

Proteomic profile of maternal-aged blastocoel fluid suggests a novel role for ubiquitin system in blastocyst quality

Gabriella Tedeschi^{1,2} · Elena Albani³ · Elena Monica Borroni⁴ · Valentina Parini³ · Anna Maria Brucculeri³ · Elisa Maffioli² · Armando Negri¹ · Simona Nonnis¹ · Mauro Maccarrone⁵ · Paolo Emanuele Levi-Setti³

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Abstract

Purpose The etiology of maternal aging, a common cause of female factor infertility and a rate-limiting step in vitro fertilization (IVF) success, remains still unclear. Proteomic changes responsible for the impaired successful pregnancy outcome after IVF with aged blastocysts have not been yet evaluated. The objective of this prospective study was to employ proteomic techniques and bioinformatic tools to enlight differences at the protein level in blastocoel fluid of aged and younger woman.

Methods Protein composition of human blastocoel fluid isolated by micromanipulation from 46 blastocysts of women aged <37 years (group A) and 29 of women aged ≥37 years (group B) have been identified by a shotgun proteomic

approach based on high-resolution nano-liquid chromatography electrospray-ionization-tandem mass spectrometry (nLC-ESI-MS/MS) using label free for the relative quantification of their expression levels.

Results The proteomic analysis leads to the identification and quantification of 148 proteins; 132 and 116 proteins were identified in groups A and B, respectively. Interestingly, the identified proteins are mainly involved in processes aimed at fine tuning embryo implantation and development. Among the 100 proteins commonly expressed in both groups, 17 proteins are upregulated and 44 downregulated in group B compared to group A. Overall, the analysis identified 33 proteins, which were increased or present only in B while 76 were decreased in B or present only in A.

Conclusions Data revealed that maternal aging mainly affects blastocyst survival and implantation through unbalancing the equilibrium of the ubiquitin system known to play a crucial role in fine-tuning several aspects required to ensure successful pregnancy outcome.

Capsule Maternal aging mainly affects blastocyst survival and implantation through unbalancing the equilibrium of the ubiquitin system

Gabriella Tedeschi and Elena Albani contributed equally to this work.

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Keywords Blastocoel fluid · Aging · Embryo implantation · Proteomics · Shotgun

✉ Elena Monica Borroni
elena.borroni@humanitasresearch.it

Introduction

Embryo implantation requires synchronous development of the blastocyst and the endometrium [1]. During the early stages of implantation, the blastocyst enters the uterine cavity apposes and adheres to the endometrial epithelium to initiate implantation. It is well established that abnormalities in the bidirectional embryo-endometrial dialog are one of the major cause of infertility resulting in implantation failure [2, 3]. Noteworthy, advancing maternal age represents one of the major causes of the altered embryo-

- ¹ Dipartimento di Medicina Veterinaria, Università degli Studi di Milano, Milan, Italy
- ² Fondazione Filarete, 20139 Milan, Italy
- ³ Humanitas Fertility Center, Department of Gynecology, Division of Gynecology and Reproductive Medicine, Humanitas Research Hospital, Via Manzoni 56, Rozzano, 20089 Milan, Italy
- ⁴ Dipartimento di Biotecnologie Mediche e Medicina Traslazionale, Università degli Studi di Milano, Milan, Italy
- ⁵ Department of Medicine, Campus Bio-Medico University of Rome, Via Alvaro del Portillo 21, 00128 Rome, Italy

endometrial communication [4]. As expected, several large studies have reported age-specific outcomes of IVF, and maternal age has clearly been associated with a decline in cumulative live birth rates in patients older than 37 [5, 6]. Unfortunately, the molecular changes that occur in the endometrium during the “window of receptivity” and the blastocyst contribution have been poorly investigated due to the difficulty and the ethical limitations in studying implantation in humans; thus, no clinically useful markers have been identified to assess embryo quality and positive pregnancy outcome [7, 8].

In the recent years, the development of a wealth of “omic” technologies has opened the way for identifying potential markers, although validation of these is still a major issue [9, 10]. In particular, proteomics is an emerging powerful technology in the identification of both biomarkers and disease targets, allowing for the detection and monitoring of differing conditions or treatments. Although the classic proteomics approach has had limited success in the field of embryology [11, 12], the new developments in mass spectrometry have been helpful and the sensitivity of this approach has enabled the development of new protocols that are capable of profiling the proteome of small groups of mouse embryos [13], and even of single human blastocysts [14–16]. Therefore, several studies have recently addressed the analysis of the proteome of the human preimplantation embryo, in particular the ability of the blastocyst to secrete and/or consume different proteins in surrounding medium (secretome), in order to communicate with the maternal endometrium and proceed with the implantation process [13–15, 17, 18]. Interestingly, degenerating embryos presented a different protein expression profile compared to that of developing blastocysts, with a significant alteration of numerous biomarkers. Besides surrounding medium, the cells of the blastocyst are exposed to the fluid of the blastocoel, an internal cavity that becomes the yolk sac of the developing embryo [19]. Thus, the blastocoel fluid is the natural environment of blastocyst growth and the assessment of its protein composition provides an opportunity to expand the knowledge of embryonic physiology, including the maternal-embryonic dialog at the time of implantation. From a clinical perspective, the analysis of blastocoel fluid is emerging as a crucial topic in the field of reproductive medicine aimed at identifying new molecular markers related to highest implantation potential. The ultimate goal is to improve blastocyst culture conditions and fertilization rate, as well as to develop an affordable and cost-effective non-invasive biochemical assay to diagnose blastocyst viability, thus facilitating the move to single embryo transfer. The major problem concerning the analysis of the blastocoel fluid relies on its limited bioavailability (1–8 nl) and, despite the fact that recent developments in mass spectrometry allow the identification and characterization of thousands of proteins from low microgram levels of protein extracted from tissues or cell cultures [16, 17, 20, 21],

the low amounts of proteins extractable from blastocoel fluid are still a limiting step in this study.

Here, by a shotgun proteomic approach and label-free quantification, we report for the first time the blastocoel fluid proteins that are differentially expressed in 29 collected surplus aged and 46 non-aged blastocysts, taking 37-year-old women as the cut off parameter to categorized human blastocysts. The differences in the protein profile of blastocoel fluid of aged versus non-aged blastocysts rely on the identification of 109 differentially expressed proteins, which are mainly involved in processes aimed at fine tuning embryo implantation and development. Upon validation, the suggested key proteins may serve as potential biomarkers of embryo quality and may contribute towards the effectiveness of protocols for blastocyst culture management. .

