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1	Immunohistochemical expression of E–cadherin in different
2	tissues of the teleost fish Scophthalmus maximus
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15	Abstract
16	E-cadherin is an evolutionary conserved protein, whose main role as the principal
17	component of adherens junctions is supporting epithelial cell-cell adhesion. It is an
18	essential molecule for the maintenance of the epithelial barrier function and the analysis
19	of its immunohistochemical expression is a valuable resource in morphopathological,
20	ontogenetic and pathogenesis studies in mammals. As well, there is an increasing
21	understanding of the importance of E-cadherin in the physiology of the immune system

and the development of the immune response. Mucosal health is a primary issue in 22 23 aquaculture research; nevertheless, there is a lack of immunohistochemical studies of cell junction proteins in fish species. In this work, an immunohistochemical technique was 24 optimized in Bouin- and formalin-fixed paraffin-embedded tissues of turbot 25 Scophthalmus maximus, employing a commercial antibody raised against human E-26 cadherin. The specificity of the antibody in recognizing the molecule in this teleost 27 species was tested by western blot and mass spectrometry-based proteomic analyses. The 28 assays showed a good specificity and indicated that the antibody recognizes the well 29 conserved cytoplasmic domain of the protein. Immunohistochemistry showed the 30 31 localisation of E-cadherin at cell-cell contact in the epithelia of the different organs, between the hepatocytes and the pancreatic acinar cells, as well as in the reticulo-32 epithelial stroma of the thymus. Also, the immunoreaction was observed in the cells 33 34 constituting the melano-macrophage centres in the spleen and kidney. No immunostaining was detected, as expected, only in the heart and brain. No significant 35 difference was noticed between the two fixative used for collecting the tissues samples. 36 This is the first description of E-cadherin immunohistochemical expression in several 37 tissues of a teleost. The immunohistochemical technique represents a useful tool to be 38 used in the different areas of fish health research. 39

Keyword: Immunohistochemistry; cadherin-1; cell junctions; epithelial barriers; mucosal
health

42

43 **1. Introduction**

Cell-cell adhesion is a fundamental structural feature of multicellular organisms, 44 mediated by a set of specialized membrane structures termed intercellular junctions. 45 Particularly, the ability of epithelial cells to organize into monolayered sheets is a 46 47 prerequisite for multicellularity, thereby providing tissue integrity, barrier function, and 48 tissue polarity in metazoan organisms (Bruser and Bogdan, 2017). Over the course of morphological evolution, metazoan animals have diversified the architecture of their cell-49 cell junctions, which includes tight junctions, adherens junctions (AJ), and desmosomes. 50 Among them, AJs are the only detected throughout the metazoan phyla, whereas other 51 junctional types show restricted phylogenetic distributions (Oda and Takeichi, 2011). 52 Thus, AJs could be considered the universal adhesion machinery for the generation and 53 maintenance of multicellular animal bodies. E-cadherin, a calcium-dependent 54 transmembrane protein, is the structural and functional core of AJs, mediating trans-55 homophilic interactions between neighbouring cells. Its adhesive functions are mediated 56 by the extracellular cadherin repeat domains, while the highly conserved intracellular 57 domains form a complex with catenins linking E-cadherin to the actin cytoskeleton, being 58 so involved in junctional maintenance, dynamics, and plasticity of epithelial tissues 59 (Bruser and Bogdan, 2017; Oda and Takeichi, 2011; van Roy and Berx, 2008). 60

In teleost, the mucosal surfaces (skin, gills and gastrointestinal tract) constitute the first line of defence against pathogens invasion and carry out multiple physiological processes, such as osmoregulation, waste excretion and nutrient adsorption. For fish, even more than for terrestrial species, mucosal barriers and their health are of primary importance to face the continue interactions with the aquatic microbiota (Peatman and Beck, 2015). Almost all of the most urgent areas of aquaculture research require a deeper understanding of

