River water analysis using a multiparametric approach: Portuguese river as a case study
Ana Barbosa-Vasconcelos, Ângelo Mendes, Flávia Martins, Elisabete Lopes, Ana Machado, Adriano A. Bordalo, Paulo Vaz-Pires, Natividade Vieira, Paulo Martins da Costa and Lucinda J. Bessa

ABSTRACT
The Ave River in northern Portugal has a history of riverbanks and water quality degradation. The river water quality was assessed by physicochemical, biological (macroinvertebrates) and microbiological (Enterococcus spp. and Escherichia coli) parameters in six locations (A–F, point A being the nearest to the source) throughout its course during a year. Epilithic biofilms were studied through polymerase chain reaction denaturing gradient gel electrophoresis (PCR-DGGE). Antimicrobial susceptibility testing helped with selecting isolates (n = 149 E. coli and n = 86 enterococci) for further genetic characterization. Pursuant to physicochemical and macroinvertebrates-based parameters, the river water was of reasonable quality according to European legislation (Directive 2000/60/EC). However, the microbiological analysis showed increased fecal contamination downstream from point C. At point D, four carbapenem-resistant E. coli isolates were recovered. Paradoxically, point D was classified as a point of ‘Good Water Quality’ according to macroinvertebrates results. Point F presented the highest contamination level and incidence of multidrug-resistant (MDR) isolates in the water column (13 MDR enterococci out of 39 and 33 MDR E. coli out of 97). Epilithic biofilms showed higher diversity in pristine points (A and B). Thus, biological and microbiological parameters used to assess the water quality led to divergent results; an outcome that reinforces the need for a holistic evaluation.

Key words | Enterococcus spp., epilithic biofilms, Escherichia coli, macroinvertebrates, multidrug-resistant isolates, river water

INTRODUCTION
The assessment of water quality is an essential measure within environmental monitoring. When water quality is poor, it affects not only the aquatic life but also the surrounding ecosystems. Rivers are unquestionably important parts of the hydrological cycle, mainly because they are fluxes of water and not reservoirs of water. Rivers, along with water, drag off sediments and other suspended materials (biotic and abiotic) that ultimately will reach all the other aquatic environments (Davies-Colley 2013). In 2000, the European Parliament and the Council of the European Union approved the Directive 2000/60/EC (http://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:02,000L0060-20141120&qid=150608744209&from=EN), which provided the guidelines to be followed by all member states in order to improve the
ecological quality of the European Community surface waters. These guidelines included the simultaneous analysis of physical and chemical factors as well as biological parameters.

River water quality is routinely assessed using physicochemical parameters, including temperature, conductivity, pH, dissolved oxygen, and total suspended solids (see www.epa.ie/water/wm/rivers/; www.epa.ie/pubs/reports/water/waterqua/Water%20Quality%20in%202016%20Ar%20Indicators%20Report.pdf). Furthermore, biological water quality assessment using macroinvertebrates is also an approach usually contemplated (Sharma & Rawat 2009; Bobori et al. 2018). The biodiversity of benthic macroinvertebrates present in an aquatic ecosystem, and their relative abundances, help to make inferences about the pollution burden, since they are good indicators of habitat/hydro-morphological alterations (Azrina et al. 2006; Balderas et al. 2016). Nevertheless, incorporation of microbiological parameters should also be included systematically in the assessment of water quality. It has been reported by others that the combination of different methods, such as physicochemical parameters and microbiological indicators, can provide a better estimation of pollution distribution (González-Fernández et al. 2010).

The microbiological quality of water is frequently assessed by quantifying indicators of fecal contamination (Escherichia coli and Enterococcus spp.), which can also signal the presence of other intestinal pathogens (Field & Samadpour 2007). Given the global problem of antimicrobial resistance, monitoring the aquatic environment, especially rivers, for the presence of resistant bacteria is of interest and may help in understanding the weight these environments have in the spread of antibiotic resistance.

The microbial consortia within a river is very complex, composed of both planktonic and attached bacteria, which are part of epilithic biofilms. Therefore, microbiological analysis of planktonic and attached bacteria should be simultaneously performed in order to provide more data that will help construct a more accurate snapshot of the environmental quality involving river water (Araya et al. 2005; Lyautey et al. 2005), in spite of being ignored by the above-mentioned EU directive.

The Ave River, located in the north of Portugal, has been considered one of the most polluted rivers both in Portugal and Europe (Soares et al. 1999), and for that reason it has been the focus of several studies (Poirel et al. 2012; Bessa et al. 2014; Kieffer et al. 2016). Such studies had exclusively assessed the microbial quality of the river, reporting worrying levels of antimicrobial resistance in fecal bacteria obtained from the river water.

Aiming at a more holistic evaluation of the Ave River water quality, in the present study a toolbox of parameters, including physicochemical, biological and microbiological, were used in spatial and temporal scales. From June 2014 to May 2015, five water samples and four epilithic biofilm samples were collected from six locations throughout the course of Ave River. Moreover, macroinvertebrate communities were also studied in three surveys coincident with three out of the five water samples collected.

**MATERIALS AND METHODS**

**Study area and surveys**

Six locations throughout the river course were selected for sampling. As shown in Figure 1, the six sites were not equidistant, because they were carefully chosen based on their location, either near a wastewater treatment plant (WWTP) or downstream of main tributaries. Contrarily to points A and B (upper part of the river), which may be deemed pristine site points, C and D (middle part) and E and F (lower part) are surrounded by a higher population density.

Physicochemical and microbiological parameters were assessed in the water samples collected in two 1-L sterile bottles from each location visited five times during a year (June 2014, September 2014, November 2014, February 2015 and May 2015). Epilithic biofilms were collected from submerged rocks at the same locations except during the May 2015 survey. Visible biofilms were scraped from the rocks using a brand new toothbrush into a sterile 100-mL flask and the volume was adjusted to 30 mL of sterile distilled water.

