

1 **Characterization of *Pediococcus acidilactici* strains isolated from rainbow trout**
2 **(*Oncorhynchus mykiss*, Walbaum) feed and larvae: safety, DNA fingerprinting and**
3 **bacteriocinogenicity**

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23 **Running page head:** Safety, DNA fingerprinting and bacteriocinogenicity of
24 **pediococci**

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30 **ABSTRACT**

31 The use of Lactic Acid Bacteria (LAB) as probiotics constitutes an alternative or
32 complementary strategy to chemotherapy and vaccination for disease control in
33 aquaculture. The objectives of this work were (i) the *in vitro* safety assessment of 8
34 *Pediococcus acidilactici* strains isolated from rainbow trout feed and larvae; (ii) the
35 evaluation of their genetic relatedness; (iii) the study of their antimicrobial/bacteriocin
36 activity against fish pathogens, and (iv) the biochemical and genetic characterization of
37 the bacteriocin produced by the strain displaying the greatest antimicrobial activity.
38 Concerning the safety assessment, none of the pediococci showed antibiotic resistance
39 nor produced hemolysin or gelatinase, degraded gastric mucin or deconjugated bile
40 salts. Four strains (50%) produced tyramine or putrescine, but the corresponding genes
41 were not successfully amplified by PCR. ERIC-PCR fingerprinting allowed clustering
42 of the pediococci into 2 well-defined groups (68% similarity). From the 8 pediococci
43 displaying direct antimicrobial activity against, at least, 3 out of 9 fish pathogens, 6
44 strains (75%) were identified as bacteriocin producers. The bacteriocin produced by *P.*
45 *acidilactici* L-14 was purified, and mass spectrometry and DNA sequencing revealed its
46 identity to be pediocin PA-1 (PedPA-1). Altogether, our results allowed the
47 identification of 4 (50%) putatively safe pediococci, including 2 bacteriocinogenic
48 strains. ERIC-PCR fingerprinting was a valuable tool for genetic profiling of *P.*
49 *acidilactici* strains. This work reports for the first time the characterization of a PedPA-
50 1-producing *P. acidilactici* strain isolated from an aquatic environment (rainbow trout
51 larvae), which shows interesting properties related to its potential use as probiotic in
52 aquaculture.

53 **Keywords:** Aquaculture, rainbow trout (*Oncorhynchus mykiss*, Walbaum), Lactic Acid
54 Bacteria, *Pediococcus acidilactici*, anti-fish pathogen activity, fish probiotics

55 **INTRODUCTION**

56 One of the major challenges for modern aquaculture is fish mortality, mainly at the
57 larval stage, attributed to opportunistic and pathogenic bacteria and resulting in
58 important economic losses (Villamil et al. 2010, Pérez-Sánchez et al. 2014). Several
59 approaches have been used to prevent and/or treat bacterial diseases, including (i)
60 effective management of stock, soil, water, nutrition and environment; (ii) sanitary
61 prophylaxis; (iii) water disinfection, (iv) vaccination, and (v) chemotherapy (mainly the
62 use of antibiotics) (Ringø et al. 2010). However, the use of antibiotics is expensive and
63 may induce resistance in the bacterial pathogens through mutations of indigenous genes
64 and/or acquisition of antibiotic resistance genes by mobile genetic elements (Panigrahi
65 & Azad 2007, Ringø et al. 2010). Despite the fact that vaccination seems to constitute
66 the ideal control method, effective commercial vaccines against some fish pathogens are
67 not available yet. Vaccine efficacy can differ due to variable pathogenicity mechanisms
68 displayed by a single pathogen species, and vaccines cannot prevent disease outbreaks
69 in immunologically immature individuals (Subasinghe et al. 2009, Toranzo et al. 2009).
70 In addition, vaccination is laborious, costly, and highly stressful to the animals,
71 retarding their growth (EFSA 2008, Gillor et al. 2008).

72 A suitable alternative for disease control is the use of probiotics, which do not induce
73 the adverse effects of antibiotics and other chemotherapeutic agents (Nayak 2010). In
74 aquaculture, probiotics are considered as live beneficial microbial adjuncts that modify
75 the host-associated or ambient microbial community, improve feed use or its nutritional
76 value, enhance the host response to diseases, and/or improve the physico-chemical and
77 microbiological quality of the surrounding environment (Verschuere et al. 2000, Pérez-
78 Sánchez et al. 2014, Hai 2015). Moreover, inactivated forms of bacteria (*i.e.*, dead
79 cells), cell components, or extra-cellular compounds have also shown probiotic effects

80 (Nayak 2010). Lactic Acid Bacteria (LAB) are the bacterial group most commonly
81 proposed as probiotics in aquaculture (Gatesoupe 2008, Pérez-Sánchez et al. 2014,
82 Ringø et al. 2014); nevertheless, to date, only *Pediococcus acidilactici* CNCM MA18/5
83 M (Bactocell®) has been legally authorized for this purpose in the European Union
84 [Commission Regulation (EC) No. 911/2009 and Commission Implementing
85 Regulation (EU) No. 95/2013]. Most LAB are considered as non-pathogenic and non-
86 opportunistic microorganisms and awarded the Qualified Presumption of Safety (QPS)
87 status granted by the European Food Safety Authority (EFSA) in Europe (Liu et al.
88 2009, Gaggia et al. 2010). Recently, LAB isolated from rainbow trout have shown the
89 ability to inhibit the growth of fish pathogens and these strains have been proposed as
90 probiotics to prevent bacterial fish diseases (Pérez-Sánchez et al. 2014, Ringø et al.
91 2014). The genus *Pediococcus* is one of the best characterized LAB groups, and
92 pediococci have been isolated from ripened cheese, processed meat, plant materials and
93 fish (Cai et al. 1999, Todorov & Dicks 2009, Araújo et al. 2015a) and are used as starter
94 cultures for the production of fermented foods (Lee et al. 2014). Furthermore, some
95 pediococci produce ribosomally-synthesized antimicrobial peptides referred to as
96 bacteriocins (pediocins), and PA-1/AcH (PedPA-1) is the most thoroughly characterized
97 pediocin (Papagianni & Anastasiadou 2009). The operon of this bacteriocin includes
98 four genes: the structural gene (*pedA*), the immunity gene encoding an immunity protein
99 that protects the bacteriocin producer from its own bacteriocin (*pedB*), the gene
100 encoding the ABC transporter for secretion (*pedC*), and the gene encoding a
101 complementary protein of unknown function (*pedD*) (Papagianni & Anastasiadou
102 2009). PedPA-1 was firstly identified in *P. acidilactici* PAC1.0 (Marugg et al. 1992),
103 and is the subclass IIa bacteriocin most effective against spoilage and food-borne
104 pathogens (Devi & Halami 2011). A previous study demonstrated that repeated doses

105 (250 µg/day for three consecutive days) of purified pediocin PA-1 given to *Listeria*
106 *monocytogenes*-infected mice resulted in a significant reduction of fecal listerial counts
107 and slowed pathogen translocation into the liver and spleen, leading to the
108 disappearance of *L. monocytogenes* infection in both organs within 6 days (Dabour et al.
109 2009).

110 The objectives of this work were (i) the *in vitro* safety assessment of 8 *P. acidilactici*
111 strains isolated from rainbow trout (*Oncorhynchus mykiss*, Walbaum) feed and larvae
112 using a previously described subtractive screening method (Muñoz-Atienza et al. 2013);
113 (ii) the evaluation of their genetic relatedness; (iii) the study of their
114 antimicrobial/bacteriocin activity against fish pathogens, and (iv) the biochemical and
115 genetic characterization of the bacteriocin produced by the strain (first determined to be
116 safe) which showed the most interesting antimicrobial properties to be used as probiotic
117 in aquaculture.

