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Authors	Leite, Debora Farias Batista;Morillon, Aude-Claire;Melo Júnior, Elias F.;Souza, Renato T.;McCarthy, Fergus P.;Khashan, Ali S.;Baker, Philip;Kenny, Louise C.;Cecatti, Jose Guilherme
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UCC

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Coláiste na hOllscoile Corcaigh

BMJ Open Examining the predictive accuracy of metabolomics for small-for-gestational-age babies: a systematic review

Debora Farias Batista Leite,^{1,2} Aude-Claire Morillon,³ Elias F Melo Júnior,⁴ Renato T Souza,⁵ Fergus P McCarthy,⁶ Ali Khashan,⁷ Philip Baker,⁸ Louise C Kenny,⁹ Jose Guilherme Cecatti¹⁰

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ABSTRACT

Introduction To date, there is no robust enough test to predict small-for-gestational-age (SGA) infants, who are at increased lifelong risk of morbidity and mortality.

Objective To determine the accuracy of metabolomics in predicting SGA babies and elucidate which metabolites are predictive of this condition.

Data sources Two independent researchers explored 11 electronic databases and grey literature in February 2018 and November 2018, covering publications from 1998 to 2018. Both researchers performed data extraction and quality assessment independently. A third researcher resolved discrepancies.

Study eligibility criteria Cohort or nested case-control studies were included which investigated pregnant women and performed metabolomics analysis to evaluate SGA infants. The primary outcome was birth weight <10th centile—as a surrogate for fetal growth restriction—by population-based or customised charts.

Study appraisal and synthesis methods Two independent researchers extracted data on study design, obstetric variables and sampling, metabolomics technique, chemical class of metabolites, and prediction accuracy measures. Authors were contacted to provide additional data when necessary.

Results A total of 9181 references were retrieved. Of these, 273 were duplicate, 8760 were removed by title or abstract, and 133 were excluded by full-text content. Thus, 15 studies were included. Only two studies used the fifth centile as a cut-off, and most reports sampled second-trimester pregnant women. Liquid chromatography coupled to mass spectrometry was the most common metabolomics approach. Untargeted studies in the second trimester provided the largest number of predictive metabolites, using maternal blood or hair. Fatty acids, phosphosphingolipids and amino acids were the most prevalent predictive chemical subclasses.

Conclusions and implications Significant heterogeneity of participant characteristics and methods employed among studies precluded a meta-analysis. Compounds related to lipid metabolism should be validated up to the second trimester in different settings.

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INTRODUCTION

Fetal growth restriction (FGR) and small-for-gestational-age (SGA) infants are

Strengths and limitations of this study

- To our knowledge, this is the first systematic review to assess the predictive accuracy of metabolomics for an adverse pregnancy outcome.
- Using small for gestational age (SGA) as surrogate for fetal growth restriction—just as in epidemiological investigations—improves the translational potential of metabolomics.
- Identification of techniques, types of maternal samples and chemical classes paves the way for future metabolomics investigations on fetal growth patterns.
- Available data could not support a meta-analysis; further studies should include accuracy measures of individual metabolites or chemical subclasses in predicting SGA.

major concerns in modern obstetrics.¹⁻³ SGA is commonly used as a proxy for FGR,⁴ despite the subtle differences between these two pathological conditions. The prevalence of both varies according to the criteria applied and on the population and setting, although it reaches as much as 25% in low-income and middle-income countries.⁵ SGA newborns may have adverse health effects, such as still-birth,⁴ perinatal asphyxia,⁶ impaired neurodevelopment⁷ and increased cardiovascular risk.^{8,9} To date, there are no robust prediction tools for SGA using clinical factors,^{10,11} ultrasound data^{12,13} or placental biomarkers.¹⁴

For hypothesis-generating or validation purposes, metabolomics is a novel area of biomarker, discovery, development and clinical diagnostics in translational medicine.^{15,16} Metabolomics is the study of all metabolites^{15,16} in a given sample, that is, low molecular weight compounds (50–2000 Da) that are intermediates of biochemical reactions and metabolic pathways, considered to directly reflect cellular activity and phenotype.^{15,16} Recent studies have evaluated the pathophysiology¹⁷⁻²⁰ of SGA with



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Correspondence to

Professor Jose Guilherme Cecatti; cecatti@unicamp.br

metabolomics. However, little is known about the potential of metabolomics to identify predictive compounds of SGA.

Since metabolomics can identify multiple metabolites from low volume samples and create a model from a collection of these samples,¹⁵ it is a promising technology for hypothesis generation in a heterogeneous condition such as SGA. The prediction of SGA in pregnancy would help refer women to specialised care facilities, improving maternal and neonatal outcomes.^{21 22}

In this context, our review question was ‘What is the accuracy of metabolomics for predicting FGR?’. The main objective of this systematic review was to assess the accuracy of metabolomics techniques in predicting SGA. As a secondary aim, we intended to determine which metabolites are predictive of this condition.

METHODS

The protocol for this systematic review was published previously.²³ This study follows international guidelines for transparency (International Prospective Register of Systematic Reviews) and respects the Preferred Reporting Items for Systematic Reviews and Meta-Analyses statement.²⁴

Literature search strategy

Two independent researchers (DFBL and A-CM) assessed 11 electronic databases (PubMed, EMBASE, Latin American and Caribbean Health Sciences Literature, Scientific Electronic Library Online, Health Technology Assessment, Database of Abstracts of Reviews of Effects, Aggressive Research Intelligence Facility, Cumulative Index of Nursing and Allied Health Literature, Maternity and Infant Care, Scopus, and Web of Science) and grey literature. There were no limits or language constraints; the search strategy covered published documents between 1998 and 2018. The keywords ‘small for gestational age’, ‘metabolomics’, ‘prediction’ and ‘antenatal’, and variations of each, were combined with Boolean operators depending on each database requirements. The full EMBASE literature search was as follows: (‘fetal growth retardation’ OR ‘fetal growth restriction’ OR ‘intrauterine growth restriction’ OR ‘intrauterine growth retardation’ OR ‘small for gestational age’) AND (‘metabolomic*’ OR ‘metabonomic*’ OR ‘metabolit*’ OR ‘H NMR’ OR ‘proton NMR’ OR ‘proton nuclear magnetic resonance’ OR ‘liquid chromatogra*’ OR ‘gas chromatogra*’ OR ‘UPLC’ OR ‘ultra-performance’ OR ‘ultra performance liquid chromatograph*’) AND (‘pregnan*’ OR ‘antenat*’ OR ‘antenat*’ OR ‘prenat*’ OR ‘pre nat*’) AND (‘screen*’ OR ‘predict*’ OR ‘metabolic profil*’). Please check online supplementary material 1 for more details.