Materials and methods

Patient population

Written informed consent was obtained from each patient and the study was approved by our local Ethics Committee. All consenting patients undergoing fertility treatment at the Humanitas Fertility Center, Humanitas Research Hospital, Rozzano, Italy, with supernumerary blastocysts were included in the study irrespective of the woman’s age (range years 26–41), infertility diagnosis (female or male), ovarian stimulation protocol (use of GnRH agonist or antagonist protocols in combination with recombinant and/or highly purified urinary gonadotropins), or performance of standard IVF or intracytoplasmic sperm injection (ICSI). The study was part of a trial on blastocoel fluid collection in order to test the safety of this procedure on pregnancy outcome [22].

Blastocyst generation

Oocytes, sperm, and embryos were cultured in the SAGE sequential culture media system (SAGE, Pasadena, USA) at 37 °C in 5% CO₂, 5% O₂ in nitrogen. Oocytes retrieval was performed 36 h after the administration of recombinant human chorionic gonadotropin through transvaginal ultrasonography. Oocytes were inseminated using either standard IVF insemination or ICSI; after ICSI, individual oocytes were transferred to a single 25 µl droplets under oil in Cleavage Medium supplemented with 10% Serum Protein Substitute (SAGE, Pasadena, USA), while standard IVF-inseminated oocytes were fertilized in 35 µl Fertilization Medium droplets under oil and transferred on day 1 to the Cleavage Medium. Fertilization results were assessed at 16–20-h post-sperm insemination. On day 3, and in some cases on day 2, 2/3 embryos were selected for transfer to each patient in the study; the embryos in excess of the number appropriate for transfer

were cultured in single 25 μ l droplets under oil in the Blastocyst Medium up to day 5 or day 6, and were cryopreserved at the blastocyst stage. Human blastocysts were scored up 120 or 144 h after insemination according to the expansion of the blastocoel cavity and number and integrity of both the inner cell mass (ICM) and trophectoderm (TE).

Isolation of the blastocoel fluid and sample collection

Blastocoel fluids from 75 blastocysts obtained from 52 IVF patients were collected. The blastocoel fluid was isolated by micromanipulation using an Olympus X40 (200 \times) microscope with Narishige manipulators and pipettes (angle 35 $^\circ$, inner diameter 5.5 μ m) from Cook (Brisbane, Australia). A droplet of 5–10 μ l Blastocyst Medium and a droplet of 3 μ l water were prepared in an ICSI dish (Falcon-Corning brand, NY, USA) and covered with oil. The blastocysts were transferred to the droplet with culture medium and the dish was placed in the micromanipulator. The microinjection needle was loaded with water before sampling. The blastocyst was immobilized by the holding pipette with the ICM placed toward the holding pipette. The microinjection needle was then gently led in to blastocyst cavity, the fluid was aspirated until the blastocyst collapsed and the blastocoel fluid was transferred to the water droplet. After micromanipulation, the samples were transferred to a labeled PCR tube using a 10- μ l pipette and immediately frozen at -80°C . To obtain adequate protein material for analysis, the samples were collected and analyzed in two pools according on the patient's age: group A (blastocoel fluid from 46 samples of women aged <37 years) and group B (29 samples of women aged \geq 37 years). Both groups were homogeneous for infertility factor, for dose of gonadotropin administrated for ovarian stimulation and for average of oocytes retrieved after induction.

Proteomic analysis

The proteins of the blastocoel fluid were lysed in a buffer containing 8 M urea, 0.1 M ammonium bicarbonate and the complete protease inhibitor cocktail (Roche, Basel, Switzerland). After reduction and derivatization, proteins were digested with sequence grade trypsin for 16 h at 37 $^\circ\text{C}$ using a protein:trypsin ratio of 1:20. The proteolytic digest was desalted using Zip-Tip C_{18} (Millipore) before mass spectrometric (MS) analysis [23, 24]. LC-ESI-MS/MS analysis was performed on a Dionex UltiMate 3000 HPLC System with a PicoFrit ProteoPrep C_{18} column (200 mm, internal diameter of 75 μ m) (New Objective, USA). Gradient: 1% ACN in 0.1% formic acid for 10 min, 1–4% ACN in 0.1% formic acid for 6 min, 4–30% ACN in 0.1% formic acid for 147 min and 30–50% ACN in 0.1% formic for 3 min at a flow rate of 0.3 μ l/min. The eluate was electrosprayed into an LTQ Orbitrap Velos (Thermo Fisher Scientific, Bremen, Germany)

through a Proxeon nanoelectrospray ion source. The LTQ-Orbitrap was operated in positive mode in data-dependent acquisition mode to automatically alternate between a full scan (m/z 350–2000) in the Orbitrap (at resolution 60,000, AGC target 1,000,000) and subsequent CID MS/MS in the linear ion trap of the 20 most intense peaks from full scan (normalized collision energy of 35%, 10 ms activation). Isolation window: 3 Da, unassigned charge states: rejected, charge state 1: rejected, charge states 2+, 3+, 4+: not rejected; dynamic exclusion enabled (60 s, exclusion list size: 200) [25]. Data acquisition was controlled by Xcalibur 2.0 and Tune 2.4 software (Thermo Fisher Scientific, MA USA). A sample containing only culture medium, kept as a control (CTR), was also treated and analyzed.

Data analysis

Mass spectra were analyzed using MaxQuant software (version 1.3.0.5). The initial maximum allowed mass deviation was set to 20 ppm for monoisotopic precursor ions and 0.5 Da for MS/MS peaks. Enzyme specificity was set to trypsin, defined as C-terminal to arginine and lysine excluding proline, and a maximum of two missed cleavages were allowed. Carbamidomethylcysteine was set as a fixed modification, N-terminal acetylation, methionine oxidation, and asparagine/glutamine deamidation as variable modifications. The spectra were searched by the Andromeda search engine against the human Uniprot sequence database (release 22.01.2014). The reversed sequences of the target database were used as decoy database. Protein identification required at least one unique or razor peptide per protein group. Quantification in MaxQuant was performed using the built in XIC-based label-free quantification (LFQ) algorithm [26] using fast LFQ. False protein identifications (1 or 5%) [17] were estimated by searching MSMS spectra against the corresponding reversed-sequence (decoy) database. The minimum required peptide length was set to 9 amino acids. Statistical analyses were performed using the Perseus software (version 1.4.0.6). Five technical replicates were carried out for each group (A and B) and for the control. Only proteins present and quantified in at least 3 out of 5 technical repeats and not detected in the sample containing only the culture medium (CTR) were positively identified as blastocoel fluid components and used for statistical analyses. Many keratins known to be due to a contamination during sample handling were excluded from the analysis. The intensity of each protein (measured in at least 3 replicates in group A and group B) in each replicate is used for the t test. Proteins were considered differentially expressed if they were present only in women aged <37 years (group A) or women aged \geq 37 years (group B) or showed significant t test

