1	RESEARCH ARTICLES
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3	Sperm of patients with severe asthenozoospermia show biochemical, molecular,
4	and genomic alterations
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31 SUMMARY

32 Severely low sperm motility is a frequent cause of infertility. This pathological 33 condition is multifactorial. However, mechanisms underlying the development of this 34 condition are not completely understood. Single abnormalities have been reported in 35 sperms of patients with asthenozoospermia. In the present study, we characterized, in 22 36 normozoospermic men and in 37 patients with asthenozoospermia, biochemical, 37 molecular, and genomic abnormalities that frequently occur in sperm of patients with 38 asthenozoospermia. We evaluated a panel of sperm biomarkers that may affect the 39 motility and fertilizing ability of sperm of patients with severe asthenozoospermia. Since 40 reactive oxygen species (ROS) production is involved in the pathogenesis of such sperm 41 abnormalities, we determined the association between ROS production and sperm 42 abnormalities. High percentage of patients with severe asthenozoospermia showed 43 increased basal and stimulated ROS production. Moreover, these patients showed 44 increased mitochondrial DNA (mtDNA) copy number but decreased mtDNA integrity and 45 they were associated with elevated ROS levels. Furthermore, mitochondrial membrane 46 potential was also significantly decreased and again associated with high ROS production 47 in these patients. However, the rate of nuclear DNA fragmentation was increased only in 48 less than one-fifth of these patients. An important cohort of these patients showed multiple 49 identical biochemical, molecular, and genomic abnormalities, which are typical 50 manifestations of oxidative stress. The most frequent association was found in patients 51 with high ROS levels, increased mtDNA copy number and decreased integrity, and low 52 MMP. A smaller cohort of the aforementioned patients also showed nDNA fragmentation. 53 Therefore, patients with asthezoospermia likely present reduced fertilizing potential 54 because of such composed abnormalities.

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56 INTRODUCTION

57 Low sperm motility (asthenozoospermia) alone or in combination with other sperm 58 abnormalities is a frequent cause of infertility. Common causes of asthenozoospermia are 59 genital tract infections, varicocele, sperm antibody (ASA), metabolic diseases and tail 60 anatomic abnormalities. Most patients with asthenozoospermia are idiopathic. Cellular 61 energy for sperm motility and propulsion is produced through oxidative phosphorylation, in 62 the mitochondria, a major producer of ATP, through the electron transport chain (Bahr & 63 Engler 1970, St John *et al.* 2000). Treatment of sperm with extracellular ATP significantly 64 increases their fertilization potential (Rossato et al. 1999). This complex biochemical and 65 molecular mechanism is genetically controlled by mitochondrial DNA (mtDNA) and nuclear 66 DNA (nDNA) (Bruijn et al. 1981). Thus, in addition to other factors (Calogero et al. 1998, 67 Narisawa et al. 2002), genomic integrity of mtDNA and nDNA plays an important role in 68 maintaining good sperm motility. The mitochondria regulate also cell apoptosis by 69 releasing several apoptotic factors (Susin et al. 1999). Many infertile men have fragmented 70 nDNA (Varum et al. 2007).

71 Several studies support the importance of the mitochondria in maintaining sperm 72 quality and motility; in fact asthenozoospermia (Folgero et al. 1993) and 73 oligoasthenozoospermia (Lestienne et al. 1997) have been reported in patients with typical 74 mitochondrial diseases characterized by point mutations or multiple deletions in mtDNA. 75 Various large deletions in and fragmentation of mtDNA have been observed in sperm with 76 poor sperm quality (Kao S et al. 1995, Kao et al. 1998, Song & Lewis 2008). Moreover, 77 comparison of several polymorphic regions in mtDNA has shown an association between 78 mtDNA haplogroup and asthenozoospermia (Ruiz – Pesini et al. 2000). Additional studies 79 indicate that sperm in abnormal semen samples show quantitative alterations in mtDNA 80 and that sperm of infertile men show increased mtDNA content or copy number (May-

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81 Panloup et al. 2003, Song & Lewis 2008). Diez-Sanchez et al. (2003) showed a clear 82 difference in mtDNA copy number between progressively motile and non-progressively 83 motile sperm. These qualitative and quantitative alterations in abnormal sperm may be because of impaired mitochondrial maintenance or oxidative stress-induced deleterious 84 85 effects on mtDNA (May-Painloup et al. 2003, Shamsi et al. 2009, Venkatesh et al. 2009). 86 Since nuclear and mitochondrial gene products are dependent on each other, nDNA 87 fragmentation may be a more reliable predictor of impaired sperm motility (Muratori et al. 88 2000). Causes of nDNA damage are not completely understood. However, several studies 89 suggest that increased intracellular or extracellular reactive oxygen species (ROS) (Aitken 90 & Curry 2011) and the consequent oxidative stress play a key role in inducing nDNA 91 damage. Sperm contain several ROS substrates such as unsaturated fatty acids, DNA, 92 and proteins and possess limited endogenous antioxidant capacity (Alvarez et al. 1987, 93 Aitken et al. 1989). Therefore, sperm are highly susceptible to oxidative damage, which in 94 turn affects mtDNA and nDNA (Aitken & De Juliis 2010). In addition, loss of mitochondrial 95 membrane potential (MMP) and subsequent decrease in energy production may decrease 96 sperm motility (Marchetti et al. 2004), which are often associated with elevated ROS levels 97 (Wang *et al.* 2003).