118

119 **MATERIALS AND METHODS**

120 **Sampling procedure and LAB isolation**

121 Samples of rainbow trout feed and larvae were obtained from a rainbow trout farm
122 located in the south of Spain. Due to commercial confidentiality, the feed brand used in
123 the farm is not given. However, the feed did not contain any bacterial additive and it
124 was confirmed that no additional supplements were added to feed or fish in the farm.
125 The feed was received in a sterilized condition from the manufacturer, and the
126 hypothesis was that feed was colonized by bacterial species from the farm environment.
127 LAB were isolated from commercial rainbow trout feed (a pool of 3 different samples, 1
128 g each), and independent composite samples from whole larvae (10 specimens; 5 days
129 post-hatching) disinfected with benzalkonium chloride (Sigma-Aldrich Co., Ltd., St.
130 Louis, Missouri, USA) (0.1% v/v, 30 s) and rinsed twice with 10 mM phosphate-

131 buffered saline (PBS; pH 7.2). The samples were 10-fold diluted in sterile peptone
132 water (Oxoid, Ltd., Basingstoke, United Kingdom), and homogenized in a Stomacher.
133 Then, the sample was pour-plated (three plates per dilution) in de Man, Rogosa and
134 Sharpe (MRS, Oxoid, Ltd., Basingstoke, United Kingdom) agar (1.5% w/v) and
135 incubated at 15 °C in microaerobiosis (plate overlying with an agar medium layer) for
136 3-7 days.

137

138 **Bacterial strains and growth conditions**

139 In this study, we used the strain *P. acidilactici* L-14, previously isolated from
140 aquacultured rainbow trout larvae by Araújo et al. (2015a) (not labelled as L-14 in that
141 study), and the strains isolated here from aquacultured rainbow trout feed. *P.*
142 *acidilactici* L-14, the strains isolated from feed, the Gram-positive fish pathogens
143 (*Lactococcus garvieae* JIP29-99, *Lc. garvieae* CECT5807, *Lc. garvieae* CF01144, *Lc.*
144 *garvieae* CF00021 and *Carnobacterium maltaromaticum* LMG14716), and the indicator
145 microorganism *Pediococcus damnosus* CECT4797 were aerobically grown in MRS at
146 30 °C. *Streptococcus iniae* LMG14521 was aerobically grown in Brain Heart Infusion
147 (BHI) broth (Oxoid) at 37 °C. The Gram-negative fish pathogens *Yersinia ruckeri*
148 LMG3279 and *Aeromonas salmonicida* LMG3776 were aerobically grown in Tryptone
149 Soya Broth (TSB; Oxoid) at 28 °C, while *Vibrio campbellii* LMG21363 was aerobically
150 grown in TSB supplemented with NaCl (1% w/v; Panreac Química S.A.U, Barcelona,
151 Spain) at 28 °C. *L. monocytogenes* CECT4032 and *L. innocua* CECT910 were cultured
152 in Brain Heart Infusion (BHI, Oxoid) at 30 °C.

153

154 **Direct antimicrobial activity assays**

155 A total of 26 LAB isolates recovered from rainbow trout feed and the strain *P.*
156 *acidilactici* L-14 were assayed for antimicrobial activity against the 9 fish pathogens
157 cited above by a stab-on-agar test (SOAT) as previously described by Cintas et al.
158 (1995). Briefly, each candidate strain was stabbed onto MRS agar and incubated at 30
159 °C for 5 h, and then 40 ml of the corresponding soft agar (0.8% w/v) medium
160 containing about 1×10^5 CFU ml⁻¹ of the pathogen was poured onto the plates. After
161 incubation at 28–37 °C for 16–24 h, depending on the optimum growth conditions for
162 each tested pathogen, the plates were checked for inhibition zones (absence of visible
163 microbial growth around the stabbed cultures), and only inhibition halos with diameters
164 above 3 mm were considered positive.

165

166 **Taxonomic identification**

167 The LAB isolates from rainbow trout feed showing antimicrobial activity against, at
168 least, 3 of the tested fish pathogens were taxonomically identified by DNA sequencing
169 of the PCR-amplified gene encoding a fragment of the 16S rRNA subunit (*16S rDNA*)
170 (Kullen et al. 2000). PCR-amplifications were performed from total bacterial DNA
171 purified using the InstaGene Matrix resin (Bio-Rad Laboratories Inc., Hercules, CA,
172 USA), in 50 µl reaction mixtures with 5 to 50 ng of purified DNA, 0.7 µmol l⁻¹ of each
173 primer and 25 µl of MyTaq PCR mix (Bioline, London, UK) in an Eppendorf
174 Mastercycler thermal cycler (Eppendorf, Hamburg, Germany). The oligonucleotide
175 primers used for PCR amplification of *16S rDNA* were obtained from Sigma-Genosys
176 Ltd. (Cambridge, United Kingdom) (Table 1). PCR products were analyzed by
177 electrophoresis on 1.5% (w/v) agarose (Pronadisa, Madrid, Spain) gels stained with
178 GelRed (Biotium, California, USA), and visualized with the Gel Doc 1000
179 documentation system (Bio-Rad, Madrid, Spain). HyperLadder II (Bioline GmbH,

180 Germany) was used as molecular size marker. The amplicons were purified by using the
181 NucleoSpin Extract II kit (Macherey & Nagel, Düren, Germany) and both DNA strands
182 were sequenced at the Unidad de Genómica (Parque Científico de Madrid, Facultad de
183 Ciencias Biológicas, Universidad Complutense de Madrid, Spain). Analysis of *16S*
184 *rDNA* sequences was performed with the BLAST program available at the National
185 Center for Biotechnology Information (NCBI; blast.ncbi.nlm.nih.gov). Only sequence
186 similarities above 97% were considered significant for bacterial identification at the
187 species level.

188

189 **Antibiotic susceptibility determination**

190 The minimum inhibitory concentrations (MICs) of 8 antibiotics against the 8 *P.*
191 *acidilactici* strains, identified following *16S rDNA* sequencing, were determined by a
192 broth microdilution test (Klare et al. 2005). The tested antibiotics were ampicillin (0.5
193 to 32 $\mu\text{g ml}^{-1}$), gentamicin (2 to 128 $\mu\text{g ml}^{-1}$), kanamycin (4 to 256 $\mu\text{g ml}^{-1}$),
194 streptomycin (4 to 256 $\mu\text{g ml}^{-1}$), erythromycin (0.12 to 8 $\mu\text{g ml}^{-1}$), clindamycin (0.12 to
195 8 $\mu\text{g ml}^{-1}$), tetracycline (1 to 64 $\mu\text{g ml}^{-1}$), and chloramphenicol (0.5 to 32 $\mu\text{g ml}^{-1}$).
196 Individual colonies were suspended in 5 ml of saline solution (0.85% NaCl) to a
197 turbidity of 1 in the McFarland scale (*ca.*, 3×10^8 CFU ml^{-1}) and subsequently 1000-
198 fold diluted in LSM broth, consisting of Iso-sensitest (IST) (Oxoid) and MRS broth
199 (IST:MRS, 9:1; pH 6.7). A volume of 50 μl of the diluted suspensions was added to
200 microplate wells containing 50 μl of LSM broth with the different antibiotic
201 concentrations. After incubation at 37 °C for 18 h, MICs were interpreted according to
202 the breakpoints established by the EFSA (2012). Strains showing MICs higher than the
203 respective breakpoint were considered as resistant. *Enterococcus faecalis* CECT795 and
204 *Staphylococcus aureus* CECT794 were used for quality control.

205

206 **Hemolysin and gelatinase production**

207 The production of hemolysin and gelatinase by the 8 *P. acidilactici* strains was
208 determined as previously described (Eaton & Gasson 2001, Muñoz-Atienza et al. 2013).
209 Briefly, cultures grown in MRS broth were streaked onto COH agar plates (Columbia
210 agar + 5% [v/v] horse blood; BioMérieux, Marcy l'Étoile, France). After plate
211 incubation at 37 °C for 1-2 days, β -hemolysin production was revealed by the presence
212 of clear zones of hydrolysis around the colonies. Moreover, in order to evaluate the
213 production of gelatinase, cultures grown in MRS broth were streaked onto Todd-Hewitt
214 (Oxoid) agar plates (1.5%, w/v) containing 30 g of gelatine per liter. After overnight
215 incubation at 37 °C, the plates were placed at 4 °C for 5 h before examination for the
216 presence of zones of turbidity (protein hydrolysis) around the colonies. *E. faecalis* P4
217 (Eaton & Gasson 2001) was used as positive control in both assays.