Table 1 List of the proteins increased in group B

Protein IDs	Protein names	Gene names	t-test Difference	FDR 1%	Previous identification
Q96NH3	Protein broad-minded	BROMI;C6orf170	1.612		x
Q9UHD9	Ubiquilin-2	UBQLN2	1.451	X	x
Q9NZL9 -5	Isoform 5 of Methionine adenosyltransferase 2 subunit beta	MAT2B	1.217		x
P05060	Secretogranin-1;GAWK peptide;CCB peptide	CHGB	1.159	X	x
Q9H1N7	Adenosine 3-phospho 5-phosphosulfate transporter 2	SLC35B3	0.932		x
Q6ZU67	BEN domain-containing protein 4	BEND4	0.837		x
P28290	Sperm-specific antigen 2	SSFA2	0.792	X	x
J3KMZ5	Serotonin N-acetyltransferase	AANAT	0.717		x
H0YNB0	Unconventional myosin-Ie	MYO1E	0.712		x
H3BUN7	SH2B adapter protein 1	SH2B1	0.617	X	x
Q5T749	Keratinocyte proline-rich protein	KPRP	0.600	X	X
Q76G19	PDZ domain-containing protein 4	PDZD4	0.582	X	x
Q9HCE0	Ectopic P granules protein 5 homolog	EPG5	0.561		x
Q12972 -3	Isoform Gamma of Nuclear inhibitor of protein phosphatase 1	PPP1R8	0.553		x
G3V314	Ena/VASP-like protein	EVL	0.491		x
Q8NI35 -5	Isoform 5 of InaD-like protein	INADL	0.450		x
P14923	Junction plakoglobin	JUP	0.445	X	x

Proteins were considered increased or decreased if they showed significant *t* test difference (cut-off at 5% permutation-based False Discovery Rate) between group A and B. Previous identification: in the Table the proteins previously identified in human blastocoel fluid (16, 17) are indicated with a capital X, while x indicates gene products previously experimentally detected at the protein level as secreted and/or present in extracellular region and/or in exosome and/or in microvesicles according to public available databases and dataset (www.neXtProt.org, www.exocarta.org, microvesicle.org, geneontology.org, www.proteinatlas.org, 29) or at the gene expression level from microarray data (16, 30) or at the transcription level in blastocystis or embryonic tissue according to <http://genomewidepdb.proteomix.org> or <https://www.ncbi.nlm.nih.gov/geoprofiles> databases. The proteins ascribed to fertilization and embryo implantation or nucleic acid interaction categories of Fig. 3 are highlighted in light and dark gray, respectively. The table lists only the proteins present and quantified in at least 3 out of 5 technical repeats using a false positive rate of 0.05 and minimum peptide length 9 amino acids, reporting in a column the proteins identified with FDR 0.01

difference (filtered for permutation-based False Discovery Rate of many independent hypotheses, cut-off at 5%) between the two groups. The proteins differently expressed in the two groups were clustered according to their functions using the DAVID platform [27] filtered for significant Gene Ontology terms: Biological Process (GOBP) and Molecular Function (GOMF), using a *p* value <0.05. Protein-protein interactions were analyzed by String [28]. Gene products previously experimentally detected at the protein level as secreted and/or in extracellular region and/or exosome and/or microvesicles were determined according to public available databases (www.neXtProt.org, www.exocarta.org, microvesicle.org, geneontology.org, www.proteinatlas.org), and dataset [29]. Gene products previously detected at the transcription level in blastocystis or embryonic tissue are listed Tables 1, 2, 3, and 4 and

S2-according to microarray datasets and gene expression databases (<http://genomewidepdb.proteomix.org> or <https://www.ncbi.nlm.nih.gov/geoprofiles>) [16, 30]. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD003535

Results

Proteomic profile of human blastocoel fluid isolated from women aged < and ≥37 years

The aim of the study was to examine the protein composition of human blastocoel fluid isolated from blastocysts of women aged <37 years (group A) and women aged ≥37 years (group B) to enlighten differences, at the protein level, that can

Table 2 List of the proteins decreased in group B

Protein IDs	Protein names	Gene names	t-test Difference	FDR 1%	Previous identification
Q02413	Desmoglein-1	DSG1	-0.158	X	X
J3KNN1	Polypeptide N-acetylgalactosaminyltransferase 9	GALNT9	-0.194	X	
Q8TAL5	Uncharacterized protein C9orf43	C9orf43	-0.341		x
P22732	Solute carrier family 2, facilitated glucose transporter member 5	SLC2A5	-0.349		x
P01566	Interferon alpha-10;Interferon alpha-21	IFNA10;IFNA21	-0.368	X	x
G8JLG2	Corneodesmosin	CDSN	-0.379		X
F8WCM 5	Insulin;Insulin B chain;Insulin A chain	INS-IGF2;INS	-0.386	X	X
Q8NBP5	Major facilitator superfamily domain-containing protein 9	MFSD9	-0.420	X	x
Q13635-4	Isoform S of Protein patched homolog 1	PTCH1	-0.421	X	x
P05109	Protein S100-A8	S100A8	-0.438	X	X
F8W878	Brain-specific angiogenesis inhibitor 1-associated protein 2	BAIAP2	-0.464	X	x
Q9HCJ0	Trinucleotide repeat-containing gene 6C protein	TNRC6C	-0.476	X	x
Q6JVE6	Epididymal-specific lipocalin-10	LCN10	-0.504		x
P0CG48	Polyubiquitin-C;Ubiquitin;Polyubiquitin-B	UBC;UBB	-0.539	X	X
F8W8U3	Homeobox protein Meis1	MEIS1	-0.558		x
E7ERA6	RING finger protein 223	RNF223	-0.558	X	
Q96F24-2	Nuclear recepto-binding factor 2	NRBF2	-0.634	X	x
Q9BY89	Uncharacterized protein KIAA1671	KIAA1671	-0.645		x
Q8N8E3	Centrosomal protein of 112 kDa	CEP112	-0.713		x
P61626	Lysozyme C	LYZ	-0.760	X	X
C9K0L2	Maestro heat-like repeat-containing protein family member 7	HEATR8	-0.760	X	
Q6PGQ7	Protein aurora borealis	BORA;FLJ22624	-0.770	X	x
P81605	Dermcidin;Survival-promoting peptide;DCD-1	DCD	-0.793	X	X