Outcomes and subgroup analysis

The primary outcome was SGA, as a surrogate for FGR and defined as birth weight <10th centile, by population-based

or customised charts. The secondary outcomes were birth weight ≤ 5 th or ≤ 3 rd centile.

The intended subgroup analysis comprised the type of metabolomics technique applied (nuclear magnetic resonance, NMR; gas or liquid chromatography coupled with mass spectrometry, GC-MS or LC-MS, respectively); maternal health status before pregnancy (women with vs without any chronic health condition); type of SGA suspected during pregnancy (early vs late SGA); and type of pregnancy (singleton vs multiple pregnancy).

Selection criteria of studies, data collection and analysis

Cohort or case–control studies were included if maternal samples were collected before the clinical diagnosis of SGA, if any metabolomics technique was applied and if the results of SGA were presented. Articles presenting data from the same research project but analysing distinct metabolites or showing data from different countries were included. Studies were excluded (1) according to study design; (2) if they had not applied any metabolomics technique; (3) if they were only experimental studies; (4) if it was not possible to extract data on SGA; or (5) if they presented duplicate data, in which case the most complete publication was included for final analysis.

Two researchers (DFBL and A-CM) independently selected studies, extracted data and discussed discrepancies. One additional reviewer (EFMJ or RTS) helped to decide, by majority, when no consensus was reached.

Piloted standardised forms were applied for data extraction, including pregnancy characteristics and experimental details. The Human Metabolome Database (HMDB)²⁵ and the Kyoto Encyclopedia of Genes and Genomes²⁶ were used for matching chemical class and metabolic pathways of each metabolite, respectively.

Risk of bias and assessment of concerns regarding applicability

Two researchers (DFBL and A-CM) independently evaluated individual studies using the Quality Assessment of Diagnostic Accuracy Studies-2 (QUADAS-2) tool.²⁷ One of the third reviewers (EFMJ or RTS) helped in decision-making when no consensus was achieved.

Each study was classified as high, low or unclear risk of bias in four domains (patient selection, index test, reference standard, and flow and timing), and as high, low or unclear concerns regarding applicability in the first three domains. We did not consider two signalling questions (‘Was a case-control design avoided?’ and ‘Was there an appropriate interval between the index test and reference standard?’). The nested case–control design was an inclusion criterion, and maternal samples should have been collected during pregnancy, that is, before the SGA diagnosis. Studies were considered ‘low risk’, for example, (1) if pregnancy or neonatal complications were not excluded in just one group of participants or data on participant selection had been provided; (2) if methods for sample preparation and interpretation were standardised or metabolite threshold was defined before the experiments

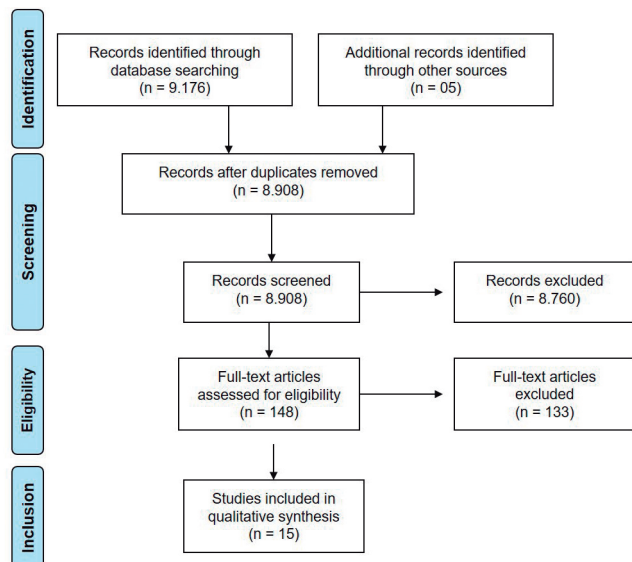


Figure 1 PRISMA flow chart of study identification, screening and selection. PRISMA, Preferred Reporting Items for Systematic Reviews and Meta-Analyses. From Moher D, *et al*²⁴ For more information, visit www.prisma-statement.org.

(for targeted analysis); (3) if the adequacy and reasons for choosing the reference birthweight chart had been explained; or (4) if large-for-gestational-age babies had been excluded from the final comparative analysis.

Data synthesis

A quantitative summary of data was performed when any predictive accuracy measures could be extracted. Authors were contacted to provide additional information, when necessary. However, only Delplancke *et al*²⁸ replied. The estimation of likelihood ratios and hierarchical summary receiver operator characteristic curve²⁹ was planned, as well as assessment of heterogeneity and publication bias.³⁰ However, due to lack of data, a meta-analysis could not be performed.

Patient and public involvement

There was no patient or public involvement in conducting this systematic review.

RESULTS

Literature search characteristics

The literature search for this systematic review was performed in February 2018 and rerun in November 2018. A total of 9181 references were retrieved (figure 1). After the removal of duplicate records (n=273), title and abstract screening, and analysis of the remaining 148 full-text articles, 15 articles were included.^{17 18 28 31–42} See online supplementary material 2 for the excluded studies.

