ORIGINAL ARTICLE

Identification of a plasma signature of psychotic disorder in children and adolescents from the Avon Longitudinal Study of Parents and Children (ALSPAC) cohort

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The identification of an early biomarker of psychotic disorder is important as early treatment is associated with improved patient outcome. Metabolomic and lipidomic approaches in combination with multivariate statistical analysis were applied to identify plasma alterations in children (age 11) (38 cases vs 67 controls) and adolescents (age 18) (36 cases vs 117 controls) preceding or coincident with the development of psychotic disorder (PD) at age 18 in the Avon Longitudinal Study of Parents and Children (ALSPAC). Overall, 179 lipids were identified at age 11, with 32 found to be significantly altered between the control and PD groups. Following correction for multiple comparisons, 8 of these lipids remained significant (lyosphosphatidylcholines (LPCs) LPC(18:1), LPC(18:2), LPC(20:3); phosphatidylcholines (PCs) PC(32:2; PC(34:2), PC(36:4), PC(0-34-3) and sphingomyelin (SM) SM(d18:1/24:0)), all of which were elevated in the PD group. At age 18, 23 lipids were significantly different between the control and PD groups, although none remained significant following correction for multiple comparisons. In conclusion, the findings indicate that the lipidome is altered in the blood during childhood, long before the development of psychotic disorder. LPCs in particular are elevated in those who develop PD, indicating inflammatory abnormalities and altered phospholipid metabolism. These findings were not found at age 18, suggesting there may be ongoing alterations in the pathophysiological processes from prodrome to onset of PD.

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INTRODUCTION

Psychotic disorders (PD) are among the most severe and debilitating medical diseases, with schizophrenia being the most common, affecting ~0.5–1% of the global population.1 At present, the diagnosis of PD is subjective and there are no reliable biological diagnostic tests.2 Over the last decade, the psychosis field of research has shifted its focus to the prodrome or ‘at-risk mental state’ (ARMs) in an attempt to identify and treat subjects at high risk of developing a psychotic illness. Investigations have indicated that 20–30% of these individuals will go on to develop schizophrenia over a 2–3 year period.3 Strong evidence supports early intervention as a means to alleviate and improve therapeutic outcome for individuals.4,5 Owing to the multifactorial complexity of PD,2,6 the identification of a disease signature and molecular biomarker(s) sensitive to the underlying pathogenic factors would be of great importance to assist in early detection and diagnosis7 but also to understand the mechanisms underlying the disease process, which has yet to be fully elucidated.8

Metabolomics, the global study of metabolites in cells, tissues or biofluids has emerged in recent years as a promising tool to identify abnormalities in psychotic illnesses. Metabolomic studies in schizophrenia and related psychoses have highlighted a number of metabolic perturbations such as glucoregulatory processes,9,10 fatty acid and lipid metabolism,11–13 mitochondrial function,14 and proline7 and tryptophan metabolism.15 Although a comprehensive mapping of disturbances in metabolic pathways in PD is still a long way off,16 the most consistent findings involve pathways common to fatty acids and the pro-oxidant/antioxidant balance.17 A recent study by Rice and colleagues reported decreased levels of erythrocyte polyunsaturated fatty acid (PUFA) levels in young people at ultra-high risk of PD,18 providing additional evidence of the putative ω–3 PUFA deficiency syndrome. These studies have identified various metabolite signatures and have contributed to a developing and enhanced understanding of the disease mechanism. However, they generally focus on the adult population who have already transitioned to schizophrenia, with a majority being medicated, and so they are limited in terms of identifying early biomarker signatures of the disease.