mucosal barriers, from pathology issues to vaccine delivery, nutrition, nutraceutics and 67 68 microflora modulation (Peatman et al., 2015). The importance of E-cadherin as diagnostic marker and the main role it plays in human diseases, from several cancer types 69 to different skin and gastrointestinal conditions, have been widely reported (Baniak et al., 70 2016; Christou et al., 2017; Maretzky et al., 2008; Singhai et al., 2011; Sugihara, 2016; 71 72 von Zeidler et al., 2014; Wu et al., 2007; Zbar et al., 2004). In fish pathology, E-cadherin 73 has recently been identified as a key molecule for resistance to infectious pancreatic necrosis (IPN) in Atlantic salmon (Moen et al., 2015), and another work on the same 74 species reported modulated intestinal E-cadherin gene expression in response to an 75 76 experimental dietary treatment affecting intestinal fluid permeability (Hu et al., 2016). 77 The investigation of E-cadherin immunohistochemical expression is a primary focus in morphological studies, including ontogenetic and morphopathological characterization of 78 the different organs, as well as an irreplaceable complement for studies based on gene 79 expression analysis (Bondow et al., 2012; Fuertes et al., 2013; Gassler et al., 2001; 80 Kuwahara et al., 2001; Sakamoto et al., 2008; Schneider et al., 2010). However, no 81 comprehensive study of E-cadherin immunolocalisation in teleost tissues has been 82 addressed and there is still a scarce knowledge of the physiological distribution of this 83 and its change under pathological conditions. In this study, 84 protein an immunohistochemical technique based on a commercial antibody was optimized in 85 Bouin- and formalin-fixed paraffin-embedded tissues from turbot (Scophthalmus 86 *maximus*), an economically-important marine species, and the distribution of E-cadherin 87 88 in different tissues of healthy specimens analysed.

89 2. Materials and methods

90 2.1. Fish and sampling procedures

For this study, 10 adult turbot $(2,127 \pm 182.2 \text{ g mean weight})$ were employed. Fish were 91 92 euthanized by overexposure to tricaine methane sulfonate (MS222, Sigma-Aldrich, 93 Denmark) and necropsied. For histological examination and immunohistochemistry, tissues samples from kidney, spleen, thymus, digestive tract, liver, pancreas, heart, gills, 94 brain and skin were collected. Samples were fixed in Bouin's fluid at 4 °C or in formalin 95 during 24 hours and then paraffin-embedded. Histological analysis was performed on 96 97 H&E and toluidine blue-stained sections. For western blot analysis, samples (1 g) of anterior and posterior intestine were collected and extensively washed with ice cold PBS 98 99 containing 1 mM of phenylmethylsulfonyl fluoride (PMSF) before storage at -80°C.

All experimental protocols were approved by the Institutional Animal Care and UseCommittee of the University of Santiago de Compostela (Spain).

102 2.2. Western blotting and E-cadherin sequences analysis

103 Western blot analysis was performed to assess the specificity of the primary antibody on 104 protein extracts from anterior and posterior intestine of turbot. Protein extracts from human skin and intestine (ileum) were used as positive control. Tissues were 105 106 homogenized in ice-cold homogenization buffer (50 mM Tris-HCl, 150 mM NaCl, 5mM EDTA, 1 mM dithiothreitol, 1 mM PMSF, 1 mM benzamidine hydrochloride hydrate, 5 107 μg/mL pepstatin A, 5 μg/mL aprotinin, 5 μg/mL leupeptin, 1% triton X-100, 0,5 % 108 sodium deoxycholate, 0,1 % sodium dodecyl sulfate pH 7.4). Homogenates were 109 110 centrifuged at 35,000 g for 15 minutes at 4 °C, and supernatants filtered through gauze 111 and frozen in aliquots at -80° C until required. Protein concentrations were determined by Bradford method according to manufacturer's instruction (Bio-Rad, Hercules, CA, 112 113 USA).