Characteristics of the included studies

The characteristics of the included studies are shown in table 1. The prevalence of SGA ranged from 7.3%³³ to 21.5% in cohort studies.²⁸ There were no studies using birth weight \leq 3rd centile to define SGA. The time interval

between initial participant enrolment and publication varied from 3¹⁷ to 54 years,⁴⁰ although these data were unclear in 38% of the reports.^{18 28 32 33 37} In nested case-control studies, participants were matched by maternal age,^{17 18 38 42} ethnicity,^{17 18 42} parity,³⁸ body mass index^{17 18 42} or infant gender.^{18 38}

Participant characteristics varied between studies. Regarding gestational age at assessment, samples were collected in the second trimester in half of the studies.^{17 18 33 35 37 39 42} In three reports, women were assessed at least twice.^{34 38 41} In one study, maternal blood was drawn either in the first or second trimester,⁴⁰ and in another three studies only samples from the third trimester were considered.^{28 36 41} In the latter case, maternal hair was divided according to length, allowing evaluation of second-trimester and third-trimester metabolites.²⁸ Studies considering the fifth centile as the cut-off sampled women in the first trimester.^{31 32}

Twin pregnancy was a clear exclusion criterion in most studies.^{17 18 31 33–35 37 40–42} Pregnancy aided by assisted reproduction^{18 37} or women with pre-existing conditions^{17 18 35 37 42} were also excluded, although these data were incompletely reported.^{28 32 36 38 39 41} When both nulliparous and multiparous women were enrolled, there was no data analysis according to parity. Half of the studies considered term deliveries exclusively,^{18 28 36 38–41} and the remaining studies did not differentiate results according to gestational age at birth.

Regarding clinical risk factors for SGA, only one paper mentioned a history of SGA, but findings were not adjusted for this variable.³² All studies, except one,²⁸ cited participants' smoking status. The rate of smoking habit ranged from 2.4%¹⁸ to 47.5%.⁴⁰ It is important to note that Gernand *et al*⁴⁰ analysed samples from women recruited between 1959 and 1965, when smoking while pregnant was encouraged, which explains the high rate of smoking participants. The duration of smoking or any differences in birth weight (absolute measures or centiles) were not clearly stated. Although more prevalent in SGA pregnancies, the results did not change with this variable control.^{31 32 35 37 40} Only Gong *et al*⁴¹ mentioned the suspicion of SGA in pregnancy, exhibiting decreasing abdominal circumference growth velocity between 20 and 36 weeks. However, on final analysis, these babies were grouped with infants not suspected during pregnancy.

Subgroup analysis

Due to unavailable data, the only subgroup analysis performed was related to the metabolomics approach applied (table 2). There was no mention of adherence to metabolomics reporting data guidelines. LC-MS was the leading technique used. Three studies have investigated metabolites related to environmental exposure, from contaminated water,³¹ consumer products³⁶ or pesticides,⁴² while others have analysed endogenous compounds.^{32–35 37–40} Only Luthra *et al*³⁸ conducted a biomarker validation study, while Gong *et al*⁴¹ chose

Table 1 Main characteristics of included studies

Authors, year	Country, year of participants' enrolment	Study design	Affected/Non-affected	Gestational age at assessment	Type of pregnancy	Parity	Birthweight curve
Outcome: SGA <5th centile							
Costet <i>et al</i> , 2012 ³¹	France, 2002–2006 (PELAGIE cohort)	Nested case–control	134/399	11 weeks	Single pregnancy	Nulliparous and parous women, unclear proportions	Customised curve
Ertl <i>et al</i> , 2012 ³²	UK*	Nested case–control	150/1000	11 ⁺⁰ –13 ⁺⁶ weeks	Unclear	55.3% nulliparous in SGA group, 48.1% nulliparous in control group	Population-based charts
Outcome: SGA <10th centile							
Grandone <i>et al</i> , 2006 ³³	Italy*	Cohort	31/393	17.1±1.2 weeks† (mean)	Single pregnancy; no maternal pre-existing conditions	Unclear	Population-based charts
van Eijsden <i>et al</i> , 2008 ³⁹	The Netherlands, 2003–2004 (ABCD study)	Cohort	429/3275	13.5±3.3 weeks (mean)	Term deliveries, no diabetes or hypertension	57.6% nulliparous	Population-based charts
Horgan <i>et al</i> , 2011 ¹⁷	Australia, 2008–2011 (SCOPE cohort)	Nested case–control	40/40	14–16 weeks	Single pregnancy; no other pregnancy complications	Nulliparous	Customised curve
Gernand <i>et al</i> , 2013 ⁴⁰	USA, 1959–1965 (Collaborative Perinatal Project)	Nested case–control	395/1751	≤26 weeks	Single pregnancy; term deliveries	Parous women	Population-based charts
Sulek <i>et al</i> , 2014 ¹⁸	Singapore* (GUSTO study)	Nested case–control	41/42	26–28 weeks	Single pregnancy; term deliveries; no maternal pre-existing conditions	Nulliparous and parous women, unclear proportions	Population-based charts
Choi <i>et al</i> , 2016 ³⁴	South Korea, 2012–2013	Cohort	39/217	First, second or third trimester	Single pregnancies	Nulliparous and parous women, unclear proportions	Population-based charts
Kiely <i>et al</i> , 2016 ³⁵	Ireland, 2008–2011 (SCOPE cohort)	Cohort	190/1578	14–16 weeks	Single pregnancy; no maternal pre-existing conditions	Nulliparous	Customised curve
Ong <i>et al</i> , 2016 ³⁷	Singapore* (GUSTO study)	Cohort	83/827	26–28 weeks	Single pregnancy; no maternal chronic illness	43.5% nulliparous	Population-based charts
Wang <i>et al</i> , 2016 ³⁶	Taiwan, 2000–2001 (Taiwan Maternal and Infant Cohort Study)	Cohort	35/188	Third trimester	Unclear; term deliveries	48% nulliparous	Population-based charts
Delplancke <i>et al</i> , 2018 ²⁸	New Zealand*	Cohort	20/73	34–37 weeks	Unclear; term deliveries	Unclear	Customised curve
Luthra <i>et al</i> , 2018 ³⁸	USA, 2010–2012 (TIDES study)	Nested case–control	53/106	First and second trimester	Single pregnancies; term deliveries	60% nulliparous	Customised curve

Continued

Table 1 Continued

Authors, year	Country, year of participants' enrolment	Study design	Affected/Non-affected	Gestational age at assessment	Type of pregnancy	Parity	Birthweight curve
Gong <i>et al</i> , 2018 ⁴¹	UK, 2008–2012 (POP study)	Nested case–control	162/259	36 weeks	Single pregnancies; term deliveries	Nulliparous	Customised curve
Morillon <i>et al</i> , 2018 ⁴²	2008–2011 (SCOPE study)	Nested case–control	40/40	20 weeks	Single pregnancies	Nulliparous	Customised curve

*Unclear period of participant recruitment.