The assessment of the benthic macroinvertebrate communities was performed during three surveys (June 2014, November 2014 and May 2015). The procedure for the collection of macroinvertebrates followed the protocol
established by a Portuguese entity (INAG 2008), which takes into account the recommendations of the European Directive 2000/60/EC.

All samples collected were kept at 4 °C, for no longer than 24 h, until further treatment in the laboratory.

The values of the precipitation on the day of each survey were retrieved from the site of ‘Instituto Português do Mar e da Atmosfera’, the Portuguese meteorological, seismic, sea and atmospheric organization (www.ipma.pt/pt/).

**Physicochemical and environmental parameters**

Temperature, pH, conductivity, total suspended solids (TSS) and dissolved oxygen (DO) were measured *in situ*, using a multiparameter instrument (Multiparameter pH/ORP/EC/DO/Temperature Waterproof Meter, Hanna Instruments, Portugal). The concentration of dissolved nutrients such as phosphate (PO$_4^{3-}$), nitrate (NO$_3^{-}$), nitrite (NO$_2^{-}$) and ammonium (NH$_4^+$) were determined using a Multiparameter Bench Photometer C 200 (Hanna Instruments, Portugal) according to the instructions from the manufacturer. The biochemical oxygen demand (BOD$_5$) was also determined according to the Winkler method (Winkler 1888).

**Macroinvertebrates**

Macroinvertebrate samples were sorted in the laboratory using sieves of 1 and 0.5 mm in order to be separated according to their size and to facilitate their visualization. Sieve contents were washed with running tap water and placed in a white tray to sort the organisms, which were then examined under a stereo microscope (Stemi 205, Zeiss, Germany). Finally, the macroinvertebrates were kept in plastic tubes containing 70% ethanol. Each macroinvertebrate was subsequently identified with the help of dichotomous keys from Tachet *et al.* (2003). Taxonomic resolution at a class-level was considered for Oligochaeta, and the remaining macroinvertebrates were identified at the family-level.
The analysis of macroinvertebrate communities was performed based on the determination of several indices and metrics, which allowed the evaluation of the ecological quality of the stream. The following metrics were determined: Shannon–Weaver Diversity Index; Pielou Evenness Index; Índice Português de Invertebrados do Norte (IPiN), which is a Portuguese multimetric index (INAG 2009); the biotic index IBMWP (Iberian Bio Monitoring Working Party), which is highly sensitive to water quality and has been extensively applied in the Iberian Peninsula (Bonada et al. 2004); the Average Score per Taxon (ASPT), which is simply the IBMWP score divided by the number of scoring taxa in the sample, and ranges from 0 to 10; the Belgian Biotic Index (IBB) (De Pauw & Vanhooren 1985); and other metrics based on enumerations such as % EPT (Ephemeroptera, Plecoptera, Trichoptera), % DF (Dominant Family), % ETO (Ephemeroptera, Trichoptera, Plecoptera, Trichoptera), EPT/C (EPT/Chironomidae), % DH (Dominant Higher), % A (Annelida), % T (Tardigrada), % BC (Bilateria, Cnidaria), % F (Filterer Collectors) (Balderas et al. 2016).

Isolation and quantification of *Escherichia coli* and *Enterococcus* spp.

The membrane filtration method was used for the isolation and quantification of indicators of fecal contamination, *E. coli* and *Enterococcus* spp., from water samples (Bessa et al. 2014). Each biofilm suspension was subjected to disaggregation in an ultrasonic water bath (Sonorex RK 52, Bandelin, Germany) for 15 min, prior to being processed as described above for water samples.

The media used, for both water and biofilm samples, were Tryptone Bile X-glucuronide agar (TBX) (BioKar Diagnostics, Beauvais, France), and Slanetz and Bartley agar (SB) (Oxoid, Basingstoke, UK) for *E. coli* and enterococci enumeration, respectively. Media supplemented with antibiotics were also used for the isolation of resistant isolates: TBX agar (for *E. coli*) supplemented with cefotaxime (2 μg mL⁻¹), ampicillin (8 μg mL⁻¹), ciprofloxacin (4 μg mL⁻¹) and imipenem (2 μg mL⁻¹) (Sigma-Aldrich, St Louis, MO, USA), and SB agar (for enterococci) supplemented with vancomycin (6 μg mL⁻¹), ampicillin (8 μg mL⁻¹) and ciprofloxacin (4 μg mL⁻¹).

**Antimicrobial susceptibility testing**

A maximum of three colonies of *E. coli* and enterococci were picked up from each specific antibiotic-supplemented and non-supplemented medium for further antimicrobial susceptibility testing, which was carried out by the agar disk diffusion method as previously described (Bessa et al. 2014). Regarding *E. coli* isolates, 19 antimicrobial agents were used: ampicillin (AMP, 10 μg), amoxicillin/clavulanic acid (AMC, 30 μg), cephalothin (KF, 30 μg), ceftazidime (CAZ, 30 μg), cefotaxime (CTX, 30 μg), imipenem (IPM, 10 μg), aztreonam (ATM, 30 μg), gentamicin (CN, 10 μg), kanamycin (K, 30 μg), amikacin (AK, 30 μg), streptomycin (S, 10 μg), tobramycin (TOB, 10 μg), nalidixic acid (NA, 30 μg), tetracycline (TE, 30 μg), ciprofloxacin (CIP, 5 μg), nitrofurantoin (F, 300 μg), sulfamethoxazole/trimethoprim (SXT, 25 μg) and chloramphenicol (C, 30 μg). While for *Enterococcus* spp., 11 antimicrobial agents were used: ampicillin (AMP, 10 μg), gentamicin (CN, 120 μg), ciprofloxacin (CIP, 5 μg), tetracycline (TE, 30 μg), nitrofurantoin (F, 300 μg), vancomycin (VA, 30 μg), teicoplanin (TEC, 30 μg), erythromycin (E, 15 μg), rifampicin (RD, 5 μg), linezolid (LZD, 30 μg) and doxycycline (DO, 30 μg). All antimicrobial disks were purchased from Oxoid. The detection of extended spectrum β-lactamase (ESBL)-producing *E. coli* was based on agar plates observation according to the disk approximation test (Drieux et al. 2008). The interpretative criteria for antimicrobial susceptibility determination followed the CLSI recommendations (CLSI 2014).