98 Sperm can be affected by endogenous ROS production or by ROS formed in 99 leukocytes present in semen (Whittington & Ford 1999). Use of recently developed probes 100 against mitochondria-produced ROS has shown that mitochondria are the main source of 101 ROS in sperm (Koppers et al. 2008, Aitken et al. 2012). Once initiated, ROS production 102 becomes a self-perpetuating peroxidation mechanism (Aitken et al. 2012) by generating 103 peroxyl and lipid radicals that perpetuate the chain reaction of lipid peroxidation, a process 104 which is very harmful to sperm (Alvarez et al. 1987, Aitken & Curry 2011), at biochemical 105 and molecular levels (Agarwal & Allamanemi 2004) because it damages different

substrates, including permanent damage of the axoneme (de Lamirande & Gagnon 1992,
Hughes *et al.* 2009).

Therefore the present study evaluated a panel of sperm biomarkers that exert detrimental effects on sperm motility in men with severe asthenozoospermia and determined the association of ROS overproduction to these biofunctional sperm alterations. To this end, we performed biochemical, genomic, and molecular analyses of sperm collected from patients with high initial percentage of non-progressive motile sperm.

131 MATERIAL AND METHODS

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133 Chemicals and reagents

134 All chemicals used in this study were purchased from Sigma (Milano, Italy), unless 135 otherwise specified. Percoll was purchased from Codisan (Milano, Italy), and 5-amino-2,3-136 dihydro-1,4-phthalazinedione (luminol) and dimethyl sulfoxide (DMSO) were purchased 137 from Bouty (Milano, Italy). 12-myristate, 13-acetate phorbol ester (PMA) was purchased 138 from VWR International (Milano, Italy), and 5,5'.6,6'-tetrachloro-1,1',3,3'-tetraethyl 139 benzimidazolyl carbocyanine iodide (JC-1) dye was purchased from Space Import-Export 140 (Milano, Italy). Annexin V, PI, LPN DNA-Prep Reagent (L DNA-Pr), and Mebstain 141 Apoptosis (Meb-Ap) Kit were purchased from Beckman Coulter (Milano, Italy). 142 DNA isolation kit was purchased from Qiagen (Milano, Italy), and TOPO TA Cloning 143 (TOPOT-CI) Kit and AccuPrime Pfx (AcP-Pfx) DNA polymerase were purchased from 144 Invitrogen (Milano, Italy). iQ SYBR Green Kit was from Thermofisher (Milano, Italy).

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146 Preparation of human sperm

147 This study included 37 men recruited from couples who underwent semen analysis 148 at the Andrology Centre of Catania University (EAA Andrology Centre) as a part of their 149 fertility evaluation. As the study was intended to be performed in patients with a high 150 percentage sperm with low motility, semen samples were collected from patients whose 151 sperm showed arbitrary progressive motility (a + b ≤20%) and non-progressive motility 152 (c >50%). Patients included in the study were diagnosed with idiopathic 153 asthenozoospermia, clinical palpable varicocele, inflammation of the accessory sex 154 glands, or as overweight following physical examination and history taking. Smokers, 155 patients with known exposure to toxic chemicals, alcohol intake and/or drug abuse, 156 systemic diseases, and recent hormonal treatment were criteria of exclusion. In addition, 157 the study included 22 healthy men with normal sperm parameters (according to the WHO 158 2010 guidelines) whose fertility status was unknown and who volunteered to participate in 159 the study. Exclusion criteria for this group were cigarette smoking, history of 160 cryptorchidism and varicocele, known exposure to toxic chemicals, and presence of genital 161 inflammation. This study was approved by the Institutional Research Review Board of the 162 University of Catania Medical School, all subjects provided written informed consent. 163 Semen samples from men in both the study groups were collected in sterile plastic jars 164 through masturbation after 3-5 days of abstinence. Routine semen analysis was 165 performed within 1 h after ejaculation by using a light microscope to determine 166 conventional sperm parameters (WHO 2010). An aliquot of the semen sample was used 167 for evaluating ROS production. The remaining semen sample was purified by performing 168 Percoll density gradient centrifugation and was used for molecular and genomic analyses.

169 Purification of human spermatozoa was achieved using a 2-step discontinuous 170 Percoll gradient (90% / 45%) obtained by diluting isotonic Percoll (90 ml Percoll 171 supplemented with 10 ml of 10x Ham's F10 (WHO 2010) solution, 370 µl sodium lactate 172 syrup, 3 mg sodium pyruvate, 210 mg sodium hydrogen carbonate, and 100 mg polyvinyl 173 alcohol) with HEPES-buffered Biggers, Whitten, and Whittingham medium (BWW) 174 (Biggers et al. 1971), according to Mitchell et al. (2011). Next, up to 3 ml liquefied semen 175 was layered on top of each gradient and was centrifuged at 500xg for 30 min. Sperm pellet 176 obtained from the base of the high-density fraction of the gradient was recovered, washed 177 with 3 ml BWW and pelleted by centrifugation at 600xg for 10 min.