†Mean for all study participants.

ABCD, Adolescent Brain Cognitive Development; GUSTO, Growing Up in Singapore Towards healthy Outcomes; PELAGIE, Étude Longitudinale sur les Anomalies de la Grossesse, l'Infertilité et l'Enfance; POP, Pregnancy Outcome Prediction; SCOPE, Screening of Pregnancy Endpoints; SGA, small for gestational age; TIDES, Tackling Inequalities and Discrimination Experiences in health Services.

to analyse the top 10 statistically different metabolites according to infant sex.

Maternal blood was the most common biological sample analysed by LC-MS in all studies,^{17 32 34–37 39–41} except for one which used GC-MS.³⁹ Maternal urine was analysed by NMR,³⁸ GC-MS³⁶ or LC-MS.⁴² There was only one report using amniotic fluid³³ and two using maternal hair,^{18 28} all applying GC-MS. The period of laboratory analysis was rarely specified, which made it impossible to estimate the total time of sample storage.

Untargeted studies reported diverse metabolic features. Authors matched the peaks with an inhouse library^{18 28} or HMDB-related database.^{17 42} Horgan *et al*¹⁷ found 785 compounds both in maternal and newborn samples; their predictive model included 19 metabolites (only 5 could be putatively identified; [table 2](#)) and used second-trimester maternal blood. Sulek *et al*¹⁸ and Delplancke *et al*²⁸ prepared and analysed samples with GC-MS using similar protocols. Sulek *et al*¹⁸ identified 32 statistically different chromatographic features from which they built a predictive model using five metabolites, including two fatty acids (2-methyloctadecanoate and margarate). In contrast, Delplancke *et al*²⁸ identified 198 metabolites, including three fatty acids (margaric, pentadecanoic and myristic acid) showing significantly higher levels in SGA cases, when second-trimester maternal hair segments were studied.

Analysis of identified metabolites

The identified compounds refer to 11 HMDB chemical classes. Fatty acids^{18 28 39} comprised the most prevalent chemical class, followed by amino acids^{18 33} and phospholipids¹⁷ ([table 3](#)).

A total of 5974 women were assessed for vitamin D status. The results were presented as total vitamin D,^{32 35 37 40} although vitamin D₂, D₃ or 3-epi-25(OH)D₃³⁵ metabolites were measured. The results were stratified according to season of maternal sampling or latitude. Either <15 ng/mL (<37.5 nmol/L)⁴⁰ or <20 ng/mL (<50 nmol/L)^{32 35 37} levels characterised vitamin D deficiency, but were statistically different in SGA pregnancies only in the first trimester.³² Horgan *et al*¹⁷ found a metabolite that could represent a vitamin D derivative, but it was only predictive in combination with 18 other compounds; this model had an area under the curve (AUC) of 0.90 (optimal OR, 44; 95% CI 9 to 214).¹⁷

The second most frequent targeted metabolite was homocysteine,^{33 34} although levels were only differentiated between normal and SGA pregnancies when measured in second-trimester amniotic fluid, with a multiple linear regression model of $r^2=0.012$ and $p=0.029$.³³ Comparatively, the only common metabolite in the second-trimester maternal hair was margarate, with conflicting results since it was found to be either increased (AUC 0.72, 95% CI 0.58 to 0.86)²⁸ or decreased.¹⁸ The N1,N12-diacetylspermine and the perfluorocarboxylic acids were associated with female SGA babies, not males. The former presented a fivefold decreased risk of SGA across

Table 2 Subgroup analysis of included studies according to which metabolomics technique was applied

Authors, year	Metabolomics technique	Maternal sample/storage temperature	Prediction model*	Targeted compounds	Coefficient of variation/limits of quantitation	Predictive compounds	Sensitivity /Specificity AUC
Nuclear magnetic resonance							
Luthra <i>et al.</i> , 2018 ³⁸	¹ H-NMR 1D NOESY with presaturation and homonuclear 2D J-resolved at 300 K Bruker 600 MHz Advance III HD spectrometer	Urine/−80°C	Targeted	Tyrosine, acetate, formate, trimethylamine	NA	None	
Gas chromatography coupled to mass spectrometry							
Costet <i>et al.</i> , 2012 ³¹	GC-MS Simple headspace SPME-capillary GC	Urine/−20°C	Targeted	Trichloroacetic acid	<5%/0.01 mg/L	None	0.1/0.93
Sulek <i>et al.</i> , 2014 ¹⁸	GC-MS Thermo Trace GC Ultra system coupled to ISQ mass selective detector Capillary GC column: Phenomenex ZB-1701 (30 m × 250 μm id × 0.15 μm with 5 m guard column)	Hair/−20°C	Untargeted	NA	NA	↓ Lactate ↓ Levulinat ↑ 2-methyloctadecanoate ↑ Tyrosine ↓ Margarate	0.998
Delplancke <i>et al.</i> , 2018 ²⁸	GC-MS Agilent 7890B gas chromatograph, capillary column ZB-1701 (30 m × 250 μm id × 0.15 μm with 5 m guard column) 5977A mass spectrometer, electron impact ionisation	Hair/−20°C	Untargeted	NA	NA	↑ Margoric acid ↑ Pentadecanoic acid ↑ Myristic acid††	0.72 0.73 0.73
Liquid chromatography coupled to mass spectrometry							
Grandone <i>et al.</i> , 2006 ³³	LC-MS/MS triple quadrupole Applera API 3000, TurbolonSpray ionisation	Amniotic fluid/−80°C	Targeted	Homocysteine	Unclear	↑ Homocysteine (1.29 μM; 1.05–1.51 μM)	
Horgan <i>et al.</i> , 2011 ¹⁷	UPLC-MS/MS Thermo Fisher LTQ Orbitrap, ESI	Plasma/−80°C	Untargeted	NA	NA	Hexacosanedioic acid, diglyceride, lyso-phosphocholine, sphinganine 1-phosphate, sphingosine 1-phosphate§	0.90
Ertl <i>et al.</i> , 2012 ³²	HPLC-MS/MS Shimadzu Prominence HPLC system with a column Phenomenex Luna C8 3×50 mm; AbSciex API-5000 triple quadrupole, ESI	Serum/−80°C	Targeted	25(OH)D ₂ ; 25(OH)D ₃	6.3%*, 6.6%† (D ₂); 6.5%*, 7.3%† (D ₃)/unclear	↓ 25(OH) ₂ vitamin D (12.16 ng/mL; 8.09–20.54 ng/mL)	0.72/0.45
Germand <i>et al.</i> , 2013 ⁴⁰	LC-MS/MS	Serum/−20°C	Targeted	25(OH)D ₂ ; 25(OH)D ₃	8.2%* (D ₂) 5.9%* (D ₃)/<1 ng/mL	None	0.39/0.66