Proteins were considered increased or decreased if they showed significant *t* test difference (cut-off at 5% permutation-based False Discovery Rate) between groups A and B. Previous identification: in the Table the proteins previously identified in human blastocoel fluid (16, 17) are indicated with a capital X, while x indicates gene products previously experimentally detected at the protein level as secreted and/or present in extracellular region and/or in exosome and/or in microvesicles according to public available databases and dataset (www.neXtProt.org, www.exocarta.org, microvesicle.org, geneontology.org, www.proteinatlas.org, 29) or at the gene expression level from microarray data (16, 30) or at the transcription level in blastocystis or embryonic tissue according to <http://genomewidepdb.proteomix.org> or <https://www.ncbi.nlm.nih.gov/geo/profiles> databases. The proteins ascribed to fertilization and embryo implantation or nucleic acid interaction categories of Fig. 3 are highlighted in light and dark gray, respectively. The table lists only the proteins present and quantified in at least 3 out of 5 technical repeats using a false positive rate of 0.05 and minimum peptide length 9 amino acids, reporting in a column the proteins identified with FDR 0.01

possibly explain blastocyst survival and implantation success known to be very different in the two groups. Blastocoel fluid was isolated by micromanipulation, and proteins were identified by a shotgun proteomic approach, using label free for the relative quantification of their expression levels. Proteins identified in the control (containing only culture medium) and keratins- likely due to a contamination during sample

preparation were discarded from the analysis (Supplementary Table 1). The proteomic analysis leads to the identification and quantification of 148 proteins (Fig. 1); 132 and 116 proteins were identified in group A (Supplementary Table 2, average CV 1.2%) and B (Supplementary Table 3, average CV 1.3%), respectively (Fig. 1a). Among the 100 proteins commonly expressed in

Table 2 (continued)

Q9NZT1	Calmodulin-like protein 5	CALML5	-0.829		X
Q9BV73	Centrosome-associated protein CEP250	CEP250	-0.991		X
O00712	Nuclear factor 1;Nuclear factor 1 B-type	NFIB	-1.041		x
O94788-3	Isoform 3 of Retinal dehydrogenase 2	ALDH1A2	-1.065		x
P19021	Peptidyl-glycine alpha-amidating monooxygenase	PAM	-1.140		x
Q6GMR7	Fatty-acid amide hydrolase 2	FAAH2	-1.178	X	x
H0Y7A7	Calmodulin	CALM2;CALM1	-1.209	X	x
P31151	Protein S100-A7;Protein S100-A7A	S100A7;S100A7A	-1.240	X	X
Q96RW7	Hemicentin-1	HMCN1	-1.250	X	x
Q9BR77	Coiled-coil domain-containing protein 77	CCDC77	-1.315	X	x
Q6UWP8	Suprabasin	SBSN	-1.407	X	X
P31025	Lipocalin-1;Putative lipocalin 1-like protein 1	LCN1;LCN1P1	-1.419	X	X
Q9UGM3	Deleted in malignant brain tumors 1 protein	DMBT1	-1.508	X	X
O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1	-1.622		x
D6R956	Ubiquitin carboxyl -terminal hydrolase isozyme L1	UCHL1	-1.796		X
Q8TE56	A disintegrin and metalloproteinase with thrombospondin motifs 17	ADAMTS17	-1.825	X	x
Q8TE76	MORC family CW-type zinc finger protein 4	MORC4	-1.857	X	x
P20382	Pro-MCH;Neuropeptide-glycine-glutamic acid	PMCH	-2.149	X	x
P01040	Cystatin-A	CSTA	-2.310	X	X
Q8NBJ4	Golgi membrane protein 1	GOLM1	-2.427	X	x
P12273	Prolactin-inducible protein	PIP	-2.704	X	X

both groups, 17 proteins are upregulated and 44 downregulated in group B compared to group A (Fig. 1b). These proteins are listed in Tables 1 and 2, respectively, while Tables 3 and 4 report the proteins expressed only in A (32) or in B (16), respectively. Overall, the analysis identified 33 proteins, which were increased or present only in B while 76 were decreased in B or present only in A (Fig. 1). As reported in Tables 1, 2, 3, and 4, Supplementary Table 2 and 3, 98% of the differentially regulated proteins and 91% of the total proteins identified have been previously experimentally detected either at the protein level in blastocoel fluid, exosomes, microvesicles or extracellular region or at the gene expression level in microarray studies concerning blastocyst transcriptome and gene expression databases.

Up to now, only two papers addressed the issue of the protein content in the blastocoel fluid by a proteomic analysis: Jansen et al. [17] described the protein content of the blastocoel together with the medium and the cells, while Poli et al. [16], very recently, reported on the proteome of the blastocoel fluid combining the results from shot gun proteomics and

gene expression analysis. The present study allows to identify 108 proteins never described before, adding unprecedented information on this important human body fluid.

Classification of the differentially expressed proteins based on bioinformatic analysis

The proteins differentially expressed in the two groups were classified based on Gene Ontology Molecular Function and Biological Processes, as shown in Fig. 2. As a further step in the bioinformatic analysis, the proteins were manually grouped according to their function taking into account, besides GOMF and GOBP, also keywords and known annotations from the literature. It was thus possible to ascribe each protein to 6 major groups: (1) fertilization and embryo implantation, (2) embryo development, (3) nucleic acid interaction, (4) signaling, (5) uncharacterized proteins, (6) proteins excluded from the groups listed above categorized as “other” (Fig. 3, Supplementary Table 4). Interestingly, comparing the analysis of proteins increased or only expressed in A