The final pellet was suspended in a low volume of BWW and was examined under a light microscope. Generally no round cells were found. However samples containing round cells or > 15% immotile sperms(d) were discarded.

181 Measurement of ROS production

182 Aliquots of 5-10x10⁶ sperm were washed with two volumes BWW and were 183 centrifuged at 300xg for 5 min. Seminal plasma was discarded. ROS production was 184 measured by performing a chemiluminescence assay, as described previously (D'Agata et 185 al. 1990). Briefly, 5 µl luminol, which was stored as a 20 mM stock solution in DMSO, and 186 8 µl horseradish peroxidase (1550 IU/ml in PBS), which was added to sensitize the assay 187 (Krausz et al. 1992), were added to 500 µl of the washed sperm suspension as probes. 188 Next, the sperm suspension was diluted with 500 µl BWW, and basal and stimulated ROS 189 production was determined by measuring chemiluminescence with Bioluminate LB 9500 T 190 luminometer (Berthold Technologies, Bad Wildbad, Germany) in an integrated mode for 10 191 min. Results are expressed as the number of photons counted per minute (cpm)/10 × 10⁶ 192 sperms.

193 Basal chemiluminescent signal (basal ROS) was monitored at 37°C until its 194 stabilization (approximately 5 -10 min). After the system returned to baseline, the sperm 195 suspension in the lumivial was stimulated with 2 µl formyl-leucyl-phenylalanine (FMLP), a 196 polymorphonuclear leukocyte-specific chemiluminescent probe (Krausz et al. 1992, Krausz 197 et al. 1994), and was monitored for additional 7 min to determine the magnitude of peak 198 obtained. After the signal returned to baseline, 4 μ l 10 μ M/l PMA was added to the sperm 199 suspension. PMA increases ROS production by stimulating kinase C in both leukocytes 200 and sperm (Ford 1990), resulting in a sustained increase in the chemiluminescent signal 201 (Krausz at al. 1994).

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203 Flow cytometric analysis

Flow cytometric analysis was performed using EPICS XL (Beckman Coulter), as reported previously (Perdichizzi *et al.* 2007). In all, 10.000 events were measured for each

sample at a flow rate of 200-300 events/s and were analyzed using SYSTEM II[™]
Software, 3.0 Version (Coulter Electronics, Milan, Italy).

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209 Determination of MMP

The lipophilic cationic fluorescent dye JC-1 was used to differentiate and label mitochondria with high and low membrane potential. Sperm with intact mitochondria show an intense red-orange fluorescence. In contrast, JC-1 treated sperm with low MMP form monomers that show green fluorescence (Troiano *et al.* 1998).

In the present study, MMP was determined by adjusting the density of the sperm suspension at $0.5-1 \times 10^6$ cells/ml with 500 µl phosphate buffer and by incubating the sperm with JC-1 in the dark at 37°C for 10-15 min. JC-1 was dissolved in DMSO to obtain 1 mg/ml stock solution. JC-1 (20 µg) was diluted in 480 µl PBS before adding it to the sperm suspension.

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220 Annexin V/PI assay

221 PS externalization was determined by staining sperm with FITC-labeled annexin V 222 and PI by using a commercial kit (Perdichizzi et al. 2007). Double staining allows the 223 distinction of (a) viable sperm (sperm not stained with annexin V and PI), (b) sperm in the 224 early stage of apoptosis (PS externalization) (sperm stained with annexin V but not with 225 PI), (c) sperm in the late phase of apoptosis (sperm stained with annexin V and PI), 226 and (d) necrotic sperm (sperm stained with PI but not with annexin V). 227 Briefly, an aliquot of the semen sample containing 0.5×10^6 sperm/ml was resuspended in 228 500 µl binding buffer, was labeled with 1 µl annexin V-FITC and 5 µl PI, was incubated in 229 the dark for 10-15 min, and was analyzed immediately. Signals were detected using FL-1 230 (FITC) and FL-3 (PI) detectors.

231 PI staining

The degree of chromatin compaction was evaluated using the sperm PI staining.
(Perdichizzi *et al.* 2007).

Briefly, an aliquot containing approximately 1×10^6 sperm/ml was incubated with 100 µl lysing and permeabilizing reagent in the dark at room temperature. After 10 min, 500 µl L DNA-Pr (containing PI,RNAse type A, NaN salts, and stabilizer) was added to the sperm suspension, and the suspension was incubated in the dark for 30 min.

238 Sperm with normal chromatin packaging emitted low PI fluorescence because less 239 amount of PI reached the DNA. In contrast, sperm containing endogenous nicks in DNA 240 emitted high fluorescence.

241

242 TUNEL assay

The evaluation of fragmentation of DNA was obtained through the Tunnel assay as previously reported (Perdichizzi *et al.* 2007). Briefly, the assay was conducted on aliquots of about 1×10^6 washed sperm, which were labeled using the Meb-Ap Kit. To obtain a negative control, deoxynucleotidyl tansferase was omitted from the reaction mixture, and positive control was obtained by pretreating the sperm with 1 µg/ml deoxyribonuclease I, RNAse-free at 37 °C for 60 min before labeling.

