Title: Association of seminal polyaromatic hydrocarbons exposome with idiopathic male factor infertility: A proteomic insight into sperm function

- Authors: Jasmine Nayak^{1,2,#}, Soumya Ranjan Jena^{1,2,#}, Sugandh Kumar³, Sujata Kar⁴,
 Anshuman Dixit³, Luna Samanta^{1,2,*}
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6 **Affiliations**

- ¹Redox Biology & Proteomics Laboratory, Department of Zoology, Ravenshaw University,
 Cuttack-753003, India
- ²Center of Excellence in Environment & Public Health, Ravenshaw University, Cuttack 753003, India
- ³Institute of Life Sciences, NALCO Square, Bhubaneswar, India
- ⁴Kar Clinic and Hospital Pvt. Ltd., Unit-IV, Bhubaneswar

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- 14 *Corresponding author
- 15 [#]Equal contribution

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17 **Conflict of interest:** The authors have nothing to disclose

18 Abstract

19 Oxidative stress (OS) is implicated in 80% of idiopathic male infertility (IMI) patients 20 where exposure to redox active environmental toxicants such as polyaromatic hydrocarbons 21 (PAHs) may play. In the present study the seminal exposome of various PAH was analyzed 22 in two separate cohorts including 43 fertile donors and 60 IMI patients by HPLC and receiver 23 operator characteristic curve was applied to find out the cut-off limits. Furthermore, 24 spermatozoa from both the groups were subjected to label free liquid chromatography mass 25 spectroscopy (LC-MS/MS) followed by bioinformatics analysis to elucidate the molecular 26 mechanism(s) involved and the key proteins from the affected pathways were validated by 27 western blot along with oxidative modification of proteins. Of the 16 standard PAH 13 were 28 detected in the semen. Receiver Operator Character (ROC) Curve analysis (AUC_{ROC}) 29 revealed the PAHs having most significant effect on fertility are of the following order 30 Anthracene<benzo(a)pyrene<benzo[b]fluoranthene<Fluoranthene<benzo(a)anthracene<indol 31 (123CD)pyrene<pyrene<naphthalene<dibenzo(AH)anthracene<fluorene<2bromonaphthalene 32 <chrysene
benzo(GH1)perylene. Benzo[a] pyrene is invariably present in all infertile 33 patients while naphthalene is present in both fertile and IMI group. Of the total 773 detected 34 proteins (Control: 631 and PAH: 717); 71 were differentially expressed (13 underexpressed, 35 58 overexpressed) in IMI patients resulting in impaired mitochondrial dysfunction and 36 oxidative phosphorylation, DNA damage, Aryl hydrocarbon receptor (AHR) signalling, 37 xenobiotic metabolism and induction of NRF-2 mediated oxidative stress response (increased 38 in 4-hydroxynonenal and nitrosylated protein adduct formation, and declined antioxidant 39 defence). The increased GSH/GSSG ratio in patients may be an adaptive response to 40 metabolize the xenobiotics via conjugation as evidenced by overexpression of AHR and Heat 41 shock protein 90 beta (HSP90 β) in patients. Seminal PAH concentrations, oxidative protein 42 modification along with protein markers (e.g. AHR and HSP90B) may help in better 43 prediction and management of IMI. Contribution of environment borne PAH in semen should 44 not undermined in infertility evaluation.

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Keywords: Idiopathic male infertility, polyaromatic hydrocarbon, proteomics, oxidative
stress, AHR signalling, protein nitrosylation.

48

49 1. Introduction

Semen quality of men in their reproductive ge is markedly deteriorating over past 50 decades^{1,2}. Approximately 15% of the co-inhabiting couples are infertile where 50% of them 51 52 have abnormal semen parameters implying the involvement of male-infertility-associated factor ³.Male infertility in general is known as a multi-causal effect with a very few large-53 scale epidemiological reports available^{4,5}.Due to the paucity of information on causative 54 factors ondecline in semen quality; accurate diagnosis and personalized treatment options are 55 56 restricted. An infertility case withunknown causative factor is identified and referred to as idiopathic infertility^{3,6}. It is reported that \sim 75% of oligospermic men are idiopathic⁷. Albeit, 57 58 the interplay between genetic, environmental and lifestyle factors are proposed to be behind this condition; very few reports established the role of environmental toxins in 59 60 idiopathicinfertility⁸. Most of the studies simply establish a correlation between environmental 61 toxin levels in body fluids such as blood plasma or urine with semen parameter without giving much insight into the mechanisms involved ^{8,9}. European Association of Urology 62 63 attributed idiopathic male factor infertility to endocrine disruption due to environmental pollution, reactive oxygen species, or genetic abnormalities ¹⁰. In recent times, more 64 emphasis is given to the "exposomes" concept that refers to the totality of environmental 65 exposures of an individual during the lifetime. This novel approach combines the body 66 67 burden of environmental toxins and modern omics technologies to study the role of the environment in human diseases¹¹. Many environmental toxinssuch as pesticides, herbicides, 68 69 phthalates and polyaromatic hydrocarbons (PAHs) undergo metabolic activation in human body and cause oxidative stress¹². Oxidative stress is time and again reported to not just 70 correlate with defective sperm function but is causally involved in the genesis male factor 71 infertility¹³⁻¹⁵. Male Oxidative Stress Infertility (MOSI) is proposed for the management of 72 73 idiopathic male infertility with measurement of seminal oxidation-reduction potential (ORP) as an easy clinical biomarker¹⁶. It is further suggested that upto 80% of the total cases of
idiopathic infertility have augmented oxidative stress¹³⁻¹⁵. Therefore, it is imperative to look
into the cause behind the aetiology of MOSI in idiopathic infertility as a function of
environmental toxins.