The aim of this study was to apply metabolomic approaches to identify plasma alterations in children (age 11) and adolescents...
Global lipidomic analysis

The plasma samples were analysed for global profiling of lipids using a method developed specifically for lipidomics analyses. The samples were prepared following the previously published Folch procedure with minor modifications. Briefly, 10 μl of 0.9% NaCl, 100 μl of CHCl₃:MeOH (2:1, v/v) and 20 μl of a 3.5 μg ml⁻¹ working standard solution of chosen lipid standards (for quality control and data normalisation purposes) were added to 10 μl of each plasma sample. The standard solution contained the following compounds: 1,2-dihexadecanoyl-sn-glycerol-3-phosphoethanolamine (PE(17:0/17:0)), N-heptadecanoyl-o-erythro-sphingosylphosphorylcholine (SM(d18:1/18:1)), N-heptadecanoyl-o-erythro-sphingosine (Cer(d18:1/17:0)), 1,2-dihexadecanoyl-sn-glycerol-3-phosphocholine (PC(17:0/17:0)), 1-heptadecanoyl-2-hydroxy-sn-glycerol-3-phosphocholine (LPC(17:0)) and 1-palmityl-d31-2-oleoyl-sn-glycerol-3-phosphocholine (PC(16:0/d31:18:1)). These were purchased from Avanti Polar Lipids (Alabaster, AL, USA). In addition, 1,2-dimyristoyl-sn-glycerol-3-phosphocholine (PC(14:0/14:0)) was purchased from Sigma Aldrich (Wicklow, Ireland) and Tripalmitin-1,1,1-13C3 (TG(16:0/16:0/16:0)) and Triocanoin-1,1,1-13C3 (TG(8:0/8:0/8:0)–13C3) from Lardan (Solna, Sweden) for the same purpose. The samples were vortex mixed and allowed to stand on ice for 30 min after which they were centrifuged (9400 g, 3 min, 4 °C). Overall, 60 μl from the lower layer of each sample was then transferred to a glass vial with an insert and 60 μl of CHCl₃:MeOH (2:1, v/v) was added. The samples were then stored at −80 °C until analysis.

Calibration curves (at concentration levels of 100, 500, 1000, 1500, 2000 and 2500 nmol ml⁻¹) for quantification of lipids were prepared using 1-hexadecyl-2-(9Z-octadecanoyl)-sn-glycerol-3-phosphocholine (PC(16:0/18:1(9Z))), 1-(1Z,13Z-octadecadienoyl)-2-(9Z-octadecanoyl)-sn-glycerol-3-phosphocholine (PC(16:0/18:1(9Z))2), 1-(1Z,13Z-octadecadienoyl)-2-(9Z-octadecanoyl)-sn-glycerol-3-phosphocholine (PC(18:0/18:1(9Z))2), 1-ocadecanoyl-sn-glycerol-3-phosphocholine (PC(18:0)), 1-(1Z,13Z-octadecadienoyl)-2-docosahexaenoyl-sn-glycerol-3-phosphocholine (PC(22:6/18:1(9Z))2), 1-stearoyl-2-archidionoyl-sn-glycerol-3-phosphohinositol (Pi(18:0/20:4)) and 1-stearoyl-2-lyso-sphingolipids (DG(18:0/20:4)) from Avanti Polar Lipids, 1-Palmityl-2-Hydroxy-sn-glycerol-3-Phosphatidylcholine (LPC(16:0)) from Lardan, and 1,2,3,7-Triheptadecanoylglycerol (TG(17:0/17:0/17:0)) and 3β-hydroxy-5-cholestene 3-ol (ChoE(18:2)) from Sigma Aldrich.