218

219 **Mucin degradation**

220 The ability of 8 the *P. acidilactici* strains to degrade gastric mucin was determined as
221 described by Zhou et al. (2001). Mucin from porcine stomach type III (Sigma-Aldrich)
222 and agar were incorporated into medium B without glucose at concentrations of 0.5 and
223 1.5% (w/v), respectively. Briefly, 10 μ l of cultures grown in MRS broth were spotted
224 onto the surface of medium B with mucin. The plates were anaerobically (Anaerogen,
225 Oxoid) incubated at 37 °C for 72 h. After incubation, the plates were stained with a
226 mixture of 0.1% (w/v) amido black (Merck KGaA, Darmstadt, Germany) in 3.5 mol l⁻¹
227 acetic acid for 30 min, and then washed with 1.2 mol l⁻¹ acetic acid (Merck KGaA). The
228 presence of a discoloured zone around the colony was considered as a positive result. A

229 fresh fecal slurry from a healthy adult cow was used as positive control of mucinolytic
230 activity.

231

232 **Biogenic amine production**

233 The detection of production of biogenic amines (histamine, tyramine, putrescine and
234 cadaverine) by the 8 *P. acidilactici* strains was first carried out according to the plate
235 assay described by Bover-Cid and Holzapfel (1999). Briefly, cultures grown in MRS
236 broth were streaked on the improved decarboxylase differential growth medium with
237 and without (negative control) the corresponding amino acid precursor (1% w/v,
238 histidine, tyrosine, ornithine and lysine). After plate incubation at 37 °C for 4 days
239 under anaerobic conditions (Anaerogen), the plates were examined for the presence of
240 histidine decarboxylase (HDC), tyrosine decarboxylase (TDC), ornithine decarboxylase
241 (ODC) and lysine decarboxylase (LDC) activities. Biogenic amine production was
242 detected by a yellow to violet color change of the decarboxylase medium due to the
243 alkalization produced by the decarboxylation of the corresponding amino acid
244 precursor. *Lactobacillus brevis* CECT4121 and *Lactobacillus* sp. 30a (García-Moruno
245 et al. 2005) were used as positive controls for tyramine, and histamine and putrescine
246 production, respectively. Subsequently, the presence of the genes encoding HDC (*hdc*),
247 TDC (*tdc*), ODC (*odc*) and LDC (*ldc*) in the 8 *P. acidilactici* strains was analyzed by
248 PCR. *Lactobacillus brevis* CECT4121 and *Lactobacillus* sp. 30a were used as positive
249 controls. PCR-amplifications were performed as previously described (Le Jeune et al.
250 1995, Coton et al. 2004, Marcobal et al. 2005, de las Rivas et al. 2006) (Table 1) and
251 PCR-product visualization and sequence analysis were performed as described above.

252

253 **Bile salt deconjugation**

254 The ability of the 8 *P. acidilactici* to deconjugate primary and secondary bile salts was
255 determined according to Noriega et al. (2006). Bile salt plates were prepared by adding
256 0.5% (w/v) sodium salts of taurocholate or taurodeoxycholate (Sigma-Aldrich
257 Corporation, St. Louis, Missouri, USA) to MRS agar (1.5%, w/v) supplemented with
258 0.05% (w/v) L-cysteine (Merck KGaA). Briefly, 10 µl of cultures grown in MRS broth
259 were spotted onto agar plates and incubated at 37 °C for 72 h under anaerobic
260 conditions (Anaerogen, Oxoid). The presence of precipitated bile acid around the
261 spotted-culture (opaque halo) was considered as a positive result. A fresh fecal slurry of
262 a healthy adult cow was used as positive control.

263

264 **Enterobacterial Repetitive Intergenic Consensus-PCR (ERIC-PCR)**

265 Genetic profiling of the 8 *P. acidilactici* strains by ERIC-PCR was performed using the
266 primers ERIC-1R and ERIC-2 (Table 1) as previously described (Versalovic et al.
267 1991). PCR-amplifications were performed from total bacterial DNA, obtained by using
268 the InstaGene Matrix resin (Bio-Rad Laboratories Inc.), in 50 µL reaction mixtures with
269 2 µL of purified DNA, 0.7 µmol l⁻¹ of each primer, 3 mmol l⁻¹ of MgCl₂ and 25 µl of
270 MyTaq PCR mix in a Eppendorf Mastercycler thermal cycler. PCR products were
271 analyzed by electrophoresis on 1.5% (w/v) agarose gels stained with GelRed at 90V for
272 90 min. PCR-product visualization and analysis were performed as described above.
273 The molecular size marker used was the 1 Kb Plus DNA ladder (Invitrogen, Madrid,
274 Spain). Cluster analyses were performed using the unweighted-pair-group method with
275 arithmetic averages (UPGMA) using the PhoretixTM 1D Advanced (Nonlinear
276 Dynamics Ltd, Newcastle upon Tyne, UK) software. *P. acidilactici* 347 (Cintas et al.
277 1998) and *P. acidilactici* MA18/5M (Bactocell®) were used as controls.

278

279 **Extracellular antimicrobial (bacteriocin) activity assay**

280 The antimicrobial activity of cell-free supernatants from the 8 *P. acidilactici* cultures
281 grown in MRS broth at 30 °C for 16 h against the indicator microorganisms *P.*
282 *damnosus* CECT4797, *L. monocytogenes* CECT4032, *L. innocua* CECT910, *Lc.*
283 *garvieae* CF01144, *Lc. garvieae* CECT5807, *Lc. garvieae* CF00021 and *A. salmonicida*
284 LMG3776 was determined by an agar well-diffusion test (ADT) as previously described
285 by Cintas et al. (1995). Briefly, supernatants were obtained by centrifugation of cultures
286 at 10,000 × g at 4 °C for 10 min, adjusted to pH 6.2 with 1 mol l⁻¹ NaOH, filter-
287 sterilized through 0.22 µm-pore-size filters (Millipore Corp., Bedford, Massachussets,
288 USA) and stored at -20°C until use. Fifty-µl aliquots of supernatants were placed into
289 wells (6-mm diameter) cut in cooled MRS (0.8%, w/v) plates previously seeded (1 ×
290 10⁵ CFU ml⁻¹) with the indicator microorganisms. After 2 h at 4 °C, the plates were
291 incubated under the conditions mentioned in the bacterial strains and growth conditions
292 section and then analyzed for the presence of inhibition zones around the wells. To
293 determine the nature and thermostability of the antimicrobial compounds, the
294 supernatants showing antimicrobial activity were (i) treated with proteinase K (10 mg
295 ml⁻¹) (AppliChem GmbH, Germany) at 37 °C for 2 h and then heated at 100 °C for 10
296 min to inactivate the enzyme, and (ii) heated at 100 °C for 10 min. After treatments,
297 samples were assayed for residual antimicrobial activity by an ADT as described above,
298 using *P. damnosus* CECT4797 and *L. monocytogenes* CECT4032 as indicator
299 microorganisms. Non-treated supernatants were used as positive controls.