Table 3 List of the proteins present only in group A

Protein IDs	Protein names	Gene names	FDR 1%	Previous identification
P04745	Alpha-amylase 1;Pancreatic alpha-amylase	AMY1A;AMY2A		X
Q13535	Serine/threonine-protein kinase ATR	ATR		x
J9JIC5	Protein Njmu-R1	C17orf75		x
O76042	Putative uncharacterized protein C3orf51	C3orf51	X	
H0Y7H7	Dedicator of cytokinesis protein 4	DOCK4		x
B4DIP4	Eukaryotic translation initiation factor 2-alpha kinase 1	EIF2AK1		x
Q13542	Eukaryotic translation initiation factor 4E-binding protein 2	EIF4EBP2	X	x
Q9H1K1-2	Isoform 2 of Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	ISCU		x
H0Y3B9	BTB/POZ domain-containing protein KCTD2	KCTD2	X	x
Q7Z4S6	Kinesin-like protein KIF21A	KIF21A		x
Q6TDP4	Kelch-like protein 17	KLHL17		x
Q9UKR0	Kallikrein-12	KLK12		x
P11047	Laminin subunit gamma-1	LAMC1		x
P02788	Lactotransferrin;Kaliocin-1;Lactoferroxin-A;Lactoferroxin-B;Lactoferroxin-C	LTF	X	X
Q3SYA6	MAGEC3 protein	MAGEC3		
F5H1U9	Multiple PDZ domain protein	MPDZ	X	x
Q96DH6	RNA-binding protein Musashi homolog 2	MSI2		x
P51843	Nuclear receptor subfamily 0 group B member 1	NR0B1		x
Q9BSM1	Polycomb group RING finger protein 1	PCGF1	X	x
Q5VWC4	26S proteasome non-ATPase regulatory subunit 4	PSMD4		x
P46060	Ran GTPase-activating protein 1	RANGAP1		x
O75556	Mammaglobin-B	SCGB2A1		x
C9JNL6	Electrogenic sodium bicarbonate cotransporter 4	SLC4A5		x
Q9NQ38	Serine protease inhibitor Kazal-type 5	SPINK5	X	x
Q5T2D2	Trem-like transcript 2 protein	TREML2		x
Q9H3U1	Protein unc-45 homolog A	UNC45A		x
Q5GH76	XK-related protein 4	XKR4	X	
Q9NYL2-2	Isoform 2 of Mitogen-activated protein kinase kinase kinase MLT	ZAK		x
Q6FIF0	AN1-type zinc finger protein 6	ZFAND6		x
O60320-2	Isoform 2 of Protein FAM189A1	FAM189A1		x
Q00994-2	Isoform 2 of Protein BEX3	NGFRAP1		x
Q96B36-3	Isoform 3 of Proline-rich AKT1 substrate 1	AKT1S1		x

Previous identification: in the Table, the proteins previously identified in human blastocoel fluid (16, 17) are indicated with a capital X, while x indicates gene products previously experimentally detected at the protein level as secreted and/or present in extracellular region and/or in exosome and/or in microvesicles according to public available databases and dataset (www.neXtProt.org, www.exocarta.org, microvesicle.org, geneontology.org, www.proteinatlas.org, 29) or at the gene expression level from microarray data (16, 30) or at the transcription level in blastocystis or embryonic tissue according to <http://genomewidepdb.proteomix.org> or <https://www.ncbi.nlm.nih.gov/geo/profiles> databases. The proteins ascribed to fertilization and embryo implantation or nucleic acid interaction categories of Fig. 3 are highlighted in light and dark gray, respectively. The table lists only the proteins present and quantified in at least 3 out of 5 technical repeats using a false positive rate of 0.05 and minimum peptide length 9 amino acids, reporting in a column the proteins identified with FDR 0.01

Table 4 List of the proteins present only in group B

Protein IDs	Protein names	Gene names	FDR 1%	Previous identification
A6NKX1	Putative uncharacterized protein CXorf52B	NCRNA00204		
O75553-5	Isoform DAB553 of Disabled homolog 1	DAB1		x
O75665	Oral-facial-digital syndrome 1 protein	OFD1		x
P16104	Histone H2A.x;Histone H2A type 1-A	H2AFX;HIST1H2A A	X	X
P48431	Transcription factor SOX-2	SOX2	X	x
P51654	Glypican-3;Secreted glypican-3	GPC3		x
P62805	Histone H4	HIST1H4A	X	X
Q05639	Elongation factor 1-alpha 2;Elongation factor 1-alpha 1;Putative elongation factor 1-alpha-like 3	EEF1A2;EEF1A1;E EF1A1P5	X	X
Q15147	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-4	PLCB4		x
Q5J5C9	Beta-defensin 121	DEFB121		x
Q96DR8	Mucin-like protein 1	MUCL1	X	X
Q96ST8	Centrosomal protein of 89 kDa	CEP89		x
Q9H6A9	Pecanex-like protein 3	PCNXL3		x
Q9UJ42	Probable G-protein coupled receptor 160	GPR160		x
B4DR52	Histone H2B;Histone H2B type 1-K	HIST2H2BF;HIST1 H2BK	X	X
H0Y3T1	Protein CROC-4	C1orf61		x

Previous identification: in the Table the proteins previously identified in human blastocoel fluid (16, 17) are indicated with a capital X, while x indicates gene products previously experimentally detected at the protein level as secreted and/or present in extracellular region and/or in exosome and/or in microvesicles according to public available databases and dataset (www.neXtProt.org, www.exocarta.org, microvesicle.org, geneontology.org, www.proteinatlas.org, 29) or at the gene expression level from microarray data (16, 30) or at the transcription level in blastocystis or embryonic tissue according to <http://genomewidepdb.proteomix.org> or <https://www.ncbi.nlm.nih.gov/geo/profiles> databases. The proteins ascribed to fertilization and embryo implantation or nucleic acid interaction categories of Fig. 3 are highlighted in light and dark gray, respectively. The table lists only the proteins present and quantified in at least 3 out of 5 technical repeats using a false positive rate of 0.05 and minimum peptide length 9 amino acids, reporting in a column the proteins identified with FDR 0.01

(Fig. 3a) with the proteins increased or only expressed in B (Fig. 3b), the major differences can be observed in 2 categories: fertilization and embryo implantation (12% group A vs 2% group B) and nucleic acid interaction (4% group A vs 13% group B).

