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Additional Information

1	Transcript levels of the soluble sperm factor protein phospholipase C zeta $f 1$
2	(PLCζ1) increase through induced spermatogenesis in European eel
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38 Abstract

Activation at fertilization of the vertebrate egg is triggered by Ca^{2+} waves. Recent studies suggest the phospholipase C zeta (PLC ζ), a sperm-specific protein, triggers egg activation by an IP3-mediated Ca^{2+} release and allow Ca^{2+} waves at fertilization.

In the present study we cloned, characterized, and phylogenetically positioned the European eel PLCζ (PLCζ1). It is 1521bp long, with 10 exons encoding an open reading frame of 506 amino acids. The amino acid sequence contains an EF-hand domain, X and Y catalytic domains, and a carboxy-terminal C2 domain, all typical of other PLCζ orthologous. The sequence is truncated not only at the Nterminus of the EF-hand domain, as in all teleost PLCζ, but also in the C-terminal region of the Xdomain and in a large part of the N-terminal X/Y linker region.

48 The tissue distribution was studied, and the gene expression was determined in testis during induced sexual maturation at three different thermal regimes. Also, brain and pituitary expression were studied 49 through sex maturation at constant temperature. $plc\zeta l$ was expressed in brain of male and female, in 50 51 testis but not in ovaries. By first time in vertebrates, it is reported $plc\zeta l$ expression in the pituitary gland. Testis $plc\zeta l$ expression increased through spermatogenesis under all the thermal regimes, but 52 being significantly elevated at lower temperatures. It was very low when testis contained only 53 spermatogonia or spermatocytes, while maximum expression was found during spermiogenesis. These 54 results support the hypothesis for an eel sperm-specific PLC(1 inducing egg activation, similarly to 55 mammals and some teleosts, but different from some other teleost species, which express this protein 56 in ovaries, but not in testes. 57

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66 Keywords:

67 Teleost, Reproduction, Fertilization, Spermatozoa, Anguilla anguilla

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69 **1. Introduction**

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Sperm fusion with the egg induces egg activation in all animals studied so far through a rise in 71 intracellular Ca²⁺ (Stricker, 1999; Tarin, 2000; Kashir et al., 2010; Horner and Wolfner, 2008a). Three 72 models have been proposed for mechanisms by which fertilization-induced Ca²⁺ waves are initiated: 73 a) Ca^{2+} bolus/conduit (Jaffe, 1983, 1991), where the sperm trigger the entering of extracellular Ca^{2+} 74 into the oocyte; b) membrane receptor (Jaffe, 1990; Evans and Kopf, 1998), with an intracellular Ca²⁺ 75 release provoked by the binding of an oocyte surface receptor with a sperm ligand; or c) a soluble 76 77 sperm factor (Swann et al., 2006; Parrington et al., 2007; Saunders et al., 2007) released into the oocyte after gamete fusion, triggering egg activation. This sperm factor corresponds to a sperm-78 specific phospholipase C (PLC) called PLCζ (Swann and Lai, 2013; Ito et al., 2011). After 79 80 fertilization, PLC⁽ induces a reaction chain by cleaving phosphatidylinositol 4,5-bisphosphate (PIP2) into inositol 1,4,5-trisphosphate (IP3) and diacylglycerol (DAG) (Igarashi et al., 2007; Miao and 81 Williams, 2012). These two metabolites, in turn, cause IP3-mediated Ca²⁺ release from the 82 endoplasmic reticulum, and the activation of such targets as DAG-sensitive protein kinase Cs (PKCs) 83 (Miyazaki et al., 1993; Saunders et al., 2002; Swann and Yu, 2008; Yu et al., 2008). 84

During the last ten years, several studies have demonstrated the importance of the soluble sperm 85 factor to allow Ca^{2+} waves at fertilization. Injection of recombinant PLC ζ cRNA (Saunders et al., 86 2002) or protein (Kouchi et al., 2004) into mouse eggs leads to Ca²⁺ oscillations at fertilization. 87 88 Saunders et al. (2002) showed that when endogenous PLC ζ was removed by immunodepletion, mouse sperm protein extracts lost their ability to release Ca²⁺. Moreover, *in vitro* fertilization of mouse eggs 89 with sperm from transgenic mice expressing lower amounts of PLCζ (due to a short hairpin RNAs 90 targeting PLC ζ) induced Ca²⁺ oscillations that ended prematurely, negatively affecting egg activation 91 and embryonic development (Knott et al., 2005). Furthermore, infertile men whose sperm failed in 92 egg activation showed abnormal expression and localization of PLCζ in the sperm (Yoon et al., 2008; 93 Heytens et al., 2009). Until now, mammalian PLCζ orthologues have been reported in mice, monkeys, 94

humans, boars, hamsters, and bulls (Cox et al., 2002; Saunders et al., 2002; Yoneda et al., 2006;
Young et al., 2009; Cooney et al., 2010). In non-mammals, PLCζ orthologues were reported in the
chicken (Coward et al., 2005), medaka (Ito et al., 2008), quail (Mizushima et al., 2009) and in two
pufferfish species *Takifugu rubripes* (Fugu) and *Tetraodon nigroviridis* (Tetraodon) (Coward et al.,
2011). In these non-mammalian species, like chicken or medaka, PLCζ mRNA is expressed in the
testis, in line with the situation in mammals. In contrast, in two pufferfish species, *plcζ1* is expressed
in the ovary, but not in the testis (Coward et al., 2011).