Samples of protein extracts were mixed with 1/4 vol of 5X SDS sample buffer (250 mM 114 115 Tris-HCl, 8 % SDS, 40% glycerol, 20% β-mercaptoethanol, pH 6.8) and denatured by heating at 37 °C for 20 min. Approximately 30 µg of total protein per tissue were resolved 116 by SDS-PAGE using 7.5% polyacrylamide slabs-gel and proteins were transferred to 117 polyvinylidene difluoride (PVDF) membranes (Immobilon-P; Millipore, Bedford, MA, 118 119 USA) by applying a 275 mA current for 3 h at 4 °C. Sodium dodecyl sulphate (SDS) was added (0,025%) to the transference buffer in order to facilitate the transfer of high 120 molecular weight proteins. After blocking for 2 h and 30 min at room temperature with 121 5% non-fat dry milk in TTBS (20 mM Tris-HCl buffer, pH 7.5, 0.15 M NaCl, 0.1% 122 123 Tween 20), membranes were incubated overnight at 4° C with the anti-human E-cadherin primary antibody (mouse monoclonal antibody, clone NCH-38, M3612, Dako, Denmark) 124 diluted 1:500 with TTBS. The blots were then incubated for 1 h at room temperature with 125 126 anti-mouse secondary antibody conjugated to horseradish peroxidase (Sigma-Aldrich, St Louis, MO, USA) diluted 1:50,000 with TTBS and, finally, developed with the 127 128 chemiluminiscent HRP substrate (Millipore) and exposed to X-ray film (Curix RP2 Plus; 129 Agfa–Gevaert, Mortsel, Belgium) for a few seconds. Membranes were washed 5 times for 10 min with TTBS between subsequent steps. Negative control was performed by 130 substituting primary antibody with TTBS. In order to estimate the apparent molecular 131 weight of detectable bands, a sample of molecular weight standards (Unstained Broad 132 Range SDS-PAGE Standards, Bio-Rad) was also applied on the gel. The membranes were 133 134 finally stained with a Ponceau-S solution to mark the positions of the molecular weight standards. 135

Additionally, for all tested samples SDS–PAGE and gel staining with Coomassie Brilliant
Blue R (Sigma–Aldrich) were carried out.

The amino acid sequence of turbot E–cadherin was inferred using ExPASy Translate tool (http://web.expasy.org/translate/) from the nucleotide sequence (GenBank accession number: MG137250) identified in a previous study (Robledo et al., 2014), and its theoretical molecular weight estimated by ExPASy Compute pI/Mw tool (http://web.expasy.org/compute_pi/). For comparison purposes, the amino acid sequence alignments were performed by using the BLASTP 2.6.1 online program (Altschul et al., 2005; Altschul et al., 1997).

145 2.3. In-gel digestion and protein identification by nano-HPLC-ESI-IT-MS/MS

146 Based on western blot results, the labelled bands of 110 kDa y 38 kDa obtained in turbot were manually excised from SDS-PAGE Coomassie-stained gels. Proteins were in-gel 147 reduced, alkylated and digested with trypsin as previously described (Jensen et al., 1999). 148 Briefly, protein bands were three times washed with water and dehydrated with 149 acetonitrile. Gel plugs were then dehydrated in a vacuum centrifuge and finally 150 rehydrated with a 0.5 µM solution of sequencing grade bovine trypsin (Promega, 151 Madison, WI) in 25 mM ammonium bicarbonate buffer, pH 8.0, for at least 40 min on 152 ice. After the rehydration step, samples were digested overnight at 37 °C and peptides 153 154 were then cleaned—up by using ZipTip C18 according to manufacturer's instructions. The peptide mixture was dried in vacuum centrifugation, and dissolved again in 15 μ L of 1% 155 formic acid prior to mass analysis. 156

157 Trypsin-digested proteins were analysed using a Dionex UltiMate 3000 RSLCnano 158 system (Thermo Fisher Scientific) coupled to a LTQ Velos–Pro mass spectrometer 159 (Thermo Fisher Scientific). The separation of the peptides was done on an Acclaim 160 PepMap100 Nano Trap Column, C18, 5 μ m, 100 Å, 100 μ m × 1 cm (Thermo Fisher 161 Scientific) coupled to an RP column Acclaim PepMap RSLC 75 μ m × 150 mm, C18, 2

