (weeks)	39.4 (39.0–40.3)
Pre-Pregnancy BMI (kg/m ²)	25.4 (22.3–31.5)
Income:Poverty Ratio (N = 32)	2.2 (1.12–3.6)
Caloric Intake (kcal/day)	2120 (1844–2786)
Total n-6 FA Intake (g/day)	16.38 (12.65–19.71)
AA Intake (g/day)	0.17 (0.11–0.22)
LA Intake (g/day)	14.98 (11.42–17.71)
Total n-3 Intake (g/day)	1.90 (1.48–2.46)
EPA Intake (g/day)	0.02 (0.01–0.05)
DHA Intake (g/day)	0.09 (0.04–0.17)
ALA Intake (g/day)	1.75 (1.33–2.35)
	Count (Percent)
Infant Sex	
Female (n (%))	16 (41.0)
Male (n (%))	23 (59.0)
Delivery Mode	
Vaginal Delivery (n (%))	29 (74.4)
Caesarean Section (n (%))	10 (25.6)
Maternal Diabetes	
Diabetes- Gestational or Chronic (n (%))	2 (5.1)
No Diabetes (n (%))	37 (94.9)
Maternal Hypertension	
Hypertension-Gestational or Chronic (n (%))	10 (25.6)
Normotension (n (%))	24 (61.5)
Unknown (n (%))	5 (12.8)
Maternal Smoking Status	
Never Smoker (n (%))	30 (76.9)
Current/Former Smoker (n (%))	9 (23.1)
Maternal Race/Ethnicity	
Non-Hispanic White (n (%))	27 (69.2)
Non-Hispanic Black (n (%))	6 (15.4)
Hispanic (n (%))	1 (2.6)
Other/Unknown (n (%))	5 (12.9)

plasma. Median plasma concentrations of EPA metabolites produced via the LOX pathway were also higher in maternal samples; however, median plasma concentrations of DHA metabolites and EPA metabolites produced by the EPOX pathway tended to be higher in cord samples.

Median plasma concentrations of inflammatory markers are shown in Table 3. Cord plasma had a higher median concentration of IL-10 (19.86 vs 9.84 nM), IL-8 (10.22 vs 5.30 nM), and TNF α (58.11 vs 26.21 nM) compared to maternal plasma. In contrast, cord plasma had a lower median concentration IL-1 β (3.38 vs 4.22), IL-2 (3.55 vs 5.16), and IL-6 (3.24 vs 3.65) compared to maternal plasma.

3.2. Relationship between maternal n-6 FA metabolites and maternal and infant inflammatory markers

Maternal AA metabolites were positively correlated with maternal IL-10, IL-1 β , IL-2, IL-6, and IL-8 (Table S1). Maternal AA metabolite plasma concentrations were also positively correlated with infant IL-1 β , IL-6, IL-8, and TNF α , but negatively correlated with infant IL-10 (Table S1). Maternal LA metabolites were not correlated with any maternal or infant inflammatory markers assessed in this study.

After adjustment for maternal smoking status, maternal AA metabolites produced via the EPOX pathway were significantly associated with multiple maternal inflammatory marker concentrations (Fig. 4; Table S2). 11 (12)-DiHET ($\beta = 1.81$, $p = 0.03$) and 8 (9)-DiHET ($\beta = 1.23$, $p = 0.02$) were positively associated with maternal IL-8. 20-HETE ($\beta = 0.97$, $p = 0.001$) and 11 (12)-DiHET ($\beta = 2.14$, $p = 0.03$) were positively associated with maternal IL-6. 5 (6)-DiHET ($\beta = 5.80$, $p = 0.003$) and 5,6-epoxyeicosatrienoic acid (EET; $\beta = 2.87$, $p = 0.01$) were positively associated with maternal IL-2. 5 (6)-DiHET was also positively associated with maternal IL-10 ($\beta = 2.95$, $p = 0.02$) and IL-1 β ($\beta = 4.18$, $p = 0.03$).