78 The crucial environmental toxins, especially phthalates, bisphenols, pesticides, flame 79 retardants and Polyaromatic hydrocarbons (PAHs) warrant special attention due to their 80 potential role as endocrine disruptors affecting hypothalamo-pituitary-thyroid axis and hypothalamo-pituitary-gonadal axis¹⁷. PAHs are the by-products of incomplete combustion of 81 organic materials generated from tobacco and cigarette smoke, barbequed food, vehicle 82 83 exhaust and oil spillers as well as during coke production and chemical manufacturing. They 84 are usually metabolically activated by cytochrome P450 enzymes during steroidogenesis and promotes free radical generation ¹⁸. The ROS (H_2O_2 and O_2^-) generated during normal 85 86 steroidogenesis are within critical levels and play an important role in the regulation of steroidogenic activity of the Leydig cell¹⁹. The elevated production of ROS have been found 87 88 to inhibit steroid productions, and causes damage to mitochondrial membrane of spermatozoa²⁰. However, our knowledge on oxidative stress-induced idiopathic male 89 90 infertility as a function of environmental borne seminal concentration of PAH is extremely 91 limited in general and with respect to non-occupational exposure in particular. With this 92 background, the present study in designed to analyse the level of PAH in the ejaculate of 93 idiopathic infertile men and its relationship with induced oxidative stress via high throughput 94 shotgun proteomic analysis in comparison to proven fertile donors to unravel the pathways 95 involved towards discovery of plausible biomarkers.

96

97 2. Materials & Methods

98 2.1 Ethics statement and Patient selection

99 Patients attending the infertility centre and the proven fertile donors at Kar Clinic and 100 Hospital Pvt. Ltd., Bhubaneswar, Odisha, India were recruited for the studyafter approval by 101 the Institutional Ethics Committee. All participants gave an informed written consent to be 102 included in this study. The exclusion criteria were leukocytospermia (Endtz positive), 103 azoospermia, historyof systemic illness, inflammation of reproductive tract (orchitis, 104 epididymitis, urethritis, and testicular atrophy), sexually transmitted disease, and 105 medications. The participants included in this study were non-smokers, non-alcoholic, and 106 had a normal body mass index. Healthy donors (with no known medical condition) who had 107 established fertility recently i.e., within one year with no cases of embryo loss were included 108 as the control group. Subsequently upon estimation of PAH concentrations and receiver 109 operator characteristic (ROC) curve analysis (as described below) in comparison to fertile 110 donors, patients were segregated into PAH positive infertile group. Of the total 60 patients 111 recruited for the study, 18 idiopathic infertile patientswere excluded based on their lower than 112 cut off value of one or more PAH present in their semen. Therefore, in the final step 43 113 proven fertile donor were compared with 42 PAH positive idiopathic infertile patients.

114 2.2 Semen analysis

The semen samples were collected from all participants of both groups (idiopathic infertile patientsn=60 and fertile donor n=43) by masturbation after 3-5 days of sexual abstinence. Samples were allowed to liquefy completely for 20-30 min at 37°C followed by semen analysis as per World Health Organization (WHO) 2010 guidelines (WHO 2010). Basic semen analysis included both macroscopic (volume, pH, colour, viscosity, liquefaction time) and microscopic parameters such as sperm concentration, motility and morphology, as well as peroxidase or Endtz test. Samples with $>1.0 \times 10^6$ /ml round cell with a positive peroxidase test were excluded from the study.After liquefaction and semen analysis, the samples were subjected to centrifugation at 400 g for 20 min at 37°C to separate the sperm and seminal plasma. The seminal plasma was processed for PAH measurement.

125 2.3 Measurement of seminal PAH exposomes

126 The HPLC analysis was carried out by injecting 20 μ L of the seminal plasma into the 127 chromatographic system (Thermo Scientific UltiMate 3000) for the determination of PAHs 128 concentration using PAH standards. PAHs were segregated by C-18 column with a gradient 129 elution process using solvent water and acetonitrile. The elution conditions applied were: 0 -130 20 min, 40% of acetonitrile isocratic; 20 - 37 min, 50-100% of acetonitrile gradient, 37 - 42131 min, 100% of acetonitrile isocratic, 42 - 45 min, 100 - 40% of acetonitrile, gradient. The flow 132 rate was set at 1 mL/min, at room temperature. Under these conditions, PAHs could be 133 separated satisfactorily within 45 min. The PAHs were identified by comparing the retention 134 time with those of standards taken. The concentration of PAH in semen was calculated according to the formula: 135

136 PAH concentration = Peak area of sample/Peak area of standard (known concentration)

137 2.4 Determination of PAH threshold for incidence of infertility

Receiver operating characteristics (ROC) curve is used in clinical biochemistry for the determination of the cut-off point in clinical deterioration. A ROC curve shows a graphical plot illustrating the diagnostic ability of a binary classifiers to identify the sensitivity and the specificity of PAH levels in the prediction of male fertility status. The ROC curves were createdusing total individual PAHs as "test variables," and "fertile donor" versus idiopathic infertile patients" (binary variable, with fertile ¹/₄ 0 and infertile patient ¹/₄ 1) as "state variable" and setting the value of the "state variable" as 1. The optimal cut-off value was 145 determined with the use of the Youden index to maximize the sum of sensitivity and 146 specificity.