The samples were analysed using an ultra-high-performance liquid chromatography/high-performance quadrupole time-of-flight mass spectrometer method (UHPLC-Q-TOF-MS). The UHPLC system was a 1290 Infinity system from Agilent Technologies (Santa Clara, CA, USA), which was equipped with a multisample (maintained at 10 °C) using 10% DCM in MeOH and ACN: MeOH:H₂O:ACN (3:1:1:1, v/v/v/v)+0.1% HCOOH as needle wash solutions after each injection for 7.5 s each, a quaternary solvent manager and a column thermostat (maintained at 50 °C). Separations were performed on an ACQUITY UPLC BEH C18 column (2.1 mm × 100 mm, particle size 1.7 μm) by Waters (Milford, CT, USA). The flow rate was 0.4 ml min⁻¹ and the injection volume was 1 μl. H₂O+1% NH₄Ac (1M)+0.1% HCOOH (A) and ACN::IPA (1:1, v/v)+1% NH₄Ac+1% HCOOH (B) were used as the mobile phases for the gradient elution. The gradient was as follows: from 0 to 2 min 35–80% B, from 2 to 7 min 80–100% B and from 7 to 14 min 100% B. Each run was followed by a 7 min re-equilibration period under initial conditions (35% B). The mass spectrometer was a 6550 Q-TOF mass spectrometer (Q-TOF) from Agilent Technologies (Agilent) interfaced with a dual jet stream electrospray (dual ESI) ion source. Nitrogen generated by a nitrogen generator (PEAK Scientific, Renfrewshire, Scotland, UK) was used as the nebulising gas at a pressure of 21 psi, as the drying gas at a flow rate of 141 ml min⁻¹ (at 193 °C) and as the sheath gas at a flow rate of 11 ml min⁻¹ (at 379 °C). Pure nitrogen (6.0) from Praxair (Fredericia, Denmark) was used as the collision gas. The capillary voltage and the nozzle voltage were kept at 3643 and 1500 V, respectively. The reference mass-solution including ions at m/z 121.0509 and 922.0098 was prepared according to instructions by Agilent and it was introduced to the mass spectrometer through the
other nebuliser in the dual ESI ion source using a separate Agilent series 1290 isocratic pump at a constant flow rate of 4 mL min\(^{-1}\) (split to 1:100 before the nebuliser). The acquisition mass range was m/z 100–1700 and the instrument was run using the extended dynamic range with an approximate resolution of 30,000 FWHM measured at m/z 1521.9715 (which is included in the tune mixture) during calibration of the instrument. MassHunters B.06.01 (Agilent) software was used for all data acquisition.

Quality control was performed throughout the dataset by including blanks, pure standard samples, extracted standard samples and control plasma samples. Relative standard deviations (%RSDs) for retention times and peak areas for lipid standards representing each lipid class in the plasma samples and in the pure standard samples were calculated. The % RSDs for the retention times were on average 0.1% for both the plasma samples and for the pure standards samples. The %RSDs for the peak areas were within accepted analytical limits at averages of 17.5 and 16.6% for the plasma samples and for the pure standard samples, respectively. This shows that the method is reliable and repeatable throughout the sample set.

Lipidomic data were pre-processed with MZmine 2 and peaks were identified based on the internal peak library. Peak areas were normalised by lipid class-specific internal standards and quantified with R based on the inverse-weighted linear model. Internal standard peaks were detected in a targeted way from the standards runs. The internal MS library’s retention times were corrected with R to match the study with a linear correction based on the observed retention times in the standards runs. Other peaks in the sample runs were processed in a non-targeted way as: import of the mzML files, mass detection, chromatogram builder, chromatogram deconvolution, isotopic peak grouping, peak fitting, peak list row filter, join aligner, peak list row filter, gap filling, peak list filter, identification with custom data base search. The peak table was filtered in R, allowing the peak to be missing in each of the eight batches in a maximum 50% of the samples. Remaining missing values were imputed with feature-wise half-the-minimum. All lipid metabolites, that were present (non-zero value) in more than 75% of samples were included in the data analyses.