In contrast, maternal metabolites produced via the COX pathway were significantly associated with infant inflammatory marker concentrations after adjustment for maternal smoking status (Fig. 4; Table S2). Maternal PGE₂ was positively associated with cord IL-6 ($\beta = 0.60$, $p = 0.03$) and cord IL-8 ($\beta = 0.43$, $p < 0.001$). A 1 nM increase in log-transformed maternal PGF₂ α predicted a 0.34 nM increase in log-transformed cord IL-8 ($p = 0.04$). A 1 nM increase in log-transformed maternal thromboxane B2 (TXB2) predicted a 0.17 nM decrease in log-transformed cord IL-10 ($p = 0.002$).

3.3. Relationship between maternal n-3 FA metabolites and maternal and infant inflammatory marker levels

Maternal plasma concentrations of EPA and DHA metabolites were significantly correlated with multiple maternal and infant inflammatory markers (Table S3). After adjustment for maternal smoking status, maternal plasma concentrations of 17,18-dihydroxy-eicosatetraenoic acid (DiHETE; $\beta = 2.33$, $p = 0.002$) and 19,20-DiHDPA ($\beta = 3.18$, $p = 0.001$) remained significantly associated with maternal IL-10 plasma concentrations (Fig. 5; Table S4). 17,18-DiHETE was also significantly associated with maternal IL-1 β ($\beta = 2.92$, $p = 0.02$). Maternal 16,17-epoxydocosapentaenoic acid (EpDPA) was significantly associated with maternal IL-6 ($\beta = 0.99$, $p < 0.001$) and cord IL-10 ($\beta = 0.10$, $p = 0.04$).

3.4. Relationships between cord n-6 FA metabolites and infant inflammatory marker levels

Cord AA metabolites were positively correlated with cord IL-1 β , IL-6, and IL-8, but negatively correlated with cord IL-10

Table 2
Median n-6 and n-3 FA metabolite concentrations in maternal and infant umbilical cord plasma.