147 2.5 Sperm protein Extraction and estimation

148 Post separation from seminal plasma, sperm pellet extracted was washed thrice with 149 phosphate buffer saline (PBS) and centrifuged at 400 g for 10 min, at 4°C. Sperm lysate was 150 prepared by adding 100µl of Radio-immunoprecipitation assay (RIPA) buffer supplemented 151 with Protease inhibitor cocktail (cOmplete ULTRA Tablets; Roche) to the sperm pellet and 152 left overnight at 4 °C for complete cell lysis. The lysate was centrifuged at 14,000 g for 30 153 min at 4 °C followed by separation of the supernatant. Protein quantification of the 154 supernatant was determined using bicinchoninic acid (BCA; Thermo Fisher Scientific, Waltham, MA). 155

156 2.6 Assessment of Glutathione and Redox potential

157 The total GSH equivalents (GSH + GSSG) were spectrophotometrically quantified by 158 glutathione reductase (GR) recycling assay at the expense of oxidation of NADPH using 5-159 5'-dithiobis 2-nitrobenzoic acid (DTNB; Ellman's reagent). Similarly, GSSG was measured 160 by masking GSH with 2-vinylpyridine. Formeasurement of the total GSH equivalents 161 (GSH+GSSG), GR was added to the assay mixture for reduction of GSSG to GSH at the 162 expense of oxidation of NADPH. The reduction potential (Ehc) of GSH/GSSG couple was 163 calculated by using Nernst equation. The sperm lysate (described above) was precipitated 164 with ice-cold 5% trichloroacetic acid containing 0.01N HCl, and cleared by centrifugation. 165 The deproteinized supernatants were used for the assay. In brief, the assay mixture (final 166 volume 200 µl) contained 3 mM NADPH in 125 mM Phosphate buffer containing 6.3 mM 167 EDTA (pH 7.5), DTNB (0.6 mM) and sperm lysate (25 µg protein). To this 2 µl GR (~1 Unit, 168 Sigma- Aldrich, St. Louis, MO, USA) was added and the yellow chromatophore (2-nitro-5thiobenzoate: TNB2-) formed by the interaction of SH groups from GSH and GSSG (after
conversion by GR) with DTNB was recorded at 405 nm in a iMark Absorbance Microplate
Reader (BioRad Instruments, Inc., Japan) at 1-min intervals for 6 min. All the determinations
were normalized to protein content. The absolute GSH amount was quantified from
difference between the total GSH equivalent and the obtained GSSG value.

The glutathione redox potential (E^{hc}) was calculated by Nernst equation for half reaction:

176
$$E^{hc} = -240 - 61.5/2 \ln\{[GSH]2/GSSG\} mV;$$

where -240mV is the standard redox potential (E°) of GSH at pH 0, -61.5/2 denotes RT/z F i.e R= Gas constant (8.314 J K-1 mol-1), T= absolute temperature of 37^{0} C or 310 K, F= Faraday constant (9.64853 X 104 C mol-1), z = number of electrons exchanged in the chemical reaction GSSG + 2e- + 2H \rightarrow 2GSH.

181 2.7 Shotgun Proteome profiling of spermatozoa

182 The extracted spermatozoa proteins were subjected to LC-MS/MS for proteomic 183 analysis. 50 μ l of sperm lysate from each sample (n=3 per group; one pooled sample and two 184 individual samples) were taken and reduced with 5 mM TCEP, then alkylated with 50 mM 185 iodoacetamide and subsequently digested with Trypsin (1:50, Trypsin/lysate ratio) for 16 h at 186 37 °C. To eliminate the salt, these digests were cleansed using a C18 silica cartridge and then 187 dried with a speed vac. Then the dried pellet was resuspended in buffer A (5% acetonitrile, 188 0.1% formic acid). All the experiments were carried out using an EASY-nLC 1000 system 189 (Thermo Fisher Scientific) combined with Thermo Fisher-QEXACTIVE mass spectrometer 190 designed with nano-electrospray ion source. A 25 cm PicoFrit column (360µm outer 191 diameter, 75µm inner diameter, 10µm tip) packed with 1.8 µm of C18-resin (Dr Maeisch, 192 Germany) was employed to resolve 1.0 µg of the peptide mixture. The peptides were loaded with buffer A and eluted at a flow rate of 300 nl/min for 100 minutes with a 0–40% gradient
of buffer B (95% acetonitrile, 0.1% formic acid). The acquisition of MS data is done by
considering the most abundant precursor ions from the survey scan using top 10 datadependent method.

197 2.8 Data Processing

198 All the samples were processed and RAW files generated were analyzed with 199 comparison to Uniprot HUMAN reference proteome (HUPO) database using Proteome 200 Discoverer (v2.2). The precursor was set at 10 ppm and fragment mass tolerances was set at 201 0.5 Da for SEQUEST search. The protease used to produce peptides, where enzyme 202 specificity was set for trypsin/P (cleavage at the C terminus of "K/R: unless followed by "P") 203 along with maximum missed cleavages value of two. For database search, carbamidomethyl 204 on cysteine was considered as fixed modification while N-terminal acetylation and oxidation 205 of methionine were considered as variable modifications. Both protein False Discovery Rate 206 (FDR) and peptide spectrum match were set to 0.01.