Discussion

According to the promising results obtained by Jensen and collaborators and by Poli and coworkers [16, 17], to better delineate possible mechanisms for the effect of maternal aging on fertility and potential biomarkers for evaluating the blastocysts quality and improving pregnancy outcome rate in IVF patients, we examined the proteomic profile of blastocoel fluid in woman <37 year old (group A) or ≥37 year old (group B). Comparison between the two matched study groups demonstrated, as already known, that pregnancy rate was lower in group B. In this group, 4/12 (33.3%) pregnancies were obtained after frozen—thawed blastocyst transfer cycles versus

group A (13/30 pregnancies, 43.3%). The shotgun proteomic approach allowed identifying 148 proteins, out of which 108 are described for the first time in the blastocoel fluid, and 109 are differentially expressed between the two groups. These proteins were functionally profiled using a suite of bioinformatics annotation tools and pathway databases, to obtain a comprehensive view of the impacted processes, pathways, functions, and networks related to maternal aging. The bioinformatic analysis showed that differential proteins participate in various biological processes, but the main perturbed networks refer to fertilization and embryo implantation, as well as to nucleic acid interactions (Fig. 3 and Table S4). Interestingly, many of the proteins differentially expressed are related to processes involving ubiquitin, that is largely known to play a crucial role in controlling several aspects required to ensure successful pregnancy outcome. In particular, the major molecular functions of these proteins consist of histone turnover and transcription factors, crucially required for cell cycle progression and proliferation. Therefore, it is presumed that alterations in their expression level could affect

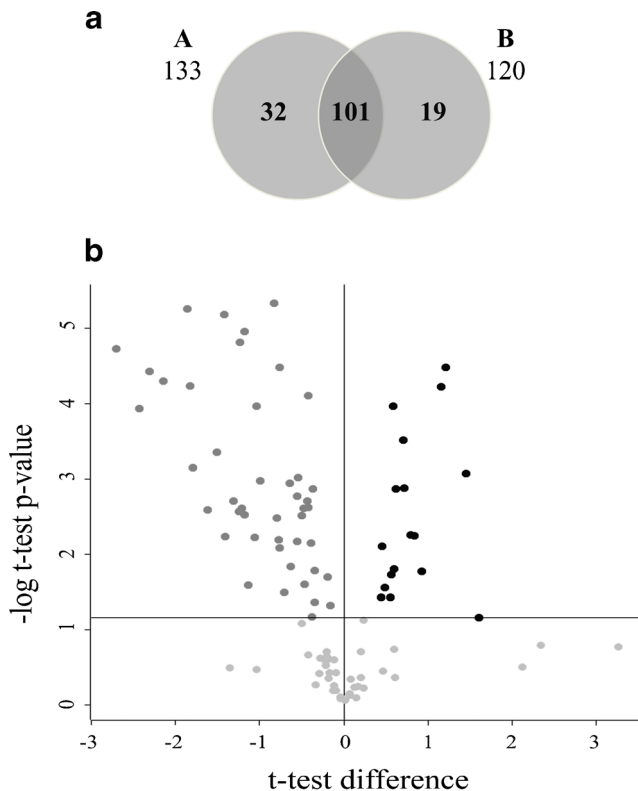


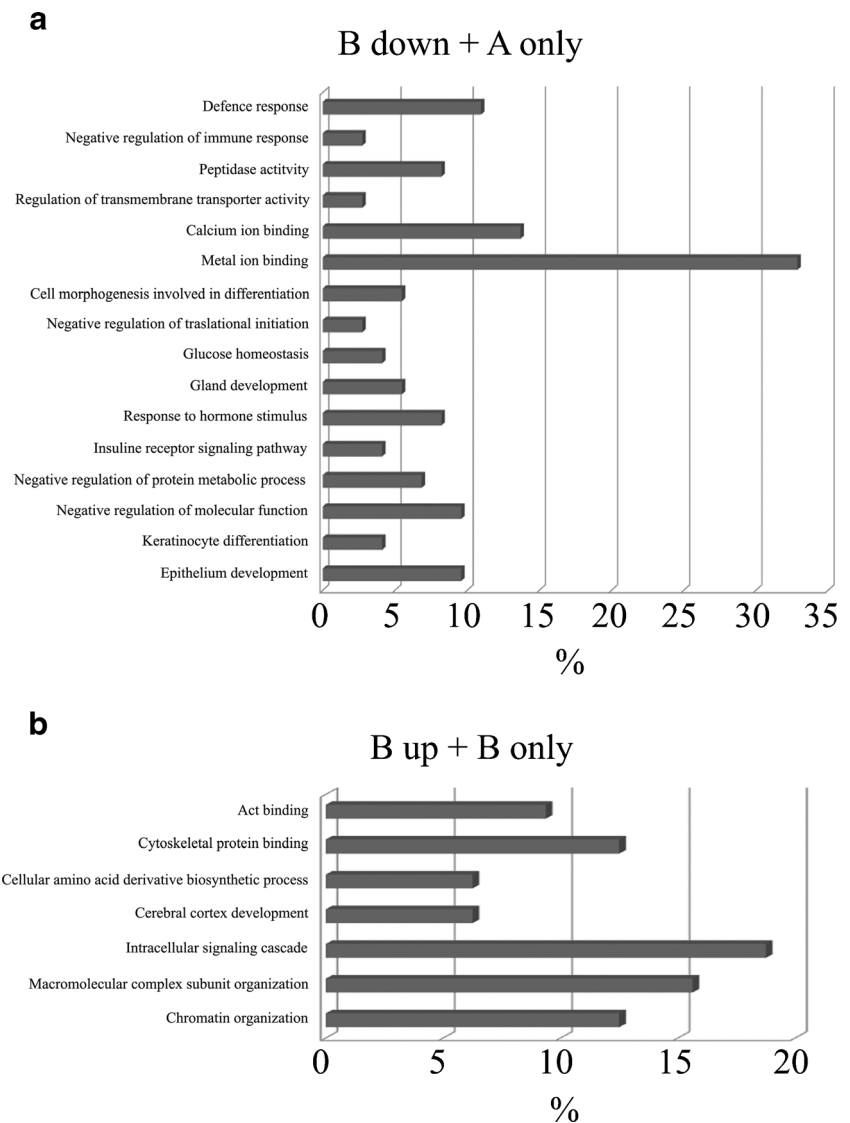
Fig. 1 Proteomic profile of human blastocoel fluid isolated from women aged < (group A) and \geq (group B) 37 years. **a** Venn diagram of the proteins identified in groups A and B. **b** Volcano plot showing the proteins common to both groups differentially expressed in group B compared to group A. Common proteins were considered differentially expressed if they showed significant *t* test difference (cut-off at 5% permutation-based False Discovery Rate) between the two groups. Proteins up- and downregulated are indicated in *black and dark gray*, respectively. Proteins which are present at levels not statistically different between groups A and B are indicated in *light gray* below the horizontal threshold line

implantation potential by altering blastocyst homeostasis towards apoptosis and autophagy settings. The following paragraph details the known biological role in reproductive processes of ubiquitin-related proteins which have been identified as blastocoel fluid components in the present study and listed in Tables 1, 2, 3, and 4 and S2-S3. In addition, a network showing the known interactions among up- or downregulated ubiquitin-related proteins is shown in Fig. 4.

