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**Antibiotic resistance of *Aeromonas* spp. strains isolated from *Sparus aurata* reared in Italian mariculture farms**

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(Article begins on next page)

1     **Antibiotic resistance of *Aeromonas* spp strains isolated from *Sparus aurata* reared in Italian**  
2   **mariculture farms**

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11

12    **Abstract**

13    Selective pressure in the aquatic environment of intensive fish farms leads to acquired antibiotic  
14    resistance. This study used the broth microdilution method to measure minimum inhibitory  
15    concentrations (MICs) of 15 antibiotics against 104 *Aeromonas spp* strains randomly selected  
16    among bacteria isolated from *Sparus aurata* reared in six Italian mariculture farms. The  
17    antimicrobial agents chosen were representative of those primarily used in aquaculture and human  
18    therapy and included oxolinic acid (OXA), ampicillin (AM), amoxicillin (AMX), cephalothin (CF),  
19    cloramphenicol (CL), erythromycin (E), florfenicol (FF), flumequine (FM), gentamicin (GM),  
20    kanamycin (K), oxytetracycline (OT), streptomycin (S), sulfadiazine (SZ), tetracycline (TE) and  
21    trimethoprim (TMP). The most prevalent species selected from positive samples was *Aeromonas*  
22    *media* (15 strains). The bacterial strains showed high resistance to SZ, AMX, AM, E, CF, S and  
23    TMP antibiotics. Conversely, TE and CL showed MIC<sub>90</sub> values lower than breakpoints for  
24    susceptibility and many isolates were susceptible to OXA, GM, FF, FM, K and OT antibiotics.  
25    Almost all *Aeromonas spp* strains showed multiple antibiotic resistance. Epidemiological cut-off  
26    values (ECVs) for *Aeromonas spp* were based on the MIC distributions obtained. The results

27 showed a high frequency of *Aeromonas spp* contamination in *Sparus aurata* reared on the Italian  
28 coast and an elevated biodiversity in isolated bacterial strains. *Aeromonas* isolates comprise  
29 potentially pathogenic species for humans, often resistant to several antibiotics and able to transfer  
30 the genes responsible for antibiotic resistance to microorganisms pathogenic for humans throughout  
31 the food chain. The few ECV studies available on many antibiotics against *Aeromonas spp* strains  
32 isolated from the aquaculture environment highlight the need for further research in this area, while  
33 regular monitoring programmes should be stepped up to check for antibiotic resistance.

34

35 **Keywords:** gilthead seabream; *Aeromonas spp* bacteria; minimum inhibitory concentration;  
36 antibiotics; epidemiological cut-off values.

37

38

## 39 1. Introduction

40 World fish consumption has been growing in the last thirty years reaching 20 kg per capita in 2014.

41 For the first time, the aquaculture production of fish for human consumption has overtaken the  
42 supply of wild-caught fish and is expected to rise to 62% by 2030 (FAO, 2016). Gilthead sea bream  
43 (*Sparus aurata*) is a very suitable species for mariculture in the Mediterranean basin and has  
44 become one of Europe's main fish species in aquaculture. Greece, Turkey and Spain are the main  
45 producers worldwide while Italy is the third main producer in the EU (EC, 2017). Large-scale  
46 aquaculture is characterized by the intensive and semi-intensive production systems with high  
47 stocking density, which leads to poor hygiene conditions and the emergence of infectious diseases  
48 (Diana et al., 2013).

49 The genus *Aeromonas* comprises a group of bacteria with a ubiquitous distribution in natural  
50 habitats, including the aquatic environment (Janda & Abbott, 2010) where species such as *A.*  
51 *hydrophila*, *A. caviae*, *A. salmonicida* and *A. veronii* biovar *sobria* cause disease in marine fish  
52 (Radu et al., 2003). *Aeromonas spp* are also important human opportunistic pathogens able to cause

53 intestinal, blood, skin and soft tissue and trauma-related infections, particularly in young children  
54 and **the** elderly (Janda and Abbott, 2010; Real et al., 1994). *Aeromonas* species have been  
55 frequently isolated from fish and other foods (Callister and Agger, 1987; Gobat and Jemmi, 1993).  
56 **These bacteria are responsible for food spoilage and may serve as vectors for disease transmission**  
57 **to humans** (Tsai and Chen, 1996). Infection can **also occur** after contact with contaminated **water** or  
58 fish (Janda and Abbott, 2010). ***Aeromonas* pathogenicity is linked** to the production of a number of  
59 extracellular hydrolytic enzymes such as lipases and proteases, which **aid in bacterial invasion and**  
60 **the establishment of infection** (Galindo et al., 2006). Among an array of other virulence factors, the  
61 **biological activities of** cytotoxic enterotoxin (Act) **include haemolysis**, cytotoxicity, enterotoxicity  
62 and lethality (Chopra et al., 1991).

63 The **worldwide** expansion of intensive fish farming has increased the use of antibiotics to treat  
64 bacterial **infections** (Díaz-Cruz et al., 2003). In aquaculture, antimicrobials are generally added to  
65 the feed or directly to the water to prevent the spread of infectious fish disease (Defoirdt et al.,  
66 2011) and in some circumstances **to promote fish growth illegally** (Serrano, 2005). **Regulations**  
67 **governing the use of antibiotics in aquaculture differ widely** with little to no enforcement in many  
68 of the world's major **aquaculture-producing** countries (Pruden et al., 2013). The extensive use of  
69 antibiotics in aquaculture has in turn resulted in the emergence of antibiotic resistance in both  
70 foodborne and opportunistic human **pathogens** (Marshall and Levy, 2011). The resistance of  
71 *Aeromonas* species to diverse groups of antibiotics **is** a major concern for human health (Figueira et  
72 al., 2011) **as resistant bacteria can spread** from the aquatic environment **to humans via the** food  
73 chain or direct contact (Taylor et al., 2011). **In addition, resistance genes can be transferred** by  
74 mobile genetic elements such as plasmids, phages and transposons (Levy and Marshall, 2004).