300

301 **Bacteriocin purification and mass spectrometry analysis**

302 The bacteriocin produced by *P. acidilactici* L-14 was purified using a modification of
303 the multi-chromatographic procedure described by Cintas et al. (1995). Briefly, the

304 bacteriocin was purified from a 1-liter culture grown in MRS at 30 °C until the early
305 stationary phase (approximately, 16 h). The cell-free culture supernatant was subjected
306 to protein precipitation with ammonium sulphate (50% [w/v]; Merck). The pellet and
307 floating materials were mixed and solubilized in 100 ml of 20 mM sodium phosphate
308 buffer (NaP) (pH 6.0), and subsequently desalted by gel filtration (PD-10 columns; GE
309 Healthcare Life Sciences, Barcelona, Spain). The resulting fractions were further
310 subjected to cationic-exchange (SP Sepharose Fast Flow, GE Healthcare) and
311 hydrophobic-interaction (Octyl Sepharose CL-4B, GE Healthcare) chromatographies,
312 followed by reversed-phase chromatography (PepRPC HR 5/5) in a Fast Protein Liquid
313 Chromatography system (ÄKTA-FPLC) (GE Healthcare). The antimicrobial activity of
314 the fractions obtained during the purification procedure was determined by a microtiter
315 plate assay (Cintas et al. 1998) using *L. monocytogenes* CECT4032 as indicator
316 microorganism. Briefly, two-fold serial dilutions of the purified bacteriocin in MRS
317 broth were prepared in microtiter plates. The wells were then filled up to 200 µl by the
318 addition of 150 µl of a diluted (in BHI broth) fresh overnight culture of the indicator
319 microorganism (*ca.*, 1×10^5 CFU ml⁻¹). After incubation at 30 °C for 16 h, growth
320 inhibition of *L. monocytogenes* CECT4032 was measured spectrophotometrically at 620
321 nm with a microtiter plate reader (Labsystems iEMS Reader MF, Labsystems, Helsinki,
322 Finland). One bacteriocin unit (BU) was defined as the reciprocal of the highest dilution
323 of supernatant or purified bacteriocin causing 50% growth inhibition (50% of the
324 turbidity of the control culture without bacteriocin). Fractions displaying a high and
325 specific bacteriocin activity were pulled together and rechromatographed on the same
326 reversed-phase column until chromatographically pure bacteriocin peptides were
327 obtained. The purified peptide was subjected to mass spectrometry analysis in a Matrix-
328 Assisted Laser Desorption Ionization-Time Of Flight Voyager-DE STR mass

329 spectrometer (MALDI-TOF MS) (PerSeptive Biosystems, Foster City, California,
330 USA), at the Mass Spectrum Service of the Centro de Genómica y Proteómica (Parque
331 Científico-UCM, Madrid, Spain).

332

333 **Nucleotide sequencing of the PA-1 structural and immunity genes**

334 The nucleotide sequence encoding the structural (*pedA*) and immunity (*pedB*) genes of
335 PedPA-1 was determined using specific primer-pairs based on the published DNA
336 sequence of the PedPA-1 operon in *P. acidilactici* PAC1.0 (GenBank accession number
337 M83924) (Marugg et al. 1992). Overlapping PCR products of approximately 400-bp in
338 length were obtained and subsequently electrophoresed, visualized and purified, and
339 both DNA strands sequenced and analyzed, as described above.

340

341 **RESULTS**

342 **Isolation of LAB from rainbow trout feed and direct antimicrobial activity**

343 A total of 26 LAB isolates were recovered from the rainbow trout feeds, of which 7
344 displayed direct antimicrobial activity against, at least, 3 out of the 9 tested fish
345 pathogens (Table 2). In addition, *P. acidilactici* L-14, isolated previously in Araújo et
346 al. (2015) from rainbow trout larvae, was the most active strain, inhibiting a total of 7
347 fish pathogens. According to the sizes of the inhibition halos, the most susceptible
348 indicators were *Lc. garvieae* JIP29-99, *Lc. garvieae* CF00021 and *Lc. garvieae*
349 CF01144, followed by *Lc. garvieae* CECT5807, *A. salmonicida* LMG3776 and *C.*
350 *maltaromaticum* LMG14716. On the contrary, *S. iniae* LMG14521, *Y. ruckeri*
351 LMG3279 and *V. campbellii* LMG21363 were the most resistant indicator
352 microorganisms. The strains *P. acidilactici* L-14 (isolated from larvae) and *P.*

353 *acidilactici* NF1-1, NF1-5, NF1-7 and NF1-25 (isolated from feed) displayed a broad
354 antimicrobial spectrum and inhibited most of the tested *Lc. garvieae* strains.

355

356 **Taxonomic identification**

357 The 7 isolates recovered from rainbow trout feed showing antimicrobial activity against,
358 at least, 3 of the tested fish pathogens were identified by nucleotide sequencing of *16S*
359 *rDNA* as *P. acidilactici*, showing 100% similarity to the sequences available at the
360 NCBI database.

361

362 **Safety assessment**

363 The 7 selected *P. acidilactici* strains isolated from rainbow trout feed and *P. acidilactici*
364 L-14 were submitted to a comprehensive *in vitro* safety assessment procedure including
365 several microbiological, biochemical and genetic assays. MIC distribution of the tested
366 antibiotics is summarized in Table 3. The microbiological breakpoints established by
367 EFSA (2012) were used to categorize the 8 pediococci as susceptible or resistant strains.
368 According to our results, all the strains were susceptible to the antibiotics tested in this
369 work (Table 3). Moreover, none of the 8 pediococci produced hemolysin or gelatinase,
370 degraded gastric mucin or deconjugated primary or secondary bile salts (results not
371 shown). On the other hand, a total of 4 (50%) strains produced one of the tested
372 biogenic amines. With regard to this, 2 strains (25%) (*P. acidilactici* NF1-5 and NF1-
373 12) produced tyramine and 2 strains (25%) (*P. acidilactici* NF1-1 and NF-10) produced
374 putrescine; however, the respective genes, *tdc* and *odc*, were not detected by PCR in
375 these strains. None of the tested strains produced histamine or cadaverine (results not
376 shown). Altogether, our results showed that 4 strains (*P. acidilactici* L-14, NF1-7, NF1-
377 18 and NF1-25) are putatively safe pediococci.

378

379 **Genetic profiling**

380 ERIC-PCR fingerprinting of the 8 *P. acidilactici* strains revealed 2 well-defined groups
381 (G1 and G2; 68% similarity). Furthermore, the 8 pediococci were clustered in 3 well-
382 defined sub-groups (SG1.1, SG1.2 and SG2.1) with similarity coefficients above 75%
383 (Fig. 1). The strains NF1-12 and NF1-25 were the most closely related, presenting
384 100% of similarity (SG1.2).

385

386 **Extracellular antimicrobial activity**

387 Six out of the 8 *P. acidilactici* strains (NF1-1, NF1-5, NF1-7, NF1-10, NF1-12 and *P.*
388 *acidilactici* L-14) (75%) displayed extracellular antimicrobial activity in their
389 supernatants against *P. damnosus* CECT4797, but only 2 (25%) of them (*P. acidilactici*
390 L-14 and NF1-1) were active against the 2 tested *Listeria* spp, with *P. acidilactici* L-14
391 displaying the strongest antilisterial activity. None of the supernatants from tested
392 strains inhibited the growth of the fish pathogens *Lc. garvieae* CF01144, *Lc. garvieae*
393 CECT5807, *Lc. garvieae* CF00021 and *A. salmonicida* LMG3776 (Table 4).
394 Interestingly, the antimicrobial activity of the supernatants disappeared completely after
395 proteinase K treatment, but was not sensitive to heating, revealing the proteinaceous
396 nature and heat stability of the secreted antimicrobial compounds (*i.e.*, heat-stable
397 bacteriocins). Interestingly, from the 6 bacteriocinogenic strains, only *P. acidilactici*
398 NF1-7 and *P. acidilactici* L-14 were considered as putatively safe.

399

400 **Purification and genetic characterization of the bacteriocin produced by *P.***
401 ***acidilactici* L-14**

402 The results of the purification of the bacteriocin produced by *P. acidilactici* L-14 are
403 summarized in Table 5. The final RP-FPLC resulted in a major well-separated
404 absorbance peak with antimicrobial activity against *L. monocytogenes* CECT4032,
405 which eluted at 19% (v/v) 2-propanol in aqueous 0.1% (v/v) trifluoroacetic acid (Fig.
406 2). This fraction showed an increment of $8.1 \times 10^8\%$ of the bacteriocin activity
407 originally present in the culture supernatant, and an outstanding 6.3×10^{11} -fold increase
408 in the specific antimicrobial activity (Table 5). The purity and molecular mass of the
409 bacteriocin was confirmed by MALDI-TOF MS, which revealed a major peptide with a
410 molecular mass of 4,621.8 Da, as well as a second peptide peak with a molecular mass
411 of 4,637.6 Da (Fig. 3).

412 Blast analysis of the sequence of 770 contiguous nucleotides (including the genes *pedA*
413 and *pedB*) of the PedPA-1 gene cluster of *P. acidilactici* L-14 revealed 100% similarity
414 to the sequence of the bacteriocin operon from *P. acidilactici* PAC1.0 (Marugg et al.
415 1992).