Isolates were classified as multidrug-resistant (MDR – resistant to at least one agent in three or more antimicrobial categories), extensively drug-resistant (XDR – resistant to at least one agent in all but two or fewer antimicrobial categories) and pandrug-resistant (PDR – resistant to all agents in all antimicrobial categories) (Magiorakos et al. 2012).

**Escherichia coli** phylogenetic group determination and enterococci species identification

*Escherichia coli* isolates that presented an ESBL phenotype and/or resistance to six or more antimicrobial drugs were selected for DNA extraction and subsequent phylo-group assignment (Clermont et al. 2013). Accordingly, seven phylo-groups were considered (A, B1, B2, C, D, E, F).
Generally, commensal strains belong to phylo-groups A and B1, while pathogenic strains usually fit into phylo-groups B2 and D.

The species of enterococci isolates that presented resistance to vancomycin and/or teicoplanin or to four or more antimicrobial drugs were then identified by performing a multiplex-PCR already described (Jackson et al. 2004).

Characterization of river biofilms by polymerase chain reaction denaturing gradient gel electrophoresis (PCR-DGGE)

The bacterial DNA of the biofilm was extracted after centrifugation at 2,655 × g for 10 min of 1 mL of biofilm suspension previously disaggregated in the ultrasonic bath for 15 min. The DNA extraction was carried out using the Powersoil DNA Isolation Kit (Mo Bio laboratories, USA), according to the instructions from the manufacturer.

PCR amplification of the variable regions V3–V5 of the 16S rRNA gene was performed with the primers 907R (5' - CCG TCA ATT CMT TTG AGT TT-3') and 341F (5' - CCT ACG GGA GGC AGC AG-3') with a 40 bp GC sequence clamped to its 5' end (Lyautey et al. 2003). The 25 μL reaction mixture contained 200 μM of each nucleotide, 0.5 mM MgCl₂, 1× Complete KCl reaction buffer (Bioron GmbH, Germany), 0.4 μM of each primer, 1.25U of DFS-Taq DNA polymerase (Bioron GmbH, Germany) and 80–100 ng template DNA. The PCR was carried out in a MyCycler Thermal Cycler (Bio-Rad Laboratories, Hercules, CA, USA) using a program previously described (Schauer et al. 2000). PCR products (550 bp) were checked by electrophoresis in 1.5% agarose gels at 100 V for 1 h.

The DGGE was performed in a DGGE-4001 system (CBS Scientific Co, San Diego, CA, USA), using a 40–60% denaturing gradient (100% denaturing gradient was 7 M urea and 40% deionized formamide) in vertical polyacrylamide gels (6% w/v acrylamide in 0.5× TAE buffer). Electrophoresis was carried out on 0.5× TAE buffer at 61 °C for 16 h at 60 V. Gels were stained with Green Safe Premium (NZYTech, Lisbon, Portugal) for 15 min as specified by the manufacturer. Image analysis was carried out using the BioNumerics 7.5 software (Applied Maths, Sint-Martens-Latem, Belgium). For each sample, a densitometric profile was generated to determine the relative contribution of each band to the total signal in the sample lane. A UPGMA Jaccard distances dendrogram was generated from the DGGE profiles of the biofilm samples collected. Moreover, based on the relative intensities of the bands, diversity indices such as the Shannon–Wiener and Simpson indices were calculated.

Statistical analysis

Descriptive statistics were computed using IBM SPSS Statistics (23.0) for categorical and continuous variables. Relative and absolute frequencies were calculated for categorical variables, and maximum, minimum, median and interquartile range for continuous variables. The assessment of normality and homoscedasticity was completed as part of the testing assumptions. None of the continuous variables showed a normal distribution. Kruskal-Wallis one-way analysis of variance (ANOVA) was applied to compare bacterial counts between different collection points and surveys. The Spearman correlation coefficient was used to assess the association between the counts of fecal bacteria found in the water column and biofilm. In both tests, the significance level was set at 0.05.

RESULTS

Analysis of physicochemical parameters

The results of all physicochemical and environmental parameters determined upon the Ave River water samples are shown in Table 1. Generally, no drastic changes occurred in each parameter analyzed along the river. The lower part of the river presented the most alkaline values of pH. The upper part of the river, being located in a mountain section, presented the lowest temperatures in relation to the other locations. The maximum variation in oxygen saturation was around 30%. Variations in this parameter occurred regardless of the location and the survey. An abnormal and rather high conductivity (213 μS cm⁻¹) was registered in point B in the survey of September 2014 and also, in the same survey, the highest values of BOD₅ were recorded.
The dissolved inorganic nutrients evaluated did not present a coincident variation among them throughout time and along the six sampling sites, as initially anticipated. Phosphates, represented by PO$_4^{3-}$, were particularly high in June 2014 in all the sampling sites analyzed. The highest values of ammonia were found in the lower part of the river. Nitrites were detected in very low concentrations (<0.025 mg L$^{-1}$), occasionally in the lower part of the river.

**Macroinvertebrates-based metrics**

From the analysis of the various metrics determined (Table 2), it was possible to infer on the ecological quality of the river points studied. The progression of the calculated indices throughout the sites is very similar. The Shannon–Weaver diversity index indicated a decrease in the water quality in the following order: A > D > B > F > E > C; A and C being the points where there was higher and lower diversity within the macroinvertebrate population, respectively. The Pielou equitability index suggested a similar trend on the water degradation: A > D > C > F > B > E. The results from the IP$\text{t}$IN index were alike (A > D > F > B > C > E), classifying point A as having a ‘Good ecological status’, points D, F and B as ‘reasonable’ and points C and E as ‘medium’.