n-6 FA Metabolites	Maternal Plasma (n = 36)	Infant Cord Plasma (n = 37)
AA COX Pathway	Median (IQR)	Median (IQR)
PGE ₂ (nM)	0.71 (0.001–1.12)	2.73 (1.05–3.35)
PGD ₂ (nM)	0.27 (0.14–0.46)	0.22 (0.12–0.36)
PGF _{2α} (nM)	0.001 (0.001–0.17)	0.48 (0.35–0.82)
TXB ₂ (nM)	0.36 (0.17–1.01)	2.42 (1.39–5.93)
11β-PGE ₂ (nM)	0.22 (0.11–0.42)	0.19 (0.10–0.37)
AA LOX Pathway	Median (IQR)	Median (IQR)
5-HETE (nM)	9.97 (6.66–17.05)	8.30 (5.71–9.92)
8-HETE (nM)	1.79 (0.99–2.71)	1.96 (1.64–2.57)
9-HETE (nM)	1.53 (1.01–2.34)	2.22 (1.17–2.60)
11-HETE (nM)	2.60 (1.68–3.50)	2.39 (1.90–3.73)
12-HETE (nM)	3.95 (2.74–7.55)	6.90 (3.92–15.91)
15-HETE (nM)	3.97 (2.44–5.20)	5.35 (3.81–7.84)
8,15-DiHETE (nM)	0.35 (0.001–0.71)	0.29 (0.001–0.45)
LXA4 (nM)	12.47 (5.14–18.71)	5.20 (4.26–7.47)
AA EPOX Pathway	Median (IQR)	Median (IQR)
5,6-EET (nM)	9.41 (7.03–15.50)	27.17 (18.90–42.29)
11,12-EET (nM)	0.16 (0.001–0.26)	0.28 (0.20–0.43)
14,15-EET (nM)	0.34 (0.18–0.50)	0.50 (0.38–0.66)
5 (6)-DiHET (nM)	1.26 (0.99–1.53)	6.20 (5.23–7.79)
8 (9)-DiHET (nM)	12.24 (6.15–19.13)	7.88 (5.24–11.81)
11 (12)-DiHET (nM)	1.85 (0.99–3.04)	1.09 (0.84–1.71)
14 (15)-DiHET (nM)	8.50 (4.18–13.37)	3.43 (2.92–4.78)
20-HETE (nM)	0.10 (0.001–0.15)	0.14 (0.10–0.17)
LA LOX Pathway	Median (IQR)	Median (IQR)
9-HODE (nM)	24.09 (17.99–36.98)	8.39 (5.80–13.08)
13-HODE (nM)	23.43 (18.90–38.12)	10.81 (8.15–16.56)
13-KODE (nM)	2.26 (1.65–3.84)	1.19 (0.92–1.75)
LA EPOX Pathway	Median (IQR)	Median (IQR)
9,10-EpOME (nM)	5.91 (3.56–10.01)	3.96 (2.58–5.39)
12,13-EpOME (nM)	9.32 (6.36–15.80)	4.76 (3.12–6.41)
9,10-DiHOME (nM)	4.66 (3.30–7.12)	1.65 (1.36–2.15)
12,13-DiHOME (nM)	6.77 (3.90–10.91)	2.70 (2.10–3.98)
GDLA LOX Pathway	Median (IQR; nM)	Median (IQR; nM)
15-HETrE (nM)	0.90 (0.58–1.33)	1.35 (1.01–1.85)
n-3 FA Metabolites	Maternal Plasma (n=36)	Infant Cord Plasma (n=37)
ALA LOX Pathway	Median (IQR)	Median (IQR)
9-HOTrE (nM)	1.72 (1.13–2.68)	0.46 (0.23–0.72)
EPA LOX Pathway	Median (IQR)	Median (IQR)
5-HEPE (nM)	0.56 (0.33–0.98)	0.37 (0.24–0.48)
9-HEPE (nM)	0.04 (0.001–0.15)	0.001 (0.001–0.10)
15-HEPE (nM)	0.17 (0.001–0.26)	0.14 (0.001–0.18)
5,15-DiHETE (nM)	0.17 (0.001–0.28)	0.12 (0.001–0.18)
EPA EPOX Pathway	Median (IQR)	Median (IQR)
14,15-DiHETE (nM)	1.57 (0.51–2.54)	4.72 (3.52–7.39)
17,18-DiHETE (nM)	1.65 (1.30–2.36)	5.62 (4.41–7.61)
14,15-EpETE (nM)	0.001 (0.001–0.19)	0.001 (0.001–0.43)
DHA LOX Pathway	Median (IQR)	Median (IQR)
7-HDHA (nM)	1.19 (0.56–1.60)	0.87 (0.49–1.31)
17-HDHA (nM)	1.99 (1.12–3.13)	2.16 (1.69–2.95)
DHA EPOX Pathway	Median (IQR)	Median (IQR)
16,17-EpDPA (nM)	0.12 (0.001–0.24)	0.34 (0.19–0.57)
19,20-DiHDPA (nM)	1.27 (0.94–1.59)	3.75 (2.64–4.47)

Table 3
Median inflammatory marker levels in maternal and infant umbilical cord plasma.

Inflammatory Marker	Maternal Plasma (n = 38)	Infant Cord Plasma (n = 39)
	Median (IQR)	Median (IQR)
IL-10 (nM)	9.84 (5.97–20.61)	19.86 (8.00–25.25)
IL-1β (nM)	4.22 (0.001–8.92)	3.38 (0.001–9.22)
IL-2 (nM)	5.16 (0.001–10.10)	3.55 (0.001–7.99)
IL-6 (nM)	3.65 (0.001–17.12)	3.24 (0.001–17.57)
IL-8 (nM)	5.30 (0.001–9.89)	10.22 (5.34–25.45)
TNFα (nM)	26.21 (19.93–42.27)	58.11 (46.15–25.45)

(Table S5). Cord LA metabolites were not significantly correlated with any infant inflammatory markers. After adjustment for maternal smoking status, cord 11-HETE ($\beta = 4.38$, $p = 0.004$) and 8,15-DiHETE ($\beta = 0.62$, $p = 0.04$) were positively associated with

cord IL-6 (Fig. 6, Table S6). Cord 14 (15)-DiHET was positively associated with cord IL-1β ($\beta = 4.33$, $p = 0.01$), while cord 11 (12)-DiHET was negatively associated with cord IL-10 ($\beta = -1.19$, $p = 0.04$).