Continued

Table 2 Continued

Authors, year	Metabolomics technique	Maternal sample/storage temperature	Prediction model*	Targeted compounds	Coefficient of variation/limits of quantitation	Predictive compounds	Sensitivity /Specificity AUC
Choi <i>et al</i> , 2016 ³⁴	HPLC-MS/MS Waters HPLC system, Applied Biosystems API-4000 MS/ MS mass spectrometer	Serum/−20°C	Targeted	Methylmalonic acid; homocysteine	<10%*; <10%†/ unclear	None	
Kiely <i>et al</i> , 2016 ³⁵	UPLC-MS/MS Waters Acquity UPLC system, Waters Triple Quadrupole TQD mass spectrometer	Serum/−80°C	Targeted	25(OH)D ₂ ; 25(OH)D ₃ ; 3-epi-25(OH)D ₃	<6%*; <5%†/0.57 ng/mL (D ₂); 0.26 ng/mL (D ₃), 0.41 ng/mL (epi-D ₃)	None	
Ong <i>et al</i> , 2016 ³⁷	LC-MS/MS Applied Biosystems Thermo Hypersil BDS C8 reverse-phase column	Plasma/unclear	Targeted	25(OH)D ₂ ; 25(OH)D ₃	≤10.3%*†/≤1.6 ng/mL	None	0.12/0.87
Wang <i>et al</i> , 2016 ³⁶	LC-MS Agilent HPLC system, Applied Biosystems Sciex API-4000 triple quadrupole mass spectrometer	Serum/unclear	Targeted	PFOA; long-chain PFCA	0.83–7.94%*; 1.57–24.7%†/0.07– 0.45 ng/mL†	PFDeA (OR 3.14; 95% CI 1.07 to 9.19), PFUnDA (OR 1.83; 95% CI 1.01 to 3.32)**	
Gong <i>et al</i> , 2018 ⁴¹	LC-MS/MS Shimadzu UK Limited UPLC system, ACE Excel 2 C18-PPP LC-column, Thermo Fisher Scientific Exactive Orbitrap mass spectrometer	Serum/unclear	Untargeted	NA		1†N1,N12-diacetylspermine**	
Morillon <i>et al</i> , 2018 ⁴²	UPLC-MS/MS Waters Acquity UPLC system, Waters Synapt G2-S mass spectrometer	Urine/−80°C	Untargeted	NA		None	
Others							
van Eijsden <i>et al</i> , 2008 ³⁹	GC-FID Solid phase extraction SPE, capillary GC	Plasma/−80°C	Semitargeted, lipid extraction	Elaidic, linoleic, alpha-linolenic, eicosatetraenoic, EPA, DPA, DHA DGLA, AA, adrenic, and Osbond acids	≤2%–22%†/unclear	↓ Eicosatetraenoic acid (OR 1.5; 95% CI 1.07 to 2.11), ↓DPA (OR 1.49; 95% CI 1.06 to 2.1)	

Continued

Table 2 Continued

Authors, year	Metabolomics technique	Maternal sample/storage temperature	Prediction model*	Targeted compounds	Coefficient of variation/limits of quantitation	Predictive compounds	Sensitivity /Specificity AUC
	*Intra-assay coefficients of variation. †Interassay coefficients of variation. ‡These metabolites were found in second-trimester hair segments. §And more 14 metabolites that could not be identified certain based on chromatographic peak and mass: phenylacetylglutamine or formyl-N-acetyl-5-methoxykynurenamine; leucyl-leucyl-norleucine or sphingosine 1-phosphate; ceronyl carnitine and/or 1-alpha,25-dihydroxy-18-oxocholecalciferol; (15Z)-tetraenoic acid or 10,13-dimethyl-11-docosyne-10,13-diol or <i>trans</i> -selacholeic acid; pentaenoic acid or cyclohexyl acetate or octanoic acid or methyl-heptenoic acid or 4-hydroxy-2-octenal or DL-2-aminooctanoic acid or 3-amino-octanoic acid; hydroxybutyrate or hydroxy-methylpropanoate or methyl methoxyacetate; lysophosphocoline and phosphocoline (more than 20 hits); phosphocoline (more than 20 hits); phosphocoline or ubiquinone-8; acetyl-leucyl-leucyl-norleucinal or oleoylglycerone phosphate or LPA(0:0/18:2(9Z,12Z)) or 1-16:1lysoPE or phosphocoline(O-11:1(10E)/2:0) or (3s)-3,4-Di-N-hexanoyloxybutyl-1-phosphocoline or N-(3-hydroxy-propyl) arachidonoyl amine or N-methyl N-(2-hydroxy-ethyl) arachidonoyl amine or similar; lysophosphocoline (16:1) or ceronyl carnitine; pregnadiol-3-glucuronide or 3-alpha,20-alpha-dihydroxy-5-beta-pregnane-3-glucuronide; 6-hydroxyshingosine or (4OH,8Z,118:1) sphingosine or 15-methyl-15-prostaglandin D2 or 15-R-prostaglandin E2 methyl ester. ¶Values for all studied metabolites. **Predictive compounds only for female babies. AA, arachidonic acid/AUC, area under the receiver operating characteristic curve; DGLA, dihomo-gamma-linolenic acid; DHA, docosahexaenoic acid; DPA, docosapentaenoic acid; EPA, eicosapentaenoic acid; ESI, electrospray ionisation; GC-MS, gas chromatography coupled to mass spectrometry; H-NMR, hydrogen nuclear magnetic resonance; HPLC, high performance liquid chromatography; LC-MS, liquid chromatography coupled to mass spectrometry; NA, not applicable; NOESY, nuclear Overhauser effect spectroscopy; PFCA, perfluorocarboxylic acid; PFDeA, perfluorodecanoic acid; PFOA, perfluorooctanoic acid; PFOA, perfluorodecanoic acid; PFUnDA, perfluoroundecanoic acid; SPME, solid phase microextraction; UPLC, ultra-performance liquid chromatography.						