207

2.9 Quantitative proteomics

208 The following procedures were performed to execute Label free quantification (LFQ) 209 suit for quantitative proteomics using MaxQuant v1.5.2.8 (http://www.maxquant.org/): 210 feature identification, initial Andromeda search, recalibration, main Andromeda search, and 211 posterior error probability calculation (likelihood of a protein being incorrectly recognized). 212 At first, razor peptides and protein groups were identified. Proteins that cannot be identified 213 unambiguously by distinct peptides but share peptides were grouped together and quantified 214 as a single protein group. For instance, if all detected peptides of protein X were also 215 identified for protein Y, X and Y are classified as one protein group (even though unique 216 peptides were found for Y, since it was still uncertain whether X was present in the sample). 217 Only one common quantification was generated for both proteins in the result. A Razor 218 peptide is formed when two protein groups (protein A and protein B) are unequivocally 219 identified by distinct peptides yet share a common peptide. Following the discovery of 220 distinct and unique peptides, a "match across the runs" procedure was used to match the same 221 accurate masses across several LC-MS/MS runs within a 1.5-minute retention time frame. 222 Relative quantification was determined by comparing the abundance of the same peptide 223 species/protein across runs, whereas absolute quantification was determined by equating the 224 quantities of various proteins in the same sample. The MaxQuant algorithms use peak 225 detection and scoring of peptides, as well as mass calibration and protein quantification, to 226 provide summary statistics. Protein abundances were normalized using the LFQ algorithm in 227 MaxQuant and then converted to Log_2 for further analysis. The label-free method analyses 228 the intensity of these peptides to determine peptide ratios by taking the greatest number of 229 detected peptides between any two samples. The median values of all peptide ratios of a 230 given protein are used to calculate protein abundance.

231

2.10 Bioinformatics analysis

232 The differentially expressed proteins (DEPs) calculated based on Log_2 fold change > 233 1 and p-value < 0.05 were subjected to functional annotation and enrichment analysis by 234 means of publicly available bioinformatics annotation tools and databases such as String, 235 UniProt, and Cytoscape. Enriched terms were ranked by p-value (hypergeometric test) using 236 Cytoscape ClueGO plugin. Venn diagram showing distribution pattern of proteins were 237 drawn using Venny 2.1. Hierarchical clustering of the DEPs between fertile donor and 238 idiopathic infertile patients were analysed by the construction of heat map using R.3.4.4 239 package (Complex Heatmap map library). Euclidean distance correlation matrix was used for 240 hierarchical clustering of the DEPs for dendrogram plotting showing complete linkage 241 between the proteins. The Biological Networks Gene Ontology (BiNGO) application in Cytoscape was used for the determination of significantly overrepresented Gene Ontology (GO) terms in the DEPs data set and the predominant functional themes of the tested DEPs were mapped to visualize the biological pathways altered in the infertile group. The proteinprotein networks were obtained from the STRING database (http://string-db.org/). A p < 0.05was considered significant. Proprietary curated database such as Ingenuity pathway analysis (IPA) was used to analyze the involvement of DEPs in biological and cellular processes, pathways, cellular distribution, protein-protein interactions and regulatory networks.

249 2.11 Western blotting

250 Two key protein markers of PAH metabolism, i.e., AhR and HSP90B(sc-101104,sc-251 59578, Santacruz, Mouse)were validated by western blotting. Besides, the impact of induced 252 oxidative stress on protein modifications, namely, 4-Hydroxynonenal (HNE)(ab46545, 253 Rabbit, Abcam) protein adduct formation and anti-3-nitro-tyrosine(ab110282, Mouse, 254 Abcam) were also studied by western blotting. From every group two individual and one 255 pooled samples were run in duplicates to maintain biological and technical variabilities. 256 Samples were normalized for protein concentration in each group. Washed spermatozoa were 257 lysed in RIPA lysis buffer (Sigma-Aldrich, St. Louis, MO, USA) overnight at 4°C containing 258 proteinase inhibitor cocktail (Roche, Indianapolis, IN, USA). Samples containing 20-30 µg of protein in 15 µl volume per sample were separated on a 4-20% SDS-PAGE and electroblotted 259 260 onto polyvinylidenedifluoride (PVDF) membranes. Then the proteins transferred to PVDF 261 membrane was blocked with 5% non-fat dry milk in Tris-buffered saline Tween 20 (TBST) buffer for 2 hrs. After that primary antibody incubation was done overnight (4⁰C) followed 262 by the specific secondary antibodies (Mouse, Rabbit, Abcam) at room temperature for 3 hrs. 263 264 Blots were then washed using TBST and protein bands were visualized using an enhanced 265 chemiluminescence kit- Pierce™ ECL Western Blotting Substrate (Thermo Scientific, 266 Rockford, IL, USA) in ChemiDoc[™] MP Imaging System (BioRad, Hercules, CA, USA).

The densitometric analysis of western blot images was done through Image J software (NIH,Bethesda,MD) by total intensity normalisation method. Results were expressed as fold change relative to the fertile donor.

270 2.12 Statistical Analysis

Statistical analysis was performed by MedCalc Statistical Software, ver. 17.4 (MedCalc Software; Ostend, Belgium). The data are expressed as mean \pm standard deviation (SD). Normalization of data was assessed using Shapiro–Wilk test followed by Levene's test for homogeneity of variance. Data on semen parameters and biochemical estimation were analyzed by Mann-Whitney U-test. Results of LC-MS/MS proteomics and Western blotting was subjected to Welch's t-test, or unequal variances t-test. A difference of p<0.05 (minimum) was considered significant.

278 3. **Results**

279 3.1 Semen analysis

Seminogram results are presented in **Table S1**. All idiopathic infertile patients included in this study have at least one semen parameter in semen analysis below WHO 2010 criteria. However, the average values were within the range, but the sperm concentration, motility, morphology and vitality were considered significant.