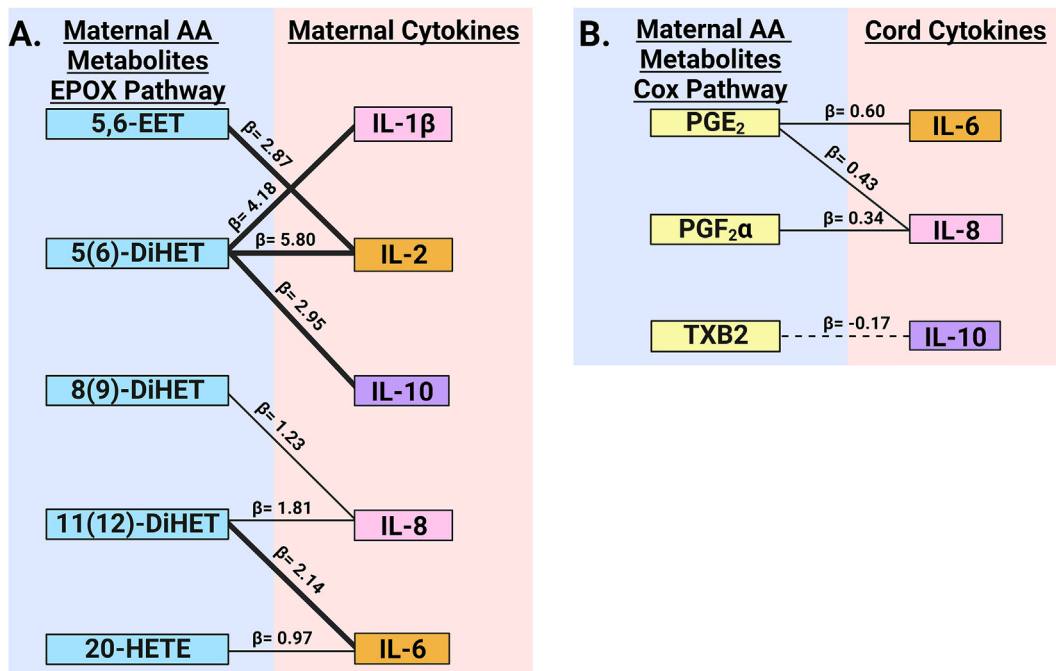


Fig. 4. Linear regression model β coefficients between maternal AA metabolites and (a) maternal (N = 35) or (b) cord (N = 36) inflammatory marker concentrations. Positive associations are indicated by a solid line, while negative associations are indicated by a dashed line. Strong associations ($\beta \geq 2.00$) are indicated with a bold line. Metabolites produced via the COX pathway are shown in yellow and via the EPOX pathway in blue. Pro-inflammatory cytokines are shown in pink, anti-inflammatory cytokines in purple, and pleiotropic cytokines in orange. Only relationships significant at $p < 0.05$ are shown. Models were adjusted for maternal smoking status. Metabolite and inflammatory marker concentrations were log-transformed to meet model assumptions. This figure was created using Biorender.com. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