Due to its unique life cycle and its phylogenetical position, the European eel (Anguilla anguilla) is a 102 103 particularly interesting model to investigate the regulatory mechanisms of reproductive physiology and for providing insights into ancestral regulatory functions in teleosts. Prepubertal silver eels 104 105 migrate across the Atlantic Ocean to reach their probable spawning area in the Sargasso Sea (Tesch, 106 1977). Gonadal development and maturation probably takes place during the supposedly 6-7 month migration period, at low temperature, whereas the spawning takes place at high temperatures, 107 108 considered to be around 20 °C (Boëtius and Boëtius, 1967, 1980). However, as detailed information 109 from the field is still lacking, it is difficult to simulate the variable environmental factors which would occur during the migration (temperature, photoperiod, pressure, etc). That is why, in captivity, silver 110 111 eels are blocked in a pre-pubertal stage (Dufour et al., 2003; Pasqualini et al., 2004; Vidal et al., 2004) and must receive a long-term hormonal treatment to induce sexual maturation and spermiation 112 (Boëtius and Boëtius, 1967; Ohta et al., 1996, 1997; Asturiano et al., 2005; Huang et al., 2009; Pérez 113 et al., 2000; Gallego et al., 2012). 114

In this study, we characterized and cloned the Anguilla anguilla plc $\zeta 1$ mRNA, analysed the structure 115 116 and investigated the position of this protein among vertebrates by phylogenetic analyses, studied the tissue distribution of this gene and finally, for the first time in teleost, we studied the expression 117 profile of $plc\zeta 1$ in the brain and gonad through spermatogenesis. The impact of water temperature on 118 119 the maturation process of European eel has been highlighted in females (Pérez et al., 2011; Mazzeo et al., 2014) and males (Gallego et al., 2012, 2014; Baeza et al., 2014), and in order to simulate the 120 natural conditions during the reproductive migration and testing its potential effect on $plc\zeta l$ 121 expression, three different thermal regimes were tested for the gene expression profile experiments, 122

two variable regimes (changing gradually from 10 to 20 $^{\circ}$ C or from 15 to 20 $^{\circ}$ C), and one constant regime (20 $^{\circ}$ C).

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126 **2. Material and methods**

127 **2.1.** Fish maintenance, hormonal and thermic treatments, and sampling

Three hundred and seventeen male European eels (mean body weight 100 ± 2 g) from the fish farm Valenciana de Acuicultura, S.A. (Puzol, Valencia; East coast of Spain) were hormonally matured at the Aquaculture Laboratory at the Polytechnic University of Valencia. They were randomly distributed and kept in six 200-L fiberglass tanks (approximately 50 males per aquaria, 2 aquaria per treatment) equipped with separate recirculation systems, thermostats/coolers, and covered to maintain constant shadow.

The fish were gradually acclimatized for one week to seawater $(37\pm0.3\%)$ of salinity) and the water temperature was kept at 20 °C or changed to 15°C in one week or to 10°C in two weeks, depending on thermal groups. Starting three weeks after arrival to the Aquaculture Laboratory, the eels were treated with weekly intraperitoneal injections of human chorionic gonadotropin (hCG, Profasi®, Serono, Italy); 1.5 IU g⁻¹ fish; during 13 weeks to induce maturation and spermiation, as previously described by Perez et al. (2000).

During the experiment, the animals were maintained in three thermal regimes (2 aquaria per treatment): T10-T20: 10 °C (first 5 weeks, with one week of temperature acclimation), 15 °C (next 3 weeks) and 20 °C (last 6 weeks); T15-T20: 15 °C (first 6 weeks, with two weeks of temperature acclimation) and 20 °C (last 9 weeks); and T20: 20 °C during the whole experimental period. These thermal regimes were previously described by Gallego et al. (2012).

Groups of 5-8 eels per treatment were anaesthetized with benzocaine (60 ppm) and sacrificed by decapitation each week along the hormonal treatment. Morphometric parameters such as total body, gonad weights were recorded to calculate the gonadosomatic index (GSI = (gonad weight/total body weight)*100) for each fish (Pankhurst, 1982). Furthermore, testicular tissue samples were fixed in 10% formalin buffered at pH 7.4 for histological processing and subsequent determination of maturational status. Samples of pituitary, testis, liver, heart, gill, muscle, spleen, fins, and kidney were collected for analyses of gene expression levels by qPCR. Brains were dissected into five parts:
olfactory bulbs, telencephalon, mes-/di-encephalon, cerebellum, and medulla oblongata. All the
samples were stored in 0.5 ml of RNAlater (Ambion Inc., Huntingdon, UK) at -20 °C until extraction
of total RNA (Peñaranda et al., 2010).

Because eels stop feeding at the silver stage and throughout sexual maturation, the fish were not fed during the experiment and were handled in accordance with the European Union regulations concerning the protection of experimental animals (Dir 86/609/EEC).

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159 2.2. Gonadal histology

Fixed testis samples were dehydrated in ethanol and embedded in paraffin. Sections of 5-10 µm 160 161 thickness were cut with a Shandom Hypercut manual microtome and stained with haematoxylin and eosin. Slides were observed with a Nikon Eclipse E-400 microscope, and pictures were taken with a 162 Nikon DS-5M camera attached to the microscope. Stages of spermatogenesis were determined 163 164 according to the most advanced germ cell type present and their relative abundance, degree of development of the seminal tubules. GSI and sperm production by the male in the same week of the 165 sacrifice. Stage 1 Spermatogonia (SPG): dominance of spermatogonia, in some cases, a few 166 167 spermatocytes were present in low number, mean GSI = 0.08 (0.0-0.36); Stage 2 Spermatocytes (SPC): spermatocytes were present in proportion \geq 50% with spermatogonia, in some cases appeared 168 low number of spermatids, mean GSI = 0.72 (0.27-1.54); Stage 3 spermatids (SD): spermatids were 169 the dominant germ cell, some sperm cells can appear, mean GSI = 3.28; and Stage 4 spermatozoa 170 (SZ): spermatozoa was the dominant germ cell, mean GSI =7.35 (3.41-12.8) (Fig. 1). 171

172

2.3. Isolation of PLCζ sequence

174 **2.3.1. European eel genome database analysis.**

The TBLASTN algorithm of the CLC DNA Workbench software (CLC bio, Aarhus, Denmark) was
used to retrieve the genomic sequence of the PLCζ from the European and Japanese eel genomes
(Henkel et al., 2012a, Henkel et al., 2012b)

Exons and splice junctions were predicted using the empirical nucleotidic splicing signatures, i.e.: introns begin with "GT" and end with "AG". The peptidic sequences of *Tetraodon nigroviridis*

180 PLCζ1 sequence (Accession: HQ185299. GI: 322510422. 1,889 bp mRNA) were used as query.

181 Percentage of European eel PLCζ1 identity with other osteichtian PLCζ sequences was calculated

182 with Secuences Identites And Similarities (SIAS) server (imed.med.ucm.es/Tools/sias.html)