In the recent years, increasing observations have demonstrated the role of ubiquitin system in reproductive processes, such as gametogenesis, modulation of steroid receptor concentrations, placental development and endo-metrial modification at the beginning of pregnancy [31]. These wide-range effects have led to extensive research and several studies recently demonstrated the increase of ubiquitylation in the uterus during embryo implantation; thus, the proper control and turnover of this key signaling protein activity suggest potential roles in controlling critical aspects of implantation [32–35]. This is also emphasized by the observation that ubiquitin is

accumulated in trophoblast of expanding blastocysts [36], suggesting that dysregulation of ubiquitin system may be responsible for failure IVF outcome. In 2009, Katz-Jaffe and collaborators reviewed findings on potential protein biomarkers in the embryo secretome [18], identifying a crucial role for ubiquitin. In our study, a huge number of proteins related to ubiquitin system has been identified and differentially regulated among the two groups analyzed. The ubiquitinase UBC and Ubiquitin Carboxyl-terminal Hydrolase isozyme L1 (UCHL1) are downregulated in aged blastocysts, as well as proteins containing a RING finger domain that plays a key role in the ubiquitination pathway during embryonic development [37, 38] such as RING Finger protein 223 (RNF223) and Kelch-like protein 17 (KLHL17). Instead, the expression of the 26S Proteasome non-ATPase regulatory subunit 4 (PSMD4), a component of the 26S proteasome complex responsible for ubiquitylated proteins degradation, and the AN1-type zinc finger protein 6 (ZFAND6), a polyubiquitin binding protein involved in regulating NF- κ B signaling [39], are completely switched off. Interestingly, several differential expressed proteins are substrate of Small Ubiquitin MOdifier (SUMO), which is also involved in regulating embryonic viability in mammals [40]. In particular, aged blastocysts lack Ran GTPaseactivating protein 1 (RANGAP1), that regulates pathways mainly involved in differentiation, apoptosis and cell cycle by altering protein function through changes in activity or cellular localization or by protecting substrates from ubiquitination [41]. Instead, they show increased expression of BEN domain-containing protein 4 that belongs to a family of proteins involved in histone deubiquitination. Accumulated evidence in the literature has currently demonstrated that the monoubiquitylation of histone H2A at lysine 119 is crucially associated with transcriptionally repressed chromatin, as a result of the repression activity of Polycomb group proteins [42–46]. The latter proteins are crucial developmental regulators that maintain transcriptional repression of hundreds of genes involved in development from early embryogenesis through birth to adulthood [37, 47–50], as well as in signaling or cancer development using chromatin-based epigenetic mechanisms [51, 52]. In particular, the Polycomb group RING finger protein 1 (PCGF1) acts as key cell growth regulator that promotes cell cycle progression and proliferation by transcriptional repression of the CDK cyclin inhibitor p21Waf1/Cip1 [53]. Interestingly, our study reveals that Polycomb group RING finger protein 1 (PCGF1) has not been detected in aged blastocysts, providing a further confirmation of the key role of ubiquitylation for initiation of pregnancy. Noteworthy, the importance of the crosstalk between Polycomb group proteins and histones has been recently demonstrated by the identification of the Jumonji protein JARID2, a component of the histone methyltransferase complex that regulates binding of the Polycomb repressive complex 2 to target genes in embryonic stem cells

Fig. 2 Classification of the proteins differentially expressed based on GOMF and GOBP. The proteins differentially expressed in A and B groups were classified based on molecular function (GOMF) and biological processes (GOBP). **a** Classification of proteins downregulated in B or present only in A. **b** Classification of proteins upregulated or present only in B



[49], as the most represented proteins in the secretome of the preimplantation human embryo able to predict positive pregnancy outcome [54]. Moreover, according to a recent observation describing the important role of histone H2A variants (H2A.X, H2A.Z and macroH2A) in genome remodeling after fertilization [55] and preimplantation embryo development [56], our study reveals that blastocoel fluid of aged woman undergoes a global change in histone composition, as it contains soluble histones (H2A.X, H2B and H4) that are completely absent in younger women.

Noteworthy, any excess of the positively charged histones can allow them to potentially associate non-specifically with negatively charged molecules such as DNA in the cell, resulting in deleterious effects on cell viability and genomic stability [57]. Indeed, recent studies have highlighted a link between increased soluble H2A.X and apoptosis induction [58, 59]. Excessive soluble H2A.X causes chromatin

aggregation and inhibition of ongoing gene transcription, but it has also non-nucleosomal functions, specifically proapoptotic activities. Therefore, to avoid the problems associated with excess histone accumulation, most eukaryotic cells largely rely on the strict regulation of their histone protein levels and excess histones are degraded by phosphorylation and ubiquitylation-dependent proteolysis [60, 61]. Moreover, a very recent report suggests that histones may be targeted for degradation also via the chaperone-mediated autophagy pathway in mammalian cells [62]. In keeping with these observations, we identified in blastocoel fluid from aged blastocysts an increased amount of Ubiquilin-2 (UBQLN2), which is involved in regulation of different protein degradation mechanisms and pathways including ubiquitin-proteasome system and autophagy, a survival mechanism whose deregulation has been linked to non-apoptotic cell death through inducing cell cycle arrest [63, 64]. Noteworthy, increased autophagy of