Global metabolomic analysis

Polar metabolites were analysed in the plasma samples using comprehensive two-dimensional gas chromatography combined with time-of-flight mass spectrometry (GC×GC-TOFMS, a LECO Pegasus 4D equipped with a cryogenic modulator from LECO, St. Joseph, MI, USA). Specifically, 400 μL methanol and 10 μL internal standard mixture heptadecanoic acid (175 mg mL\(^{-1}\)), α-Valine-d8 (36 mg mL\(^{-1}\)), succinic acid-d4 (59 mg mL\(^{-1}\)) and α-glutamic acid-d5 (110 mg mL\(^{-1}\)) were added to 30 μL of plasma samples. The samples were vortex mixed and centrifuged for 5 min at 10,000 r.p.m. and half of the supernatant was evaporated to dryness. This was followed by lipid class-specific internal standards and quantified with R based on the inverse-weighted linear model. Internal standard peaks were detected in a targeted way from the standards runs. The internal MS library’s retention times were corrected with R to match the study with a linear correction based on the observed retention times in the standards runs. Other peaks in the sample runs were processed in a non-targeted way as: import of the mzML files, mass detection, chromatogram builder, chromatogram deconvolution, isotopic peak grouping, peak fitting, peak list row filter, join aligner, peak list row filter, gap filling, peak list filter, identification with custom data base search. The peak table was filtered in R, allowing the peak to be missing in each of the eight batches in a maximum 50% of the samples. Remaining missing values were imputed with feature-wise half-the-minimum. All lipid metabolites, that were present (non-zero value) in more than 75% of samples were included in the data analyses.

ChromatOF software (LECO) was used for within-sample data processing, and the Guineu software (https://code.google.com/p/guineu/) was used for alignment, normalisation and peak matching across samples. The normalisation was performed by correction for internal standards and specific target metabolites were additionally quantified using external calibration curves. Other mass spectra from the GC×GC-TOFMS analysis were searched against the NIST 14 Mass Spectral Library and the Golm Metabolome Database, using also retention index data in the identification. Artefact peaks due to chemical background and compounds outside the linear range of the method were removed from the dataset. Control serum samples (n = 32 for human) and pure standards (to monitor the instrument performance and robustness) were analysed together with the samples. The relative standard deviation (RSD) for internal standards, spiked into the samples, was on average of 15.7% for the plasma samples. The RSD% of the quantified metabolites in the control serum samples (n = 32) was on average 23.4%. The RSD% was 13.3% for isolucine, 11.2% for leucine and 24.2% for valine in control serum samples (n = 4), and for internal standards in mice the RSD was on average 16.6%. Neither sample preparation nor analysis order showed any significant effect on the results.

All plasma metabolite peaks that were present (non-zero value) in more than 75% of samples were included in the data analyses, including the unidentified ones. The unidentified peaks were annotated with their structural class from the Golm Metabolome Database using functional group prediction based on the fragmentation patterns.12,23

Targeted metabolomic analysis

A targeted metabolomic approach was taken to target a specific metabolic pathway, that is, the tricarboxylic acid (TCA) cycle (citric acid, succinic acid, fumaric acid, malic acid, α-ketoglutaric acid). A subset of control samples at both ages 11 and 18 were used for the analysis. This resulted in the following study numbers: PD at age 11 (38 controls vs 38 cases) and PD at age 18 (36 controls vs 36 cases) (Supplementary Table 4). Briefly, 50 μL of 0.1 mg mL\(^{-1}\) of Labelled internal standards (succininc acid-2,2,3,3-d₄, fumaric acid-2,3-d₂, adipic acid-2,2,5,5-d₄ and α-malic acid-2,3,3-d₃, Sigma Aldrich) were added to 100 μL of plasma. To this, 440 μL of anhydrous EtOH, 100 μL pyridine, 500 μL of deionised H₂O and 150 μL of ethylchloroformate (ECF) were added and samples were vortexed. To this, 1000 μL of CHCl₃ was added. The pH was then adjusted to 5–6 by adding 7% NaOH solution and shaken for 5 s. Overall, 100 μL of ECF was added and vortexed for 20 s. To this, 2 mL of deionised H₂O was added and vortexed. The samples were then centrifuged at 1700 g for 3 min at 4 °C. The CHCl₃ layer was transferred to a 10 ml glass tube containing anhydrous sodium sulphate drying reagent. Following drying, samples were analysed using an Agilent 72500 QTOF GC/MS system (Agilent, Santa Clara, CA, USA).