183

184 **2.3.2. Partial cloning of the PLCZ1 gene**

cDNA was generated using 1 µg of total RNA. A mixture of cDNA from different tissues of female 185 186 silver eels were used as template for amplification of PLCZ. Partial PLCZ cDNA was amplified by PCR using specific primers which were designed based on the predicted PLC sequence of European 187 188 eel using Primer3 Software (Whitehead Institute/Massachusetts Institute of Technology, Boston, MA): PLCZ1fw1: GGCTTCCTCCGGTACATGGA; PLCζ1rv1: TGTAGTTGGAGGACAGCGTGC; 189 PLCZ1fw2: AGATTCATCAGCAGGATCTATCC; PLC(1rv2: TACTGGCCCATGAAGTCGTT. 190 191 PCR amplification was run in a Hybaid PCR express, using 25 µl of reaction mixture containing 1x PCR buffer (Invitrogen), 200 µM dNTPs (Invitrogen), 0.1 IU of Taq DNA polymerase (Invitrogen), 192 500 nM of each primer and 1 µl of cDNA template. PCR products were visualized in 2% agarose gel 193 194 stained with SYBR Safe DNA gel Stain (Invitrogen) and bands of expected size were purified using Qiaquick Gel Extraction kit (Qiagen) and ligated into the pGEM-T easy vector (Promega, WI, USA). 195 Cloning was performed in competent E. coli JM109 cells (Promega). Positive colonies were isolated 196 and plasmids extracted by Qiagen Plasmid Mini Kit (Qiagen). Plasmids with insert were sent to 197 Eurofins Genomics (Germany) for sequencing. 198

199

200 2.3.3. Phylogenetic analysis

Amino-acid sequences of known or predicted sequences of gene coding for the PLCζ from 14 species
retrieved from NCBI or ENSEMBL were first aligned using ClustalW (Thompson et al., 1994), then
manually adjusted. Human, *Homo sapiens*, and mouse, *Mus musculus* PLCβ1 were used as outgroup.
The JTT (Jones, Taylor and Thornton) protein substitution matrix of the resulting alignment was
determined using ProTest software (Abascal et al., 2005). Phylogenetic analysis of the PLCζ sequence

alignment was performed using the maximum likelihood method (PhyML software, Stamatakis et Ott,

207 2008), with 1000 bootstrap replicates.

208

209 2.4. Gene expression analyses by quantitative real-time PCR

210 **2.4.1. Primers and reference gene**

211 Acidic ribosomal phosphoprotein P0 (ARP): ARPfw: GTG CCA GCT CAG AAC ACT G; ARPrv: 212 ACA TCG CTC AAG ACT TCA ATG G (Aroua et al., 2007; Weltzien et al., 2006) was used as reference gene in the quantitative real-time Reverse Transcriptase-Polymerase chain reaction (qPCR) 213 214 because its mRNA expression has been shown to be stable during experimental maturation (Weltzien et al., 2005). The qPCR expression stability of the reference gene was determined using the 215 216 BestKeeper program (Pfaffl et al., 2004), reporting a standard deviation (SD [±Cq]) lower than 1. In the testis, T10-T20: SD= 0.79; T15-T20: SD= 0.97; T20: SD= 0.79; p<0.05 with a Cq geometric 217 mean of T10-T20: 24.3±1.73; T15-T20: 24.37±1.96; T20: 25.17±1.73; in the brain and pituitary 218 219 olfactory bulb: SD= 0.85; telencephalon: SD= 0.56; mes-/di-encephalon: SD= 0.53, pituitary: SD= 220 0.77; p<0.05 and a Cq geometric mean of olfactory bulb: 23.74±1. 8; telencephalon: 22.43±1.48; mes-/di-encephalon: 22.17±1.44; pituitary: 22.77±1.71. The BestKeeper calculated variations in the 221 222 reference gene are based on the arithmetic mean of the Cq values. Genes with a SD value higher than 1 are defined as unstable. European eel PLCZ specific qPCR primers qPLCZ1fw: GAA GAG CCA 223 CCT GTT TGC AT; qPLC(1rv: CAG CAG TCG ATC TCC AGA CA; were designed based on the 224 full-length European eel CDS sequences. All the primers were designed on two different exons, in 225 226 order to avoid amplification of potential genomic contamination, using Primer3 Software (Whitehead 227 Institute/Massachusetts Institute of Technology, Boston, MA, USA). All primers were purchased from Integrate DNA Technology, Inc. (IDT, Coralville, IA). 228

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230 2.4.2. SYBR Green assay

To quantify gene expression, qPCR assays were performed using a model 7500 unit (Applied Biosystems; Foster City, CA, USA), with PCR protocol previously described by Peñaranda et al. (2013).

The total volume for every PCR reaction was 20 µl, performed from diluted (1:20) DNA template (5 234 ul), forward and reverse primers (250 nM each), and SYBR Green/ROX Master Mix (12 ul) 235 236 (Fermentas GMBH). Transcript levels were determined using an efficiency-adjusted relative quantification method as described by Weltzien et al. (2005). Serial dilutions of cDNA pool of gonad 237 tissues were run in duplicate and used as a common standard curve. One of these dilutions was also 238 included in each run as a calibrator. Target and reference genes in unknown samples were run in 239 duplicate PCR reactions. Non-template control (cDNA replaced by water) for each primer pair was 240 run in duplicate on all plates. 241

242

243 **2.4.3.** PLCζ tissue distribution

244 In order to investigate the tissue distribution of PLC(mRNA expression, gonads (testes and ovaries) and somatic tissues (liver, heart, gill, muscle, spleen, fins, kidney, brain, pituitary) were collected 245 from three immature male eels (mean body weight 118 ± 14 g; mean GSI <0.1) from the fish farm 246 247 Valenciana de Acuicultura, S.A. (Puzol, Valencia; East coast of Spain) and three female eels (mean body weight 608 ± 35 g; mean GSI 0.9 ± 0.3) from the Albufera lagoon (Valencia, Spain). Samples 248 were stored in RNAlater (Ambion, Austin, Texas, USA) immediately after decapitation and stored at 249 250 20 °C until RNA extraction. The brain was dissected into five parts: olfactory bulbs, telencephalon, mes-/di-encephalon, cerebellum and medulla oblongata as previously reported by Weltzien et al. 251 (2005). 252

Total RNA was extracted following the method used by Hildahl et al. (2011). Total RNA was treated
with DNase I (Turbo DNA-free; Ambion) at 37°C for 30 min. First-strand cDNA was prepared from
1µL total RNA using superscript III (Invitrogen) according to the manufacturer's protocol. All tissues
were analysed by qPCR.