Equally, all the other metrics, except % FC, attributed to point A the highest ecological quality, followed by points D and F, which indeed presented a reasonable number of different individuals (Ephemeroptera, Plecoptera, Trichoptera and...
Odonata) that indicate a good ecological environment. The % FC throughout all river points was notably higher in the survey of November 2014, which was also a time point presenting generally high levels of fecal contamination.

An additional outcome, which could be an indication of the decreasing quality of the water and habitat of the river, was the fact that an invading species of bivalve, Corbicula fluminea, was detected in all the three macroinvertebrates surveys, from point C downstream. It was most prevalent at point D: June 2014 (n = 4), November 2014 (n = 2) and May 2015 (n = 120).

**Enumeration of the indicators of fecal contamination**

Enterococci enumeration in the water column at different collection points revealed an increase from A to F. The contamination increased significantly (p < 0.05) from B to C. The same trend was observed regarding the levels of contamination by *E. coli*, in particular from B to C, although a significant difference was also noticed between point A and point B. The contamination levels of the water column by both fecal bacteria at different collection times did not differ significantly (p > 0.05).

The Spearman coefficient indicates a positive correlation between the number of fecal bacteria present in the water column and in the biofilm. This correlation was more evident in the case of *E. coli* (Spearman’s rho = 0.770; p < 0.001), compared to enterococci (Spearman’s rho = 0.579; p = 0.003).

Spatially, it was visible that site C seems to be a turning point, since it was from that location that the counts of both *E. coli* and enterococci obtained by the culture method started to be more substantial in the water stream (Figure 2) and also in the biofilm. Regarding the variation throughout the timeframe of a year, it was possible to observe that the fluctuations in the CFU numbers did not follow a pattern coincident with the rainfall. It is noteworthy that *E. coli* and *Enterococcus* spp. counts were significantly higher in the river biofilm than in the streaming water.

**Antimicrobial resistance, diversity of *E. coli* phylogenetic groups and *Enterococcus* species**

In total, from the four surveys (June 2014, September 2014, November 2014 and February 2015), and of both water and biofilm samples, 149 *E. coli* and 86 enterococci isolates were
selected for further studies after analysis of the antimicrobial susceptibility results. When isolates obtained from the same sample had the same antimicrobial resistance profile, only one was selected. In a few cases, isolates obtained from antibiotic-supplemented media end up not presenting resistance to the concrete antibiotic in the medium.

The most relevant profiles as well as the origin of 52 MDR *E. coli* isolates amongst the 149 isolates studied are shown in Table 3. All the 149 *E. coli* isolates presented resistance to AMP (ampicillin) and to TE (tetracycline), and the majority (77.9%) was MDR, one was XDR and the other was PDR. Four carbapenemase-producing *E. coli* were obtained from the water sample collected from point D in February 2015. As shown in Figure 3, the majority of the MDR isolates was obtained from the water samples. Overall, the collection points D, E and F were those from which more MDR *E. coli* isolates were recovered. Though MDR isolates started to appear at point B, it was at point C that such occurrence may lead to foreseeing a tendency of increase.

*Escherichia coli* isolates presenting an ESBL phenotype were obtained from all sampling sites and in all collection times. Overall, 67 ESBL-producing *E. coli* were obtained. The major part of MDR *E. coli* isolates belonged to the phylogenetic groups A or B1 (Table 3). The PDR isolate belonged to the phylo-group E, which is closely related to phylo-groups D and B2 that are known to enclose mostly pathogenic strains.

The numbers of MDR enterococci were lower than the counts of MDR *E. coli*. Besides that, MDR enterococci were, as were MDR *E. coli*, detected in higher numbers in the water than in the epilithic biofilms. The incidence of MDR enterococci was more marked in water samples from points D and F, especially in the survey of June 2014 (Figure 4). Curiously, at point E a breakout in the trend was observed. Nonetheless, point C could also be deemed
a turning point, from where MDR enterococci started to appear. Exceptionally, at point A, one MDR Enterococcus spp. was recovered from the water sample collected in November 2014.

The most frequent antibiotic resistance found among the enterococci was towards tetracycline (TE – 52.3%). Resistance to AMP, nitrofurantoin (F), and chloramphenicol (C) were less frequent. Some of the most relevant profiles amongst the 59 antimicrobial-resistant enterococci isolates and their respective origins are presented in Table 4. Isolates displaying simultaneous resistance to ciprofloxacin (CIP), teicoplanin (TEC), and vancomycin (VA) were consistently found in June and September 2014 at points D, E and F.

Overall, 17 isolates presenting phenotypic resistance to vancomycin (VA) were obtained; 15 from water samples and two from biofilms. They were only detected in samples from points D, E and F. In the last survey, in February 2015, only one vancomycin-resistant Enterococcus spp. was obtained and it was from point F.