μm, 100 Å (Thermo Fisher Scientific). Mobile phases A and B were respectively 0.1% 162 163 formic acid in water and in 100% acetonitrile. A 90 min linear gradient from 5% to 35% 164 B, at a flow rate of 300 nL/min, was used. For ionization, a spray voltage of 2.10 kV and a capillary temperature of 200 °C were used. Peptide detection was performed by using 165 survey scans from 350 to 1600 Da (2 µscans), followed by MS/MS scans (2 µscans) of 166 167 the six more intense peaks using an isolation width of 1 Da and a normalised collision 168 energy of 35%. Singly charged ions were excluded from MS/MS fragmentation and a dynamic exclusion enabled, with repeat count set to 2 and exclusion duration of 30 s. 169 170 Protein identification was performed using the database searching function of the PEAKS 171 7 software (Ma et al., 2003; Zhang et al., 2012) (Bioinformatics Solutions Inc, Waterloo, 172 Ontario, Canada), to compare experimental MS/MS spectra against reference MS/MS spectra from the UniProtKB/TrEMBL database (release 2017_04; 84827567 sequence 173 174 entries), which also included their respective decoy sequences. The following limitations were used for the searches: tryptic cleavage, up to 2 missed cleavage sites, and tolerances 175 176 ± 1.0 Da for precursor ions and ± 0.8 Da for MS/MS fragments ions. The FDR was kept below 1% and only proteins with at least one unique peptide were considered. When 177 protein identification failed, the PEAKS algorithm was used to perform de novo 178 179 sequencing for each input spectrum. The same parameters (mass error tolerance and PTMs) specified for database search are also used for *de novo* sequencing. Average Local 180 confidence (ALC) for each *de novo* sequence was set at $\geq 60\%$. 181

182 2.4. Immunohistochemistry

Thin sections (3 µm thick) were obtained from all the sampled organs. The sections were placed on slides treated with silane to improve section adherence and dried overnight at 37 °C. After deparaffination with xylene (two 5–min washes) and hydration through a graded ethanol series, slides were incubated with a peroxidase–blocking solution (Dako,

Denmark) for 30 minutes to quench endogenous peroxidase activity. Antigen retrieval 187 188 was performed using high pH antigen retrieval buffer (Dako, Denmark), following the manufacturer instruction. The optimal working dilution for the monoclonal antibody anti-189 190 human E-cadherin was determined to be 1:50 with an incubation time of 2 h at room temperature. Then, slides were incubated during 30 min with horseradish peroxidase 191 192 (HRP)-labelled polymer conjugated to rabbit secondary antibody and peroxidase reaction 193 was developed using a diaminobenzidine-positive chromogen (EnVision+ System-HRP) kit, K4007, Dako). All incubations were performed in a humid chamber at room 194 temperature, and the sections were washed three times for 5 min in 0.1 M phosphate 195 196 buffered saline containing 0.05% Tween–20 between all subsequent steps. Sections were finally counterstained with haematoxylin, dehydrated and coverslipped with DePeX 197 mounting medium for microscopic observation. Tissue sections from formalin-fixed 198 199 paraffin-embedded human intestine were used as positive controls. In sections included as negative controls, primary antibody was replaced with either PBS or antibody diluent. 200

201 **3. Results**

202 *3.1. Histological analysis*

203 The histological evaluation of the sampled tissues did not show any significant204 pathological alteration or presence of pathogenic agents.

205 *3.2. Western blotting*

In human tissues, an expected signal corresponding to a molecular weight of approximately 97 kDa was detected in both the skin and intestinal extracts. Furthermore, an additional intensely labelled band of about 38 kDa was observed for the skin. In turbot, the band corresponding to the mature form of E–cadherin reached approximately 110 kDa, identical for the anterior and posterior intestine. This result was consistent with the
theoretical molecular weight indicated by ExPASy Compute pI/Mw tool for the protein.
As well, additional 38–kDa labelled bands were observed in both intestinal regions (Fig
1).

The alignment performed by BLASTP 2.6.1 showed that turbot and human E–cadherin (Uniprot code P12830) amino acid sequences exhibited more than 53% of identity (Fig 2

A). Furthermore, the alignment of the human 38 kDa C–terminal fragment of E–cadherin,

known as CTF1 (Marambaud et al., 2002; Maretzky et al., 2005), with the correspondent

last 182 amino acids of turbot protein resulted in more than 75% of identity (Fig 2 B).