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258 2.4.4. PLCζ expression through spermatogenesis

To study PLCζ expression during spermatogenesis, total RNA of gonads, olfactory bulb,
telencephalon, mes-/di-encephalon and pituitary was isolated from the RNAlater preserved tissues as
described by Peñaranda et al. (2013). Testis RNA of males from thermal groups T10-T20, T15-T20

and T20 was treated and purified with DNase I of NucleoSpin RNA XS kit (Macherey-Nagel, Düren,
Germany). First-strand cDNA was synthesized from 500 ng of testis total RNA, using qScript cDNA
Synthesis Kit (Ouanta Bioscience, MD, USA) with 15 µl RNA used as template.

Total RNA extracted from the olfactory bulb, telencephalon, mes-/di-encephalon and the pituitary of males from the thermal group T20 was treated with deoxyribonuclease (gDNA Wipeout Buffer, Qiagen), using a total volume of 14 μ l for 500 ng of total RNA for the olfactory bulb ant pituitary, or 1 μ g for the telencephalon and the mes-/di-encephalon. First-strand cDNA was synthesized in 20 μ l reactions using Quantiscript Reverse Transcriptase (Qiagen) with 14 μ l used as template, which were obtained in the previous step. RNA concentration and quality were evaluated by using a NanoDrop 2000C Spectrophotometer (Fisher Scientific SL, Spain).

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273 **2.5. Statistics**

Each variable was first checked for normality. If the variables did not have a normal distribution, theywere log-transformed and their normality was checked again.

276 Then, data were analyzed by analysis of variance (One-way ANOVA), using the Student-Newman-

Keuls test to compare means. Variance homogeneity was checked with the Bartlett test. Differences
were considered significant when p<0.05.

- Statistical analyses (One-way ANOVA) were also performed to study the evolution of PLC ζ expression in one tissue throughout sex development, and to study the differences in expression between thermal regimes in the same developmental stage (SPG, SPC, SD or SZ).
- T-test analyses were performed to compare differences between males and females in a same tissue
 from the data obtained in the study of PLCζ tissue distribution.
- All statistical procedures were performed using Statgraphics Plus 5.1 (Statistical Graphics Corp.,
- Rockville, MO, USA). Results are presented as mean \pm standard error (SEM).
- 286

287 **3. Results**

288 3.1. Characterization of European eel PLC₁

The $plc\zeta l$ gene was identified *in silico* in both the European and Japanese eel genomes. The European 289 eel *plc\zeta1* predicted sequence differed from the Japanese eel predicted sequence by 30 nucleotides and 290 291 13 amino acids. From the Anguilla anguilla plc $\zeta 1$ predicted sequence, specific primers were designed 292 to clone and confirm this sequence. Two overlapping fragments covering 1167 bp were cloned and sequenced. The European eel $plc\zeta l$ cDNA sequence (Fig. 2) differed from the corresponding partial 293 294 sequence characterized in the European eel genome by only 2 nucleotides and a gap of 3 nucleotides 295 in position 700 of the European eel $plc\zeta l$ cDNA sequence. This gap led to a lack of 1 amino acid, which did not affect the reading frame. The complete $plc\zeta l$ CDS was 1521 bp long, composed by 10 296 exons giving an open reading frame (ORF) of 506 amino acids (GenBank accession number 297 AFV13732.1) (Fig. 2). 298

299 European eel *plc* ζ 1 showed a high identity when compared with *plc* ζ from other teleosts: from 76.69% 300 for the Fugu Takifugu rubripes to 79.32% for the Atlantic cod Gadus morhua, with the highest identity. The European eel $plc\zeta 1$ share 78% of identity with the non-teleost actinopterygian spotted 301 302 gar Lepisosteus oculatus. When compared with sarcopterygian Plc amino acid sequences, European 303 eel Plc(1 presented 70.44% of sequence identity with the human, 66.82% with the mouse and the lizard, and 69.13% with the chicken. The highest identity with a sarcopterygian Plc was found with 304 305 the coelacanth, with 72.22% of identity. Classical domains of European eel Plc(1 protein were predicted using Interproscan software (http://www.ebi.ac.uk/interpro/) and revealed a typical Plc 306 307 domain structure with the following conserved domains: EF hand-like domains from position 16 to 98, X domain in position 101-240, Y domain in position 243-360, and C2 domain in position 383-467 308

309

310 **3.2. Phylogeny**

We performed phylogenetic analyses on five actinopterygian Plc ζ 1 amino acid sequences (four Plc ζ 1 from teleost species and one from a non-teleost species, the spotted gar), and five sarcopterygian PLC ζ 1 amino acid sequences, with the PLC β 1 (phospholipase C, beta1) from two mammalian species as outgroup (Fig. 3). In this phylogenetic analysis, the actinopterygian and sarcopterygian Plc ζ 1 clustered in two monophyletic groups. In the actinopterygian group, the European eel Plc ζ 1 clustered with the spotted gar at the basis of the teleost clade, constituting an actinopterygian Plc ζ 1 clade as sister clade of the sarcopterygian Plcζ1. This phylogeny confirmed that European eel Plcζ1 is
orthologous with actinopterygian Plcζ1 and sarcopterygian Plcζ1.

319

320 **3.3**. *plcζ1* tissue distribution in the European eel

plc² mRNA expression was compared in various tissues of female and male European eels (Fig. 4). 321 The $plc\zeta l$ showed a differential expression in male and female European eel. In female eels, very low 322 323 expression of $plc\zeta l$ was detected in peripherical tissues such as liver, heart, gill, muscle, spleen, fins, kidney, ovary or pituitary whereas there was high expression in the different brain parts. In male eels, 324 no expression was found in the muscle and in the kidney. Low expression of male $plc\zeta l$ mRNA was 325 detected in the liver, gill, heart, spleen, fins, medulla oblongata, cerebellum and pituitary. However 326 327 there was high expression in the testis, olfactory bulb, telencephalon and mes-/di-encephalon. $plc\zeta l$ in the olfactory bulb, telencephalon and gonads was expressed at higher levels in females compared to 328 the males (p < 0.05). 329