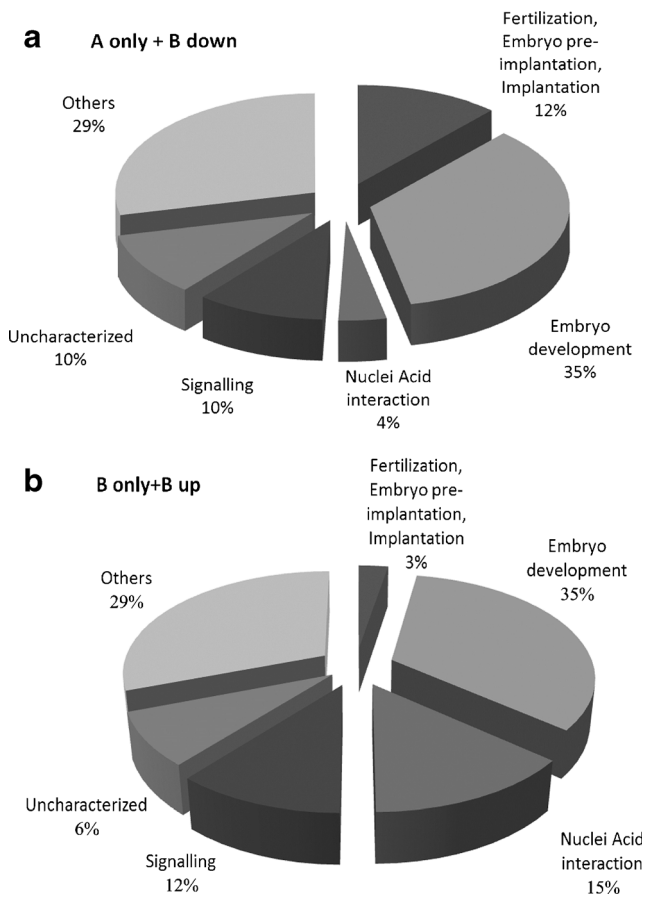
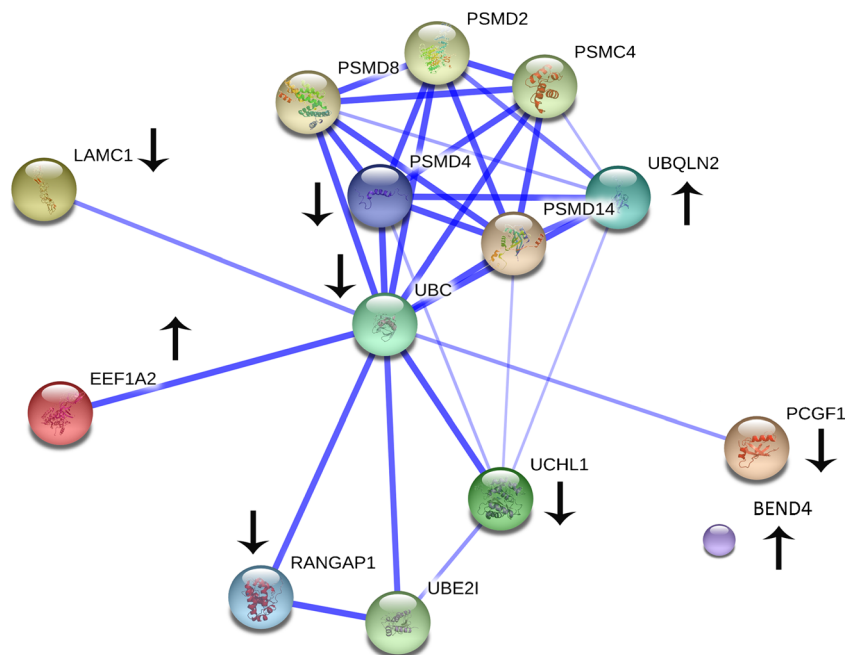


Fig. 3 Functional analysis of the proteins differentially expressed in A and B. The proteins were manually grouped according to their function in biological processes taking into account, besides GOMF, and GOBP, also keywords and annotations known from literature (Supplementary Table 4). **a** Classification of proteins downregulated in B or present only in A. **b** Classification of proteins up regulated or present only in B

Fig. 4 Protein-protein interaction analysis of the proteins differentially expressed in A and B involved in the ubiquitin system. The analysis was performed by STRING. Stronger associations are represented by *thicker lines*. Proteins increased or decreased in B are indicated by an *arrow*. PSMD8, PSMD4, PSMD2, and PSMD14 are isoforms of PSMD4 which was found decreased in B



aged blastocysts is further confirmed by absence in the blastocoel fluid of Laminin subunit gamma-1 (LAMC1), which is crucially involved in protection from autophagy [65, 66].

Besides ubiquitin, our proteomic data reveals that also FAAH2, a key protein in the endocannabinoid system, is differentially expressed in young and aged women blastocoel fluid. Recently, comprehensive studies have indicated that endocannabinoids, a group of bioactive lipids including anandamide (AEA), are actively involved in the process of reproduction and pregnancy, from gametogenesis, uterine receptivity, early embryo-blastocyst development, oviductal transport and implantation through to birth [67–69]. As a consequence of its potential physiological impact, endocannabinoid signaling is finely regulated at multiple levels through several metabolic routes, including the main degradative enzyme fatty acid amide hydrolase (FAAH), that cleaves and inactivates AEA [70]. Changes in the activity and/or expression of FAAH determine significant fluctuations in AEA levels, which in turn can lead to success or failure of pregnancy [71]. In line with this, it has been reported that women in an IVF program who have successful implantation have low serum AEA levels associated with elevated levels of in their peripheral lymphocytes at 6 weeks gestation, whereas low FAAH [72, 73] and high AEA levels in blood are associated with spontaneous threatened miscarriage [74]. In keeping with these observations, our data revealed lower levels of FAAH2, an isoform highly expressed in higher placental mammals [75] in the blastocoel fluid of aged woman. Given the potential impact of this observation, additional studies will be devoted to validate this preliminary result.

In summary, by applying a proteomic approach to compare blastocoel fluid from <37-year-old and ≥37-year-old women

blastocysts, we suggest that increased rate of implantation failure in aged IVF patients relies on the pro-apoptotic signature of their blastocysts, as a consequence of the dramatic dysregulation of mechanisms involved in the regulation of ubiquitin system as well as, potentially, in the control of a correct AEA tone. Noteworthy, several additional proteins not related to the ubiquitin system but equally involved in apoptotic processes have been found differentially regulated among the two groups, such as the Isoform 2 of Protein BEX3 (NGFRAP1) [76], Dermicin (DCD) [77], the Isoform 3 of Proline-rich AKT1 substrate 1 (AKT1S1) [78], Calmodulin (CALM) [79], and the eukaryotic translation elongation factor 1A (EEF1A) [80, 81], providing a further confirmation of the pro-apoptotic signature of aged blastocysts.

In conclusion, the results of our deep proteomic investigation provide valuable information on the molecular player involved in biological processes related to blastocyst features in aged women which, in turn, can be used as a starting point towards the identification of non-invasive tools to investigate and ameliorate blastocyst viability, and improving clinical outcome of IVF cycles.

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Compliance with ethical standards

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Conflict of interest The authors declare that they have no conflict of interest.

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