284 *3.2 PAH Exposome in semen*

Out of the 16 standard PAHs used for screening, a total of 13 PAH metabolites, i.e., Anthracene, Benzo (A) Anthracene, Benzo (A) Pyrene, Benzo (B) Fluoranthene, Benzo (GH1) Perylene, Chrysene, Dibenzo (AH) Anthracene, Fluorene, Fluoranthene, Indo (123 CD) Pyrene, Napthalene, 2 Bromonapthalene, Phenanthrene, Pyrene were detected in the semen samples at ng/ml level (**Fig 1**). However, the concentration of PAH in the semen of idiopathic infertile patients were significantly higher in comparison to the fertile donor.The cut-off level of these PAHs (if any) determined by ROC curve analysis segregates the fertile
from the idiopathic infertile patients. The results of the ROC analysis are presented in Fig. **1,Table S2.** Benzo (A) Pyrene particularly is found to be highly discriminative among 13
PAHs in idiopathic infertile patients.

295 3.3 Effect of PAH concentration on Sperm redox status

To corroborate the alteration in the redox environment of sperm in the idiopathic infertile patients, ratio of GSH:GSSG was measured. An increase in the absolute concentrations of GSH and GSH:GSSG ratio was noticed in idiopathic infertile patients (**Fig. 2A,B**). The reduction potential in spermatozoa of idiopathic infertile patients is more negative with respect to fertile donor (**Fig. 2C**). A reduction in the level of total antioxidant capacity of sperm was observed in the infertile group as compared to fertile control (**Fig. 2D**).

302 3.4 Global proteome profiling of spermatozoa

303 The quantitative differential proteomic analysis identified a total of 773 proteins in 304 fertile donor and idiopathic infertile patients by label free LC-MS/MS. Out of the total 773 305 proteins, 631 were fromfertile donor and 717 from idiopathic infertile patients with 575 306 proteins common in both (Fig. 3). A total of 71 DEPs (based on Log_2 fold change >1 and p-307 value < 0.05) were detected, of which 13 and 58 were under- and over-expressed, 308 respectively in idiopathic infertile patients compared to fertile donor (Fig. 3, Table S3). The 309 hierarchical clustering by heat map showed over and under expressed proteins into the two 310 groups distinctively (Fig. 3).

The functional enrichment analysis of Gene Ontology (GO) by ClueGO revealed that the identified proteins were involved in various crucial biological functions such as chromosome condensation (GO:0030261), hexokinase activity (GO:0004396), nucleosome assembly (GO:0006334), canonical glycolysis (GO:0061621) and NADH regeneration (GO:0006735).The enriched cellular component and molecular functions were ATPase dependent transmembrane transport complex (GO:0098533), sperm flagellum (GO:0036126), endocytic vesicle lumen (GO:0071682), nucleosome (GO:0000786), metallo-exopeptidase activity GO:0008235, hexokinase activity (GO:0004396) and glucose binding (GO:0005536).The enriched processes and the identified proteins involved in various molecular functions along with its localisation were shown in **Fig. 4, Table S4.**

321 3.5 Functional pathway analysis of Differentially Expressed Protein

322 The BiNGO mapping revealed the involvement of DEPs in reproduction, 323 spermatogenesis, nucleosome assembly, chromatin assembly, DNA packaging and glycolysis 324 (Bonferroni step down with p value ≤ 0.001) resulting in DNA damage, impaired energy 325 metabolism and reproductive function (Fig. 5). String protein-protein interaction analysis of 326 DEPs revealed that the major pathways deregulated are Glycolysis/Gluconeogenesis 327 (HAS:00010; FDR 1.15e-06), Fatty acid degradation (HAS:00071; FDR 0.0054),HIF-1 328 signaling pathway (HAS:04066; FDR 0.0281), Estrogen signaling pathway (HAS:04915; 329 FDR 0.0498), Oxidative phosphorylation (HAS:00190; FDR 0.0498), Metabolic pathways 330 (HAS:01100; FDR 0.0029), DNA packaging (GO:0006323; FDR 0.00072), Regulation of 331 regulation of reactive oxygen species metabolic process (GO:2000377; FDR 0.0414), Post-332 translational protein modification (GO:0043687;FDR 0.0080), and Spermatogenesis 333 (GO:0007283; FDR 0.0284) (Fig. S1). The protein interaction of upregulated DEPs by IPA 334 identified the topmost molecular network to be associated with Cancer, Endocrine System 335 Disorders, Organismal Injury and Abnormalities where out of the 35 nodal proteins 18 were 336 detected in our dataset. In the second most pathway the proteins were involved in Cell Death 337 and Survival, Cellular Development, Organismal Survival where out of 21 nodal proteins 12 338 were from our dataset. The downregulated DEPs topmost network is associated with Cancer, 339 Cell Death and Survival, Organismal Injury and Abnormalities where out of 19 nodal 340 proteins 9 were found in our dataset (Fig. 6 & 7, Table S5).

IPA canonical pathway revealed that Aryl Hydrocarbon Receptor Signaling, Hypoxia
Signaling in the Cardiovascular System, Telomerase Signaling, PPAR Signaling, Xenobiotic
Metabolism Signaling, eNOS Signaling and Oxidative Phosphorylation were deregulated
(Fig. 8, Table S6)

The top toxicity list and functions determined by IPA-Toxicological pathway showed that Aryl Hydrocarbon Receptor (AhR) Signalling, Xenobiotic Metabolism Signalling, Fatty Acid Metabolism, Hypoxia-Inducible Factor Signalling, NRF2-mediated Oxidative Stress Response, Mitochondrial Dysfunction and Oxidative Phosphorylation are the most affected toxicological functions (**Fig. 8, Table S7**).