330

331 3.4. *plcζ1* expression during spermatogenesis

Once demonstrated the expression of male eel $plc\zeta l$ in the brain, pituitary and testis, we studied the 332 333 testis $plc\zeta l$ mRNA expression of the males from all the thermal regimes through spermatogenesis; and the brain (olfactory bulb, telencephalon, mes-/di-encephalon) and pituitary $plc\zeta l$ mRNA expression in 334 group T20 (kept at 20 °C) through spermatogenesis. In the brain and pituitary of the males kept at 20 335 °C, plcZl expression was stable from spermatogonia to spermatozoa and did not show significant 336 337 differences throughout maturation. The higher $plc\zeta l$ expression was observed in the telencephalon and 338 in the olfactory bulb (Fig. 5). The mes-/di-encephalon and the pituitary showed the lower $plc\zeta l$ expression levels (p<0.05). 339

Testis $plc\zeta l$ expression (Fig. 6) increased through spermatogenesis in all the thermal regimes. The plc ζl expression was very low when testis showed only spermatogonia (S1) or spermatocytes (S2) (Fig. 6). Maximum $plc\zeta l$ expression was found between S3 and S4 (spermiogenesis) when it was 75fold higher than at S1 (p<0.05). Furthermore, when comparing thermal regimes for a same stage of 344 development, testis $plc\zeta l$ was significantly highly expressed at stage spermatozoa in the lower thermal

regime (T10-T20) than in the higher thermal regimes (T15-T20 and T20, p<0.05).

346

347 **4. Discussion**

European eel *plcζ1* sequence showed a Plcζ typical domain structure but its sequence is shorter when compared with other vertebrate Plcζ, suggesting that eel Plcζ1 could have conserved its activity, but maybe at a lower level. The expression of eel testis *plcζ1* mRNA increase through spermatogenesis reaching maximum levels during spermiogenesis, and its expression is significantly higher at lower temperature compared to higher temperatures, suggesting that temperature may play a role in the regulation for *plcζ1* transcription in the testis, when *plcζ1* seems to acquire its function.

354

355 **4.1. Molecular structure and function**

The European eel $plc\zeta l$ contains an EF-hand domain located in the amino-terminal region of the 356 357 molecule, X and Y catalytic domains, and a carboxy-terminal C2 domain, all typical of other PLC orthologues (for review see Kashir et al, 2013; Ito et al, 2011, Parrington et al, 2007). Similar to 358 Medaka (Ito et al, 2008), and Fugu and Tetraodon $plc\zeta$ (Coward et al, 2011), the European eel $plc\zeta l$ 359 360 sequence is shorter when compared with mammalian $PLC\zeta$, showing an EF-hand domain truncated at the N-terminus, like in all the teleosts $plc\zeta$ studied so far (Fig. 2). EF-hands are involved in binding 361 Ca^{2+} and are thought to be important for the oscillatory Ca^{2+} activity of the enzyme (Ito et al, 2011). 362 In teleost species, studies showed that a deletion of a part of the EF-hand domain reduces the Ca²⁺ 363 oscillatory activity of Plc^(Kouchi et al, 2005; Kuroda et al, 2006). It remains possible that eel Plc⁽¹⁾ 364 does not trigger Ca^{2+} oscillation, however medaka Plc ζ , which is similarly truncated at its N-terminus, 365 can induce Ca²⁺ oscillation in mouse oocytes but at a lower activity than for full-length mammalian 366 PLCζ (Coward et al, 2011; Kuroda et al, 2006; Ito et al, 2008). These results suggest that these 367 domains are involved in the Ca^{2+} signal but are not obligatory to induce Ca^{2+} oscillation. This means 368 eel Plc(1 could have conserved its activity, but maybe at a lower level. Furthermore, EF-hand 369 domains seem also to play a role in nuclear translocation (Kouchi et al, 2004, 2005; Yoda et al 2004). 370 According to Kuroda et al. (2006), Trp13, Phe14, and Val18, which may be necessary for appropriate 371

372 conformation for nuclear translocation, may also be necessary to keep normal Ca^{2+} oscillation-373 inducing activity as well. Nevertheless, despite the lack of a part of the N-terminal of all teleosts 374 studied so far, at least some of these Plc ζ s still can trigger Ca^{2+} oscillations.

The XY domain, known to form together the active site responsible for PIP2 cleavage (Parrington et 375 al, 2007), is highly conserved. On the contrary, the X/Y linker region, between the two catalytic 376 377 domains, is a poorly conserved domain with a high diversity of amino acid residues among vertebrate. 378 In the C terminus of the X domain and in the X/Y linker region, PLC possesses a cluster of basic amino acid residues (lysine and arginine), which is found in many nuclear proteins (Kuroda et al, 379 2006, Jones and Nixon, 2000). Eel PLC(1 is truncated in the C-terminal region of the X-domain and 380 in a large part of the N-terminal X/Y linker region, on approximately 85 amino acids, when compared 381 382 with the other osteichthyan PLCζ sequences. This loss of protein part leads to a change in the protein conformation (data not shown) which may affect the protein function. Furthermore, due to its loss, eel 383 PLCC1 misses these two nuclear targeting regions localised in the lost part, which may affect the 384 385 nuclear translocation of the protein. According to Kuroda et al. (2006), in the mouse, nuclear targeting was absent for point mutation of Lys299 and/or Lys301 in the C terminus of X domain, and nuclear 386 translocation was lost when the residues from the NLS were replaced by glutamate. Nevertheless, 387 these substitutions did not affect PLC ζ ability to induce the Ca²⁺ oscillation. Furthermore, European 388 eel PLC ζ 1 still possesses region for enzymatic catalisis and substrate/Ca²⁺ binding, which are very 389 well conserved residues among osteichthyans, so European eel PLCZ1 catalytic function could be 390 preserved. Further studies to confirm the PLC ζ 1 function for initiating the Ca²⁺ oscillation after 391 fertilization in eel are necessary. 392

To better understand the evolutionary history for the PLC ζ family, we performed phylogenetic analyses on osteichthyans of key-phylogenetical positions: the human and the mouse, representative of mammalians; the anole lizard and the chicken, representative of sauropsids; the coelacanth, a representative of early sarcopterygians; the spotted gar, a non-teleost actinopterygian; the European eel, a member of an early group of teleosts (elopomorphs), and three members of teleosts (*Medaka*, *Takifugu* and *Tetraodon*). The *Anguilla anguilla* PLC ζ 1 branch with the spotted gar at the basis of the teleost PLC ζ group. Each species exhibits only one PLC ζ , which seem to suggest that this protein has 400 not been affected by the teleost-specific third whole-genome duplication. The duplicated gene must401 have been lost during evolution.