416

417 **DISCUSSION**

418 In this work, 26 LAB isolates were recovered from rainbow trout feed samples. From
419 these isolates, a total of 7 were selected for further characterization due to their direct
420 antimicrobial activity against, at least, 3 of the tested fish pathogens, and were
421 taxonomically identified as *P. acidilactici*. In addition, *P. acidilactici* L-14, a strain
422 previously isolated from a rainbow trout larvae (Araújo et al. 2015a), showed direct
423 antimicrobial activity against 7 of the tested fish pathogens. The extracellular
424 antimicrobial (bacteriocin) activity, safety assessment and genetic relatedness of these 8
425 *P. acidilactici* strains were determined in order to select the most suitable strain to be
426 used as a probiotic for aquaculture.

427 Our group has recently demonstrated the *in vivo* effectiveness of nisin Z, a peptide
428 produced by *Lactococcus lactis*, in protecting rainbow trout against lactococcosis
429 caused by *Lc. garvieae* (Araújo et al. 2015b). In this study, the 8 *P. acidilactici* strains
430 displayed a broad antimicrobial spectrum against fish pathogens, which could be due to
431 different antimicrobial metabolites such as organic acids (mainly lactic acid), hydrogen
432 peroxide, diacetyl, acetaldehyde and/or bacteriocins, with the organic acids and
433 bacteriocins being the key weapons in inhibiting pathogens of relevance for aquaculture
434 (Gillor et al. 2008, Desriac et al. 2010). In this respect, 6 out of 8 *P. acidilactici* strains
435 were found to be bacteriocin producers, based on the proteinaceous nature and heat
436 stability of the antimicrobial agent, which is in agreement with previous studies, where
437 a remarkable high number of LAB displaying antimicrobial activity against fish
438 pathogens were potential bacteriocin producers (Muñoz-Atienza et al. 2013, Gómez-
439 Sala et al. 2015). However, the results indicated that the antimicrobial activity against
440 *Lc. garvieae* exerted by the pediococci was not due to the production of bacteriocins as
441 the antimicrobial effect was only observed in the presence of pediococcal cells.
442 Similarly, Muñoz-Atienza et al. (2013) described several lactic acid bacteria strains with
443 direct but not extracellular antimicrobial activity against *Lc. garvieae*, which can be
444 explained by the fact that the direct antimicrobial activity may be due to the competition
445 for nutrients, which is considered as a desirable probiotic property.

446 The species *P. acidilactici* is awarded with the QPS status since these bacteria are
447 considered neither pathogenic nor opportunistic microorganisms (Liu et al. 2009,
448 Gaggia et al. 2010). With regard to this, according to EFSA, the demonstration of their
449 safety only requires confirmation of the absence of genes encoding resistance to
450 antibiotics of clinical significance in human and veterinary medicine. Nevertheless, in
451 this work we followed a comprehensive previously described *in vitro* subtractive

452 screening (Muñoz-Atienza et al. 2013) with criteria more exhaustive than that
453 established by EFSA to assess the safety of *P. acidilactici* strains, which included not
454 only the evaluation of antibiotic resistance but also hemolysin and gelatinase
455 production, mucin degradation and biogenic amine production.

456 The irresponsible use of antibiotics in aquaculture has contributed to the emergence and
457 spread of antibiotic resistance (Cabello 2006). The genetic determinants encoding
458 antibiotic resistance may be acquired by LAB, such as pediococci, and subsequently
459 horizontally transferred to other bacteria, including animal and human pathogens (Liu et
460 al. 2009). Danielsen et al. (2007) reported the presence of the gene *erm(B)* in a *P.*
461 *acidilactici* strain, which confers acquired resistance to erythromycin, and Tenorio et al.
462 (2001) described the presence of the gene *aac(6')Ie-aph(2'')Ia* in a strain of *P.*
463 *acidilactici*, which confers high-level resistance to gentamicin. Furthermore, the
464 presence of the genes *mef(A/E)* and *lnu(A)*, conferring resistance to erythromycin and
465 lincosamides, respectively, was reported in pediococcal strains (Muñoz-Atienza et al.
466 2013). Interestingly, none of the *P. acidilactici* strains evaluated in our study showed
467 resistance to any of the tested antibiotics. Moreover, none of them produced the
468 virulence factors hemolysin or gelatinase, which is in agreement with previous studies
469 (Albano et al. 2009, Muñoz-Atienza et al. 2013, Mabrouk et al. 2014). In addition, the 8
470 tested strains did not display mucinolytic activity indicating their low invasive and
471 toxigenic potential at the mucosal barrier, which supports that LAB do not degrade
472 mucin *in vitro* and is in agreement with previously published works (Zhou et al. 2001,
473 Delgado et al. 2007, Muñoz-Atienza et al. 2013). The production of biogenic amines
474 (low molecular weight organic bases with biological activity), by the decarboxylation of
475 precursor amino acids through substrate-specific enzymes, by many LAB strains has
476 been associated with undesirable toxic effects for humans (Buňková et al. 2009, Talon

477 & Leroy 2011). In this sense, tyramine poisoning is characterized by hypertension and
478 headache, while histamine or scombroid poisoning is associated with facial flush,
479 vomit, diarrhea, edema, and heart palpitations amongst other symptoms. In the
480 European Union, the presence of histamine is already regulated in some fish products
481 (European Commission, 2005). Other biogenic amines, such as putrescine and
482 cadaverine interfere with the enzymes that metabolize tyramine and histamine,
483 enhancing the adverse effects even if not being toxic by themselves (Landete et al.
484 2007, Buňková et al. 2009). In this work, we found that 4 *P. acidilactici* strains (50%)
485 produced tyramine or putrescine. In a previous study, it was reported that strains of the
486 genus *Pediococcus* were the main producers of tyramine in beer (Izquierdo-Pulido et al.
487 2000). Moreover, *P. acidilactici* strains were identified as low concentration tyramine
488 producers in Robiola di Roccaverano cheese (Bonetta et al. 2008), but other strains were
489 shown as producing high tyramine concentrations in a sardine infusion decarboxylase
490 broth (Kuley et al. 2013). In contrast, several studies showed that pediococcal strains
491 isolated from fermented sausages (Fadda et al. 2001, Albano et al. 2009), traditionally
492 processed fish products (Thapa et al. 2006) and fish and fish products (Muñoz-Atienza
493 et al. 2011) were unable to produce tyramine, cadaverine, histamine and/or putrescine.
494 Interestingly, the respective genetic determinants in the 4 biogenic-amine producing
495 strains identified in our study were not detected by PCR analysis, which may be due to
496 the existence of still unknown genes, to point mutations of the respective genes that
497 could hamper their PCR-amplification or to false-positives. With regard to this, and
498 accordingly to the precautionary principle, we did not consider as safe these 4 *P.*
499 *acidilactici* strains. On the other hand, the ability of probiotic strains to deconjugate bile
500 salts could disrupt the formation of micelles, lipid digestion and absorption of fatty
501 acids and monoglycerides in the intestine, due to the ineffectiveness in the

502 emulsification of dietary lipids, and seriously affect the animal production (Begley et al.
503 2005). None of the 8 tested *P. acidilactici* deconjugated bile salts. It should be
504 mentioned that, according to EFSA, the 8 *P. acidilactici* strains tested in this work could
505 be considered as safe microorganisms to be used in food and feed; however, the *in vitro*
506 subtractive screening procedure used in this work to assess the safety of these *P.*
507 *acidilactici* strains revealed that, based on our more stringent criteria, as discussed
508 above, only 4 of them were considered as safe.