350 *3.6 Expression profile of key pathway proteins*

The key proteins in top canonical pathway are AhR (predicted) and Heat shock protein (HSP)90 β validated by western blot (**Fig. 9 C & D**) which corroborated the LC-MS/MS data. Both the proteins were found to be over expressed in the idiopathic infertile patients compared to fertile donor. The expression of 4-Hydoxynonenal (HNE) protein adduct and protein nitrosylation were also found to be overexpressed in idiopathic infertile patients (**Fig. 9 A & B**).

357 4. Discussion

Polyaromatic hydrocarbons (PAHs) are known endocrine disruptors which mimic the reproductive hormones and interfere with their synthesis by acting as agonist and antagonists. Several research studies on adult rodents with PAHs such as B(a)P, 2,3,7,8-Tetrachlorodibenzodioxin and 3-Methylchloranthrene results in an increase in the number of abnormal sperm and immature germ cells ^{21,22}, affects spermatogenesis by causing testicular atrophy ²³, diminishes testicular weight and increase apoptosis in seminiferous tubules ^{24,25}. Apart from this PAHs also disrupt the normal embryonic development by inducing oxidative 365 stress. A study by Delfino, demonstrated that exposure to PAHs disrupt the redox balance and generate reactive oxygen species (ROS)²⁶. This leads to oxidative stress causing damage to 366 biomolecules such as DNA, lipid and protein involved in the development of reproductive 367 368 process. In the current study, seminal PAH concentration was measured in the semen of 369 idiopathic infertile patients followed by proteomics of spermatozoa to understand the 370 mechanism(s) by which PAHs elicit male infertility. Several studies have shown that urinary 371 1-hydroxypyrene (1-OHP) is a good biological index for the occupational exposure assessment of PAHs²⁷. In a study by Xia et al, men with higher urinary concentrations of 1-372 373 hydroxypyrene, 2-hydroxyfluorene and sum of all four PAH metabolites (assessed as tertiles) were more likely to have idiopathic male infertility ²⁷. In another study, the same authors 374 375 ²⁷reported that higher urinary 1-hydroxypyrene (assessed as quantiles) levels were more 376 likely to have below reference sperm concentration and total sperm count. Similarly, Song et 377 al found a direct correlation between blood concentrations of PAH with sperm motility and a decrease in pregnancy outcome ²⁸. But no concrete data were available on semen 378 379 concentration of PAH with respect to infertility to justify their involvement in spermatogenesis, sperm maturation and sperm function. 380

381 This pioneer study reports association between idiopathic male factor infertility with 382 comprehensive screening data of PAHs in the semen resulting in sperm dysfunction through 383 shotgun proteomic analysis. A total of 13 PAHs out of the 16 standards were identified in our 384 sample implying the ubiquitous incidence in non-occupational peoples (only 4 people in the 385 patient group are smokers). The concentrations of all the 13 PAHs detected were significantly 386 higher (p<0.0001) in idiopathic infertile patients with respect to fertile donors. Based on 387 AUC_{ROC} the PAHs having most significant effect on fertility are of the following order 388 Anthracene<benzo(a)pyrene<benzo[b]fluoranthene<Fluoranthene<benzo(a)anthracene<indol 389 (123CD)pyrene<pyrene<naphthalene<dibenzo(AH)anthracene<fluorene<2bromonaphthalene

390 <chrysene
benzo(GH1)perylene. Irrespective of fertility status all analyzed samples 391 possessed naphthalene, albeit at different concentration showing the highest cut-off value of 392 868ng/ml. On the other hand, the lowest was noticed for bothchrysene and benzo(a)pyrene at 393 6 ng/ml and benzo(a)pyrene being the ubiquitous one in idiopathic infertile patients 394 distinctively segregating infertile men from their fertile counter parts. Four out of 43 semen 395 samples analyzed in fertile donor (~9%) showed measurable benzo(a)pyrene (0.35 \pm 396 1.17ng/ml). On the other hand, substantially high level of benzo(a)pyrene (43.37 \pm 397 38.57ng/ml) was detected in all the 60 semen samples analyzed in idiopathic infertile 398 patients. Thus, benzo(a)pyrene can be used as a marker to distinguish infertile men from 399 fertile one with 66.67% sensitivity and 100% specificity at 95% CI (confidence interval).A 400 large cohort study may further substantiate our findings. Though most of the idiopathic 401 infertile males participated in the present study have normal spermiogram, ~30% have 402 declined motility while~60% have above normal anomalous spermatozoa. It will not be out 403 of context to mention that prenatal exposure of benzo(a)pyrene to Gclm knockout mice 404 resulted reduction in testicular weight, testicular sperm head counts, epididymal sperm 405 counts, and epididymal sperm motility when analyzed at 10-weeks of age, relative to wild type littermates ²⁹.In another study on Mexican workers in a rubber factory with potential 406 407 occupational exposure to PAHs, impaired spermatogenesis was reported evinced by increased anomalies in sperm concentration, motility and morphology ³⁰.In fact, we have observed 408 409 increased retention of histone proteins (H1-3, H1-4, H1-7, H2BC19P, H2BC11, H2BC12, 410 H2BS1) in the spermatozoa of idiopathic infertile patients implying improper nuclear remodelling ³¹. Furthermore, the gene ontology and protein-protein interaction analysis data 411 412 (BiNGO, ClueGO, String) reveal that DNA packaging, chromatin assembly and nucleosome 413 assembly is deregulated in patient group. PAHs are also known to cause potential DNA damage in case of idiopathic infertile males³². Interactive metabolites of PAHs may reach the 414

testicles and epididymis forming sperm DNA adducts³³. In addition, the compounds resulting 415 416 from PAH oxidation have the ability to enter oxidation cycles, which increase the generation 417 of ROS and thus cause sperm DNA damage. To corroborate the findings we observed 418 significantly higher 4-HNE and S-Nitrotyrosine levels in the spermatozoa of infertile patients 419 in comparison to their fertile counterparts. Apart from improper compaction and packaging of 420 sperm DNA, themajor alterations in carbohydrate metabolism and active transport across 421 membrane leads to production of dysfunctional spermatozoa. The predicted alteredNADH 422 regeneration pathway further corroborates the imbalance in cellular redox state which is expected from redox acting toxicants like PAHs³⁴. 423