219 3.3. Validation of western blot results by MS-proteomics analysis

Proteomics data supported the presence of E-cadherin in both 110 kDa and 38 kDa bands 220 (Table 1) by finding a unique peptide sequence which matched with the E-cadherin 221 222 protein sequence of *Fundulus heteroclitus*. That fish sequence, which is currently available in the UniProtKB/TrEMBL database, exhibited more than 45% of identity with 223 the human E-cadherin (Uniprot code P12830), and more than 57% with turbot's, after 224 225 their sequence alignment. The further alignment of that unique peptide sequence with the E-cadherin protein sequence of S. maximus resulted in 100% of identity (Fig 2 B). 226 Moreover, in the 110 kDa band, de novo PEAKS data analysis found an additional peptide 227 228 sequence (NQGLSQDNTVQTK) in the sample which also exhibited 100% of identity 229 with the E-cadherin protein sequence of turbot.

230 > 3.4. Immunohistochemistry

The expected negative or positive reactions were observed in the negative or positive controls, respectively. E–cadherin was detected in all the studied tissues of turbot, with the exception of the brain and heart, in both formalin- and Bouin-fixed samples. As

expected, the immunostaining was mostly observed in the epithelia, located at the cell-234 235 cell junction area with a basolateral position. The epidermis and the epithelium covering 236 the gill lamellae showed this kind of immunoreactivity (Fig 3 A, B), as well as the lining epithelium of the digestive tract (Fig 3 C) from the oesophagus to the anus. In the stomach 237 the gastric pits were also labelled, but not the entire epithelium of the gastric glands (Fig 238 3 D). As well, in the kidney the expression of E-cadherin was observed in the epithelia 239 240 of the tubules, ducts and Bowman's capsule (Fig 4 A). In this organ and in the spleen, the melano-macrophage centres (MMCs) also showed immunoreactivity, which appeared 241 242 located at the contact area between the cells constituting the centres (Fig 4 B). E-cadherin 243 immunostaining was also noticed in the opercular epithelium that separates the thymus from the gill chamber, as well as drawing a reticular pattern in the thymus parenchyma, 244 245 with a stronger intensity in the inner part of the organ (Fig 4 C). Finally, E-cadherin was 246 immunolocalised at the intercellular junction between the hepatocytes in the liver and the acinar cells in the pancreas, as well as in the epithelium of the biliar and pancreatic ducts. 247 248 On contrary, no immunostaining was observed in the endocrine components of the 249 pancreas, the islets of Langerhans (Fig 5).

250 **4. Discussion**

To our knowledge, this is the first work addressing the immunolocalisation of E–cadherin in different tissues of a teleost fish. The commercial antibody employed was thoroughly evaluated to test its specificity in recognizing the protein in turbot by western blot and MS–based proteomic analyses.

The results suggest that the monoclonal antibody recognizes the C–terminal region of the protein, corresponding to the cytoplasmic domain (CD). In fact, the CD of E–cadherin remained quite conserved from placozoa to man (Hulpiau and van Roy, 2011) and

cleavage fragments of human E-cadherin CD have been reported. Particularly, the 258 259 intramembrane protease complex gamma secretase, through the action of a presenilin-260 1(PS1), is responsible for the cleavage of the 38 kDa fragment known as CTF1. Upon formation of cell-cell contacts, PS1 is recruited to sites of cell-cell adhesion, where it 261 forms complexes with E-cadherin and b-catenin at the cell surface (van Roy and Berx, 262 263 2008). There is a lack of information about cleavage sites and fragments of E-cadherin 264 in teleost, however, the observation of 38 kDa labelled bands in turbot tissues indicate the possibility that they might be similar to those described in mammals. As well, a high 265 similarity between the amino acid sequences of the C-terminal region of turbot and 266 267 human E-cadherin was observed, which would support the cross-reactivity of the antibody employed. 268

The immunohistochemical expression observed in turbot was full consistent with that 269 described in mammalian tissues, being E-cadherin immunolocalised at cell-cell contacts 270 271 in the lining epithelia covering the body surfaces exposed to the external environment (skin, gills, gastrointestinal tract), as well as in the epithelia of the biliar and pancreatic 272 ducts and the collecting duct system of the kidney. In this last organ, also the simple 273 squamous epithelium of the Bowman's capsule was labelled, as previously seen in human 274 275 kidney (Tsuchiya et al., 2006). Membranous labelling of pancreas acinar cells and of hepatocytes was also observed, in accordance with what described in mammals (Lim et 276 al., 2007; Tsuchiya et al., 2006). Besides, immunostaining of hepatocytes was also 277 reported in the cell line RTL–W1, originated from a primary culture of rainbow trout 278 279 normal liver (Malhao et al., 2013).