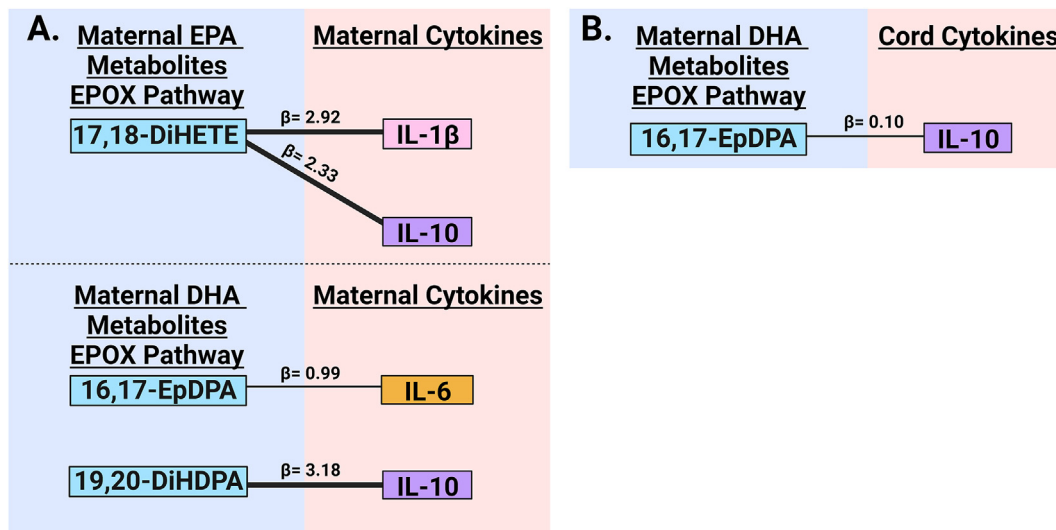


Fig. 5. Linear regression model β coefficients between maternal n-3 metabolites and (a) maternal (N = 35) or (b) cord (N = 36) inflammatory marker concentrations. Strong associations ($\beta \geq 2.00$) are indicated with a bold line. Metabolites produced via the EPOX pathway are shown in blue. Pro-inflammatory cytokines are shown in pink, anti-inflammatory cytokines in purple, and pleiotropic cytokines in orange. Only relationships significant at $p < 0.05$ are shown. Models were adjusted for maternal smoking status. Metabolite and inflammatory marker concentrations were log-transformed to meet model assumptions. This figure was created using Biorender.com. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

3.5. Relationships between cord n-3 FA metabolites and infant inflammatory marker levels

Cord plasma concentrations of EPA and DHA metabolites were significantly correlated with cord IL-1 β (Table S7). After adjustment for maternal smoking status, a 1 nM increase in log-transformed maternal 7-HDHA predicted a 4.14 nM increase in log-transformed cord IL-1 β ($p < 0.001$) (Table S8).

4. Discussion

Our results showed that multiple n-6 and n-3 FAs metabolites in maternal and umbilical cord plasma predicted inflammatory marker concentrations in linear regression models. In maternal plasma, we found that higher concentrations of AA metabolites produced via the COX pathway (PGE₂, PGF₂ α , and TXB2) were predictive of a pro-inflammatory cytokine environment in mothers.