75 Janda and Abbott (2010) reviewed the general susceptibility profiles of Aeromonads to various  
76 antimicrobial classes, showing resistance to **sulfamethoxazole**, **cephalosporins**, **penicillins**  
77 (**amoxicillin**, **ampicillin**, **ampicillin-sulbactam**, **ticarcillin**, **oxacillin** and **penicillin**) and **macrolides**  
78 (**clarithromycin**). ***Aeromonas* species resistant to penicillins** and first generation **cephalosporins** are

79 associated with the production of chromosomally encoded beta-lactamases (Janda and Abbott,  
80 2010). Other important resistance determinants to beta-lactam antimicrobials and tetracyclines are  
81 *bla* genes and *tet* genes respectively encoded in mobile genetic elements (Agersø et al., 2007; Wu et  
82 al., 2011) or integrons, responsible for resistance to tetracyclines, aminoglycosides,  
83 chloramphenicol and trimethoprim (Chang et al., 2007; Kadlec et al., 2011). Indeed, acquired  
84 antibiotic resistance among fish pathogens could determine serious therapeutic problems in humans  
85 following the use of molecules whose class and structure are similar or, in some cases, identical to  
86 those used in mariculture (Cabello, 2006). Despite recent efforts by international agencies such as  
87 the European Centre for Disease Prevention and Control and the National Antimicrobial Resistance  
88 Monitoring System (EFSA, 2014), the role of antibiotic usage in aquaculture in the development  
89 and dissemination of antibiotic resistance genes is still poorly understood. The potential risk of  
90 transferring such resistance from the aquaculture environment to humans is underestimated  
91 (Cabello et al., 2013) so the effectiveness of antibiotics used in fish farming should be carefully  
92 monitored.

93 Little information is available on the susceptibility of *Aeromonas* spp isolated from mariculture to  
94 antibiotics used in both fish farming and human therapy. Antimicrobial susceptibility is generally  
95 tested by measuring the drug's minimum inhibitory concentration (MIC). MIC breakpoints are the  
96 MICs at which an organism should be considered susceptible, intermediate or resistant. Breakpoint  
97 values are published by organizations such as the European Committee on Antimicrobial  
98 Susceptibility Testing (EUCAST) and the American Clinical Laboratory Standard Institute (CLSI),  
99 based on pharmacokinetic/pharmacodynamic data and clinical studies. MIC<sub>50</sub> and MIC<sub>90</sub> indicate  
100 the lowest concentrations of the antimicrobial agent inhibiting visible growth of 50% and 90% of  
101 the bacterial population respectively. However, few interpretation criteria for *Aeromonas* spp have  
102 been published to date. The only available breakpoints proposed by the CLSI are from clinical  
103 isolates adapted from *Enterobacteriaceae*, while no criteria have been established by EUCAST.  
104 Epidemiological cut-off values (ECVs) must be set to discriminate wild-type strains (with no

105 acquired resistance mechanism to the tested antibiotic) from non-wild-type strains (with one or  
106 more acquired resistance mechanisms) (Kahlmeter et al., 2003). These cut-off values are the upper  
107 limit of the MIC distribution of fully susceptible strains.

108 The purpose of the present study was to estimate the MICs of *Aeromonas* spp strains isolated from  
109 *Sparus aurata* against 15 antimicrobial agents, and to determine the ECVs for *Aeromonas* spp.

110

## 111 2. Materials and methods

### 112 2.1 Fish sampling

113 The study was conducted on gilthead sea bream (*Sparus aurata*) collected from six offshore  
114 mariculture farms in three Italian regions (Sardinia, Sicily and Tuscany). All fish farms were  
115 characterized by intensive rearing systems in sea cages. Water salinity was ca. 33‰ and the  
116 temperature ranged between 16°C and 22°C. Twenty commercial size (~250 g) *Sparus aurata*  
117 specimens were randomly collected at each farm during two different visits conducted four months  
118 apart. After collection, fish were slaughtered by immersion in fusing ice, placed in expanded  
119 polystyrene boxes and covered with a plastic film then transported to the laboratory under  
120 refrigeration and processed within three hours after collection.

### 121 2.2 Microbiological analysis

122 Samples of skin, gills, muscle and intestinal content were aseptically collected from each specimen  
123 for microbiological analysis. The initial suspension and decimal dilution for microbiological  
124 examination were prepared according to ISO 6887–1:1999. Each matrix was tested for *Aeromonas*  
125 species (presence/absence) inoculating 0.1 mL of homogenized PBS (pH 7.4) on plates of  
126 *Aeromonas* Medium Base (Ryan's medium) (Oxoid, Basingstoke, UK) supplemented with  
127 ampicillin selective supplement at 5 mg/L. The agar plates were incubated at +30°C for 48 hours.  
128 Colonies with typical growth characteristics, opaque dark green with darker centres, were picked  
129 and subcultured on brain heart infusion (BHI) agar plates (BHI, Oxoid, Basingstoke, UK). After  
130 incubation, isolates were tested as follows: morphology in Gram staining, cytochrome oxidase,

131 amylase and trealose fermentation. After presumptive genus identification, strains were stored at -  
132 80°C for subsequent genetic confirmation and species identification.