Table 3 | Antimicrobial resistance profiles, origin and phylogenetic group of 52 multidrug-resistant (MDR) E. coli isolates selected among the 149 isolates studied

<table>
<thead>
<tr>
<th>Date of sampling</th>
<th>Sampling sites</th>
<th>Sample</th>
<th>Antimicrobial resistance profiles</th>
<th>No. of isolates</th>
<th>Phylogenetic group</th>
</tr>
</thead>
<tbody>
<tr>
<td>R4</td>
<td>D</td>
<td>Water</td>
<td>AMP FOX IPM CIP CN F TE KF K SXT CAZ CTX AK S NA C TOB AMC ATM&lt;sup&gt;a&lt;/sup&gt;</td>
<td>1</td>
<td>E</td>
</tr>
<tr>
<td>R4</td>
<td>D</td>
<td>Water</td>
<td>AMP FOX IMP CIP CN TE KF K SXT CAZ CTX AK S NA TOB AMC ATM&lt;sup&gt;b&lt;/sup&gt;</td>
<td>1</td>
<td>A</td>
</tr>
<tr>
<td>R4</td>
<td>D</td>
<td>Water</td>
<td>AMP FOX CIP CN TE KF K SXT CAZ CTX S NA C TOB AMC&lt;sup&gt;c,d&lt;/sup&gt;</td>
<td>1</td>
<td>F</td>
</tr>
<tr>
<td>R4</td>
<td>C</td>
<td>Biofilm</td>
<td>AMP CIP CN TE KF K SXT CTX S NA TOB ATM&lt;sup&gt;e&lt;/sup&gt;</td>
<td>1</td>
<td>A</td>
</tr>
<tr>
<td>R1</td>
<td>E/F</td>
<td>Biofilm</td>
<td>AMP CIP CN TE S NA C TOB SXT K&lt;sup&gt;f&lt;/sup&gt;</td>
<td>2</td>
<td>A</td>
</tr>
<tr>
<td>R1</td>
<td>C/E</td>
<td>Water</td>
<td>AMP FOX CIP CN TE AMC KF S NA&lt;sup&gt;c&lt;/sup&gt;</td>
<td>2</td>
<td>B1</td>
</tr>
<tr>
<td>R1</td>
<td>B/D</td>
<td>Water</td>
<td>AMP CIP TE KF S NA SXT&lt;sup&gt;c&lt;/sup&gt;</td>
<td>4</td>
<td>A</td>
</tr>
<tr>
<td>R3</td>
<td>E/F</td>
<td>Water</td>
<td>AMP CIP TE CTX S NA&lt;sup&gt;c&lt;/sup&gt;</td>
<td>3</td>
<td>B1/A</td>
</tr>
<tr>
<td>R4</td>
<td>C/F</td>
<td>Water</td>
<td>AMP TE KF SXT CTX S NA&lt;sup&gt;c&lt;/sup&gt;</td>
<td>2</td>
<td>B1/A</td>
</tr>
<tr>
<td>R1</td>
<td>C</td>
<td>Water</td>
<td>AMP CIP TE NA SXT&lt;sup&gt;c&lt;/sup&gt;</td>
<td>2</td>
<td>B1/A</td>
</tr>
<tr>
<td>R1</td>
<td>F</td>
<td>Water</td>
<td>AMP FOX TE AMC KF NA&lt;sup&gt;c&lt;/sup&gt;</td>
<td>2</td>
<td>B1/A</td>
</tr>
<tr>
<td>R3</td>
<td>B/C/D/F</td>
<td>Water/Biofilm</td>
<td>AMP CIP TE SXT S NA</td>
<td>6</td>
<td>B1/A</td>
</tr>
<tr>
<td>R3/R4</td>
<td>C/E</td>
<td>Water</td>
<td>AMP TE KF SXT CTX S</td>
<td>3</td>
<td>B1/A</td>
</tr>
<tr>
<td>R1/R2/R4</td>
<td>E/F</td>
<td>Water/Biofilm</td>
<td>AMP CIP TE NA</td>
<td>4</td>
<td>A/B1</td>
</tr>
<tr>
<td>R1</td>
<td>D</td>
<td>Water</td>
<td>AMP TE KF NA&lt;sup&gt;c&lt;/sup&gt;</td>
<td>2</td>
<td>F</td>
</tr>
<tr>
<td>R1/R2</td>
<td>D/E/F</td>
<td>Water</td>
<td>AMP CIP NA SXT</td>
<td>4</td>
<td>A</td>
</tr>
<tr>
<td>R2/R3/R4</td>
<td>D/E/F</td>
<td>Water</td>
<td>AMP TE CTX KF&lt;sup&gt;c&lt;/sup&gt;</td>
<td>4</td>
<td>A</td>
</tr>
<tr>
<td>R1/R2</td>
<td>D/F</td>
<td>Water</td>
<td>CIP TE NA</td>
<td>4</td>
<td>A</td>
</tr>
<tr>
<td>R3</td>
<td>F</td>
<td>Water</td>
<td>AMP CN TE KF SXT CTX S NA TOB&lt;sup&gt;c&lt;/sup&gt;</td>
<td>1</td>
<td>B2</td>
</tr>
<tr>
<td>R4</td>
<td>F</td>
<td>Biofilm</td>
<td>AMP TE KF NA</td>
<td>1</td>
<td>B2</td>
</tr>
<tr>
<td>R2</td>
<td>D</td>
<td>Water</td>
<td>AMP CTX KF</td>
<td>1</td>
<td>D</td>
</tr>
</tbody>
</table>

<sup>a</sup>PDR: Pandrug-resistant.
<sup>b</sup>XDR: Extensively drug-resistant.
<sup>c</sup>ESBL producers.
<sup>d</sup>These isolates presented intermediate resistance to imipenem. R1: June 2014; R2: September 2014; R3: November 2014; R4: February 2015. AMP: Ampicillin; FOX: Cefoxitin; IPM: Imipenem; CIP: Ciprofloxacin; CN: Gentamicin; F: Nitrofurantoin; TE: Tetracycline; KF: Cephalothin; K: Kanamycin; SXT: Sulfamethoxazole/Trimethoprim; CTX: Cefotaxime; AK: Amikacin; S: Streptomycin; NA: Nalidixic Acid; C: Chloramphenicol; TOB: Tobramycin; AMC: Amoxicillin/Clavulanic Acid; ATM: aztreonam.
Regarding the identification of the species of *Enterococcus*, it was found that the most common species were *Enterococcus faecalis* and *Enterococcus faecium*, followed by *Enterococcus durans* and *Enterococcus mundtii*.