quintiles. The perfluorodecanoic and perfluoroundecanoic acids presented OR of 3.14 (95% CI 1.07 to 9.19) and 1.83 (95% CI 1.01 to 3.32).³⁶ Tyrosine, an essential amino acid for infants, was part of the predictive model of maternal hair, combining five metabolites with an AUC of 0.998 (95% CI 0.992 to 1.0).¹⁸ However, tyrosine did not predict SGA when urine samples were studied.³⁸ Methylmalonic acid,³⁴ acetate, formate or trimethylamine³⁸ did not differentiate SGA when compared with uncomplicated pregnancies ($p>0.05$).

Risk of bias and applicability concerns

Figure 2 shows synthesised data for all included studies. See online supplementary material 3 for individual QUADAS-2 data.

Regarding the risk of bias, all cohort studies conducted a consecutive participant inclusion.^{28 33–37 39} Nested case-controls matched cases and controls randomly,^{33–35 41} or according to maternal and infant characteristics.^{17 18 38 42} One study⁴¹ failed to mention matching procedures ('Patient Selection' domain). Researchers were not blinded to SGA status when interpreting metabolomics results,^{17 18 28 32 35–41} and thresholds of targeted metabolites were not prespecified^{31 33 36 38 39} ('Index Test' domain). Conversely, SGA identification was not influenced by the metabolomics test, although it was unclear when laboratory experiments were performed in some studies.^{18 28 31 33 34 41} Birthweight charts were adequate, except for two studies. The first did not report which centile was chosen,¹⁸ and the second used a centile designed for a different population³³ ('Reference Test' domain). Two studies were ranked as 'high risk' because not all participants were included in the analysis^{31 37} ('Flow and Timing' domain).

The QUADAS-2 tool also highlights the importance of how the findings of the included studies are suitable to the review question. In the patient selection domain, it was ranked as 'high applicability concerns' when infants born between the 4th and the 10th centile, but with normal abdominal circumference growth velocity, were not included in the final analysis.⁴¹ It was 'unclear' when the gestational age of maternal assessment was not standardised,³⁴ or was inferred by hair segment length,²⁸ or when few metabolites from untargeted studies were chosen for interpretation⁴¹ ('Index Test' domain). Finally, it was 'high' when the birthweight charts applied did not correspond to the study population^{18 33} ('Reference Standard' domain).

Meta-analysis

From the 15 included studies, only 3 were designed for prediction purposes^{17 18 42} and provided the AUC. The remaining reports described statistical differences of metabolites between SGA pregnancies and controls.^{28 31–41} Accuracy measures were extracted when available (table 2). However, due to marked heterogeneity (tables 1 and 2) of gestational age at sampling, type of samples used, type of birthweight chart chosen, thresholds for vitamin D deficiency, metabolomics approach

Table 3 Predictive metabolites summarised according to their chemical class, subclass and biological process

Predictive metabolites	Chemical class	Chemical subclass	Metabolic pathway
Margarate	Fatty acyls	Fatty acids and conjugates	Lipid transport, metabolism, peroxidation
Pentadecanoic acid	Fatty acyls	Fatty acids and conjugates	Lipid transport, metabolism, peroxidation; fatty acid metabolism and biosynthesis
Myristic acid	Fatty acyls	Fatty acids and conjugates	Lipid transport, metabolism, peroxidation; fatty acid metabolism and biosynthesis
Eicosatetraenoic acid	Fatty acyls	Fatty acids and conjugates	Lipid transport, metabolism, peroxidation; lipid metabolism pathway
Docosapentaenoic acid	Fatty acyls	Fatty acids and conjugates	Lipid transport and metabolism, fatty acid metabolism, alpha linolenic acid and linoleic acid metabolisms
Tyrosine*	Carboxylic acids and derivatives	Amino acids, peptides and analogues	Catecholamine biosynthesis, phenylalanine and tyrosine metabolism, thyroid hormone synthesis, transcription and translation
Homocysteine	Carboxylic acids and derivatives	Amino acids, peptides and analogues	Glycine and serine metabolism, methionine metabolism
Hexacosanedioic acid	Carboxylic acids and derivatives	Dicarboxylic acid and derivatives	Fatty acid biosynthesis
Sphinganine 1-phosphate	Sphingolipids	Phosphosphingolipids	Sphingolipid signalling pathway, neuroactive ligand-receptor interaction
Sphingosine 1-phosphate	Sphingolipids	Phosphosphingolipids	Lipid metabolism pathway, sphingolipid metabolism
PFDeA	Alkyl halides	Alkyl fluorides	Not reported†
PFUnDA	Alkyl halides	Alkyl fluorides	Not reported†
25,OH,vitamin D	Steroids and steroids derivatives	Vitamin D and derivatives	Lipid metabolism pathway
Diglyceride	Glycerolipids	Diradylglycerols	Adipocytokine signalling pathway
Lactate	Hydroxy acids and derivatives	Alpha hydroxy acids and derivatives	Gluconeogenesis, glycogenesis types IB and IC, pyruvate metabolism, triosephosphate isomerase
N1,N12-diacetylspermine	Carboximidic acids and derivatives	Carboximidic acids	
Lyso-phosphocholine	Glycerophospholipids	Glycerophosphocholines	Not reported†
2-methyloctadecanoate	Saturated hydrocarbons	Alkanes	Not reported†
Levulinate	Keto acids and derivatives	Gamma-keto acids and derivatives	Not reported†

*Essential amino acid for infants.

