



**Andreia Filipa
Henriques Mortágua**

**DNA METABARCODING APPROACH AS A
COMPLEMENTARY TECHNIQUE FOR ASSESSMENT
OF PORTUGUESE RIVERS USING DIATOMS**

**ABORDAGEM DE *METABARCODING* DE DNA COMO
TÉCNICA COMPLEMENTAR NA AVALIAÇÃO DOS
RIOS PORTUGUESES USANDO DIATOMÁCEAS**

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Universidade de Aveiro Departamento de Biologia
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Dissertação apresentada à Universidade de Aveiro para cumprimento dos requisitos necessários à obtenção do grau de Mestre em Biologia Aplicada, realizada sob a orientação científica da Doutora Salomé Fernandes Pinheiro de Almeida, professora auxiliar do Departamento de Biologia da Universidade de Aveiro e coorientação científica da Doutora Maria João Feio, investigadora no MARE-UC (*Marine and Environmental Sciences Centre*) da Universidade de Coimbra.

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palavras-chave

Diatomáceas, *metabarcoding* de DNA, DNA ambiental, biomonitorização, rios portugueses, avaliação ecológica da água, sistemas de água doce

resumo

A Directiva Quadro de Água (DQA) é o principal instrumento político de gestão das massas de água na Europa e inclui a avaliação biológica de rios e riachos através das diatomáceas, mediante o cálculo de um índice autoecológico, o *Indice de Polluosensibilité Spécifique* (IPS), adotado oficialmente para Portugal. Este índice requer um alto nível de conhecimento taxonómico para a identificação morfológica dos indivíduos. Avanços na área da genómica, como o *metabarcoding* de DNA combinado com técnicas de sequenciamento de alto rendimento (HTS), oferecem uma alternativa promissora aos métodos clássicos, limitando a exigência de especialização e, portanto, reduzindo o tempo e os custos. O objetivo deste estudo foi testar o potencial do *metabarcoding* de DNA de diatomáceas na avaliação biológica de rios portugueses, comparando as classificações do IPS, obtidas com abordagens morfológica e moleculares. No total, 88 amostras de rios do centro de Portugal foram recolhidas na primavera de 2017, seguindo as normas da DQA. A abordagem morfológica incluiu a identificação taxonómica de pelo menos 400 valvas ao microscópio ótico. A abordagem molecular compreendeu a extração de eDNA seguida de sequenciação (Illumina MiSeq) usando o *barcode* de DNA *rbcL* com 312pb. As sequências foram analisadas com o software Mothur, produzindo Unidades Taxonómicas Operacionais (UTOs) atribuídas à biblioteca de referência R-Syst::diatom. Testou-se também o efeito de um fator de correção (FC) para o biovolume aplicado aos dados moleculares. Os inventários das comunidades de diatomáceas revelaram um total de 306, 125 e 111 espécies identificadas através da morfologia e método molecular sem e com FC, respetivamente. A percentagem total de UTOs atribuídos com sucesso à biblioteca de referência foi de 32%, com uma média de 47,5% por amostra, enquanto a percentagem média de leituras “não classificadas” dos UTOs convertidos em lista de taxa foi de 52,5% e variou entre 2 e 95%, entre todas as amostras. Ao comparar as abundâncias das espécies, os resultados mostraram diferenças estatísticas em relação ao número de espécies dos inventários moleculares e morfológico, embora a aplicação do FC tenha aproximado as duas abordagens. A fonte dessas diferenças pode estar na necessidade de completar as bibliotecas de referência, representando, atualmente, a maior dificuldade na atribuição taxonómica das sequências de eDNA. Em relação aos valores de IPS, os resultados indicaram uma boa correlação entre os métodos morfológico e moleculares, especialmente quando se aplicou o FC. Os diagramas de NMDS e PCO baseados na abundância das espécies revelaram um gradiente de classificações de qualidade em todas as 3 metodologias, apoiando a hipótese de que o *metabarcoding* de DNA pode vir a ser abordagem válida para avaliação da qualidade ecológica. No entanto, ainda há trabalho a ser feito nesta área no sentido de proporcionar uma transição suave entre a abordagem tradicional e a mais recente, sem perder de vista o conhecimento acumulado nas últimas décadas sobre a avaliação da qualidade da água.