**Analysis of the bacterial communities within the biofilms**

Diversity in the composition of bacterial epilithic biofilms collected at three surveys (June 2014, September 2014 and November 2014) was explored by DGGE of the PCR-amplified 16S rRNA gene fragments. Based on the DGGE profiles, an UPGMA dendrogram from cluster analysis using the Jaccard coefficient was constructed (Figure 5). Spatial and temporal differences within the epilithic biofilms microbial community could be clearly observed. The closest related genetic fingerprints presented a similarity of 70%. Overall, the genetic fingerprints obtained from the survey of November 2014 were notably distinct from those obtained from June and September 2014. Assuming that...
each band represents an operational taxonomic unit (OTU), the profiles obtained from samples collected in June and September 2014 from point A presented higher similarities between each other and a higher number of OTU in comparison to the sample collected from the same site in November 2014. The genetic fingerprint obtained from

Table 4 | Antimicrobial resistance profiles, origin and species identification of 34 enterococci isolates selected among the 59 isolates studied

<table>
<thead>
<tr>
<th>Date of sampling</th>
<th>Sampling sites</th>
<th>Sample</th>
<th>Antimicrobial resistance profiles</th>
<th>No. of isolates</th>
<th>Species identification</th>
</tr>
</thead>
<tbody>
<tr>
<td>R1</td>
<td>D</td>
<td>Water</td>
<td>AMP TE RD E DO CN CIP TEC VA</td>
<td>1</td>
<td>E. faecalis</td>
</tr>
<tr>
<td>R1</td>
<td>F</td>
<td>Water</td>
<td>AMP RD E CN LZD CIP VA</td>
<td>1</td>
<td>E. fecium</td>
</tr>
<tr>
<td>R1</td>
<td>F</td>
<td>Water</td>
<td>TE RD E DO CN CIP C</td>
<td>1</td>
<td>E. faecalis</td>
</tr>
<tr>
<td>R3</td>
<td>E</td>
<td>Water</td>
<td>AMP TE RD E CIP TEC VA</td>
<td>1</td>
<td>E. faecalis</td>
</tr>
<tr>
<td>R4</td>
<td>C/E/F</td>
<td>Water</td>
<td>AMP TE RD E CIP</td>
<td>4</td>
<td>E. faecium/E. faecalis</td>
</tr>
<tr>
<td>R1</td>
<td>C/D/E</td>
<td>Water/Biofilm</td>
<td>AMP RD E CIP</td>
<td>6</td>
<td>E. faecium/E. faecalis</td>
</tr>
<tr>
<td>R1</td>
<td>F</td>
<td>Water</td>
<td>TE DO CIP TEC VA</td>
<td>1</td>
<td>E. faecium</td>
</tr>
<tr>
<td>R2/R3</td>
<td>C/D/E/F</td>
<td>Water</td>
<td>AMP RD E CIP</td>
<td>4</td>
<td>E. faecalis/E. faecum/E. hirae</td>
</tr>
<tr>
<td>R1</td>
<td>D</td>
<td>Water/Biofilm</td>
<td>AMP RD E CIP</td>
<td>2</td>
<td>E. faecium/E. faecalis</td>
</tr>
<tr>
<td>R1</td>
<td>D</td>
<td>Water</td>
<td>TE DO TEC VA</td>
<td>1</td>
<td>E. faecalis</td>
</tr>
<tr>
<td>R1/R2</td>
<td>D/E/F</td>
<td>Water</td>
<td>CIP TEC VA</td>
<td>6</td>
<td>E. durans/E. mundtii/E. faecum/E. faecium</td>
</tr>
<tr>
<td>R2</td>
<td>D</td>
<td>Water</td>
<td>TE CIP VA</td>
<td>1</td>
<td>E. durans</td>
</tr>
<tr>
<td>R3</td>
<td>E</td>
<td>Water</td>
<td>TEC F VA</td>
<td>1</td>
<td>E. faecalis</td>
</tr>
<tr>
<td>R1</td>
<td>F</td>
<td>Biofilm</td>
<td>F VA</td>
<td>1</td>
<td>E. faecium</td>
</tr>
<tr>
<td>R1</td>
<td>E</td>
<td>Water</td>
<td>TEC VA</td>
<td>1</td>
<td>E. faecalis</td>
</tr>
<tr>
<td>R2</td>
<td>D</td>
<td>Biofilm</td>
<td>CIP VA</td>
<td>1</td>
<td>E. mundtii</td>
</tr>
<tr>
<td>R4</td>
<td>E</td>
<td>Biofilm</td>
<td>TEC F</td>
<td>1</td>
<td>E. faecium</td>
</tr>
</tbody>
</table>

R1: June 2014; R2: September 2014; R3: November 2014; R4: February 2015.

AMP: Ampicillin; TE: Tetracycline; RD: Rifampicine; E: Erythromycin; DO: Doxycycline; CN: Gentamicin (120 μg); LZD: Linezolid; CIP: Ciprofloxacin; TEC: Teicoplanin; VA: Vancomycin; F: Nitrofurantoin.

Figure 5 | UPGMA Jaccard distances dendrogram of DGGE profiles obtained after PCR amplification of bacterial 16s rRNA of the biofilms collected at the six sampling sites in the first three surveys.
point C in June 2014 was the one that showed the lowest number of OTU (six bands), while the samples collected from point A in June and September 2014 originated profiles with the highest number of OTUs registered, i.e. 22 OTUs.

The values of the calculated diversity indices are shown in Figure 5. Higher values obtained for the Shannon–Wiener index represent higher diversity. The values of the Shannon–Wiener index ranged between 0.8918 and 1.332. Equally, the Simpson index (that ranges between 0 and 1) indicates that the closer to 0 the values, the higher diversity is present in the community. Thus, the two diversity indices were in accordance. The biofilms collected from point A, both in June and in September, were the most diverse in their composition, while the biofilms collected from point C, in the same dates, presented lower diversity.