### 133 2.3 Bacterial identification

134 Genus identification of isolates was confirmed by PCR (Khan et al., 2009). To avoid over-  
135 representation of clones, 16S ribosomal DNA sequencing was conducted on a selection of strains to  
136 identify bacterial species. A hierarchical method was used to select up to three strains from each of  
137 the following nested criteria: region of collection (three levels), fish farm (two levels), fish  
138 specimens (40 levels) and fish matrix (4 levels). For species identification, colonies with  
139 morphological and biochemical features of *Aeromonas* spp were grown overnight at 37°C in  
140 tryptone soya broth (Oxoid). DNA was extracted using the following protocol: 1mL of broth culture  
141 ( $10^8$  CFU/mL) was centrifuged at 12,000 g for five minutes, then the pellet was resuspended in 1mL  
142 of phosphate-buffered saline, boiled for five minutes, and centrifuged again (Bottero et al., 2004).  
143 The supernatant was stored at -20°C until use. The DNA was quantified using a spectrophotometer  
144 (Nanodrop 2000, Thermo Fisher Scientific). All extracted DNA were subjected to sequencing  
145 analysis with the MicroSeq 500 16S rDNA bacterial sequencing kit (Thermo Fisher Scientific). 16S  
146 rDNA amplicons were purified by Exo-Sap treatment according to the manufacturer's  
147 recommendations (USB Europe, Staufeu, Germany). Forward and reverse sequencing reactions  
148 were performed using the ABI Prism BigDye Terminator Cycle Sequencing Ready Reaction Kit,  
149 version 1.1 (Thermo Fisher Scientific). The extended products were purified with DyeEx 2.0 Spin  
150 kit (Qiagen, Valencia, CA, USA) and resolved by capillary electrophoresis using an ABI 310  
151 Genetic Analyzer (Thermo Fisher Scientific). The electropherograms were analyzed using Chromas  
152 2.22 software (Technelysium, Epoch Life Science Inc.) and the sequences were submitted to the  
153 BLAST similarity search software on the National Center for Biotechnology Information (NCBI)  
154 website.

### 155 2.4 Antibiotic susceptibility

156 Antibiotic susceptibility was determined for *Aeromonas* strains at the genus level. MICs of 15  
157 antibiotics were measured by the broth microdilution method (CLSI, 2011). The antimicrobial  
158 agents chosen among those mainly used in aquaculture and human therapy were: oxolinic acid  
159 (OXA), ampicillin (AM), amoxicillin (AMX), cephalothin (CF), cloramphenicol (CL),  
160 erythromycin (E), florfenicol (FF), flumequine (FM), gentamicin (GM), kanamycin (K),  
161 oxytetracycline (OT), streptomycin (S), sulfadiazine (SZ), tetracycline (TE) and trimethoprim  
162 (TMP). To obtain stock solutions, the antibiotic powders (Sigma Aldrich, MI, Italy) were weighed  
163 and dissolved in the following solvents (Sigma Aldrich): phosphate buffer, pH 8.0, 0.1 mol/L (AM),  
164 phosphate buffer, pH 6.0, 0.1 mol/L (AMX and CF), ethanol 95% (CL and E), methanol 96% (FF),  
165 aqueous alkaline solution NaOH 0.1M + ethanol 2:1 (FM), aqueous alkaline solution NaOH 0.1M,  
166 pH 10 (OXA), methanol-water 2:1 (OT and TE), aqueous acidic solution HCl 10% (TMP), and  
167 deionized water (GM, K, S and SZ). Once dissolved, each stock solution (2,560 µg/mL) was  
168 dispensed in 1.5 mL aliquots into polypropylene vials and frozen at - 80 °C until use. Each  
169 microtitre plate was prepared with 12 serial twofold dilutions of each antibiotic stock solution  
170 (Work Station - Micro Star, Hamilton, Bonaduz GR, Switzerland) with deionized water (phosphate  
171 buffer, pH 6.0, 0.1 mol/L, only for AMP and AMX antibiotics). The antibiotic concentrations  
172 obtained ranged between 0.06 µg/mL and 128 µg/mL (0.12-256 µg/mL for SZ antibiotic). Strains  
173 were subcultured twice in BHI plates before preparation of the inoculum. After overnight  
174 incubation at 37 °C, two or more colonies were picked from BHI plates and dissolved in salt  
175 solution (0.85% w/v) to obtain 0.5 McFarland turbidity, measured using a portable photometric  
176 reader (Densimat, bioMérieux, Lyon, France). Each bacterial suspension was further diluted (1:100)  
177 in cation-adjusted Mueller Hinton broth (CAMHB, Oxoid, Basingstoke, UK) supplemented with  
178 NaCl (1%) to obtain an inoculum concentration of ca.  $10^6$  cfu/mL. Fifty µL of the final suspension  
179 were transferred into microtitre wells (one strain for each row of the microplate) containing 50 µL  
180 of each antimicrobial agent. The density of the final inoculum in each well was ca.  $5 \times 10^5$  cfu/mL.  
181 The reference strain *E. coli* ATCC 25922 was used as quality control. Each microplate was



182 subsequently incubated under aerobic conditions for 20 hours at 35 °C. The MIC of each antibiotic  
183 was compared with breakpoint values to determine resistance (CLSI, 2005, 2007, 2011, 2016;  
184 NCCLS, 1998, 1999, 2002). The MIC range and mode, MIC<sub>50</sub> and MIC<sub>90</sub> of each antimicrobial  
185 agent were also determined. Multiple antibiotic resistance (MAR) among *Aeromonas* spp strains  
186 was evaluated applying the MAR index defined as  $a/b$ , where “ $a$ ” was the number of antimicrobials  
187 the isolate was resistant to and “ $b$ ” was the number of antibiotics against which the isolate was  
188 tested. According to Krumperman (1985), a MAR index below 0.2 is interpreted as strains  
189 originating from animals in which antibiotics are seldom or never used, while a MAR index above  
190 0.2 is interpreted as strains originating from an elevated selective pressure environment where  
191 antibiotics are frequently used.