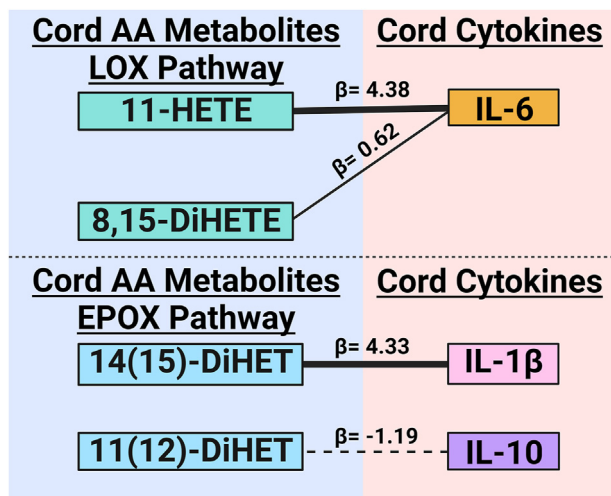


Fig. 6. Linear regression model β coefficients between cord AA metabolites and cord ($N = 37$) inflammatory marker concentrations. Positive associations are indicated by a solid line, while negative associations are indicated by a dashed line. Strong associations ($\beta \geq 2.00$) are indicated with a bold line. Metabolites produced via the LOX pathway are shown in green and via the EPOX pathway in blue. Pro-inflammatory cytokines are shown in pink, anti-inflammatory cytokines in purple, and pleiotropic cytokines in orange. Only relationships significant at $p < 0.05$ are shown. Models were adjusted for maternal smoking status. Metabolite and inflammatory marker concentrations were log-transformed to meet model assumptions. This figure was created using [Biorender.com](#). (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

Given that maternal plasma concentrations were taken upon admission for delivery, these findings align well with previous studies which have established prostaglandins, especially PGE_2 and $\text{PGF}2\alpha$, as important regulators of inflammation during parturition [47]. In addition to promoting cervical ripening, myometrial contraction, and membrane rupture [47], PGE_2 and $\text{PGF}2\alpha$ contribute to the acute inflammatory response during labor by increasing pro-inflammatory cytokine production [48,49]. Denison et al. found that PGE_2 participates in a positive feedback loop to increase IL-8 production [48], while Xu et al. found that $\text{PGF}2\alpha$ elevates IL-1 β , IL-6, and IL-8 production [49]. This study similarly found that maternal AA metabolites were associated with higher maternal plasma concentrations of the pro-inflammatory cytokine IL-1 β and the pleiotropic cytokine IL-6, but lower concentrations of the anti-inflammatory cytokine IL-10.

Higher concentrations of cord LOX (11-HETE and 8,15-DiHETE) and EPOX (11 (12)-DiHET and 14 (15)-DiHET) AA metabolites were also predictive of a pro-inflammatory cytokine environment in infants. Cord AA metabolites were associated with higher cord plasma concentrations of IL-1 β (pro-inflammatory) and IL-6 (pleiotropic), and lower concentrations of IL-10 (anti-inflammatory). These findings align with previous studies which have established n-6 FAs as pro-inflammatory nutrients in a variety of settings [30]. Although little is known about the effects of HETEs on inflammation during parturition, HETEs have been shown to promote inflammation by regulating neutrophil chemotaxis [50] and mast cell activation [51]. The effects DiHETs have on markers of inflammation are unknown, but higher serum concentrations of 11 (12)-DiHET are associated with preterm labor, a common inflammation-driven pregnancy complication [52], indicating that DiHETs may also contribute to the inflammatory response during pregnancy.

We also found significant relationships between n-3 FA metabolites and inflammatory markers. In maternal plasma, higher concentrations of EPA (17,18-DiHETE) and DHA (19,20-DiHDP)

metabolites were associated with higher concentrations of maternal IL-10. These findings are supported by previous studies which have reported that n-3 FA metabolites are anti-inflammatory [34–36,53]. Our previous work found that placental trophoblast treatment with resolvin D2 (RvD2), an EPA-derived specialized pro-resolving mediator, increased the mRNA expression of IL-10 [53]. Askari et al. reported that 19,20-DiHDP inhibits inflammatory cytokine production in endothelial cells [37]. Similarly, Jurado-Fasoli et al. and Aoki et al. found that 17,18-DiHETE is negatively correlated with markers of inflammation-driven diseases including metabolic syndrome and nonalcoholic steatohepatitis [54,55].