The most controversial results were the lack of immunostaining of the gastric glands and islets of Langerhans in the pancreas, where the expression of E–cadherin was described in human by Tsuchiya et al. (2006), who performed an immunohistochemical study on

different healthy human tissues. However, the same authors also observed in both cases 283 284 immunoreactivity to another member of cadherin family, N-cadherin. Particularly, in the 285 stomach, N-cadherin was detected in parietal cells, which are specialized in secreting hydrochloric acid (Tsuchiya et al., 2006). In teleost, on the other hand, only one cell type 286 is observed in gastric glands, secreting both pepsinogen and hydrochloric acid (Grosell et 287 al., 2010). The presence of other cadherins other than E-cadherin in these locations cannot 288 289 be discarded and the development of molecular markers is needed for a better characterization of the cadherin family in teleost. Concerning the lack of immunostaining 290 291 for E-cadherin in turbot heart and brain, this is in accordance with that described in 292 human, where N-cadherin was in turn detected in the intercalated discs of cardiac muscle and in the central nervous system (Tsuchiya et al., 2006). 293

E-cadherin was also immunolocalised, as expected, at cell-cell contacts in the epithelium 294 of the gill chamber separating the thymus from the aquatic milieu. In the thymus, the 295 296 immunostaining corresponded to the stromal tissue, constituted by a framework of reticulo-epithelial cells that support the parenchyma (Vigliano et al., 2011). This staining 297 was more intense in the inner zone of the organ. Zonation of the thymus has been reported 298 in turbot, consisting in an outer part mainly composed by thymocytes and the inner 299 thymus, where mostly lymphoblasts and macrophages are present (Padrós and Crespo, 300 1996). This might resemble the cortical and medullary portions of human thymus, where 301 302 a strongest staining intensity of E-cadherin was found in the medulla and has been related with mechanisms involved in T cells development and proliferation (Kutlesa et al., 2002). 303 304 Further research has to be carried out to investigate the functions of fish E-cadherin others 305 than junctional maintenance, but, based on the emerging evidences in mammals (Van den 306 Bossche and Van Ginderachter, 2013), it is plausible a broader implication in the 307 functioning of teleost immune system.

In the same way, immunohistochemical localisation of E-cadherin was observed in the 308 309 MMCs in kidney and spleen. These are nodular accumulations of closely packed pigment-containing cells, mostly macrophages, which play significant roles in 310 physiological processes, such as destruction, detoxification or recycling of endogenous 311 and exogenous materials, and in the immune response, being proposed as the evolutionary 312 precursors of mammalian germinal centres (Agius and Roberts, 2003; Steinel and 313 314 Bolnick, 2017). MMCs in spleen and kidney increase in size and/or number in response to infection, vaccination, environmental and physiological changes, as well as they have 315 been seen developing elsewhere in fish body, often in association with chronic 316 inflammation (Agius and Roberts, 2003; Bermúdez et al., 2010). A comprehensive 317 understanding of MMCs functions and of the kinetics of the cells that join, leave or form 318 the centres needs further and systematic investigations (Steinel and Bolnick, 2017), but 319 320 this is the first evidence of E-cadherin involvement in the interaction between the cells constituting MMCs in a teleost. 321

In conclusion, the immunohistochemical technique optimized with a commercial antibody showed a good specificity and allowed the study of E–cadherin distribution in several tissues of turbot. The recognition of the CD of the protein, well evolutionary conserved, points toward a successful employment of this technique in other fish species. This is a useful tool for the investigation of mucosal barriers and their physiological and pathological changes, for ontogeny studies, as well as to explore the occurrence and significance of cell–cell adhesion in the functioning of the immune system.

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Table 1. NanoHPLC-ESI-IT-MS/MS analysis of the 110 kDa and 38 kDa labeled
bands found by western blot with an anti-E-cadherin antibody in *Scophthalmus maximus*.