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250 Extraction of total DNA

DNA from the sperm samples of patients and controls was extracted using a DNA isolation kit, according to the manufacturer's instructions. Extracted DNA was quantified using NanoDrop 1000 spectrophotometer (Thermo Scientific, Euroclone, Milano, Italy) in triplicate.

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256 Long-range polymerase chain reaction for determining mtDNA integrity

Long-range polymerase chain reaction (long PCR) was performed to amplify approximately half of the mitochondrial genome (8.7 kb) by using AcP-Pfx DNA polymerase, which is inactive at ambient temperatures and is activated after initial denaturation to determine mtDNA integrity.

Long PCR was performed in a 50-μl reaction mixture containing 1 × buffer with dNTPs.

• forward primer (5'-AAGGATCCTCTAGAGCCCACTGTAAAG-3'),

• reverse primer (5'-TTGGATCCAGTGCATACCGCCAAAAG-3'),

• 2.5 U DNA polymerase,

• 200 ng sperm DNA.

Amplification conditions were as follows: initial denaturation at 95 °C for 2 min, followed by 25–35 cycles of denaturing (95 °C for 15 s), annealing (62 °C for 1 min), and extension step at 68 °C for 9 min. PCR products obtained were visualized by electrophoresis on 0.8% agarose gels. DNA extracted from sperm treated with H_2O_2 for 1 h at 37 °C was used as control. Results of long PCR showed that DNA amplification decreased after H_2O_2 treatment.

273

274 Determination of mtDNA copy number

Quantitative PCR (qPCR) was performed to determine the relative copy number of mtDNA, which was calculated using the copy number ratio of mitochondrial gene encoding 16S rRNA to nuclear gene encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (Song & Lewis 2008). To synthesize standard DNA, PCR was performed using 16S RNA primers under the following amplification conditions: the first cycle at 94 °C for 5 min; 30 cycles of denaturation at 94 °C for 1 min, annealing at 58 °C for 1 min, and extension at 72 °C for 1 min; and final extension at 72 °C for 10 min. Before cloning, PCR products obtained were electrophoresed on 1% agarose gel, which produced a single 150-bp band. The 150-bp fragment was cloned into the PCR 2.1-TOPO vector by using the TOPOT-CI Kit, was sequenced to confirm the accuracy of the inserted sequence, and was used as standard DNA for performing qPCR. Plasmid DNA obtained was quantified using NanoDrop 1000 spectrophotometer was diluted to obtain 1 × 10² to 1 × 10⁸ copies/µl, and was stored in a -80°C in a freezer.

288 The amount of mtDNA and GAPDH was determined using 2 primer 289 sets specific to the mitochondrial 16S rRNA gene and nuclear GAPDH. The mitochondrial 290 amplification reaction was performed in duplicate with 16S rRNA 291 5'-ACTTTGCAAGGAGAGCCAAA-3' (forward primer and reverse primer 292 5'-TGGACAACCAGCTATCACCA-3'). Nuclear GAPDH amplified was using 293 5'-GGATGATGTTCTGGAAGAGCC-3' forward primer and reverse primer 294 5'-AACAGCCTCAAGATCATCAGC-3'. Primers were included in triplicate along with 295 negative control samples and a range of standards. The qPCR was performed using ABI 296 7300 (Applied Biosystems, Milano, Italy) with iQ SYBR Green Kit, according to 297 manufacturer's instructions.

The SYBR green dye binds to double-stranded DNA but not to single-stranded DNA and can be used for monitoring DNA amplification during qPCR (10 ng template; initial denaturation at 95 °C for 5 min, followed by 40 cycles of denaturation at 95 °C for 10 s and annealing at 60 °C for 30 s). Moreover, the dye emits bright fluorescence upon binding to DNA. Melting curve analysis was performed to verify the accuracy and specificity of amplification.

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Statistical analysis

All the variables were initially tested using Kolmogorov-Smirnov test to determine data normality. Data of normally distributed variables were expressed as mean ± SD and those of non-normally distributed variables were expressed as median and 25-75 percentile. Groups were compared using unpaired Student's t-test and non-parametric test (Mann–Whitney U test) for normal and non-normal distribution, respectively. Correlation analysis between the study variables was performed using Spearman's non-parametric test with untransformed values. For all the statistical tests, differences with P <0.05 were considered significant. Difference in deletion frequency was determined using x^2 test. All analyses were performed using SAS statistical software package version 9.1 (SAS Institute Inc., Cary, NC, USA).

331 RESULTS

Median age of controls was 33.3 years (range, 20.1-40.7 years), which was not significantly different from that of patients (26.4 years [range, 22.9-38.1]). As expected, all the parameters of sperm from patients were significantly lower than those of sperm from healthy controls. However, sperm with normal morphology were comparable. Moreover, ejaculates of patients showed high leukocyte infiltration (P <0.0001; Table 1). In contrast, ejaculates of only 6 controls (27.2%) showed leukocyte contaminations (less than 1×10^{6} /ml).