Surprisingly, higher concentrations of maternal 17,18-DiHETE and 16,17-EpDPA (DHA metabolites) were also associated with higher maternal plasma concentrations of the pro-inflammatory IL-1 β and pleiotropic IL-6, respectively. Similarly, higher cord concentrations of the DHA metabolite 7-HDHA were predictive of higher cord plasma concentrations of pro-inflammatory IL-1 β . It is possible that some n-3 FA metabolites contribute to increased maternal and infant inflammation, despite n-3 FAs generally promoting inflammation resolution [34–37]. Hu et al. demonstrated that accumulation of 19,20-DiHDP in retinal tissue contributes to the development of non-proliferative diabetic retinopathy by altering cell membrane compositions [56], which may support the hypothesis that some n-3 FA metabolites promote inflammation. Alternatively, it is possible that n-3 FA metabolites are upregulated as a compensatory measure in response to inflammation. Previous studies by Zhang et al. show that although 17,18-DiHETE is an anti-inflammatory metabolite, it is positively associated with mortality in patients with systolic heart failure [57], which may support our theory that n-3 metabolites were elevated to counteract inflammation. Finally, it is possible that the observed relationships between n-3 metabolites and pro-inflammatory cytokines are an artifact of low n-3 fatty acid intake. The World Health Organization recommends pregnant women consume 200–500 mg/day of EPA + DHA [58], but the average EPA + DHA intake in our cohort was only 110 mg/day. Our previous work found a similar trend of insufficient EPA + DHA intake in pregnant women across the United States [59], suggesting that EPA + DHA nutritional status may be inadequate to promote an anti-inflammatory cytokine environment in pregnant women and their infants.

Interestingly, maternal n-6 and n-3 FA metabolite concentrations were also predictive of infant inflammatory marker concentrations, highlighting the importance of maternal nutrition for infant health. Higher maternal concentrations of AA metabolites produced via the EPOX pathway (5,6-EET, 5 (6)-DiHET, 8 (9)-DiHET, 11 (12)-DiHET, and 20-HETE) were predictive of a pro-inflammatory cytokine environment in infants. Additionally, higher maternal concentrations of the DHA metabolite 16,17-EpDPA was predictive of an anti-inflammatory infant cytokine environment. Given that n-6 FA and n-3 FA metabolites regulate inflammation to promote a healthy pregnancy [60], modifying maternal diet may be an effective strategy to reduce perinatal inflammation [61,62] and improve pregnancy outcomes [63–65]. Increasing n-3 FA intake may be beneficial [59], as increased intake is associated with increased maternal blood concentrations of n-3 FAs [38,39]. However, results have been mixed in clinical trials assessing the effect of n-3 FA supplementation on pregnancy outcomes [40,44,66,67]. For example, Haghiac et al. reported that obese women who consumed EPA + DHA supplements beginning in the first trimester of pregnancy had reduced inflammatory cytokine levels in adipose and placental tissue [40]. Similarly, Hamazaki et al. reported a beneficial effect of maternal fish intake (a major source of n-3 FAs) on infant neurodevelopment up to 1 year of age [66]. However, meta-analyses by Lehner et al. and Serra et al. found no association between n-3 FA supplementation during

pregnancy and risk of preterm birth, neurodevelopmental delays, or low birthweight [44,67]. Further research studies are needed to assess how n-3 FA supplementation may improve pregnancy outcomes for women at-risk for high levels of inflammation during pregnancy.

Reducing maternal n-6 FA intake may also be beneficial, as the western diet is high in these pro-inflammatory nutrients. Dietary intake of n-6 FAs, including AA and LA, has dramatically increased in the past century from an n-6: n-3 ratio of 6:1 to 20:1 [68]. Excessive exposure to n-6 FAs is associated with inflammation-driven morbidities including poor infant neurodevelopmental outcomes [42,66], low birthweight [69], and gestational hypertension [43,70,71]. Our data suggests that n-6 and n-3 FA metabolites may play a role in regulating inflammation in pregnancy, but further studies are needed to understand how changes in n-6 and n-3 FA intake during pregnancy may affect markers of inflammation in mothers and infants.

This study was limited by a small sample size from a single academic medical institution (University of Nebraska Medical Center/Nebraska Medicine). Multiple factors contribute to maternal and infant inflammation during pregnancy including maternal diet [40], smoking status [72], delivery mode [73], psychological stressors such as poverty or discrimination [6], and chronic disease processes such as obesity, hypertension, or diabetes [74–77]. We were unable to adjust for all potential variables associated with inflammation due to sample size limitations, but the baseline characteristics of our study population were reported. We did adjust for maternal smoking status, as exposure to tobacco smoke is associated with changes in fatty acid metabolism and inflammation [46].