#### 192 2.5 Epidemiological cut-off values

193 The distribution of MIC values served to determine the ECVs. The statistical determination of ECV  
194 values for each antimicrobial agent at genus level was conducted according to Turnidge et al.  
195 (2006) using the freely available ECOFFinder Microsoft Excel spreadsheet calculator  
196 (<https://clsi.org/education/microbiology/ecoffinder/>). The spreadsheet is designed to estimate the  
197 ECVs based on the observed MIC of the tested bacterial population, i.e. it estimates the MIC value  
198 best describing where wild type distribution ends.

199

### 200 3. Results

#### 201 3.1 Isolation and identification of *Aeromonas* spp

202 *Aeromonas* spp were observed in 98 skin samples (30.6%), 154 gills (48.2%) and 40 gut contents  
203 (12.5%) whereas the bacteria were never detected in muscle. One hundred and four *Aeromonas* spp  
204 strains isolated from *Sparus aurata* were speciated by 16S ribosomal DNA sequencing. Of the total  
205 strains, 59 originated from Tuscany, 40 from Sicily and five from Sardinia. The *Aeromonas* strains  
206 were isolated from skin (n. 48), gut content (n. 20) and gills (n. 36). Sequencing identified 23  
207 different *Aeromonas* species or species-complex. The most frequently recovered species were

208 *Aeromonas media* (15 strains, 14.4%), *Aeromonas salmonicida/bestiarium/hydrophila/caviae*  
209 species-complex (12 strains, 11.5%), *A. molluscorum* (11 strains, 10.6%) and *A. bivalvum* (10  
210 strains, 9.6%). Table 1 reports a complete list of *Aeromonas* species and species-complex identified  
211 and the relative number of strains. Fig. 1 shows their distribution by region of origin.

### 212 3.2 Antimicrobial susceptibility

213 For some of the selected antimicrobial agents, the reference strain used as quality control for the  
214 MIC determination assay indicated the *Aeromonas* strains in compliance with CLSI  
215 recommendations (CLSI, 2005). Over 90% of the speciated *Aeromonas* strains showed  
216 susceptibility to CL, FF and GM antibiotics. Table 1 lists the resistance profile for each *Aeromonas*  
217 species. All tested *Aeromonas* strains showed resistance to two or more antibiotics. One strain of *A.*  
218 *bivalvium* and one strain of the *A. punctata/hydrophila/enteropelogenes* species-complex were  
219 resistant to 11 antibiotics while one *A. molluscorum* strain was resistant to 12 antibiotics. Table 2  
220 reports the MAR index indicating the multiple antibiotic resistance of *Aeromonas* spp strains by  
221 region of origin. Table 3 shows the MIC<sub>50</sub>, MIC<sub>90</sub>, mode and range and cut-off of MICs for each  
222 tested antibiotic, and the number of sensitive, intermediate and resistant strains with reference to the  
223 CLSI breakpoints. The most frequent combination of antibiotic resistance profiles was AM, AMX,  
224 CF, E, S, SZ and TMP. For CF and SZ, the MIC<sub>50</sub> and MIC<sub>90</sub> values were above the tested range  
225 (128 and 256 µg/mL respectively).

### 226 3.3 Determination of wild-type strains

227 The ECVs were computed for 12 out of 15 antimicrobial agents. In addition to CF and SZ, no  
228 values were computed for TMP due to a high number of isolates with MIC values greater than the  
229 upper limit of the tested dilutions (128 µg/mL).

230 The wild-type strains ranged between 59.6% and 96.2% of the tested strains. Thirty-one strains  
231 (29.8%) were wild-type for all antibiotics with a computable ECV. One strain (*A. bivalvium*)  
232 resulted wild-type exclusively for E, one strain for GM and K (*A.*  
233 *punctata/hydrophila/enteropelogenes* species-complex) and one strain (*A. molluscorum*) for GM, K

234 and S. The remaining 70 strains were wild-type for five up to 11 different antibiotics, yielding 31  
235 different combinations of antibiotic wild-type profiles. More than 80% of wild-type strains were  
236 resistant to eight antibiotics (CL, E, FF, GM, K, OT, S, TE). Table 3 reports the complete results on  
237 the ECVs and percentage of wild-type strains.

238

#### 239 4. Discussion

240 The worldwide growth of aquaculture has seen the development of intensive fish farming. This in  
241 turn has been associated with an extensive use of antibiotics to treat or prevent bacterial infections.  
242 Regulations governing the antimicrobial agents authorized in fish farming differ from country to  
243 country. The selective pressure exerted by intensive fish farming has resulted in the emergence of  
244 antibiotic-resistant food-borne pathogens, opportunistic pathogens and human commensal flora of  
245 food animals (Sorum, 2006; Teuber, 2001; Witte, 2000). The potential transfer of antibiotic  
246 resistance from the aquatic environment to humans through direct contact or via the food chain is a  
247 serious concern for human health (Marshall and Levy, 2011). Antibiotic resistance monitoring fails  
248 to collect extensive information of the classes of antimicrobials used in aquaculture and the efficacy  
249 of antibiotics (Cabello et al., 2013).

250 The present study provided useful information on the resistance of *Aeromonas* spp isolated from  
251 gilthead sea bream (*Sparus aurata*) reared in Italian fish farms. *Aeromonas* spp were widely  
252 distributed in skin, gills and intestinal content of *Sparus aurata* whereas they were never detected in  
253 muscle. *Aeromonas* spp can potentially cause human illness by direct contact or through the  
254 ingestion of contaminated fish (Janda & Abbott, 2010).