339

340 Seminal ROS production

341 ROS production was measured using the total population of unfractionated cells to 342 determine the overall oxidative status of the ejaculate. Basal ROS production (in 58.3% 343 samples) and stimulated ROS production (in 70.8% and 83.3% samples treated with 344 FMLP and PMA, respectively) were significantly higher (P < 0.0001) in patients than in 345 controls (Fig.1). In all the patients with increased spontaneous, basal level of activity, 346 FMLP- and PMA-stimulated ROS production was higher than the basal ROS production. 347 Consistently, chemiluminescent signals after PMA stimulation were elevated significantly 348 over those after FMLP stimulation (P < 0.001). Significant correlation was observed 349 between basal and stimulated ROS production (r =0.44, P <0.03 and r =0.76, P <0.00001 350 for FMLP- and PMA-stimulated ROS, respectively) in semen samples of patients with 351 asthenozoospermia. Furthermore, FMLP- (r =0.5, P <0.01) and PMA-stimulated ROS 352 production (r = 0.46, P < 0.02) but not basal ROS production were correlated with leukocyte 353 concentration in the semen samples. Moreover, strong correlation was observed between 354 PMA- and FMLP-stimulated ROS production (r =0.89, P <0.000002), but in three cases 355 production was stimulated by the addition of PMA only, with the response being lower than that with FLMP. However, no correlation was observed between basal as well as
 stimulated ROS production and sperm parameters or between ROS production and
 mtDNA copy number or flow cytometric sperm variables, except DNA fragmentation.

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360 Integrity of mtDNA in sperm of patients with asthenozoospermia and controls

361 Long PCR amplified an 8.7-kb fragment from the 16-kb mitochondrial genome in all 362 the samples. This 8.7-kb fragment contains several genes encoding subunits of energetic 363 complexes as well as the common deletion types 4.3 kb and 7.4 kb in sperm (Song & 364 Lewis 2008). Fig. 2 shows the representative products of long PCR from 2 365 normozoospermic controls and 2 patients. The high intensity of the full-length band 366 indicated the presence of normal intact mtDNA (Fig.2, lanes 1 and 2). In contrast, the low 367 intensity of full-length mtDNA band indicated poor mtDNA integrity because of low amount 368 of mtDNA, fragmentations and deletions. The results of long PCR showed differences in 369 mtDNA integrity in sperm of controls and patients. Normozoospermic controls showed high 370 intensity of full length band and did not contain deletions in mtDNA, indicating normal 371 intact mtDNA. In contrast, 36 (97.2%) patients showed multiple deletions in mtDNA (Fig.2, 372 lanes 3 and 4). This difference in the frequency of deletions in mtDNA between patients 373 and controls was highly significant (P < 0.0001). Only 1 patient with asthenozoospermia 374 had intact mtDNA; however, this patient showed high PS externalization and had abnormal 375 chromatin compactness values (results not shown). Moreover, this patient had the highest 376 mtDNA copy number and showed the highest PMA-stimulated ROS production. In 377 addition, this patient showed low progressive sperm motility of 12%, with 1 million 378 leukocytes in the ejaculate. Furthermore, abnormal mtDNA was associated with high ROS 379 production in sperm samples of 83.4% patients.

380

381 Alterations in mtDNA copy number in sperm of patients and controls

The median mtDNA copy number in sperm of patients with asthenozoospermia was 14.8 (percentile, 5.4-29.68; range, 1-61), which was significantly higher than that in controls (median, 5.75 [percentile, 4.72-7.05; range, 1.1-10]; P <0.006). This increase in mtDNA copy number was observed in 45.8% patients. Moreover, patients with increased mtDNA copy number showed high ROS production.

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388 Integrity of nDNA

Integrity of nDNA, which was measured using the TUNEL assay, was not significantly different between the 2 study populations (median, 2.4% [percentile, 1.4-3.2; range 0.5-4.0] vs. 2.0% [percentile, 0.9–5.0; range 0.6-34.6] in controls and patients, respectively; Table 1). In all, 16.6% patients showed very high rate of nDNA fragmentation (>10%). However, the rates of nDNA fragmentation in the remaining patients were within normal limits or between 4%–5.1%. Moreover, the rate of nDNA fragmentation was correlated with basal ROS production in patients (r =0.48, P <0.016).

396

397 MMP

The sperm of only 8 (21.6%) patients showed normal (high) MMP compared with that of controls (mean, 55.3% \pm 21.7 vs. 86.1% \pm 7.9; P <0.0001). Low MMP was associated with high ROS production in a high percentage (78.9%) of patients.

401

402 Other flow cytometric parameters

403 No significant differences were observed in percentage viability, PS externalization,
404 late apoptosis, necrosis, or abnormal chromatin compactness between the sperm of the 2
405 study populations (Table 1). Interestingly, a negative correlation was observed between

406 alive sperm and PS externalization (r = -0.555, P <0.005), late apoptosis (r = -0.666, P 407 <0.0003) and necrotic cell numbers (r = -0.446, P <0.028). In contrast, a positive 408 correlation was observed between PS externalization and late apoptosis (r =0.555, 409 P <0.0048).

410

411 Subpopulations of patients with multiple abnormalities in sperm

Next, we determined whether patients with asthenozoospermia showing abnormal ROS in their ejaculates had multiple identical ROS-associated abnormalities in their sperm. Almost all patients showing low MMP and high ROS production had deletions in the mtDNA of their sperm, and almost half of these patients (44.6%) showed increased mtDNA copy number (cohort a). Moreover, 12.6% of these patients also showed high rate of nDNA fragmentation (>10%) (cohort b).