Calibration was achieved by comparison of metabolite peak areas with reference to an external standard (TCA cycle metabolite library, Sigma Aldrich) and by comparison of their mass spectra with those in the NIST library (version 2.0). For quality control purposes, an aliquot from a pool of control serum samples was spiked into the samples, was on average of 15.7% for the plasma samples. The RSD% of the quantified metabolites in the control serum samples (n = 32) was on average 23.4%. The RSD% was 13.3% for isolucine, 11.2% for leucine and 24.2% for valine in control serum samples (n = 4), and for internal standards in mice the RSD was on average 16.6%. Neither sample preparation nor analysis order showed any significant effect on the results.
The levels of the lipids in the PD case group were analysed relative to the control group as a function of the acyl chain length and double bond content within each lipid group. The level ratio was computed by computing each lipid's average level within each subject group, and the ratio of these average levels between the PD case and the control groups. Each lipid group was examined (Figures 2 and 3; Supplementary Figure 1). LPCs of CE(18:2) + unknown CE (667.6219) were elevated in the PD group. An upward sloping relationship was seen in the mean ratio of SM levels in cases vs controls for higher carbon numbers. Clear patterns are not seen for the PCs and TGs, although the figure does highlight that the PCs are elevated in the PD group and TGs are downregulated, particularly so for those with a lower number of carbon double bonds.

The global lipidome was then evaluated by clustering the data into a set of lipid clusters. Cluster analysis identified seven lipid clusters (LC) and a description of each cluster is given in Table 3. Three of the identified clusters were significantly higher in the PD case group. LC4 was dominated by LPCs (P-value < 0.025), LC6 was dominated by both PCs and CEs (P-value = 0.036), whereas LC7 was a cluster containing PCs (P-value = 0.006).

At age 18, a total of 23 lipids were significantly different between the control and PD groups (Table 4; nominal P-value < 0.05). These lipids were three LPCs, thirteen PCs, one PE, three SMs and three TGs. All of these lipids, with the exception of PC (36:4), were decreased in the PD group (Figure 2), although no clear pattern with respect to the acyl carbon chain length or double bond content was observed. The lipid cluster LC4 was significantly decreased in the PD group (P-value = 0.017) and was dominated by LPCs (Supplementary Table 1). None of these however passed significance at the selected FDR threshold of 0.1.

Age 11 and 18 lipidomic signatures of PD:

At age 11, a total of 32 lipids were significantly altered between controls and cases (nominal P-value < 0.05). These lipids included three CEs, five LPCs, 19 PCs, four SM and a TG (Table 2). All of these lipids, with the exception of TG(56:7), were elevated in the PD group. Eight of these passed FDR significance (P-value < 0.1) (Figure 1). Relationships with the acyl chain length of lipid species was examined (Figures 2 and 3; Supplementary Figure 1). LPCs of lower carbon numbers and double bond content were higher in the PD group. An upward sloping relationship was seen in the mean ratio of SM levels in cases vs controls for higher carbon numbers. Clear patterns are not seen for the PCs and TGs, although the figure does highlight that the PCs are elevated in the PD group and TGs are downregulated, particularly so for those with a lower number of carbon double bonds.

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Age 11 and 18 polar metabolomic signatures of PD:

The metabolomic datasets used for analysis contained a total of 151 metabolites. At the age of 11, a total of 8 metabolites were significantly different between the control and PD groups, 6 of which were significantly decreased (1-monopalmitin, 2,3-dihydroxybutanoic acid, d–(-)-ribofuranose, ethanolamine, hydroxyamine and ribitol) and two significantly elevated (sugar derivatives).
Figure 1. The levels of significant lipids at FDR level for age 11 samples.