509 PCR fingerprinting methods, such as ERIC-PCR, are valuable tools for genetic typing
510 of microorganisms, and more useful than pulsed-field gel electrophoresis due to a fast
511 and easy execution and the possibility of evaluate many samples simultaneously
512 (Ventura & Zink 2002). A previous work reported the suitability of ERIC-PCR to
513 determine the genetic variability of *P. acidilactici*, *Pediococcus pentosaceus* and
514 *Pediococcus lolii* (Doi et al. 2009). In our work, ERIC-PCR fingerprinting allowed the
515 clustering of the 8 *P. acidilactici* strains isolated from rainbow trout feed and larvae in 2
516 well-defined groups. The 2 groups displayed equal percentages of safe pediococcal
517 strains (50%). Furthermore, the 6 pediococcal strains identified as bacteriocinogenic
518 were grouped in the 3 different subgroups (2 strains by each subgroup [NF1-1 and NF1-
519 12 in SG1.1; L-14 and NF1-10 in SG1.2, and NF1-5 and NF1-7 in SG2.1]). Only 2 out
520 of the 6 bacteriocinogenic strains, included in 2 different subgroups (*P. acidilactici* L-
521 14 and *P. acidilactici* NF1-7), were considered as safe. The bacteriocinogenic strains *P.*
522 *acidilactici* NF1-5 and NF1-7 were the most closely related to the commercial probiotic
523 *P. acidilactici* MA18/5M (Bactocell), with a similarity of 82%. Moreover, the PedPA-1
524 producer strains *P. acidilactici* L-14 and *P. acidilactici* 347 (Cintas et al. 1998)
525 presented 83% of similarity, suggesting genetic differences that may be due to the
526 different source of isolation (*i.e.* rainbow trout larvae and dry-fermented sausage).

527 Based on its strong antimicrobial activity and safety, we selected the bacteriocinogenic
528 strain *P. acidilactici* L-14 for the characterization of its bacteriocin, using biochemical
529 and genetic methods. The purified bacteriocin produced by *P. acidilactici* L-14 was
530 analyzed by MALDI-TOF MS (Fig. 3) revealing a major peptide with a molecular mass
531 (4,621.8 Da) closely similar to that of the PedPA-1 (4,628.1 Da) firstly identified in *P.*
532 *acidilactici* PAC1.0 (Henderson et al. 1992). This difference may be explained by the
533 formation in the purified PedPA-1 of 2 disulphide bonds between the cysteine residues
534 Cys9 and Cys14, and Cys24 and Cys44, and by the deamidation of the 3 asparagine
535 residues (Asn27, Asn28 and Asn41). Moreover, a second peptide with a molecular mass
536 of 4,637.6 Da was identified, which may have resulted from a spontaneous oxidation of
537 the methionine residue (Met31) to a methionine sulfoxide (MetSO31), thus increasing
538 the molecular mass by 16 additional Da. In this respect, it has been reported that during
539 bacteriocin purification, Met usually becomes spontaneously oxidized, leading to loss or
540 reduction of the bacteriocins antimicrobial activity (Basanta et al. 2010). Taking into
541 account that the PedPA-1 activity quantified in the last RP-FPLC fraction was higher
542 than that of the culture supernatant, the oxidation events cited above could have taken
543 place during the subsequent treatment of the purified bacteriocin for MALDI-TOF MS
544 analysis, similar to suggested reasons for reduction in enterocin L50 (L50A and L50B)
545 produced by *E. faecium* L50 (Basanta et al., 2010). The genetic analysis of *pedA* and
546 *pedB* in *P. acidilactici* L14 supported the results obtained by mass spectra, since both
547 genes were identical to the respective genes from *P. acidilactici* PAC1.0 (Marugg et al.
548 1992). The gene *pedA* gene encodes a 62 amino acid peptide (prepediocin PA-1)
549 containing a 18 N-terminal amino acid leader sequence which is cleaved off during
550 secretion yielding a 44 amino acid peptide corresponding to the mature pediocin PA-1
551 (Marugg et al. 1992). The gene *pedB* encodes a 112 amino acid protein responsible for

552 the immunity of the cells (Marugg et al. 1992). The operon of this bacteriocin is
553 completed with two more genes involved in secretion, *pedC* and *pedD*, encoding a 174
554 amino acid membrane fusion protein and a 724 amino acid ATP-binding cassette (ABC)
555 transporter, respectively (Marugg et al. 1992, Venema et al. 1995). Pediocin-producing
556 pediococci strains are highly widespread in nature and have been isolated from several
557 sources, including a large variety of plants and fruits (Bennik et al. 1997, Carr et al.
558 2002, Todorov & Dicks 2009), fermented meat and meat products (Bauer et al. 2005,
559 Albano et al. 2007), boza (cereal-based fermented beverage) (Todorov & Dicks 2005),
560 the gastrointestinal tract of poultry (Juven et al. 1991), ducks (Kurzak et al. 1998) and
561 sheep (Hudson et al. 2000), and human feces (Millette et al. 2007).

562

563 **CONCLUSION**

564 The results of this work reveal that rainbow trout feed and larvae constitute an
565 interesting source for the isolation of bacteriocinogenic pediococci with potential
566 application as probiotics in aquaculture. To our knowledge, this is the first study
567 reporting the characterization of a PedPA-1-producing *P. acidilactici* strain isolated
568 from an aquatic environment (rainbow trout larvae). Further *in vitro* and *in vivo* studies
569 should be carried out in order to evaluate the probiotic effects and to confirm the lack of
570 toxicity of this strain before its proposal as probiotic to prevent fish diseases in
571 aquaculture.

572

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582

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802

Figure legends

Fig. 1. Cluster analysis of ERIC-PCR fingerprinting of the 8 *P. acidilactici* strains isolated from rainbow trout feed and larvae. The dendrogram was constructed using the Unweighted Pair Group Method (UPGMA) using arithmetic averages with correlation levels expressed as percentage values of the Dice correlation coefficient.

Fig. 2. RP-FPLC of the bacteriocin produced by *P. acidilactici* L-14. The black arrow indicates the peak showing bacteriocin activity against *L. monocytogenes* CECT4032. Bacteriocin activity was expressed in bacteriocin units (BU, *i.e.* the reciprocal of the highest dilution of the bacteriocin causing 50% growth inhibition).

Fig. 3. Mass spectrometry analysis of purified PedPA-1 from *P. acidilactici* L-14.