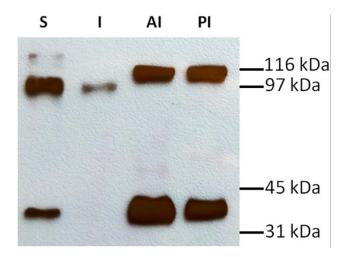
Band ID	Presence of	Protein	Uniprot	Uniprot -	#Peptides	#Unique	#Sequences	SC	MWt
Ballu ID	E-cadherin	description	Code	10lgP				(%)	(kDa)
		Cadherin-1 OS=					R.PANPD		
110 kDa Band	YES	Fundulus	A0A146 XRX5	47,63	1	1	ELGNFID	2	83.6
Dund		heteroclitus PE=4 SV=1					DNLK.A)	,
		Cadherin-1							
38 kDa	YES	OS=	A0A146			\sim	R.PANPD		
Band		Fundulus heteroclitus	XRX5	37,07		1	ELGNFID DNLK.A	2	83.6
		PE=4 SV=1			20				
110 kDa		E–cadherin protein		\mathbf{X}			D.NQGLS		
Band	YES	sequence of	$\mathbf{}$	-	1	1	QDNTVQ TK.V*	1.3	110
		S. maximus		T					

457 Different parameters supporting the successful protein identification of E-cadherin by MS are

458 indicated: PEAKS protein score (-10lgP), number of matching total and unique peptides (FDR <

459 1%), peptide sequences, % sequence coverage (SC) and theoretical protein mass (MWt).

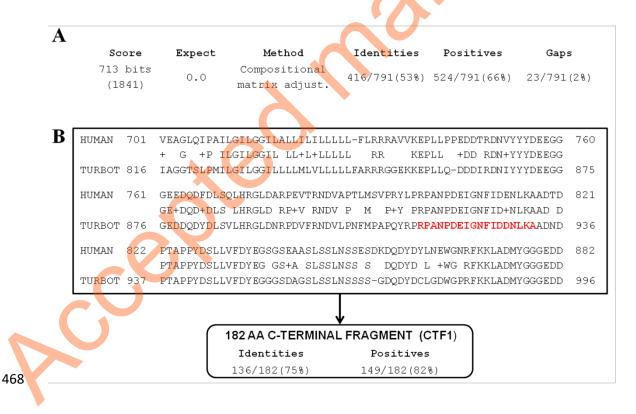
- 460 *Obtained by *de novo* sequencing using PEAKS algorithm and alignment with E–cadherin protein
- 461 sequence of *S. maximus* using the BLASTP 2.6.1 (Score: 28.9 bits(63); Expect: 1^{e-06}; Method:
- 462 Compositional matrix adjust; Identities: 13/13(100%); Gaps: 0/13(0%)).



- 463
- 464 Fig 1. Western blot analysis of E-cadherin expression in protein extracts from

465 **human and turbot** (*Scophthalmus maximus*) **tissues.** S = human skin; I = human ileum;

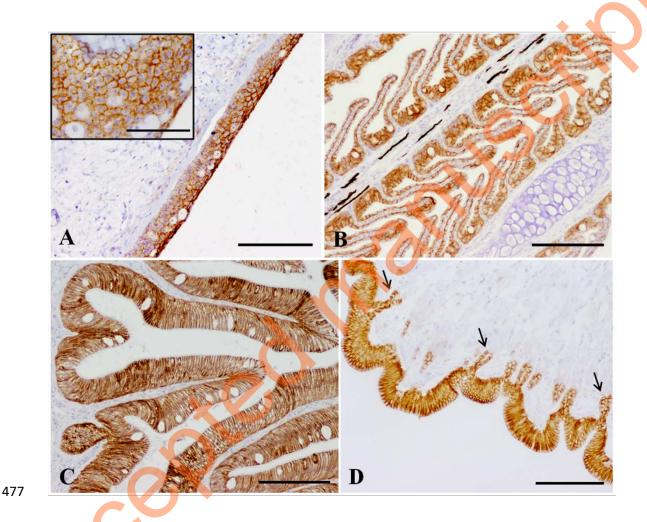
- AI = turbot anterior intestine; PI = turbot posterior intestine. At the right, the position of
- the molecular weight standards is indicated.