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431 DISCUSSION

432 The results of this study provide further evidence that severe asthenozoospermia is 433 associated with various abnormalities in sperm. The sperm of patients with 434 asthenozoospermia showed increased ROS production, mitochondrial and nuclear 435 genomic alterations, and multiple molecular abnormalities. However, the frequency of 436 abnormalities in these different nonconventional biofunctional sperm parameters varied in 437 patients with asthenozoospermia (Fig. 3).

438 We found that ejaculates of 58.3%, 70.8%, and 83.3% patients, showed increased 439 basal, FMLP-stimulated, and PMA-stimulated ROS production respectively, compared to 440 controls. This result indicated that ROS was overproduced under basal condition 441 irrespective of its source, i.e., leukocytes or sperm, which was consistent with the results 442 of Whittington & Ford (1999). As from leukocyte specific FMLP agonist stimulation, 443 leukocytes, were the main ROS producer in semen samples from a little more than two-444 thirds of the patients, as elsewhere reported (Krausz et al. 1992, Whittington & Ford 1999). 445 However, the lack of correlation between ROS levels and sperm motility, a major target of 446 ROS, is unclear. Moreover, the results of previous studies are inconsistent in this regard 447 (Whittington et al. 1999; Kao et al. 2008). Although PMA is the most powerful stimulant for 448 oxidant stimulation by human sperm (Krausz et al. 1992), ROS production in patients after 449 PMA can not be specifically compartmentalized to some extent to leukocytes or sperm. 450 since the probe is a stimulus for both leukocytes and sperm. However, consistently PMA-451 stimulated ROS production were elevated significantly over those after FMLP, suggesting 452 some amount of ROS production by sperm.

In the present study, we observed that almost 50% patients with severe asthenozoospermia showed significantly increased mtDNA copy number, which was consistent with the results of previous studies that non-progressively motile sperm show

456 increased mtDNA copy number (May-Panloup et al. 2003, Amaral et al. 2007, Song & 457 Lewis 2008). Recent studies have shown a negative correlation between mtDNA copy 458 number and sperm motility in men with varicocele; moreover, varicocele correction 459 improves sperm motility and decreases mtDNA copy number in these patients (Gabriel et 460 al. 2012). Furthermore, mtDNA copy number increases in men living in hypoxic conditions 461 at high altitudes for 1 year compared with that in men living in plains (Luo et al. 2011). This 462 increase in mtDNA copy number might be induced by elevated oxidative stress (Lee et al. 463 2000, Liu *et al.* 2003).

464 Our results showed decreased mtDNA integrity in almost all sperm samples from 465 patients with asthenozoospermia. These mitochondrial genomic alterations are hallmarks 466 of spermatogenetic dysfunction (Hecht & Liem 1984, May-Panloup et al. 2003, Song & 467 Lewis 2008) and severely alter mitochondrial function in abnormal sperm. Genomic alterations were also observed in nDNA; however, the frequency of alterations in 468 469 nDNA was lower than that in mtDNA. The rate of nDNA fragmentation was not 470 significantly different between controls and patients with asthenozoospermia. However, a 471 small percentage of patients with asthenozoospermia showed high rate of nDNA 472 fragmentation (>10%). Furthermore, nDNA fragmentation was correlated with basal ROS 473 production, which was consistent with what was previously reported (Aitken et al. 2010). 474 This finding was also consistent with the notion that nDNA fragmentation is often 475 associated with oxidative stress (De Iuliis et al. 2009). Oxidative stress or ROS production 476 in the mitochondria induces breaks in nDNA (Wang et al. 2003, Aitken & De Iuliis 2010). 477 However, mtDNA is more susceptible to the harmful effects of excess ROS production 478 than nDNA (Yakes et al. 1997, Sawyer et al. 2003). This may be one of the reasons for 479 the higher incidence of abnormalities in mtDNA than in nDNA in patients with 480 asthenozoospermia. Thus, mitochondrial dysfunction may be involved in the pathogenesis

of asthenozoospermia in these men. Men with multiple mutations and large deletions in
mtDNA showed severe phenotypic defect (Kao *et al.* 1995, St John *et al.* 1997, Salehi *et al.* 2006).

484 A significantly lower number of sperm of patients with severe asthenozoospermia 485 had normal (high) MMP values as further expression of mitochondrial dysfunction. In fact, 486 only one-fifth of patients with asthenozoospermia had normal MMP values. MMP is a good 487 predictor of sperm quality. Such cell abnormality will result in less energy production for 488 sperm function and motility. Sperm with high MMP values have intact acrosome, high 489 fertilizing capacity, and normal motility and morphology. In contrast, sperm with low MMP 490 values are of low quality and are associated with low IVF rates (Kasai et al. 2002, 491 Marchetti et al. 2004). This is in turn correlated with ROS production (Wang et al. 2003). 492 Dysruption of MMP may occur during early stages of apoptosis in germ cells (Erkkilä et al. 493 1999) and thus before the induction of nDNA damage in sperm.