402

403 **4.2.** Sex-specific and species-specific tissue distribution of $plc\zeta 1$

PLC ζ is known to be sperm-specific, but eel *plc\zeta1* mRNA was highly expressed in different brain 404 parts, also showing low expression in the pituitary and peripherical tissues of male and female eels. 405 406 Tissue distribution of eel $plc\zeta l$ mRNA revealed a differential expression in male and female European eel, with high $plc\zeta l$ expression in testis, and very low in ovary, like in every $plc\zeta$ orthologous from 407 408 mammals (Cox et al, 2002; Saunders et al, 2002; Yoneda et al, 2006; Young et al, 2009), birds (Coward et al, 2005; Mizushima et al, 2009), and some teleosts like medaka (Ito et al, 2008) and eel, 409 410 but different to other fish like in the two pufferfish species Takifugu rubripes and Tetraodon *nigroviridis* (Coward et al, 2011). While $plc\zeta$ mRNA is thought to be only expressed in male gametes, 411 eel *plcCl* also expressed in the brain and pituitary of male and female. Yoshida et al. (2007) found 412 413 expression of $Plc\zeta$ mRNA in brains of both male and female mice, and Coward et al. (2011) found 414 expression of *plc* ζ in *Tetraodon* brain, but its function in the brain is unknown. Nevertheless, it is the first evidence of pituitary expression of PLC in vertebrates. These results showed different tissue 415 416 specific patterns of expression in $plc\zeta$ mRNA, which is not only expressed in fish testis, but also in the brain or in the ovary. PLCζ function is well documented in sperm vertebrates, nevertheless further 417 studies of PLC² expression and functions in somatic tissues are necessary. 418

419

420 **4.3.** *plcζ1* expression is stable in brain but increase in testis through spermatogenesis

This is the first study of the effect of the eel sexual maturation on the expression of brain and pituitary *plc* ζ *l* mRNA. In the European eel, *plc* ζ *l* mRNA expression is stable in the pituitary and in the brain through the spermatogenesis. The significance of *plc* ζ *l* mRNA expression in the brain and in the pituitary is unknown, further studies of Plc ζ *l* protein synthesis in the brain-pituitary-gonad axis should be performed to clarify the role of this protein in the reproductive function.

According to our results, *plcζ1* mRNA expression increases in the testis through spermatogenesis
regardless of thermal regime, reaching maximum levels during spermiogenesis. Mizushima et al.

(2009) searched the *PLC* ζ mRNA expression in quail sperm cells and found expression in elongate 428 spermatids but not in spermatocytes or in round spermatids. Furthermore, they demonstrated that 429 430 injection of chicken or quail elongated spermatids lead to successful fertilization and development of mouse and quail eggs, but none of the round spermatids alone induced blastodermal development. 431 These results of *PLC* ζ mRNA expression and spermatogenic cell injection support the evidence that 432 the egg activation potency of PLC² during spermatogenesis is acquired in elongated spermatids in 433 quail. This is in accordance with our results showing a European eel $plc\zeta l$ mRNA expression 75-fold 434 higher at the spermatozoa stage than at the spermatogonia stage, suggesting that eel Plc(1 function is 435 acquired during the stage of spermiogenesis. 436

437 PLC ζ function in the process of fertilization is known, but it seems to play further roles in 438 spermatogenesis. For instance, Ito et al. (2010) observed that PLC ζ knock-out mice was unable to 439 complete spermatogenesis with spermatocytes failing to proceed beyond elongation, underlying the 440 involvement of PLC ζ in spermatogenesis.

The observed increase in eel $plc\zeta 1$ mRNA expression during spermiogenesis regardless of thermal regimes clearly indicates that this increase is independent of temperature. However, at the final step of spermatogenesis (stage spermatozoa) European eel $plc\zeta 1$ mRNA expression in the testis was significantly higher for the males subjected to the temperature T10-T20 compared to T15-T20 and T20, suggesting that temperature may play a role in the regulation for $plc\zeta 1$ transcription in the testis, especially during the process of spermiogenesis, precisely when $plc\zeta 1$ seems to acquire its function.

447

The present study shows that $plc\zeta l$ mRNA synthesis in the eel testis starts after the onset of spermatogenesis. Our results support the hypothesis of a sperm-specific Plc ζl egg activation in the European eel, similar to many other vertebrates. However, expression of $plc\zeta l$ mRNA showed different tissue specific patterns, expressing in the brain or in the ovary like the two pufferfish species *Takifugu rubripes* and *Tetraodon nigroviridis*. Further studies of the function of PLC ζ in the Brain-Pituitary-Gonad axis are necessary to clarify the physiologic processes which control sexual maturation and fertilization. Due to its phylogenetical position and its complex life cycle, the

- European eel may be a very useful model to explore the evolutionary origins of PLCζ and itsfunctional role in the egg activation.
- In conclusion, the Plcζ1 expression pattern found in the European eel suggests an important functionof this protein in the spermatozoa of this species.
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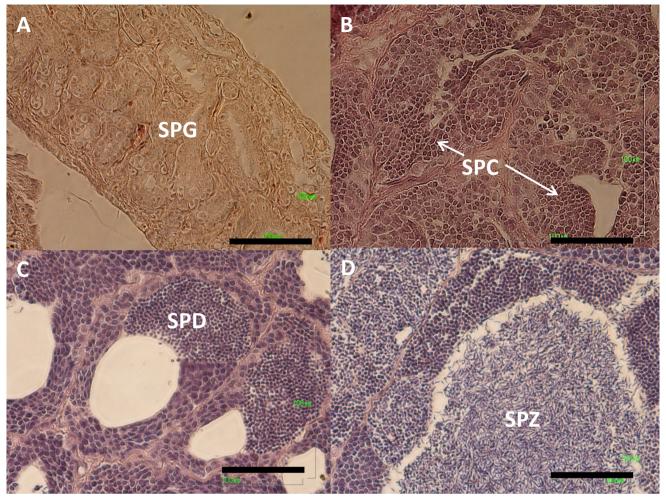
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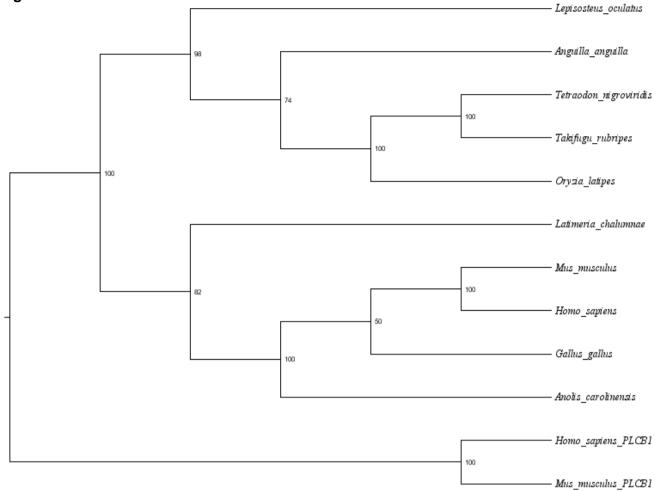
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755 Table I