255 Clinical breakpoints are useful to assess the efficacy of antibiotics during treatments, while the  
256 determination of ECVs will establish the emergence of antibiotic resistance mechanisms within a  
257 bacterial population. Based on these values, the present study documented high resistance rates for  
258  $\beta$ -lactams, erythromycin, sulfadiazine and trimethoprim. The MIC<sub>90</sub> of ampicillin, amoxicillin and  
259 cephalothin (>128  $\mu$ g/mL) were higher than the reference breakpoints for resistance and the number

260 of resistant strains ranged between 40.4% and 86.5%. The literature reports resistance rates for  
261 these antibiotics as high as 100% (Hatha et al., 2005; Snoussi et al., 2011). The MIC<sub>50</sub> for ampicillin  
262 and amoxicillin was 16 µg/mL, an intermediate value between the reference breakpoints for  
263 susceptibility and resistance, while the MIC<sub>50</sub> for cephalothin was greater than the reference value  
264 for resistance (>128 µg/mL). Amoxicillin and ampicillin are susceptible to β-lactamase and to rapid  
265 onset antibiotic resistance especially when the antibiotic is repeatedly used in a short time period,  
266 typical of intensive fish farming systems. Three different types of β-lactamase have been observed  
267 in *Aeromonas* spp (Walsh et al., 1997), but little information is available on the ECV<sub>ST</sub> for  
268 *Aeromonas* spp and limited to few antibiotics, hampering a comparison with the MIC distribution  
269 observed in our microbial population. Despite the high resistance rates observed for β-lactam  
270 antibiotics, based on the ECVs computed for amoxicillin and ampicillin, an elevated percentage of  
271 strains could be considered wild-type.

272 Among the quinolone antibiotics, various countries have authorised oxolinic acid (a first generation  
273 quinolone) for therapeutic use in aquaculture, while flumequine is the only one of the five  
274 fluoroquinolone antibiotics listed in Reg. EC 37/2010 authorised for fish farming. These antibiotics  
275 are used in mariculture for the treatment of furunculosis caused by *Aeromonas salmonicida* (Giraud  
276 et al., 2004). Oxolinic acid and flumequine showed resistance in 32.7% and 22.1% of the tested  
277 *Aeromonas* spp strains respectively. The antibiotic resistance of *Aeromonas* spp in the present study  
278 is in agreement with previous investigations conducted in mariculture farms where resistance was  
279 between 25% and 50% (Inglis et al., 1991; Snoussi et al., 2011; Cattoir et al., 2008).

280 The ECV computed in the present study was 0.25 µg/mL for both oxolinic acid and flumequine  
281 while the literature reported values of 0.031 µg/mL and 0.06 µg/mL respectively (Baron et al.,  
282 2017; Smith and Kronvall, 2015). However, these results are not comparable as the values obtained  
283 in our study coincided with the lowest dilution tested.

284 Due to their broad-spectrum activity, low toxicity and cost, tetracyclines are the most commonly  
285 used antibiotics in both human and veterinary medicine. In mariculture, oxytetracycline is

286 authorized for therapeutic immersion in Europe, while elsewhere (USA and Asian countries) it is  
287 also administered with medicated foods. The widespread use of tetracycline has resulted in the  
288 dissemination of resistance to many marine bacteria (Furushita et al., 2003) with the number of  
289 resistant strains ranging from 7.7% (TE) to 11.5% (OT). These results are comparable with previous  
290 studies where *Aeromonas* spp strains showed sensitivity to tetracycline and oxytetracycline (Awan  
291 et al., 2009). *Aeromonas* spp strains showed high in vitro sensitivity against both oxytetracycline  
292 (80.8%) and tetracycline (85.6%) in the tetracycline class with MIC<sub>50</sub> values below the reference  
293 breakpoint of susceptibility ( $\leq 1\mu\text{g/mL}$ ) and MIC<sub>90</sub> of 4  $\mu\text{g/mL}$  and 16  $\mu\text{g/mL}$  for tetracycline and  
294 oxytetracycline, respectively. The MIC<sub>50</sub> and MIC<sub>90</sub> observed in our study were within the range  
295 reported in previous investigations conducted on Aeromonads isolated from freshwater fish (Baron  
296 et al., 2017; Čížek et al., 2010). The ECV of *Aeromonas* spp was 2  $\mu\text{g/mL}$  for both tetracycline and  
297 oxytetracycline, values greater than those reported by Barone et al. (2017).

298 Among the Macrolides, erythromycin is the bacteriostatic drug of choice against Gram-positive  
299 bacteria. Although it is not approved for aquaculture use in most European countries, the EU has  
300 established maximum residue limits (MRLs) (Reg. EC 37/2011). In the present study, erythromycin  
301 showed little effectiveness against *Aeromonas* spp. The MIC<sub>90</sub> of erythromycin was higher than the  
302 reference breakpoints (8  $\mu\text{g/mL}$ ) with 84.6% of the tested *Aeromonas* strains showing resistance.  
303 This high resistance rate and the MIC<sub>50</sub>, MIC<sub>90</sub> and ECV for erythromycin are in agreement with  
304 other studies (Mejdi et al., 2010; Baron et al., 2017).

305 Trimethoprim is mainly used in fish culture and often combined with sulfadiazine in commercial  
306 preparations. Because of the potential carcinogenic effect of both antibacterial agents, the EU set  
307 MRLs in fish muscle. The present study tested the two antimicrobials independently. Low efficacy  
308 was obtained for sulfonamides with resistance rates of 92.3% and 69.2% of strains for sulfadiazine  
309 and trimethoprim, respectively. For both sulfadiazine and trimethoprim the MIC<sub>50</sub> and MIC<sub>90</sub> were  
310 above the reference breakpoints, so the ECVs could not be estimated. These values could not be

311 compared with other studies on *Aeromonas* spp as these antibacterials are generally used in  
312 combination.