494 Other flow cytometric parameters were not significantly different between patients 495 with asthenozoospermia and normozoospermic controls. Sperm vitality is a good predictor 496 of gamete quality. An inverse correlation was observed between sperm viability and signs 497 of cell apoptosis, such as PS externalization, early and late stages of apoptosis, necrosis, 498 and chromatin compactness. This has important clinical implications in that the selection of 499 good guality sperm for ICSI conventionally focuses on mobile and consequently viable 500 sperm. Furthermore, positive correlation was observed between PS externalization and 501 late apoptosis, indicating that PS externalization promoted the entry of sperm into the 502 senescence phase, followed by apoptosis and death.

503 These abnormalities in sperm of patients with severe asthenozoospermia are typical 504 manifestations of ROS- induced damage and are based on a continuum of decreased 505 sperm motility; decreased MMP; decreased mtDNA integrity; increased mtDNA copy

506 number; PS externalization; caspase activation; oxidative nDNA damage, including nDNA 507 fragmentation; late apoptosis; and death. The final damaging consequences on sperm of 508 such exposure depend on the capacity of sperm of these men to withstand oxidative 509 stressor, possibly compounded by a compromised total antioxidant capacity in their 510 seminal fluid (Pasqualotto et al. 2000, Kao et al. 2008). ROS-induced cellular damage also 511 depends on whether ROS production is extracellular (leukocytes) or intracellular (sperm). 512 Extracellular ROS production exerts less damage on nDNA (Henkel et al. 2005). 513 In addition, time and site of ROS exposure, oxidants produced by morphologically poor 514 sperm, and other round cells are also important determinants of the degree of severity of 515 ROS-induced cellular damage (Henkel et al. 2005). So as the generation of these reactive 516 free radicals overwhelms the defense system, this induces oxidative stress, which is 517 characterized by a cascade of cellular damage (Aitken et al. 2010). This may be the 518 reason why only a subpopulation of patients with asthenozoospermia showed increased 519 nDNA fragmentation, which is caused by prolonged exposure to ROS (Aitken et al. 2010). 520 Basal ROS status in the ejaculates of our patients correlates with nDNA damage 521 observed, thus supporting the role of ROS in inducing nDNA alterations. However, these 522 multiple abnormalities observed in sperm of patients with asthenozoospermia may also 523 result from deranged spermatogenesis and then aborted apoptosis (Sakkas et al. 2003).

The general findings of this study are consistent with the hypothesis that sperm of patients with asthenozoospermia have several biochemical, molecular, genomic, and functional abnormalities, which may decrease their fertilization potential (Tesarik *et al.* 2002, Zidi-Iran I *et al.* 2016). This was also observed in patients with asthenozoospermia included in the present study. During follow-up, sperm of 2 patients in subgroup b could not lead to pregnancy after as many as 3 ICSI attempts. In contrast, sperm of 1 patient who had low MMP as the only abnormality led to pregnancy during the first ICSI attempt

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531 (results not shown). We observed that patients with this pathological condition could be 532 subgrouped according to the presence of only 1 or more cellular abnormalities, with high 533 ROS production, increased mtDNA deletions and copy number, and reduced MMP being 534 the most common associated abnormalities. Rate of nDNA fragmentation was high only in 535 less than one-fifth of the patients with asthenozoospermia. As time elapses and the cause 536 persists, the current picture might get worse in the absence of any treatment. No robust 537 clinical implications can be drawn from the results of the present study because the study 538 included limited number of patients. However, the present findings strengthen the 539 association of high frequency biochemical and biofunctional sperm alterations in patients 540 with severe asthenozoospermia, and emphasize evaluating male factor by sperm function 541 tests to determine hidden anomalies which may better define the fertility status in vivo and 542 in vitro.

543 To our knowledge, this is the first study to examine, all together, biochemical, 544 functional, molecular, and genomic abnormalities in sperm of patients with asthenozoospermia. These abnormalities make up an evolutionary spectrum of 545 546 progressive alterations in presence of oxidative free radical offense, whose final result will 547 be either survival or senescence and then death, eventually going through several 548 intermediate steps. Our results further indicate that sperm of infertile patients with severe 549 asthenozoospermia who are candidates for ICSI may harbor cellular abnormalities, which 550 may jeopardize oocyte fertilization and embryonic development depending on the severity 551 of these abnormalities. 552 553

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556	Authors' roles
557	R.D. designed the study, analyzed and interpreted the data, and drafted the
558	manuscript. O.B., G.R., P.A., F.M.P., and N.B. performed some analyses. O.B. obtained
559	the data for her Ph.D. thesis. E.V. performed clinical evaluation of patients and designed
560	the study. R.C. and G.S. organized and revised the manuscript. F.G.V collaborated in the
561	drafting of the manuscript. E.V. and R.D contributed equally in the study.
562	
563	Declaration of interest
564	The authors declare that they do not have any conflicts of interest that could
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FIGURE LEGENDS

Figure 1. Basal, FMLP-stimulated, and PMA-stimulated ROS production in controls and patients (open bars) with asthenozoospermia. Bars represent median and the 25th and 75th percentiles. Vertical lines represent range. Vertical axis is in logarithmic scale. Bars in the right vertical axis indicate medians in patients.