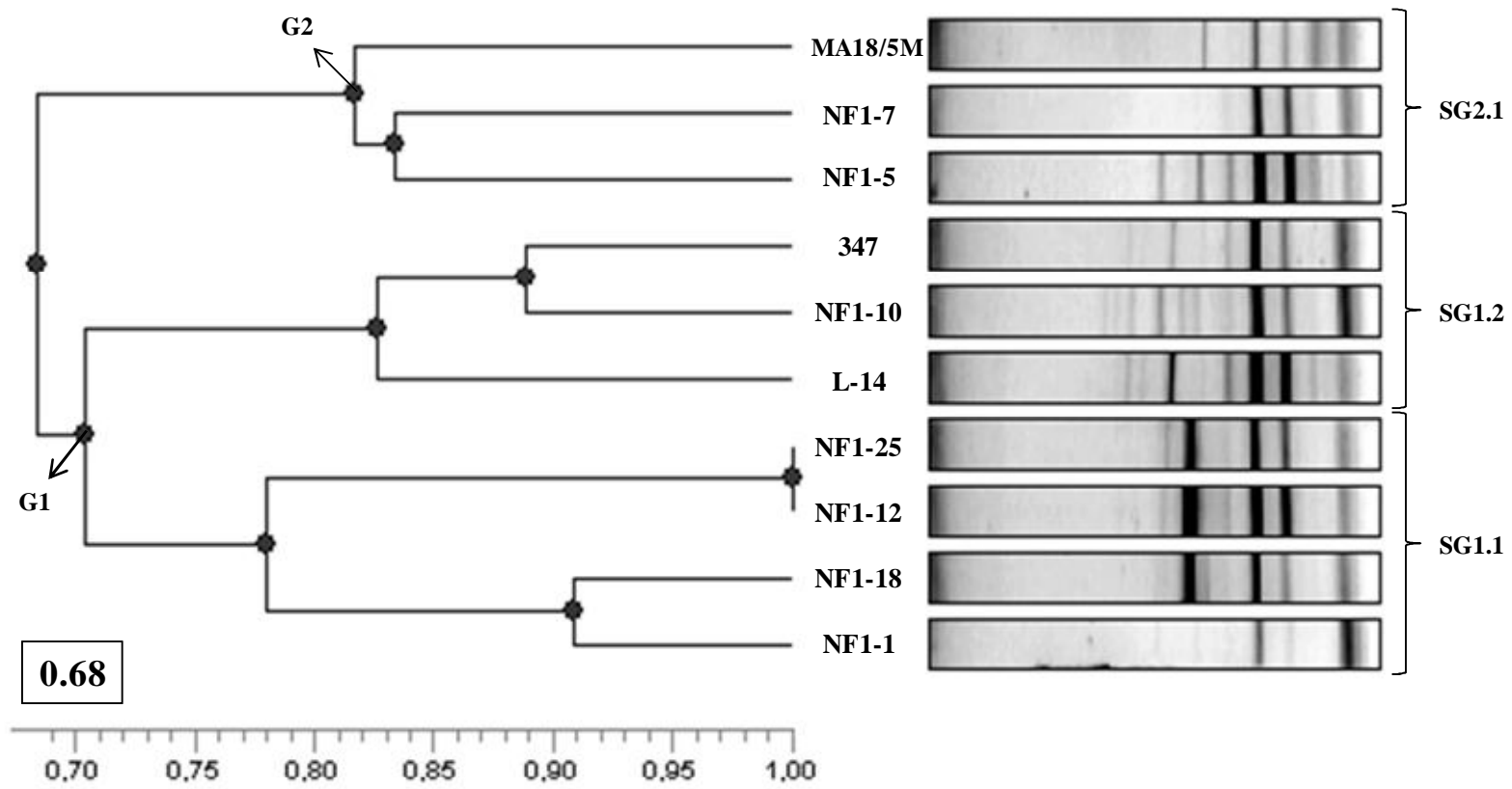


Fig. 1

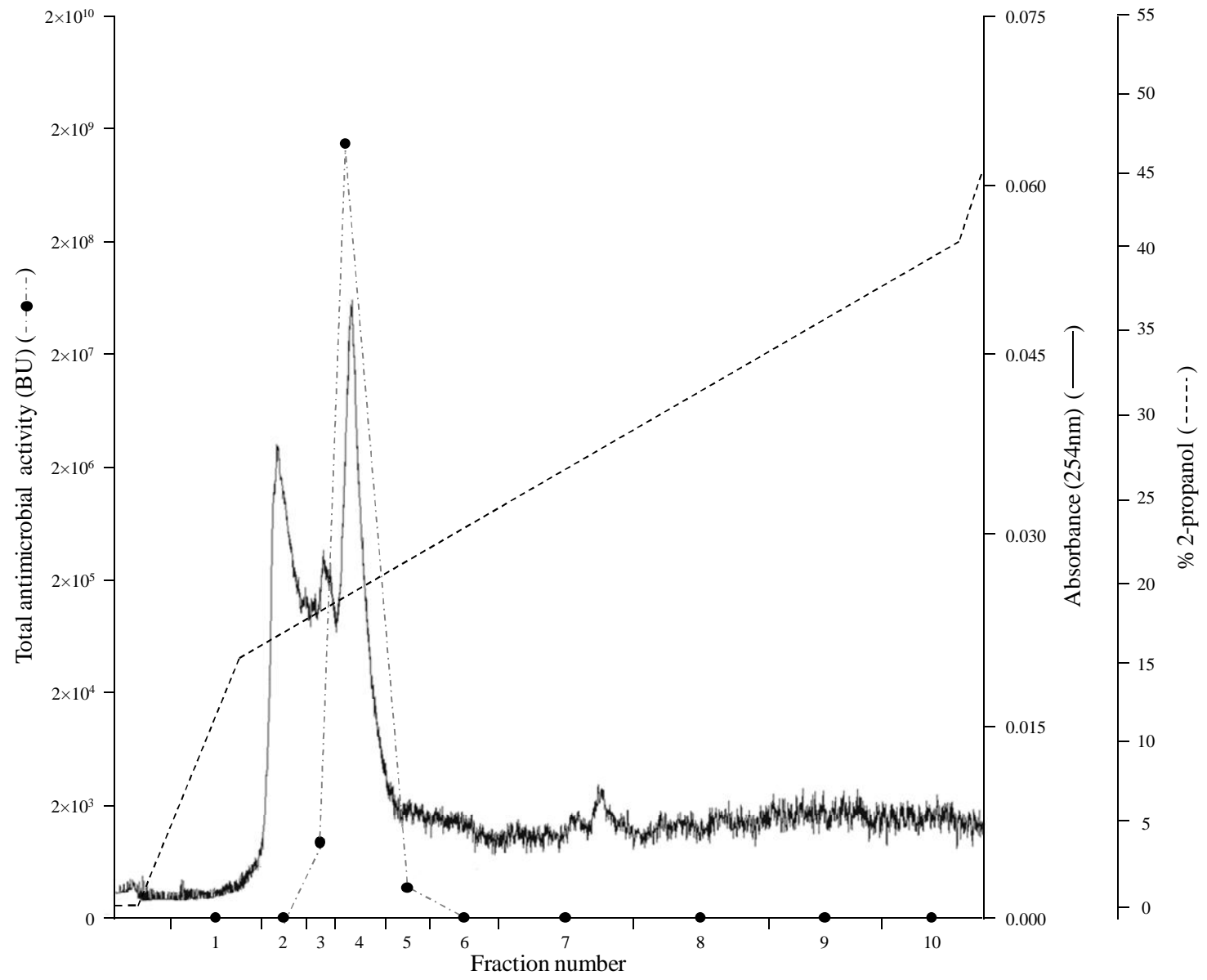


Fig.2

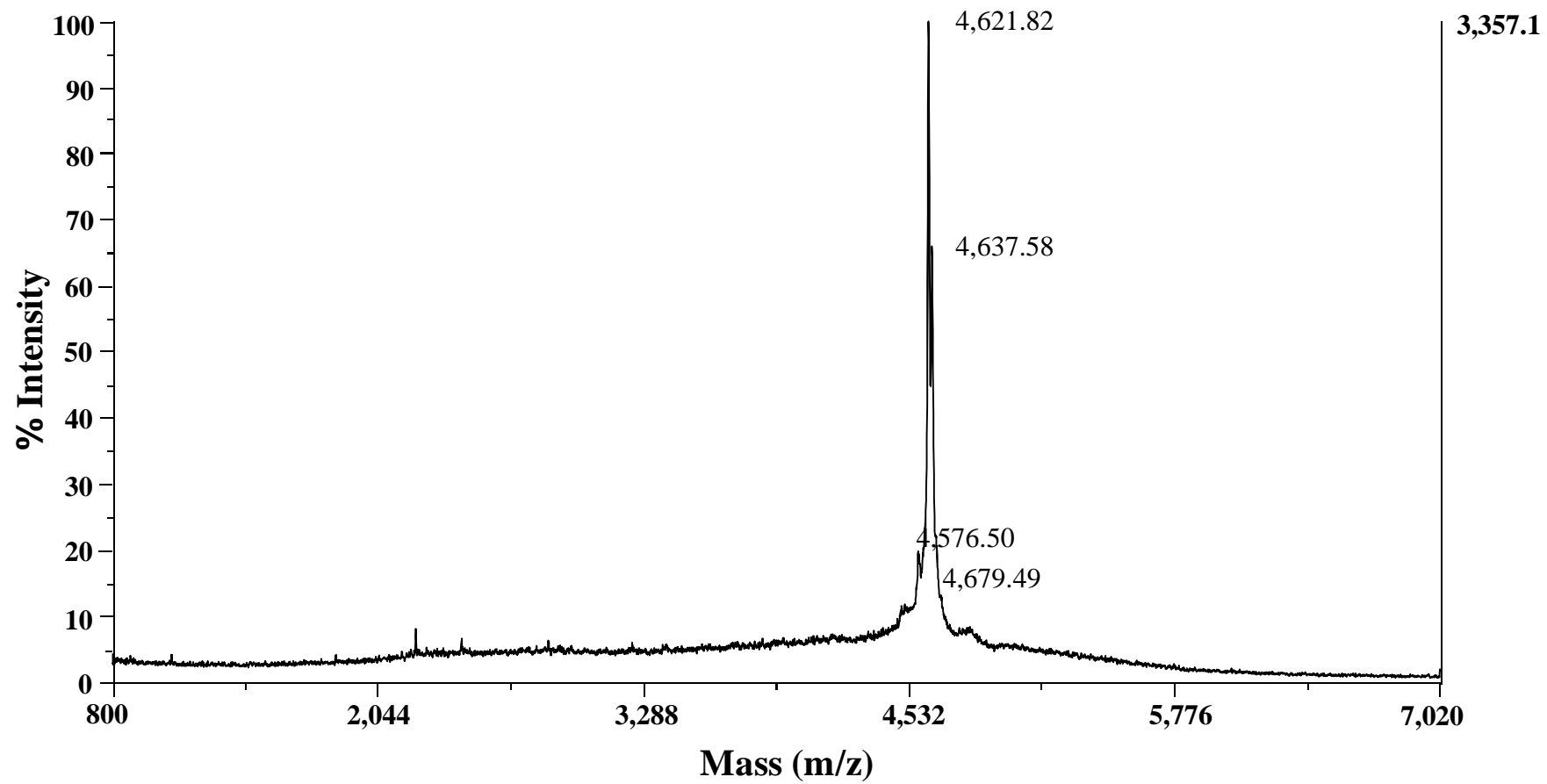


Fig. 3

Table 1. Oligonucleotide primers used in this study

Target gene	Primer	5'-3' sequence ^a	PCR fragment size (bp)	Annealing temperature (°C)	Reference
<i>16S rDNA</i>	plb16	AGAGTTTGATCCTGGCTCAG	Variable	48	Kullen et al. (2000)
	mlb16	GGCTGCTGGCACGTAGTTAG			
<i>hdc</i>	CL1	CCWGGWAAWATWGGWAATGGWTA	500	48	Le Jeune et al. (1995)
	JV17HC	AGACCATACACCATAACCTT			
<i>ldc</i>	CAD2-F	CAYRTNCCNGGNCAYAA	1,185	53	de las Rivas et al. (2006)
	CAS2-R	GGDATNCCNGGNGGRTA			
<i>odc</i>	3	GTNTTYAAYGCNGAYAARACNTAYTTYGT	1,446	52	Marcobal et al. (2005)
	16	TACRCARAATACTCCNGGNGGRTANGG			
<i>tdc</i>	TD5	CAAATGGAAGAAGAAGTAGG	1,100	48	Coton et al. (2004)
	TD2	ACATAGTCAACCATRTTGAA			
ERIC-PCR	ERIC-1R	ATGTAAGCTCCTGGGGATTAC	Variable	46	Versalovic et al. (1991)
	ERIC-2	AAGTAAGTGACTGGGGTGAGCG			

^aR=A or G; W=A or T; Y=C or T; D=A, G, or T; N=A, G, C, or T.

Table 2. Direct antimicrobial activity against fish pathogens of the 8 *P. acidilactici* strains isolated from rainbow trout feed and larvae^a

Strain ^b	Indicator microorganisms								
	<i>L. garvieae</i> CF00021	<i>L. garvieae</i> CF01144	<i>L. garvieae</i> JIP29-99	<i>L. garvieae</i> CECT5807	<i>S. iniae</i> LMG14521	<i>C. maltaromaticum</i> LMG14716	<i>Y. ruckeri</i> LMG3279	<i>A. salmonicida</i> LMG3776	<i>V. campbellii</i> LMG21363
L-14	++	++	++	+++	-	-	+	++	+++
NF1-1	+	+++	+++	+++	-	+	-	-	-
NF1-5	-	+++	++	+++	-	-	-	-	-
NF1-7	+	+++	++	+++	-	-	-	+	-
NF1-10	+	+++	-	-	-	-	-	+	-
NF1-12	-	-	+	+	-	+	-	-	-
NF1-18	+	-	+	-	+	+	-	+	-
NF1-25	+	+++	++	-	-	-	-	-	-

^aDirect antimicrobial activity was determined by a stab-on-agar test and the scores reflect different degrees of growth inhibition (diameter in mm): -, no inhibition; +, 3–5 mm inhibition zone; ++, 6–9 mm inhibition zone; +++, ≥10 mm inhibition zone. ^bStrains inhibiting less than 3 fish pathogens are not shown.

Table 3. MICs distribution of 8 antibiotics for the 8 *P. acidilactici* strains isolated from rainbow trout feed and larvae

Antibiotics	Number of strains with the indicated MIC (mg/L) ^a													EFSA breakpoints (mg/L) ^b	
	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128	256		512
Ampicillin						2	6								4
Gentamicin					2		3	3							16
Kanamycin								1			7				64
Streptomycin						1			4	3					64
Erythromycin	6			1	1										1
Clindamycin	6				2										1
Tetracycline						1		7							8
Chloramphenicol						7	1								4