313 Aminoglycoside antibiotics showed intermediate MIC<sub>90</sub> values for gentamicin (8 µg/mL) and  
314 kanamycin (32 µg/mL), whereas they were above the breakpoint for streptomycin (64 µg/mL) to  
315 which 39.4% of strains were resistant. The ECVs for gentamicin and streptomycin were greater than  
316 those observed by Baron et al. (2017), while the MIC<sub>50</sub> for streptomycin was comparable with data  
317 obtained by Goñi-Urriza et al. (2000).

318 In the present study, chloramphenicol and florfenicol MIC<sub>90</sub> were lower than the reference  
319 breakpoints. These results were expected for chloramphenicol as it has been banned from use in  
320 animal food production since 1994 (EC 1430/94) due to its serious side effects on human health  
321 (irreversible aplastic anaemia). While florfenicol is registered for use in aquaculture only in some  
322 European countries, resistance to the fenicol category ranged between 2.9 % and 3.8% of the tested  
323 strains. The MIC<sub>50</sub> and ECVs for these two antimicrobials were in agreement with values reported  
324 by Baron et al. (2017).

325 Overall, *Aeromonas* spp showed elevated multiple resistance to the antibiotics tested. Most of the  
326 strains (82.7%) showed a MAR index between 0.3 and 0.5 (corresponding to resistance to four to  
327 eight different antibiotics) while six strains were resistant to nine to 11 antibiotics. One strain, *A.*  
328 *punctata/hydrophila/enteropelogenes*, was resistant to 11 out of 15 antibiotics tested, indicating that  
329 the isolates were exposed to high-risk sources of contamination with broad use of antibiotics, as in  
330 intensive fish farming. This result is in agreement with previous studies indicating the high  
331 antibiotic resistance of *Aeromonas* spp (Dumontet et al., 2000; Nguyen et al., 2014). The antibiotics  
332 most frequently associated with multiple resistance were amoxicillin, ampicillin, cephalothin,  
333 erythromycin, streptomycin, sulfadiazine and trimethoprim.

334

## 335 5. Conclusions

336 The present study confirms that selective pressure in the aquatic environment of intensive fish farms  
337 leads to acquired antibiotic resistance by *Aeromonas* spp in gilthead sea bream reared in Italy.  
338 Compared to clinical breakpoints, measuring epidemiological cut-off values allows a better  
339 distinction between wild-type strains and strains which have acquired drug resistance due to  
340 selective pressure. The multiple antibiotic resistance of almost all strains raises serious concerns due  
341 to the possible transfer via food of antibiotic-resistant bacteria to humans or the acquisition of  
342 antibiotic resistance by human pathogens. In the light of these findings, regular monitoring  
343 programmes should be stepped up to check for antibiotic resistance in the aquaculture production of  
344 fish for human consumption.

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509 *Agents Ch.* 55(12), 5813-5818.



1 Table 1 – Resistance of *Aeromonas* species and species-complex to 15 antimicrobial agents

Species	N (%)	OXA	AMX	AM	CF	CL	E	FM	FF	GM	K	OT	S	SZ	TE	TMP
<i>A. media</i>	15 (14.4%)	8	8	6	13	1	13	5	-	1	3	1	6	13	1	12
<i>A. enteropelogenes</i>	1 (0.9%)	-	1	1	1	-	1	-	-	-	-	-	-	1	-	1
<i>A. bivalvium</i>	10 (9.6%)	2	6	6	10	-	10	1	-	1	1	2	6	10	1	8
<i>A. media/veronii</i>	4 (3.8%)	2	4	4	4	-	4	2	1	-	-	-	-	4	-	4
<i>A. salmonicida/bestiarium/hydrophila/caviae</i>	12 (11.5%)	1	7	8	12	1	11	-	1	-	-	1	7	12	1	9
<i>A. punctata/hydrophila/enteropelogenes</i>	1 (0.9%)	1	1	1	1	1	1	1	-	-	-	1	1	1	-	1
<i>A. salmonicida/bestiarium</i>	8 (7.7%)	-	4	5	8	-	8	-	-	-	-	1	6	8	1	3
<i>A. popoffii</i>	3 (2.9%)	2	1	2	3	-	3	-	-	-	-	-	1	2	-	2
<i>A. molluscorum</i>	11 (10.6%)	7	1	1	4	1	3	6	1	1	2	5	4	11	3	6
<i>A. encheleia</i>	2 (1.9%)	1	1	1	2	-	2	-	-	-	-	-	2	2	-	2
<i>A. hydrophila/salmonicida/bestiarum</i>	4 (3.8%)	1	-	-	4	-	3	-	-	-	-	-	-	4	-	4
<i>A. punctata</i>	6 (5.8%)	1	3	1	6	-	6	1	-	-	-	-	1	4	-	6
<i>A. bivalvium/ popoffii</i>	3 (2.9%)	-	-	-	2	-	3	-	-	-	-	-	-	3	-	1
<i>A. salmonicida/bestiarium/popoffii</i>	2 (1.9%)	1	-	-	1	-	2	1	-	-	-	-	-	2	-	-
<i>A. media/hydro</i>	2 (1.9%)	1	2	2	2	-	2	1	-	-	-	-	-	2	-	2
<i>A. allosacrophila</i>	1(0.9%)	-	-	-	1	-	1	-	-	-	-	-	-	1	-	1

<i>A. tasmaniensis/ hydro/ punctata</i>	2(1.9%)	1	2	-	2	-	2	1	-	-	-	1	1	2	1	2
<i>A. media/ punctata</i>	5 (4.8%)	4	3	2	3	-	5	3	-	1	2	-	2	3	-	4
<i>A. encheleia/ molluscorum</i>	3 (2.9%)	-	2	2	3	-	3	-	-	-	-	-	1	2	-	1
<i>A. salmonicida/ sobria/popoffii</i>	4 (3.8%)	-	-	-	4	-	3	-	-	-	-	-	1	4	-	2
<i>A. salmonicida</i>	3 (2.9%)	-	-	-	3	-	1	-	-	-	-	-	-	3	-	1
<i>A. salmonicida/sobria</i>	1 (0.9%)	-	-	-	1	-	1	-	-	-	-	-	1	1	-	-
<i>A. molluscorum /eucrenophila</i>	1 (0.9%)	1	-	-	-	-	-	1	-	-	-	-	1	1	-	-
Total	104 (100%)	34	46	42	90	4	88	23	3	4	8	12	41	96	8	72