Figure 2. Four representative products of long PCR analysis of human sperm for determining mtDNA integrity. Lanes 1 and 2: results of long PCR of mtDNA of sperm from 2 controls. Lanes 3 and 4: results of long PCR of mtDNA of sperm from 2 representative patients with asthenozoospermia. Lanes 1 and 2 show a high-intensity 8.7-kb band, which represents full-length wild-type mtDNA, indicating the presence of normal intact mtDNA. Lanes 3 and 4 show low-intensity 8.7-kb bands, indicating the presence of low amount of full-length mtDNA, and smaller bands, indicating deletions in mtDNA. HindIII/*A* was used as a size marker.

Figure 3. Frequency (%) of abnormal biochemical, genomic, and cytofluorimetric parameters in sperm of patients with asthenozoospermia.

	CONTROLS	PATIENTS	p-VALUE
SEMEN VARIABLES	(n = 22)	(n = 37)	
CYTOLOGICAL			
Concentration (×10 ⁶ /ml)*	119.3 ± 49	69 ± 33.6	p < 0.0002
	(39–235)	(20–150)	
Total sperm number (×10 ⁶)*	439.3 ± 196.5	214.2 ± 108.8	p < 0.0001
	(126–750)	(60–440)	
Progressive motility (%)	47.4 ± 9.1	11.8 ± 4.8	p < 0.0001
$(a + b)^*$	(30–68)	(2–20)	
Nonprogressive motility (%)	22.8 ± 11.7	61.5 ± 6.5	p < 0.0001
(c)*	(5–46)	(52–72)	1
Non-motile sperm (%)	30.2 ± 8.9	26.6 ± 6.5	p < 0.12
(d)*	(14-48)	(16-42)	r
Normal morphology (%)*	21.2 ± 5.4	19.8 ± 7.8	p < 0.50
	(10–32)	(8–40)	p 0.00
Leukocytes (×10 ⁶ /ml) **	0 (0-0.4)	1 (0.7–1.5)	p < 0.0001
	0-0.9	0.3–7	-
Flow cytometry			
Viable spermatozoa*	73.5 ± 7.8	66.2 ± 19.9	p < 0.11
	60.2-86.1	20.7-93.1	1
Spermatozoa with PS	1.9 (1.2–2.6)	3.2 (1.3-4.9)	p < 0.13
externalization (%)**	0.04–13.8	0.12-40.3	
Spermatozoa in late apoptosis	6.0 (2.0–7.8)	7.1 (4.4–12.6)	p < 0.23
(%) ^{**}	0.1–14.7	0.1–32.0	
Necrotic spermatozoa (%)**	16.0 (12.2–23.4)	13.7 (6.3–20.5)	p < 0.39
	2.2-30.4	2.2–54.7	
Spermatozoa with DNA	2.4 (1.4–3.2) 0.5–4.0	2.0 (0.9–5.0) 0.6–34.6	p < 0.6
fragmentation (%)**	0.3-4.0	0.0-54.0	
Spermatozoa with high	86.1±7.9	55.3 ± 21.7	p < 0.0001
(normal) MMP values (%)*	72.2–97.8	15.5–95.8	
Spermatozoa with abnormal	15.4 (11.4–17.8)	15.2 (11.4–21)	p < 0.57
chromatin compactness (%)**	8.4–18.9	4.3-39.3	

Values expressed as mean ± SD, with range in parentheses
Values expressed median (25%–75%), with range in the second line

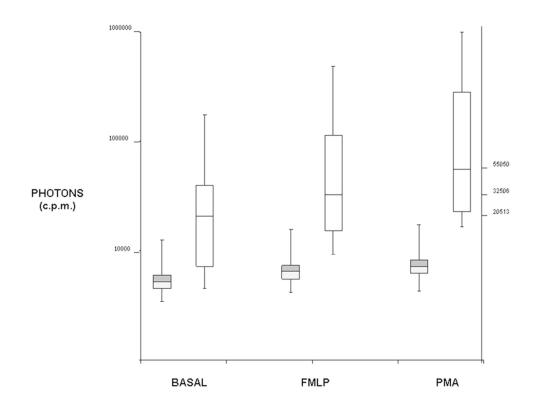
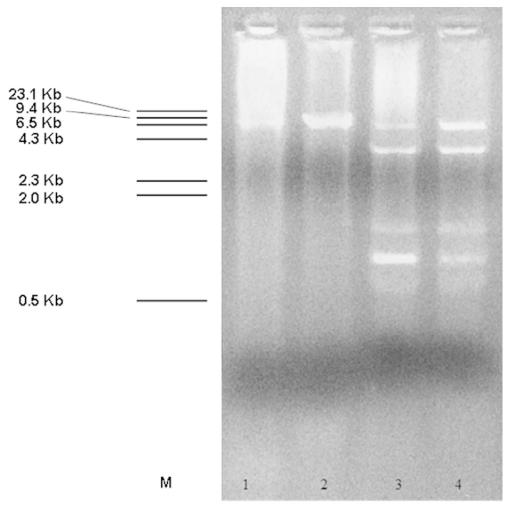


Figure 1 38x29mm (600 x 600 DPI)



1-2 NORMAL SAMPLES3-4 ASTENOZOOSPERMIC SAMPLESM λ DNA /Hind III

Figure 2

114x131mm (300 x 300 DPI)