Figure 2. The relationship between psychotic disorder and acyl chain content in lipid species. The mean ratio of lipid levels in cases vs controls in plasma samples (ages 11 and 18) for lysophosphatidlycholines (LPCs).
in the PD group (Table 5), although none were significant at the selected FDR threshold. Cluster analysis identified six metabolite clusters (CL), none of which were significant between study groups (Supplementary Table 2).

At the age of 18, a total of 19 metabolites were significantly different between the case and control groups, none at FDR level (Table 6). These metabolites mainly belonged to the following classes of metabolites; organic acids, fatty acids and sugar/sugar derivatives and were all significantly decreased in the PD group with the exception of glycine and levoglucosan which were elevated in the PD group. 1-Monopalmitin is the only common significant metabolite between the studies and was found to be decreased in PD groups at both ages. The metabolite cluster CL1 was significantly decreased in the PD group (P-value = 0.034) and contained 22 metabolites consisting of fatty acids, organic acids and unknown metabolites (Supplementary Table 3).

**DISCUSSION**

Our findings indicate that the lipidome is altered between subjects with PD compared to subjects who do not experience any PEs, particularly at the age of 11, giving promise to the potential of an early biomarker signature of PD. At the age of 11, a number of LPCs were found to be significantly elevated in the PD group. This is indicative of altered phospholipid metabolism, which has been considered as the pathophysiological basis of schizophrenia for some time.\(^13\) A number of studies have reported impaired phospholipid levels in schizophrenia subjects, although the specific results have not been consistent.

LPC, an inflammatory phospholipid generated by hydrolysis of PC via the actions of phospholipase A\(_2\) (PLA\(_2\)), promotes inflammatory effects such as expression of endothelial cell adhesion molecules, growth factors, chemotaxis and activation of monocytes/macrophages.\(^25\) LPC has been suggested to have a functional role in the pathogenesis of various diseases including atherosclerosis,\(^26\) diabetes\(^27\) and systemic autoimmune diseases.\(^28\) The association between inflammatory abnormalities and PD has been found repeatedly in many studies, which reported increased levels of pro-inflammatory compounds (mainly cytokines) in the serum, plasma and cerebrospinal fluid of patients with psychosis\(^29\) or who transition to schizophrenia from the at-risk mental state.\(^30\) In support of the inflammatory theory in relation to psychotic outcome in the ALSPAC cohort, Khandaker et al.\(^31\) reported higher levels of the systematic inflammatory...
increased platelet membrane LPC in schizophrenia patients.

bonds are associated with risk of PD. An earlier study reported in this study at the age of 11 (LPC 18:1 and LPC 18:2), which the reported signi... naive schizophrenia patients as compared to healthy controls.

investigation were donated from participants at the ages 11 and were thus very different in terms of medication exposure and duration of psychotic illness from those of chronic schizophrenia. In comparison, the mean age of first-episode schizophrenia patients in the study by Cai and colleagues was 27.5 ±9.5 years (n = 11). In the twin study, which involved twin pairs discordant for schizophrenia, the participants had an average age of 51 years (n = 19), with the majority taking antipsychotic medication. The differences between these studies could explain some of the inconsistencies in the reported findings related to the direction of the LPCs and also highlights the need for validation studies for biomarker confirmation. Identification of the biomarkers at a young age prior to conversion to schizophrenia would be of more benefit clinically to assist early detection and diagnosis.

A total of four PCs were found to be significantly elevated in the plasma of the PD group at age 11. At age 18, the PCs were decreased in the PD group, although not significant at the selected FDR threshold. A few studies have reported PCs to be related to psychotic outcome, with most of the studies reporting reduced levels in schizophrenia. The finding of elevated LPCs and PCs at age 11 and subsequent decreased levels relative to the controls (although not significant at FDR level) at age 18 suggest clinically to assist early detection and diagnosis.