DISCUSSION

Through the years, the Ave River has not been in compliance with the requirements needed to attest its water quality (Costa 2008). For that reason, many campaigns and actions to clean up Ave River have been carried out by competent national entities, namely TRATAVE (entity responsible for the wastewater treatments on Ave River and its tributaries). The physicochemical quality of the water has improved, however, some issues regarding its microbiological quality are still continuing, as demonstrated by our results.

Despite suffering occasional variations, probably due to punctual discharges into the river, all the physicochemical parameters analyzed throughout time in all sampling sites were within the values recommended to classify the river water as having reasonable quality, according to the European water framework directive (Directive 2000/60/EC). Only the concentration of phosphates consistently surpassed the limit values (0.10 mg L\(^{-1}\)), particularly in the summer time, indicating a possible detergent contamination from sewage water.

Macroinvertebrates are used in the biomonitoring of surface waters since they are good indicators of habitat/hydro-morphological alterations (Balderas et al. 2016). The analysis of the macroinvertebrate metrics studied showed that the ecological quality of the river did not diminish throughout its course (from point A to point F). Indeed, point D was deemed by the macroinvertebrate-based monitoring metrics as a point of ‘Good Water Quality’.

Therefore, physicochemical and macroinvertebrates-based parameters retrieved results that could classify the river water of, at the least, satisfactory quality (Directive 2000/60/EC; INAG 2009). However, on the contrary, microbiological parameters, which are not included in the European Directive, revealed an increase in fecal contamination, especially downstream from point C, where the levels of contamination by \(E.\ coli\) (CFU 100 mL\(^{-1}\)) have increased by about 17.5 times in relation to point B. At point D the levels of fecal contamination were rather high. There, in the total of the four surveys, in the water column, 20.6% (20 out of 97) MDR \(E.\ coli\) and 30.8% MDR enterococci (12 out of 39) were obtained. Thus, the high numbers of fecal indicators obtained, around 1,000 CFU 100 mL\(^{-1}\) or higher, are not reliable with the apparent good quality of the river making the river water not appropriate for either irrigation or treatment aimed at human consumption, according to the existing legislation (Directive 2000/60/EC).

This increase in the number of fecal contamination indicators throughout the river is not unexpected, once the population density surrounding the river also increases, especially from point C onward, and moreover the agriculture environment gives place to industrial activities. Thus, the entry of non-treated waters (originated from agriculture, animal farming and urban waters) can occur and explain the increase in fecal contamination throughout the river.

The contamination of a water stream by \(E.\ coli\) is intimately correlated with hydrological conditions, such as rainfall and its consequent dragging effects (Ratajczak et al. 2010). However, that was not verified in this study; the peak of rainfall occurred in the third sampling collection, on November 2014, while the highest contamination by \(E.\ coli\) was observed in the fourth collection (February 2015), when the precipitation was relatively low. At point C, the highest number (CFU 100 mL\(^{-1}\)) of \(E.\ coli\) was registered in June 2014, when there was dry and hot weather. This contamination may be explained by some occasional discharges into the river and/or by the ‘concentration effect’ occasioned by the reduction in water level during the summer time, which is usually quite marked in Portugal.
due to the low rainfall in that season of the year. An association between rainfall and increase of enterococci CFU counts was also not observed. Furthermore, the progression of contamination by *E. coli* and by enterococci did not overlap. Overall, the CFU numbers of *E. coli* were higher than those of *Enterococcus* spp., which is not surprising since *E. coli* predominate over enterococci in the gastrointestinal tract (Dubreuil et al. 2012).

When comparing the CFU numbers (both of *E. coli* and enterococci) obtained in the river water and in the biofilm, it becomes clear that those numbers are much greater in the biofilm than in the water, which is in accordance with previous studies (Craig et al. 2004; Balzer et al. 2010). Nevertheless, a positive correlation was still detected between the number of fecal bacteria present in the water column and in the biofilm, especially in the case of *E. coli*. This was an interesting outcome that will help to outline the risk management of the river.

At each point, the variation of % FC throughout time followed the same progression as the fecal contamination, which may suggest that the proliferation of filterer collectors may be due to the increase of fecal contamination.

Significant numbers of MDR isolates were also obtained in this study. The appearance of MDR *E. coli* at point B, deemed as pristine, could be a worrying fact, nonetheless, its appearance was not consistent throughout time (they were only recovered in June 2014 and November 2014). The incidence of MDR *E. coli* and enterococci was particularly noticeable in water samples from points D, E and F. In the surroundings of these points of the river, there are WWTPs, whose treated effluents are launched into the river. However, it is known that WWTPs are not 100% effective in eliminating bacteria. Previous studies have demonstrated that WWTPs in Portugal could only reduce and not totally eliminate the bacterial load in the outflow (Martins da Costa et al. 2006, 2007). Moreover, they also concluded that those WWTPs could select MDR strains and favor the accumulation of genes of antibiotic resistance. Indeed, WWTPs can receive in the same tank not only municipal wastewater, but also wastewater from hospitals and industries, allowing the contact of antibiotic residues with bacteria and consequently favoring the occurrence of horizontal transference of resistance genes.

In 2010, a KPC-producing *E. coli* was isolated from this river (Poirel et al. 2012), being the first report of that kind of carbapenemase-producing *E. coli* in Portugal. Now, in our study of February 2015, four other carbapenemase-producing *E. coli* (one PDR, one XDR and two MDR) were isolated approximately 9.5 km upstream of point D. A molecular analysis confirmed that the PDR and XDR isolates harbored the *bla*IMPM-8 and *bla*VIM-1 genes, respectively, and that the two MDR isolates, showing intermediate resistance to imipenem, harbored one of the two genes, *bla*IMPM-8 and *bla*VIM-34 (Kieffer et al. 2016).

MDR enterococci were also frequent in water samples collected from point D, including isolates that presented resistance to vancomycin (mainly *E. faecalis*).