^a Shaded areas show the range of dilutions tested for each antibiotic. MICs which exceeded the upper or lower limit of the tested range are listed in the next dilution series.

^b Strains with MICs higher than the EFSA breakpoints are considered as resistant.

Table 4. Extracellular antimicrobial (bacteriocin) activity of the 8 *P. acidilactici* strains isolated from rainbow trout feed and larvae^a

Strain	Origin	Indicator microorganisms														
		<i>P. damnosus</i> CECT4797			<i>L. monocytogenes</i> CECT4032			<i>L. innocua</i> CECT910			<i>Lc. garvieae</i> CF01144, CECT5807 and CF00021			<i>A. salmonicida</i> LMG3776		
		SN	SN-H	SN-PK	SN	SN-H	SN-PK	SN	SN-H	SN-PK	SN	SN-H	SN-PK	SN	SN-H	SN-PK
L-14	Larva	18.7	18.7	-	17.8	17.8	-	17.4	ND	ND	-	ND	ND	-	ND	ND
NF1-1	Feed	7.9	7.8	-	7.2	7.1	-	7.2	ND	ND	-	ND	ND	-	ND	ND
NF1-5	Feed	7.2	7	-	-	-	-	-	ND	ND	-	ND	ND	-	ND	ND
NF1-7	Feed	7.1	7.1	-	-	-	-	-	ND	ND	-	ND	ND	-	ND	ND
NF1-10	Feed	7.3	7.3	-	-	-	-	-	ND	ND	-	ND	ND	-	ND	ND
NF1-12	Feed	7.1	7	-	-	-	-	-	ND	ND	-	ND	ND	-	ND	ND
NF1-18	Feed	-	-	-	-	-	-	-	ND	ND	-	ND	ND	-	ND	ND
NF1-25	Feed	-	-	-	-	-	-	-	ND	ND	-	ND	ND	-	ND	ND

^a Antimicrobial activity (mm) of supernatants (SN), supernatants subjected to heat treatment (SN-H) and supernatants subjected to proteinase K treatment (SN-PK) as determined by an agar well-diffusion test.

ND, not determined.

Table 5. Purification of PedPA-1 produced by *P. acidilactici* L-14^a

Supernatant and purification stage	Volume (ml)	Total A ₂₅₄ ^b	Total activity (10 ³ BU) ^c	Specific activity ^d	Increase in specific activity ^e (fold)	Yield (%)
Culture supernatant	1,000	22,600	240	11	1	100
Ammonium sulfate precipitation	100	1,300	49,200	36,800	3,500	20,480
Gel filtration chromatography	156	780	9,600	12,200	1,100	3,994
Cation-exchange chromatography	50	12	1.6×10 ⁶	1.3×10 ⁸	1.2×10 ⁷	6.6×10 ⁵
Hydrophobic-interaction chromatography	15	0.3	900	3.2×10 ⁶	3.0×10 ⁵	384
Reversed-phase chromatography (FPLC)	1.5	0.3	1.9×10 ⁹	6.7×10 ¹²	6.3×10 ¹¹	8.1×10 ⁸

^a During the purification process, the antimicrobial activity, but not the protein concentration of the bacteriocin samples, was quantified.

^b Absorbance at 254 nm (A₂₅₄) multiplied by the volume in milliliters.

^c Antimicrobial activity in bacteriocin units per milliliter (BU/mL), as determined by an microtiter plate assay, multiplied by the total volume in milliliters.

^d Specific antimicrobial activity expressed as the total antimicrobial activity (BU) divided by the total A₂₅₄.

^e Specific antimicrobial activity of a fraction (BU/A₂₅₄) divided by the specific antimicrobial activity of the culture supernatant (BU/A₂₅₄).