1. monopalmitin 448.89 ± 162 368.91 ± 123.4 0.0128 0.544
2. Dihydroxybutanoic acid 0.09 ± 0.03 0.07 ± 0.02 0.014 0.544
3. Ribitol 98.34 ± 169.78 52.87 ± 40.02 0.0429 0.7
4. Ethanolamine 250.51 ± 88.88 214.15 ± 46.75 0.0215 0.544
5. Hydrolxylamine 175.9 ± 41.79 155.67 ± 31.77 0.0202 0.544
6. Sugar derivative 805.27 ± 247.15 961.92 ± 337.63 0.0274 0.591
7. Sugar derivative 89.91 ± 74.69 141.94 ± 85.59 0.0216 0.544

Abbreviations: CE, cholesterol ester; LPC, lysophosphatidylcholine; PC, phosphatidylcholine; PD, psychotic disorder; SM, sphingomyelin; TG, triacylglycerol.

Values are expressed as standard units ± s.d. (standard deviation). P-values are adjusted for gender and BMI. FDR-adjusted P-values are adjusted for multiple comparisons using the Benjamini–Hochberg procedure.

Table 5. Differential plasma metabolites between control and PD groups at age 11

<table>
<thead>
<tr>
<th>Metabolite name</th>
<th>Control (n = 67)</th>
<th>Cases (n = 38)</th>
<th>P-value</th>
<th>FDR-adjusted</th>
</tr>
</thead>
<tbody>
<tr>
<td>1-monopalmitin</td>
<td>448.89 ± 162</td>
<td>368.91 ± 123.4</td>
<td>0.0128</td>
<td>0.544</td>
</tr>
<tr>
<td>2,3-Dihydroxybutanoic acid</td>
<td>0.09 ± 0.03</td>
<td>0.07 ± 0.02</td>
<td>0.014</td>
<td>0.544</td>
</tr>
<tr>
<td>d-(−)-ribofuranose</td>
<td>98.34 ± 169.78</td>
<td>52.87 ± 40.02</td>
<td>0.0429</td>
<td>0.7</td>
</tr>
<tr>
<td>Ethanolamine</td>
<td>250.51 ± 88.88</td>
<td>214.15 ± 46.75</td>
<td>0.0215</td>
<td>0.544</td>
</tr>
<tr>
<td>Ribitol</td>
<td>175.9 ± 41.79</td>
<td>155.67 ± 31.77</td>
<td>0.0202</td>
<td>0.544</td>
</tr>
<tr>
<td>Hydroxylamine</td>
<td>805.27 ± 247.15</td>
<td>961.92 ± 337.63</td>
<td>0.0274</td>
<td>0.591</td>
</tr>
<tr>
<td>Sugar derivative</td>
<td>89.91 ± 74.69</td>
<td>141.94 ± 85.59</td>
<td>0.0216</td>
<td>0.544</td>
</tr>
</tbody>
</table>
energy pathways were significantly decreased with reduced protein and transcript expression of TCA and oxidative phosphorylation enzymes, confirming compromised energy metabolism in individuals with schizophrenia. A major strength of this investigation is the ALSPAC cohort upon which it was based. The ALSPAC cohort includes detailed longitudinal clinical assessments and biosampling. The plasma samples were collected at age 11, prior to the development of psychotic disorder, and were not subject to confounds of drug exposure and chronic illness. Our observation of an altered lipidome at age 11, therefore, highlights a perturbed metabolism related to inflammation in the PD group, which may be an early biomarker signature of the disease, with the LPCs representing potential future early biomarkers of PD. The detected associations indicate that lipidomic profiles are useful for identifying important disease signatures. However, as a step to move these signatures closer to utilisation in the clinic validation in an external cohort is necessary. Notwithstanding this, the present study is an important step towards the identification of a signature associated with the development of PD.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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DISCLAIMER

This publication is the work of the authors and will serve as guarantors for the contents of this paper.
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