The presence of carbapenemase-producing *E. coli* and vancomycin-resistant enterococci impelled us to contact the hospitals nearby in that region in order to know if they had had cases of infections by bacteria with similar profiles of antimicrobial resistance. None of the hospitals had reports of cases of infection by carbapenemase-producing *E. coli* in the timeframe of this study and it is known that vancomycin-resistant enterococci have been rarely found in the clinical setting of that region. Although the national scenario of the epidemiological situation of carbapenemase-producing *Enterobacteriaceae* has worsened from 2013 to 2015 from ‘sporadic occurrence’ to ‘sporadic hospital outbreaks’, respectively (Albiger et al. 2015), the regional hospitals near Ave River do not contribute to such statistics. That fact is also corroborated by the scarcity of *E. coli* belonging to the phylo-groups B2 and D found amongst the set of MDR *E. coli* isolates obtained in this study. Therefore, as apparently these isolates were not originated in the hospital setting, their presence in the river remains quite enigmatic. It can be hypothesized that low concentrations of these last-resort antibiotics or others to which they are resistant by co-selection mechanisms could be in the water and thus allow the development of resistance or the enrichment of resistant strains in the water. Another hypothesis could be the presence of some chemicals or pollutants that had the capacity to allow/favor the acquisition of these kind of antibiotic resistances, especially to carbapenems, since the carbapenemase-producing *E. coli* found in Ave River in 2010 and 2015 harbored different genes (Poirel et al. 2012; Kieffer et al. 2016).
The presence of MDR isolates in the epilithic biofilms was rather lower than those detected in the water column. These differences account for the risk evaluation of dissemination of resistance. The resistant bacteria floating in the water column represent a high risk for the rapid dissemination of resistance, since such bacteria will quickly spread downstream. The resistant strains present within the biofilm can contribute to the dissemination prolonged in time, representing a temporal risk and favoring the horizontal transfer of genes conferring antibiotic resistance among bacteria. Biofilms can also work as suppliers of resistant bacteria to the water column, especially when there are torrents and increased flow. The fact that higher levels of antibiotic resistance were found in the water column than in the biofilm reveals the difficulty of resistant strains in integrating multispecies biofilms.

Considering that the bacterial community existing in the water column and in the river biofilms are substantially different (Beier et al. 2008), and based on the premise that the changes in the community within the biofilm are indicative of changes in the aquatic ecosystem (Lear et al. 2008), the variations in those communities through the PCR-DGGE approach were also analyzed. Overall, for each sampling point, the results showed that the bacterial composition of the epilithic biofilms collected in June and September 2014 were quite similar, however changing considerably in November 2014. This was probably due to rainfall that occurred in the month of November, previously to the survey, in which the river flow increased, causing resuspension of the sediment and thus altering the composition of the microbial communities within the epilithic biofilms (Lear et al. 2008).

Through the analysis of the diversity indices calculated, we verified that the upper part of the river generally presented higher diversity in their bacterial communities in respect to points D, E and F. At point C, there was little diversity in the first two surveys and more variability in the last one. This loss of diversity in the bacterial community at points D, E and F match with the increase of fecal indicators of contamination in the biofilms at those points, which may lead us to infer that the fecal bacteria are able to dominate over some of the original environmental bacteria. Furthermore, several other factors account for changes in the community composition, for instance, an increase in the temperature of the water has great influence on the metabolism of some bacterial families that are less thermotolerant and may not survive in such conditions (Araya et al. 2003).

CONCLUSIONS

This study confirms the need of evaluating simultaneously multiple parameters to fully assess the quality of river water. Nowadays more than ever, the quantification of indicators of fecal contamination, and the determination of their antimicrobial susceptibility profiles may be important parameters to complement the physicochemical and biological ones. Changes in the biological communities, either microbial or of macroinvertebrates, portray alterations suffered by the watercourse due to climatic changes or pollution and anthropogenic activities.

Though macroinvertebrate-based monitoring metrics may be helpful in obtaining an ecological assessment of the river, they may not be adequate to mirror the overall water quality. More specific studies in the critical points of the river identified in this study still have to be performed in order to better understand the microbial community and the river water dynamics, as well as studies on the relation between fecal contamination and functional feeding groups under a controlled environment.

The fecal contamination increased downstream as the population density and industrial, livestock and agricultural explorations increased. Point F presented the highest contamination level and presence of MDR E. coli (including ESBL phenotypes) and enterococci (including vancomycin-resistant E. faecalis and E. faecium). However, point D was considered the most worrisome in terms of isolates showing resistance to last-line antibiotics exclusively for human use, such as imipenem (IMP). Pinpointing throughout the river the presence of isolates presenting resistance to last-line antibiotics and being able to analyze the distribution of isolates with a huge heterogeneity in their resistance profiles, for both E. coli and enterococci, is of great importance to understanding the critical points in the river and gain awareness that rivers can be the means of dissemination and sources of emergence of MDR strains.
ACKNOWLEDGEMENTS

This work was supported by the project INNOVMAR – Innovation and Sustainability in the Management and Exploitation of Marine Resources (reference NORTE-01-0145-FEDER-000035), within Research Lines NOVELMAR and INSEAFOOD), supported by North Portugal Regional Operational Programme (NORTE 2020), under the PORTUGAL 2020 Partnership Agreement, through the European Regional Development Fund (ERDF).

REFERENCES


CLSI (Clinical and Laboratory Standards Institute) 2014 Performance Standards for Antimicrobial Susceptibility Testing; Seventeenth Informational Supplement. CLSI document M100-S24. Wayne, PA, USA.


INAG 2008 Protocolo de amostragem e análise para os macroinvertebrados bentónicos (Protocol for Triage and Analysis of Benthic Macroinvertebrates). Ministério do Ambiente, Ordenamento do Território e do Desenvolvimento


First received 4 January 2018; accepted in revised form 26 August 2018. Available online 24 September 2018