424 In this study, 71 DEPs were reported in patient group with higher levels of PAH and 425 IPA toxicity list of these DEPs was predicted to be involved in Aryl Hydrocarbon Receptor 426 (AhR) Signalling, Xenobiotic Metabolism Signalling, Hypoxia-Inducible Factor Signalling, 427 NRF2-mediated Oxidative Stress Response, Mitochondrial Dysfunction and Oxidative 428 Phosphorylation. The AhR is ligand-activated transcription factor that responds to endogenous ligands in addition to exogenous xenobiotic ligands, such as PAHs³⁵. Upon ligand binding, 429 430 AhR translocates to nucleus where it binds to AhR nuclear transporter (ARNT) and activates xenobiotic metabolizing enzymes: cytochrome P450 (CYP) 1A1, 1A2, and 1B1 for 431 catalyzing oxidative biotransformation of xenobiotics ^{36,37}. After biotransformation PAHs 432 generate potential reactive intermediates ^{38,39}. In fact, Hansen et al., reported the role of AhR 433 434 signalling in maintenance of Sertoli cell architecture and resultant spermatogenesis in AhR 435 knockout mice where the poorly remodelled spermatozoa are suggested to be more 436 susceptible to oxidant attack ⁴⁰. In the present study an increased expression of 4-HNE and 3-Nitrotyrosine implies induction of oxidative stress. On the other hand, 4-HNE is known to 437 produce DNA adduct ⁴¹ as observed in case of PAH exposure and AhR signalling⁴².It is 438 439 pertinent to mention here that the levels of 4-HNE within spermatozoa are positively

correlated with mitochondrial superoxide formation ⁴³, and elevated 4-HNE is responsible for 440 441 numerous adverse effects on sperm function such as decline in motility, morphology, acrosome reaction, sperm-oocyte interaction and apoptosis ^{44,45}. The BiNGO and IPA 442 443 canonical pathway analysis further supports the hypothesis. Protein S-nitrotyrosination is 444 responsible for protection of the proteins under oxidative stress, however irreversible S-445 nitrotyrosination leads to pathological condition. Of late, it has been elucidated that 446 hydrophobic bio-structures like cell membranes and lipoproteins undergo S-nitrosylation and has strong association with lipid peroxidation⁴⁶. Therefore, it is quite natural to observe an 447 448 increase in both 4-HNE and 3-nitrotyrosine concentrations in the spermatozoa of infertile 449 patients implying PAH-induced oxidative stress. Further, experimental strategies may reveal 450 the proximal oxidizing mechanism during tyrosine nitration including mapping and 451 identification of the tyrosine nitration sites in specific proteins in the spermatozoa of 452 idiopathic infertile men. Moreover, parallel over-expression of AhR and HSP90^β as observed 453 by western blot in the present study corroborated the finding as it is suggested that ligand-454 bound AhR translocates to the nucleus with HSP90ß showing its co-localization in the nucleus ⁴⁷. In contrast to AhR-dependent and CYP1A-mediated production of intracellular 455 456 ROS, the AhR signaling pathway also regulates the expression of genes involved in 457 antioxidant responses. Besides AhR signaling, NRF2 is another important transcription factor 458 regulating genes that are critically involved in the metabolism of xenobiotics as well as 459 endogenous compounds which is reported as top toxicological pathway in our DEP data set. 460 Both signaling pathways respond to environmental and endogenous stressors. Albeit, AhR 461 and NRF2 are clearly separated signaling pathways, recent reports demonstrate the cross-462 regulation between these two signaling axes suggesting an integrated response to environmental stressors ⁴⁸. 463

464 Glutathione, an important antioxidant is involved in the elimination of PAHs and spermatozoa depend heavily on glutathione metabolizing system for its survival⁴⁹. The 465 466 reactive intermediates formed after metabolism of PAHs are conjugated to glutathione and eliminated by glutathione-S-transferases (GST) and glutathione peroxidase (GPx)⁵⁰. 467 Glutathione (GSH) acts as a redox sensor by oxidizing to glutathione disulfide molecule 468 (GSSG). So the ratio of GSH to GSSG is used as a biosignature of oxidized intracellular 469 environment ⁵¹.A recent report by Branco et al., 2021 have reported that PAH and their 470 metabolites show idiosyncratic behaviour with respect to glutathione metabolism where 471 472 phenanthrene induced higher ROS production. On the other hand, the authors reported 473 increased GSH levels by benzo(b)fluoranthene along with augmented levels of protein 474 sulfydryl group. The upregulation of GSH was opined to be a consequence of Nrf2 signalling 475 activation and increased levels of glutathione metabolising enzymes and their mRNA after exposure to benzo(b)fluoranthene, but not during exposure to phenanthrene ⁵². Moreover, data 476 477 of the present study shows a distinct energy deprived and hypoxic state in the spermatozoa of 478 infertile men due to declined redox potential which is similar to the results of previously report by our group for unilateral varicocele patients ⁵³. 479