†No human metabolic pathways reported at KEGG.

KEGG, Kyoto Encyclopedia of Genes and Genomes; PFDeA, perfluorodecanoic acid; PFUnDA, perfluoroundecanoic acid.

and identified compounds, a meta-analysis could not be performed.

DISCUSSION

Main findings

In this first systematic review of metabolomics and adverse pregnancy endpoints, we presented techniques and metabolites which were studied for the prediction of SGA. Any effect on birth weight has important implications for perinatal research, since it is related to short-term and long-term outcomes,^{43–46} and in different generations.^{47 48} Intrauterine environment influences fetal growth through

epigenetic processes: altered gene expression potentially leads to distinct phenotypes.⁴⁹ Metabolomics is the most adequate approach to study this outcome since it is most directly related to phenotype.⁵⁰

Interpretation of metabolomics findings in pregnancy can be challenging. First, maternal metabolite concentrations are influenced by placental transfer to and from the fetus. The ‘mirror effect’, seen for maternal plasma and venous cord blood metabolites at birth,⁵¹ cannot be ruled out when only maternal specimens are studied. Second, maternal exposure to distinct compounds may affect metabolite levels. Statistically significant differences

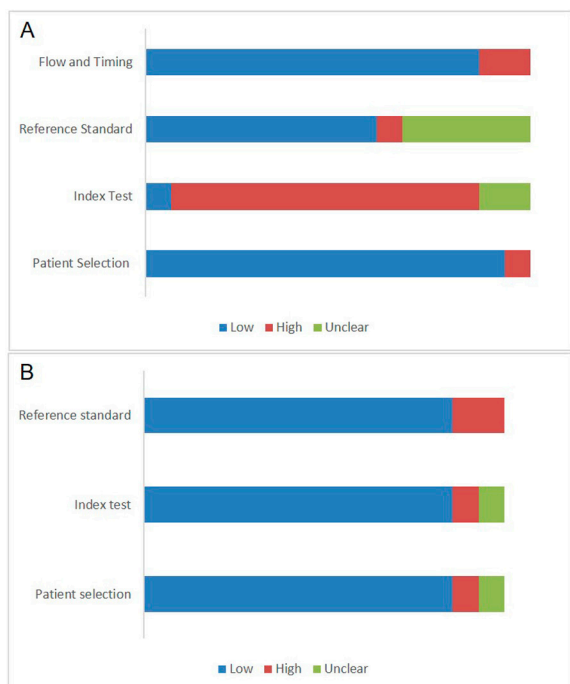


Figure 2 Assessment of risk of bias (A) and applicability concerns (B) of individual studies.

between SGA infants and controls may not express the totality of underlying pathological pathways and have no clinical meaning. Finally, it is unclear when the processes leading to SGA are initiated. The disruption in maternal metabolism can theoretically occur at any time. In general the lower the gestational age at which the condition is suspected, the more severe the phenotype will be at birth.^{52 53} Thus, the description of clinical data in translational studies must deal with all these confounding factors.

Gestational age at sampling is probably the most important parameter for prediction purposes. With timely prediction, women could be referred to specialised care and have increased surveillance, and this in turn may lead to a reduction in perinatal mortality. There are temporal changes in the maternal metabolome during pregnancy^{28 54–57}; therefore, it is reasonable to expect distinctive metabolites at different stages of pregnancy, as reported here. Unfortunately, a wide or unclear definition of gestational age of sampling^{34 36 38 40} renders a more precise interpretation impossible and may limit the clinical application of these results.

In contrast, gestational age at birth and birthweight centile seem to be the hallmarks of severity and prognosis of growth restriction.^{6 58} Indeed, term and preterm SGA babies show distinct clinical phenotypes, and there are concerns that some babies <10th centile of birth weight are constitutionally small infants.^{59–61} If only term deliveries are evaluated, the most severe cases of growth restriction may be potentially missed. Moreover, when term and preterm births are analysed together, or when lower cut-offs are not specified (eg, ≤ 3 rd or ≤ 5 th centile), the lack of predictive metabolites might mean that they are

distinct conditions. Thus, we hypothesise that the predictive performance of metabolomics may be improved if data are analysed by gestational age at delivery and by different cut-offs of birthweight centiles.

Evidence suggests that tobacco smoke has an impact on birth weight,^{62–64} although it is uncertain how and when fetal growth is impaired. It is possibly related to oxidative stress,⁶⁵ and both maternal and fetal metabolism may be disturbed at delivery.^{66 67} Studies that were included did not investigate cigarette-related chemicals or quantify exposure to tobacco smoke. Therefore, no relationship between SGA and tobacco was found. Hence, we suggest that tobacco interferes with ongoing metabolic pathological processes, or its disturbance is related to additional metabolic pathways other than the one examined by the included studies.

Subgroup and metabolite findings

No reports have explored data on any maternal chronic condition, suspicion of SGA in pregnancy or number of fetuses. The lack of clear statements about participant selection has hindered data interpretation and precluded these analyses.

The majority of included studies performed a targeted approach, that is, a hypothesis-testing evaluation,^{16 50} driven by epidemiological or experimental data regarding SGA newborns. None of the targeted metabolites^{31–40} were in common with those found by ‘hypothesis-generating’ metabolic profiling^{17 18 28 41 42} investigations. This reinforces the suggestion that various maternal metabolic pathways may be triggered by the SGA condition and be detected by different biological samples. However, since blood is a very complex sample and GC-MS only evaluates volatile molecules,⁵⁰ our findings may be biased by study methodologies.

Untargeted studies, as expected, have characterised several metabolites that may be validated in future investigations. Nine lipids and fatty acid metabolites,^{17 18 28 39} two amino acids^{18 33} and a steroid^{17 32} have been identified as potential biomarkers of SGA.