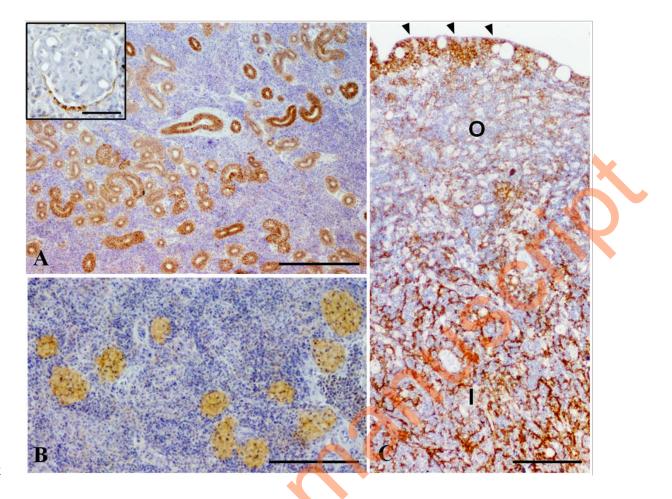
469 Fig 2. Comparisons between human and turbot E-cadherin amino acid sequences.

- 470 A) Output of BLASTp alignment of human (P12830) and turbot (*Scophthalmus maximus*)
- 471 E-cadherin. B) Comparison between the amino acid sequences of the C-terminal fragment

known in human as CTF1 and its counterpart in turbot. The amino acids highlighted in
red corresponds to the unique peptide sequence found by nano-LC-MS/MS analysis of
the excised bands from Western blot in turbot tissues that matched with the E-cadherin
sequence of the teleost *Fundulus heteroclitus*. Conservative amino acid changes are
shown by a "+" sign between the aligned residues.

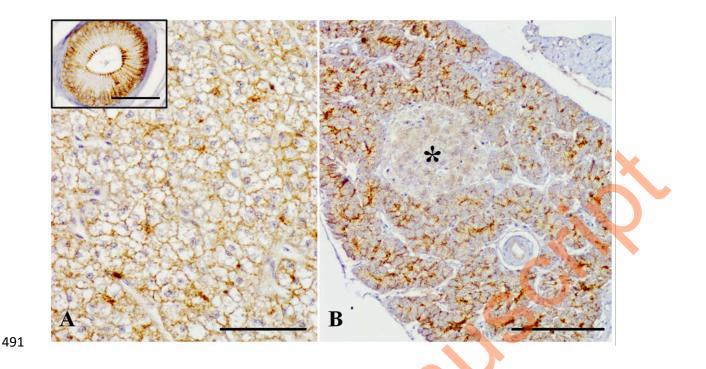


478 Fig 3. E-cadherin immunolocalisation at cell-cell contacts in the lining epithelia of 479 turbot skin (A), gills (B), intestine (C) and stomach (D). Note the immunoreaction of 480 the gastric pits (3D, arrows), while this is not present in the underlying gastric glands. 481 Bars = $100 \mu m$ (Inset $3A = 50 \mu m$).



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Fig 4. E-cadherin immunohistochemical expression in turbot (Scophthalmus 483 maximus) kidney (A), spleen (B) and thymus (C). A) The immunoreaction was 484 485 observed in the epithelia of the renal ducts and tubules, as well as in the epithelium of the Bowman's capsule (inset). Bar = $200 \mu m$; Inset's bar = $25 \mu m$. B) Immunostaining of the 486 splenic melano-macrophage centres. Bar = $100 \,\mu m. C$) Immunolocalisation of E-cadherin 487 in thymus stroma, showing a stronger staining intensity in the inner (I) than in the outer 488 489 (O) part of the organ. Note also the immunoreaction of the epithelium separating the 490 thymus from the gill chamber (arrowheads). Bar = $100 \,\mu$ m.



492 Fig 5. E-cadherin immunohistochemistry in turbot (*Scophthalmus maximus*) liver
493 (A) and pancreas (B). A) Membranous staining pattern of the hepatocytes and in the
494 epithelium of a biliar duct (Inset). Bars = 50 µm. B) Immunostaining of E-cadherin at

495 cell-cell contacts between acinar cells, while this is not noticed in a pancreatic islet of

496 Langerhans (star). Bar = $100 \,\mu m$.

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