- 2 oxolinic acid (OXA), amoxicillin (AMX), ampicillin (AM), cephalothin (CF), cloramphenicol (CL), erythromycin (E), flumequine (FM), florfenicol
- 3 (FF), gentamicin (GM), kanamycin (K), oxytetracycline (OT), streptomycin (S), sulfadiazine (SZ), tetracycline (TE) and trimethoprim (TMP).



4 Table 2. Multiple antibiotic resistance (MAR) index of *Aeromonas* spp strains isolated from gilthead sea bream reared in 3 Italian regions.

MAR index	Region			Total
	Sardinia	Sicily	Tuscany	
0.1	-	<i>n</i> = 1	<i>n</i> = 2	<i>n</i> = 3
0.2	-	-	<i>n</i> = 13	<i>n</i> = 13
0.3	-	<i>n</i> = 14	<i>n</i> = 31	<i>n</i> = 45
0.4	<i>n</i> = 3	<i>n</i> = 7	<i>n</i> = 4	<i>n</i> = 14
0.5	<i>n</i> = 1	<i>n</i> = 14	<i>n</i> = 7	<i>n</i> = 22
0.6	-	<i>n</i> = 1	<i>n</i> = 1	<i>n</i> = 2
0.7	<i>n</i> = 1	<i>n</i> = 2	<i>n</i> = 1	<i>n</i> = 4
0.8	-	<i>n</i> = 1	-	<i>n</i> = 1
0.9	-	-	-	-

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10 **Table 3.** MIC ( $\mu\text{g/mL}$ ) and antimicrobial susceptibility of *Aeromonas* spp strains isolated from *Sparus aurata*. \*=M45-P (CLSI, 2005); a=M100-  
 11 S26 (CLSI, 2016); b= M42/49 (CLSI, 2011); c=M31A2 (NCCLS, 2002); d=M31A (NCCLS, 1998).