All lipid-related metabolites identified are intermediates for energy storage and breakdown. Most metabolites were found in maternal blood¹⁷ or hair of the SGA group.^{18 28} Blood levels of saturated and monounsaturated non-esterified fatty acids apparently remain stable throughout pregnancy, while long-chain polyunsaturated fatty acid (docosahexaenoic acid and eicosapentaenoic acid, for example) measurements seem to show ethnicity-related changes.⁵⁷ Experimental data show the importance of hypoxia and oxidative stress to placental function, and ultimately to birth weight.^{68 69} Findings from included studies may represent a dysregulation of lipid pathways at the placental level, but an association with maternal background is unclear. Therefore, we hypothesise that disorders of lipid metabolism may be the ‘metabolic snapshot’ of defective deep placentation⁷⁰ and might reflect maternal efforts to respond to impaired fetal growth.

Recommendations on the assessment of vitamin D and cut-offs to define vitamin D deficiency in pregnancy are controversial.⁷¹ However, vitamin D supplementation decreases SGA risk.⁷² In early pregnancy, vitamin D status has been related to SGA,^{73 74} which is in accordance with this review, despite the inconsistent findings.⁷⁵ There is evidence that trophoblasts actively produce and secrete vitamin D metabolites,⁷⁶ but it is not clear how they mediate fetal growth impairment. Altered hepatic gene expression and liver function in vitamin D-deficient female rats⁷⁷ and single nucleotide polymorphisms⁷⁸ in vitamin D receptor gene have been suggested as mechanisms to be explored by a multidimensional omics approach.

Finally, homocysteine is an intermediate metabolite of the folate cycle. It is indirectly involved with DNA methylation and is a marker of folate deficiency.⁷⁹ Maternal levels rarely reach hyperhomocysteinaemia limits,⁸⁰ but folate depletion^{81–83} and homocysteine itself⁸⁰ are thought to be associated with a higher SGA risk. In this review, homocysteine was only statistically different in SGA pregnancies when measured in amniotic fluid,³³ although within the normal ranges proposed for 17–21 weeks.⁸⁴ Since amniocentesis is generally performed in women at higher obstetrical risk, future studies should investigate whether homocysteine in amniotic fluid represents a confounding factor or a new biomarker.⁸⁵

Methodological quality

Most studies were ranked as ‘low risk’ of bias or applicability to the review question. However, the lack of clear descriptions of laboratory experiments, including sample preparation and storage, and blinding of the researchers to the case/control status are major pitfalls of the included studies.

Strengths and limitations

To our knowledge, this is the first systematic review of metabolomics and an adverse pregnancy outcome (SGA). We presented possible biomarkers of SGA pathophysiology, metabolites implicated in lipid transport and metabolic pathways, as well as gluconeogenesis.

However, this analysis has some limitations. First, included studies showed heterogeneity, which is fundamental in systematic reviews. Indeed, there was a wide variety of participant characteristics and methods used, and not all authors provided a detailed description of methods employed. Although the Metabolomics Standards Initiative was released in 2007,⁸⁶ there is still poor adherence to guidelines.^{87 88} Clear reporting^{15 87 88} and data sharing in repositories are crucial steps in identifying features of interest, specifically possible biomarkers to be validated in the clinical studies.¹⁵ Second, we could not perform a meta-analysis of the extracted data, impacting the translational potential of metabolomics.

Third, we considered that birth weight was a surrogate measure of intrauterine development. SGA and FGR are not interchangeable concepts. However, SGA has been

used as a surrogate for FGR in many clinical studies due to difficulties in defining optimal intrauterine growth: (1) FGR diagnosis relies mostly on ultrasound measurements of fetal biometry,^{3 89} which in turn is subject to systematic errors⁹⁰; (2) intrauterine development is adaptive, rather than uniform⁹¹ or only genetically driven⁴⁹; and (3) growth impairment at birth better identifies adverse neonatal outcomes than during pregnancy.⁵⁸ It is recognised that changes in obstetric care occur when growth restriction is suspected, and neonatal outcomes are improved.^{21 22} Thus, an accurate prediction of SGA during pregnancy will be a turning point in modern obstetrics.

CONCLUSIONS AND IMPLICATIONS FOR PRACTICE

Using the available clinical tools, efforts to predict SGA remain disappointing. Since SGA is a heterogeneous condition, it benefits from metabolomics. This novel area of research allows analysis of numerous types of biological fluids and detects thousands of metabolites in complex samples.^{15 16 25} However, findings of this systematic review must be interpreted with caution. The type of samples used may have influenced LC-MS (second-trimester maternal blood) and GC-MS (second-trimester maternal hair) findings in individual studies. Furthermore, the prediction of SGA in the context of maternal disorders, suspected FGR and twin pregnancies is an open field for future metabolomics studies, and environmental exposure investigation as well.

Surprisingly, none of the studies used ≤ 3 rd centile of birth weight as a cut-off or analysed preterm deliveries and hypertensive syndromes. Considering our findings and the different phenotypic manifestations of SGA, we envision a better performance when (1) cut-offs other than the 10th centile are tested; (2) data on gestational age at sampling and at birth are standardised; and (3) other pregnancy-related syndromes are considered, especially hypertension. Thus, future metabolomics results should advance in these critical points.

Finally, all detected biomarkers were related to lipid pathways and energy metabolism. We consider that research efforts to predict SGA should focus on compounds involved in these pathways, up to the second trimester of pregnancy.

Author affiliations

¹Department of Tocogynecology, Campinas' State University, Campinas, Brazil

²Department of Maternal and Child Health, Universidade Federal de Pernambuco, Recife, Pernambuco, Brazil

³Irish Centre for Fetal and Neonatal Translational Research (INFANT), University College Cork National University of Ireland, Cork, Ireland

⁴Clinics Hospital, Universidade Federal de Pernambuco, Recife, Brazil

⁵Obstetrics and Gynecology, Universidade Estadual de Campinas, Campinas, Brazil

⁶Department of Gynaecology and Obstetrics, St Thomas Hospital, Cork, UK

⁷Department of Epidemiology and Public Health, University College Cork, Cork, Ireland

⁸College of Medicine, University of Leicester, Leicester, UK

⁹Department of Women's and Children's Health, University of Liverpool School of Life Sciences, Liverpool, UK

¹⁰Obstetrics and Gynecology, University of Campinas, Campinas, Sao Paulo, Brazil

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