480 Conclusion

The present findings surmise the adverse impact of environment borne PAHs 481 482 exposure on sperm function in idiopathic infertility which are largely ignored in regular 483 infertility assessment. The high level of benzo(a)pyrene in the infertile group could serve as a 484 predictive marker for idiopathic infertility along with the signature proteins AhR and the 485 HSPs, particularly the HSP90. The presence of oxidative protein modification and differential 486 expression of proteins involved in chromatin packaging and DNA damage further 487 corroborates the noxious effect of PAH in semen (Figure 10). Therefore, it is suggested that 488 along with seminogram and other biological markers, analysis of seminal levels of 489 environmental toxins such as PAH in general and benzo(a)pyrene in particular may help in

- 490 proper management of idiopathic male factor infertility.
- 491 Declaration of Competing Interest: The authors declare that they have no known
- 492 competing financial interests or personal relationships that could have appeared to influence
- the work reported in this paper.
- 494 Acknowledgement: The authors thank Director, DBT-Institute of Life Science,
- 495 Bhubaneswar, India for the computational facilities.
- 496 **Funding information**: Department of Science and Technology (INSPIRE programme Grant
- 497 No. DST/AORCIF/IF150007); University Grants Commision, Government of India (Grant
- 498 No. 19/06/2016(i) EU V; Higher Education Department, Government of Odisha (Grant No
- 499 26913/HED/HE PTC WB 02 17(OHEPEE).

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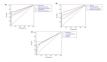
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645 Legends to figures

- Fig. 1 Receiver Operating Characteristic (ROC) curves of polyaromatic hydrocarbons in semen of idiopathic infertile men (n=60) in comparison to fertile donor (n=43).
- 648Fig. 2Comparison of redox status in the spermatozoa of fertile donor (n=43) and infertile649patients (n=60). A. Levels of reduced (GSH) and Oxidized glutathione (GSSG); B.650Spermatozoal redox status; C. Half cell reduction potential. D. Total antioxidant651capacity. FD: Fertile donors; IIP: Idiopathic infertility patients. Data are expressed652as mean \pm SD. *p<0.05.</td>
- Comparative global proteomic profiling of spermatozoa between FD: Fertile Donors 653 Fig. 3 654 and IIP: Idiopathic infertility patients. (A) Venn diagram showing distribution of 655 differentially expressed proteins (DEPs) (B) Heat map showing a hierarchical cluster of DEPs. The dendrogram for sample replicates (column clustering) separated the 656 657 samples according to their clinical diagnosis into FD and IIF. Hierarchical clustering 658 analysis between protein expression profiles of DEPs (row clustering) separated 659 overexpressed DEPs in IIP from underexpressed DEPs in FD. The green and red 660 colour denoted low and high expression levels respectively as shown in attached graduated colour scale bar. 661
- Fig. 4 Gene Ontology (GO) enrichment analysis result of differentially expressed proteins
 (DEPs) in IIP: Idiopathic infertile patients compared to FD: fertile donor. Bar graph
 showing the top GO terms for cellular component (A) molecular function (B) and
 biological process (C).
- Fig. 5 Cytoscape (BiNGO app) enrichment analysis revealed over-represented biological
 processes for the differentially expressed proteins (DEPs) in the spermatozoa of
 idiopathic infertile patients in comparison to fertile donor.
- Fig. 6 Ingenuity pathway Analysis of overexpressed proteins in Idiopathic infertile patients compared to fertile donor top Disease and Function (A) Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities (B) Cell Death and Survival, Cellular Development, Organismal Survival.
- Fig. 7 Ingenuity pathway Analysis of underexpressed proteins in Idiopathic infertile
 patients compared to fertile donor top Disease and functions are Cancer, Cell Death
 and Survival, Organismal Injury and abnormalities.
- Fig. 8 Ingenuity Pathway Analysis (IPA) (A) Canonical pathways analysis and (B) toxicity
 lists analysis of the differentially expressed proteins (DEPs) of idiopathic infertile
 patients in comparison to fertile donors.
- Fig. 9 Expression profile of (A) 4-Hydroxynonenal (B) 3-nitrotyrosine (C) AhR (D) HSP90β
 and their respective densitometry analysis in spermatozoa of FD: fertile donor and
 IIP: idiopathic infertile patient with total protein normalization (in arbitrary unit).
 p<0.05 with respect to fertile donor.
- Fig. 10 Schematic representation of molecular mechanisms involved in environmental borne
 polyaromatic hydrocarbon induced sperm dysfunction in idiopathic male infertility.

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81. No.	PAR (rg/ml)	Control 5.00415555	Infertilegateinty	Mana Widary U Test (p-value) P=0.0001	
1	Antencer		405.684303.97		
2	Dono(A)Anhracone	20/20106.24	585303486.40	P<8.0081	
3	Beneve(A)Pyrene	6.3541.17	61.0498.17	P<8.0003	
4	Record/Officembere	3.68113.58	0.5210575	918,0003	
5	Record CHSPer/rec	1343.02	196.184293.58	P-8.0005	
6	Orward	6.0013.33	15,77122,39	918,0001	
7	Discont/All/Astensor	6.1610.07	16.15126.81	P<8.0083	
8	Haorme	454010530	1051.6812301.74	P-8,0083	
9	Huxanhau	10111.01	27.56125.77	P<8.0081	
34	Infol02008Parent	6249233	7.3218.00	9-8,0081	
11	Nephalan	17140127140	1/12/06/17/08/10	P+8.0081	
12	20mmmerghairer	68.204185.99	307.624585.58	P-8.0003	
13	Press:	4.48133.68	54,32154,68	918,0001	





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