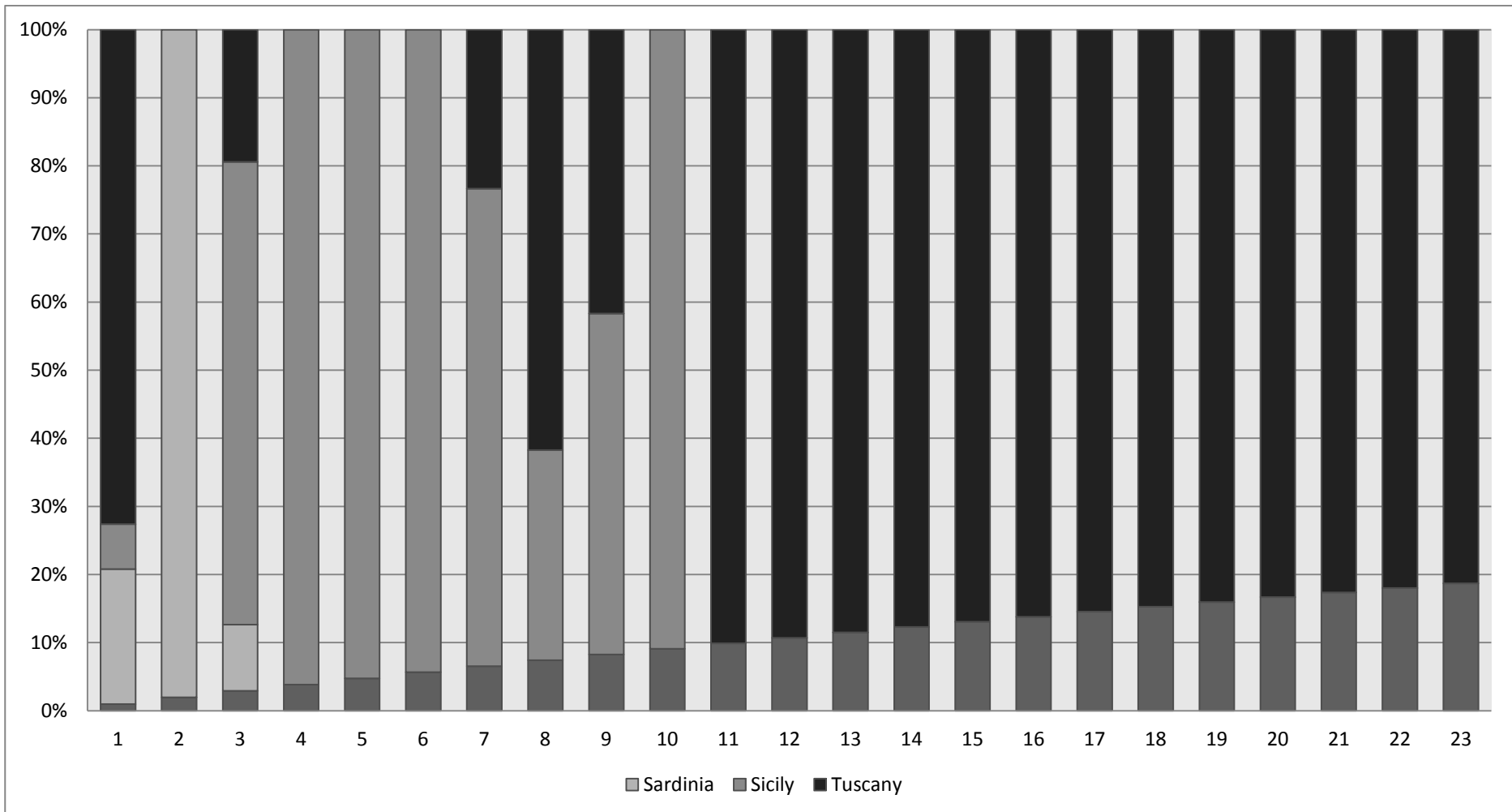
<b>Antibiotic</b>	<b>Breakpoints</b>	<b>MIC<sub>50</sub></b>	<b>MIC<sub>90</sub></b>	<b>Moda</b>	<b>Range</b>	<b>S (%)</b>	<b>I (%)</b>	<b>R (%)</b>	<b>ECV</b>	<b>WT strains (%)</b>
<b>OXA</b>	$\leq 0.12$ - $\geq 1^b$	0.06	16	0.06	0.06- $\geq 128$	65 (62.5)	5 (4.8)	34 (32.7)	0.25	69 (66.3)
<b>AMX</b>	$\leq 8$ - $\geq 32^*$	16	$\geq 128$	8	0.06- $\geq 128$	44 (42.3)	14 (13.5)	46 (44.2)	32	66 (63.5)
<b>AM</b>	$\leq 8$ - $\geq 32^*$	16	$\geq 128$	16- $\geq 128$	0.06- $\geq 128$	42 (40.4)	20 (19.2)	42 (40.4)	64	77 (74.0)
<b>CF</b>	$\leq 8$ - $\geq 32^*$	$\geq 128$	$\geq 128$	$\geq 128$	0.06- $\geq 128$	14 (13.5)	-	90 (86.5)	ND	ND
<b>CL</b>	$\leq 8$ - $\geq 32^*$	0.5	4	0.5	0.25-64	98 (94.8)	2 (1.9)	4 (3.8)	2	91 (87.5)
<b>E</b>	$\leq 0.5$ - $\geq 8^c$	16	64	8	0.06- $\geq 128$	9 (8.7)	7 (6.7)	88 (84.6)	32	93 (89.4)
<b>FM</b>	$\leq 2$ - $\geq 4^c$	0.12	16	0.06	0.06- $\geq 128$	81 (77.9)	-	23 (22.1)	0.25	62 (59.6)
<b>FF</b>	$\leq 4$ - $\geq 8^b$	1	4	0.5	0.06-64	101 (97.1)	-	3 (2.9)	2	93 (89.4)
<b>GM</b>	$\leq 4$ - $\geq 16^*$	2	8	2	0.12-32	92 (88.5)	8 (7.7)	4 (3.8)	8	100 (96.2)
<b>K</b>	$\leq 16$ - $\geq 64^a$	8	32	16-32	0.5- $\geq 128$	89 (85.6)	7 (6.7)	8 (7.7)	32	96 (92.3)
<b>OT</b>	$\leq 1$ - $\geq 8^b$	0.5	16	0.5	0.12- $\geq 128$	84 (80.8)	8 (7.7)	12 (11.5)	2	84 (80.8)
<b>S</b>	$\leq 6$ - $\geq 25^d$	16	64	16	1- $\geq 128$	9 (8.7)	54 (51.9)	41 (39.4)	64	90 (86.5)
<b>SZ</b>	$\leq 38$ - $\geq 76^a$	$\geq 256$	$\geq 256$	$\geq 256$	0.12- $\geq 256$	8 (7.7)	-	96 (92.3)	ND	ND
<b>TE</b>	$\leq 1$ - $\geq 8^b$	0.5	4	0.5	0.12- $\geq 128$	89 (85.6)	7 (6.7)	8 (7.7)	2	85 (81.8)
<b>TMP</b>	$\leq 8$ - $\geq 16^a$	32	64	64	0.12- $\geq 128$	32 (30.8)	-	72 (69.2)	ND	ND

12 MIC (Minimum Inhibitory Concentrations), S (susceptible strains), I (intermediate strains), R (resistant strains), **ECV** (epidemiological cut-off  
 13 value) ( $\mu\text{g/mL}$ ), WT strains (wild-type strains), oxolinic acid (OXA), amoxicillin (AMX), ampicillin (AM), cephalothin (CF), cloramphenicol (CL),

- 14 erythromycin (E), flumequine (FM), florfenicol (FF), gentamicin (GM), kanamycin (K), oxytetracycline (OT), streptomycin (S), sulfadiazine (SZ),  
15 tetracycline (TE) and trimethoprim (TMP). N.D.= not determined.

1 Figure 1. Percentages of *Aeromonas* species - species complex isolated from 6 mariculture farms in 3 Italian regions.

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3

4 1=*A. media*; 2=*A. enteropelogenes*; 3=*A. bivalvium*; 4=*A. media/veronii*; 5=*A. salmonicida/bestiarium/hidrophila/caviae*; 6=*A. punctata/hydrophila/enteropelogenes*; 7=*A.*  
 5 *salmonicida/bestiarium*; 8=*A. popoffii*; 9=*A. molluscorum*; 10=*A. encheleia*; 11=*A. hydrophila/salmonicida/bestiarum*; 12=*A. punctata*; 13=*A. bivalvium/popoffii*; 14=*A.*  
 6 *salmonicida/bestiarium/popoffii*; 15=*A. media/hydro*; 16=*A. allosacarophila*; 17=*A. tasmaniensis/hydro/punctata*; 18=*A. media/punctata*; 19=*A. encheleia/molluscorum*; 20=*A.*  
 7 *salmonicida/sobria/popoffii*; 21=*A. salmonicida*; 22=*A. salmonicida/sobria*; 23=*A. molluscorum /eucrenophila*.

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