A small sample size also limited our ability to examine the effects of metabolite interactions on maternal and infant inflammation. We did perform a principal component analysis as a proof of concept to detect patterns of clustering maternal metabolites and their association with maternal inflammatory markers; however, these results should be interpreted with caution due to our sample size limitations [78,79]. We found that the maternal metabolites assessed in this study clustered into 4 principal components (Figure S1), which accounted for 71% of the variance in maternal cytokine concentrations. Component 4 included the n-3 metabolites 14,15-DiHETE, 17,18-DiHETE, and 19,20-DiHDPA, as well as the n-6 metabolites 20-HETE, 5,6-DiHET, and 12-HETE. This component was positively correlated with maternal IL-10 ($r_s = 0.62$; $p < 0.0001$), IL-1 β ($r_s = 0.44$; $p = 0.008$), IL-2 ($r_s = 0.39$; $p = 0.02$), and IL-6 ($r_s = 0.36$; $p = 0.04$; Table S9), which supports our findings that individual maternal n-3 metabolites are positively correlated with both inflammatory and anti-inflammatory maternal cytokines. Although additional studies in larger samples sizes are needed to confirm our results, this study and our supporting principal component analysis suggests that bioactive n-3 and n-6 metabolites interact to regulate maternal and infant inflammation.

Additionally, further studies are needed to assess the relationship between inflammation and bioactive metabolites of n-3 and n-6 FAs in special populations, including maternal-infant dyads affected by psychological stressors or chronic diseases. Similarly, more research is needed to determine whether bioactive metabolites of n-3 and n-6 FAs directly affect plasma concentrations of the inflammation markers assessed in this study, or if the observed relationship between metabolites and inflammation is mediated through other molecules not measured in the present study, such as platelet activating factor [80,81]. Finally, our study examined the relationship between n-6 and n-3 FA metabolites and inflammatory markers at a single time-point in pregnancy (delivery). Future studies are needed to assess how n-6 and n-3 FA nutritional status affects maternal and infant inflammation throughout pregnancy.

Statement of authorship

Rebecca Slotkowski: Conceptualization, Methodology, Validation, Formal Analysis, Investigation, Data Curation, Writing – Original Draft, Writing – Review & Editing, Visualization. **Matthew VanOrmer:** Conceptualization, Methodology, Investigation, Data Curation, Visualization, Writing – Review & Editing, Project Administration. **Anum Akbar:** Conceptualization, Investigation, Writing – Review & Editing. **Taija Hahka:** Conceptualization, Investigation, Writing – Review & Editing. **Maranda Thompson:** Conceptualization, Investigation, Writing – Review & Editing. **Rebekah Rapoza:** Conceptualization, Investigation, Writing – Review & Editing. **Arzu Ulu:** Conceptualization, Methodology, Investigation, Writing – Review & Editing. **Melissa Thoene:** Conceptualization, Methodology, Resources, Visualization, Writing – Review & Editing, Supervision. **Elizabeth Lyden:** Conceptualization, Methodology, Formal Analysis, Writing – Review & Editing. **Maheswari Mukherjee:** Conceptualization, Writing – Review & Editing, Supervision. **Ana Yuil-Valdes:** Conceptualization, Writing – Review & Editing, Supervision. **Sathish Natarajan:** Conceptualization, Writing – Review & Editing, Supervision. **Tara Nordgren:** Conceptualization, Resources, Methodology, Writing – Review & Editing, Supervision. **Corrine Hanson:** Conceptualization, Methodology, Resources, Visualization, Writing – Review & Editing, Supervision. **Ann Anderson Berry:** Conceptualization, Methodology, Resources, Visualization, Writing – Review & Editing, Supervision, Funding Acquisition.

Conflict of interest statement

The authors have no competing interests to declare.

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Appendix A. Supplementary data

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