Sequence name	Species name	Accession number	
PLCZ1-001	Mus musculus	ENSMUSP0000032356	
1-phosphatidylinositol 4,5-			
bisphosphate phosphodiesterase	Anolis carolinensis	XP_008108585	
zeta-1-like, partial			
PLCZ1-201	Gallus gallus	ENSGALP00000021386	
PLCZ1-201	Oryzias latipes	ENSGALF0000021380	
1 LC21-201	Oryzius iunpes	ENSORLT0000005752	
PLCZ1-201	Latimeria chalumnae	ENSLACT0000000957	
PLCZ1-201	Takifugu rubripes	ENSTRUP00000043591	
PLCZ1-201	Homo sapiens		
	nomo suprens	ENSP00000402358	
PLCZ1-201	Lepisosteus oculatus	ENSLOCP00000018988	
PLCZ1-201	Gasterosteus aculeatus	ENICO + CD00000012017	
DI C71 201		ENSGACP00000013217	
PLCZ1-201	Tetraodon nigroviridis	ENSTNIP0000003915	
PLCB1-005	Homo sapiens	ENSP00000367908	
PLCB1-005	Mus musculus	EINSE 00000307908	
1 LCD1-005	wius musculus	ENSMUSP00000105743	



762 763 764 765	Figure 2	
766	Eel	
767	Fugu Mouse	MFRKSKR 7 MESQLHELAEARWFLSKVQDDFRGGKINVEITHKLLEKLDFPCHFAHVKHIFKENDRQNQ 60
768	nouse	EF-Hand domain
769	Eel Fugu	LPASRRKDVKYIFDHYASGADSLHAGGLLRFLQMEQAEPGADDAMAEN 56 PSTRRAEIOHLYQKYLSG-ETLSVSDLLKFLHKEOMELTADEHTAEG 53
770	Mouse	GRITIEEFRAIYRCIVHREEITEIFNTYTENRKILSENSLIEFLTQEQYEMEIDHSDSVE 120
771	Eel	LIDKYEIDETERKSRMMTFPGFLRYMESRDCSVLNQEHTRVYQDMGRPLCHYFISSSHNT 116
772	Fugu Mouse	LINRYEIEESAIQAKSMTFEGFFRYMESKDCCVFNQAHTSVYQDMDQPLSSYFISSSHNT 113 IINKYEPIEEVKGERQMSIEGFARYMFSSECLLFKENCKTVYQDMNHPLSDYFISSSHNT 180
773		·*···** * · · · · · · · · · · · · · · ·
774	Eel	YLTADQLVGKSHLFAYESALRKGCRCLEIDCWDGPDLEPIVYHGYTLTSKILFRDVISTI 176
775	Fugu Mouse	YLTGDQIVGKSHLDAYVIALRKGCRCLEIDCWDGSDMEPVVYHGYTLTNKILFKEVIATV 173 YLISDQILGPSDIWGYVSALVKGCRCLEIDCWDGSQNEPIVYHGYTFTSKLLFKTVVQAI 240 ** .**::* *.: .* ** **********: **:*****:*:*:*:
	Eel	AEHAFQVSPYPVILSLENHCHLPQQQVMAQYITTILGDRLLDAGLDLSSSAELPSP 232
	Fugu Mouse	EQHAFERSPYPVILSLENHCSKEQQEIMAHYLISILGEKLLRAPIDHPTTGELPSPNDLK 233 NKYAFVTSDYPVVLSLENHCSPGQQEVMASILQSTFGDFLLSDMLEEFP-DTLPSPEALK 299 ::** * ***:***** **::** :: :** :: . ****
	Eel	
	Fugu Mouse	HKILIKNKKLKPNTDAEESVDEGEEEEENEEEEEEEEEEEEEEKIQFCPRIMTGSKTKVSKT 293 FKILVKNRKVGTLSETHERIGTDKSGQVLEWKEVIYEDGDEDSGMDPETWDVFLSRIKEE 359
	Eel Fugu	QQKGKVKVAVELSNLVIYTKSVKFVSFSHSRESQRFYENTSLGE 276 GTIQQDTIKHILVKKKKKKKKVVAEALSDLVIYTRSVKFISFRYSRDNQHNYENTSLVE 353
	Mouse	READPSTLSG-IAGVKKRKRKMKIAMALSDLVIYTKAEKFRNFQYSRVYQQFNETNSIGE 418 ::* *: :* **:*****: ** .* :** *: *:.** Y-domain Y-domain
	Eel	KKAHKLALKSGPEFVLHNARFISRIYPAGSRTLSSNYNPQEFWNMGSQLVALNFQSLGLP 336
	Fugu Mouse	TKARKLLKSSGPDFIRHNQRFLSRIYPAGSRTASSNYNPQEFWNVGCQLVALNFQSLATP SRARKLSKLRVHEFIFHTAAFITRVYPKMMRADSSNFNPQEFWNVGCQMVALNFQTPGLP 478 .:*:** :*:** *:*:** :*:***
	Eel	MDLNNARFRDNGGCGYVLKPHFLRSHEATFDPSALPPDLKPVQVLMKVISGSNLPISKAG 396
	Fugu Mouse	MDLNDGRFQDNGGCGYILKPAVLMSTQGDFDPGRSRRSFRAKHLLLKVISGSNLPLSRSR 473 MDLQNGKFLDNGGSGYILKPDILRDTTLGFNPNEPEYDDHPVTLTIRIISGIQLPVSSSS 538 ***::::* ****.**:*** .* .*:*: .: ::::*** :**:*: C2-domain
	Eel	KPIDPYVRVEITGVPSDCRRIQSEPVKHNSLSPKWDASMNFTVGVPELALIRFTVRDHGL 456
	Mouse	KTLDPFVRVEIHGIPFDSCRKSTHAVKNNSLSPCWDAHMNFKIRTPELCLIRFCVRDQTG 533 NTPDIVVIIEVYGVPNDHVKQQTRVVKNNAFSPKWNETFTFLIQVPELALIRFVVETQQG 598 * * :*: *:* * **:*:** *: **:*:** *: **:*.*** *: ***.**** *: ***.**** *: ***.**** *: ***.**** *: ***.**** *: **:*:*** *: **:*:*** *: ***.***** *: ***.***** *: ***.***** *: ***.********
	Eel	RPA-NDFMGQYTLPFTSMKKGHVELDLRASVCVTQHKEQNSQGMKAHGKVS 506
	Mouse	ILS-SEFVGQYTLPFTSLKKGYCWVPLCSRDGCSLDPASLFVLVWYS 579 LLSGNELLGQYTLPVLCMNKGYRRVPLFSKSGANLEPSSLFIYVWYFRE 647 : .:::******::**: : *::.:



778779 Figure 4780

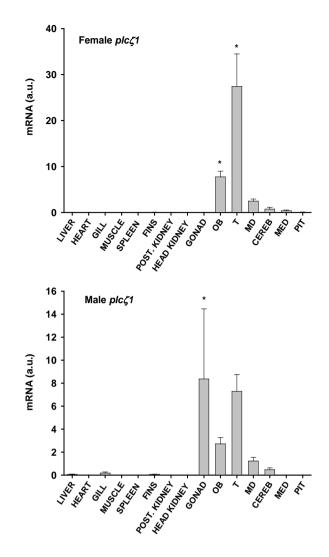
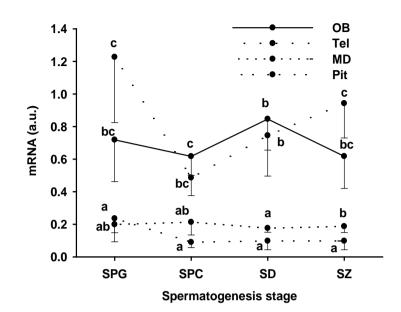
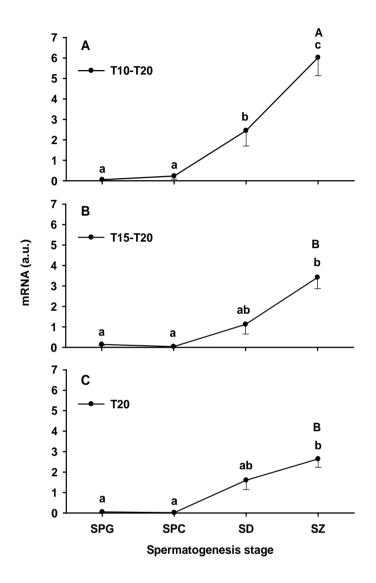


Figure 5





788	Table legend
789	
790	Table I. Accession number of the sequences used for phylogenetic analyses
791	
792	Figure legend
793	
794	Figure 1. Histological sections of eel testis at different developmental stages during chorionic
795	gonadotropin (hCG) hormonal treatment. A: spermatogonia; B: spermatocyte; C: spermatids, D:
796	spermiation. SPG= spermatogonia; SPC: spermatocytes; SPD: spermatids; SPZ: spermatozoa, Scale
797	bar: A=100µm; B, C, D= 50µm
798	
799	Figure 2. Multiple sequence alignment of European eel, Mouse and Fugu PLC ζ at amino acid
800	level. "*" Conserved residues, ":" conservation between groups of strongly similar properties, "."
801	conservation between groups of weakly similar properties. Residues in red: AVFPMILW, small and
802	hydrophobic. Residues in blue: DE, acidic. Residues in pink : RK, Basic – H. Residues in green:
803	STYHCNGQ, Hydroxyl + sulfhydryl + amine + G. EF-hand like domain, X-domain, Y-domain and
804	C2-domain are shown above the alignment.
805	
806	Figure 3. Consensus phylogenetic tree of the vertebrate Phospholipase C zeta. This phylogenetic
807	tree was constructed based on the amino-acid sequences of PLC ζ (for the references of each sequence
808	see Table I) using the Maximum Likelihood method with 1000 bootstrap replicates. The number
809	shown at each branch node indicates the bootstrap value (%). The tree was rooted using the two
810	sequences of the mouse and human phospholipase beta1.
811	
812	Figure 4. Tissue distribution of (A) <i>plcζ1 in female</i> , (B) <i>plcζ1</i> in immature <i>male</i> European eel.
813	Data are normalised to eel arp. Asterisk indicates significant differences between males and females
814	in a same tissue (p<0.05; n=3). Values are presented as means \pm SEM ($n = 3$). OB : olfactory bulb, T :
815	Telencephalon, M/D: mes-/di-encephalon, CEREB: cerebellum, MED: medulla oblongata, PIT,
816	pituitary.
817	
818	Figure 5. European eel $plc\zeta 1$ expressions during experimental maturation in 3 brain parts and
819	in the pituitary in fishs kept at 20 degrees. Data are normalised to eel arp. Small letters indicate
820	significant differences between the olfactory bulb, the telencephalon, the mes-/di-encephalon and the
821	pituitary, in the same gonad development stage (p<0.05; n=6-12). Results are given as mean \pm SEM.
822	SPG= Spermatogonia stage, SC= Spermatocyte stage, SD= Spermatid stage, SZ= Spermatozoa stage.

- See main text for definition of gonad developmental stages, OB: olfactory bulb, Tel: telencephalon,
 MD: mes-/di-encephalon, Pit: pituitary.
- 825

Figure 6. European eel *plcZ1* expressions during experimental maturation in fish testis kept in different thermal regimes. Data are normalised to eel *arp*. Capital letters indicate significant differences between the thermal treatments in the same gonad development stage (p<0.05; n=8-17). Small letters indicate significant differences through spermotogenesis in the same thermal treatment (p<0.05; n=6-17). Results are given as mean \pm SEM.. SPG= Spermatogonia stage, SC= Spermatocyte stage, SD= Spermatid stage, SZ= Spermatozoa stage. See main text for definition of gonad developmental stages.

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