keywords

Diatoms, DNA metabarcoding, environmental DNA, biomonitoring, Portuguese rivers, ecological assessment of water, freshwater systems

abstract

The Water Framework Directive (WFD) is the main political instrument for management of the waterbodies in Europe and includes the bioassessment of rivers and streams based on diatoms, through the calculation of an autoecological index, the *Indice de Polluosensibilité Spécifique* (IPS) officially adopted for Portugal. This index requires a high level of taxonomic expertise for morphological identification of individuals. Advances in genomics, such as the DNA metabarcoding combined with high-throughput sequencing (HTS) techniques offer a promising alternative to classical methods, limiting expertise requirement and therefore reducing time and costs. The aim of this study was to test the potential of DNA metabarcoding of diatoms in the bioassessment of Portuguese rivers by comparing the IPS classifications obtained with morphological and molecular approaches. A total of 88 samples from rivers in central Portugal were collected in the spring of 2017 following WFD standards. The morphological approach comprised taxonomic identification of at least 400 valves, under the light microscope. The molecular approach included eDNA extraction followed by DNA sequencing (Illumina MiSeq) using a 312bp *rbcL* DNA barcode. Sequences were analysed with Mothur software, producing Operational Taxonomic Units (OTUs) that were taxonomically assigned to the R-Syst::diatom reference library. It was also tested the effect of a correction factor (CF) for biovolume applied on molecular data. Inventories of diatom communities revealed a total number of 306, 125 and 111 species identified with morphology, molecular method without and with the CF, respectively. The total percentage of successfully assigned OTUs to the reference library was 32%, with an average of 47.5% per sample, while the average percentage of unassigned reads from the converted OTUs to taxa list was 52.5% and varied between 2 and 95%, among all samples. When comparing species' abundances, the results showed statistical differences in the number of species between molecular and morphological inventories although the application of the CF approximated both approaches. The source of these differences may lay on the incompleteness of reference libraries, which currently represents the major difficulty in taxonomic assignment of eDNA sequencings. Regarding IPS values, the results indicated a good correlation between morphological and molecular methods, especially when applying the CF. NMDS and PCO diagrams based on species abundances revealed a gradient of quality classifications in all 3 methodologies. These support the hypothesis that DNA metabarcoding may be a valid approach for ecological quality assessment. Yet, there is still work to be done on this new methodology in order to be able to make a smooth transition between the traditional and this new approach without misspend accumulated knowledge from the last decades on water quality assessment.

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INTRODUCTION

Water is an essential resource for the existence of all living beings. It covers over 70% of the Earth's surface and it is distributed by oceans, lakes, glaciers, rivers, groundwater and as vapour in the atmosphere (Cia.gov, 2017). Particularly freshwater is a valuable and finite resource and humans have been using it over time not only for direct consumption, but also for the development of other means of subsistence such as in agriculture or in industry which led to the evolution of civilizations. However, the exploration of water resources was and still is not always sustainable.

Although it is a very old practice ascending to ancient Mesopotamia, the use of pesticides in agriculture began with elemental sulphur to control insects and rapidly became a routine. Later in the 1940's, the production of synthetic pesticides, which displayed higher selectivity and better control of pests, grew significantly (Unsworth, 2010). However, over-application of agrochemicals (pesticides and fertilizers containing nitrates and phosphates, among others) has shown to contribute to the degradation of soil/water quality and ecosystems. Many studies identified other problems associated with agriculture, namely, the loss of biodiversity due to monocultures, unsustainable water consumption (Horrigan et al., 2002), salinization and erosion of soil (UNEP/WHO, 1996) and eutrophication of freshwater systems (Daniel et al., 1994).

Along with agricultural practices, other means of anthropogenic water contamination have also begun long time ago. During centuries, due to population growth and urbanization, drinking water sources were contaminated with raw sewage leading to the spread of diseases such as cholera, infectious hepatitis or typhoid (Bryan, 1977). In the mid-19th century, the Industrial Revolution introduced new sources of water pollution intensifying the damages on human and environmental health. Since then, chemical wastes, toxic components and hazardous solvents and metals have been disseminated in marine and freshwaters (UNEP/WHO, 1996). Direct discharges of contaminants from mining, smelting or even pharmaceuticals also play a significant role in this issue with pollutants leaching from surface to groundwater.

Human activities always had consequences in the environment and ecosystems' balance, however, the impact of these activities dramatically increased in the last few decades due to over-exploitation of resources and wastes generated, as mentioned above. Particularly freshwater resources from which humans use 70 to 80% for economic purposes have become scarce for consumption and its quality decreased (Baroni et al., 2007). The importance of *clean* water gradually became a matter of concern when in 1960 the first environmental movements emerged and symbolic events such as the Earth Day or legislative acts in U.S.A like Clean Water Act (CWA), in 1972 (Congress, 1972), raised awareness on the water pollution issue.

1. Water Monitoring Programs

International organizations and political entities realized the urgency of taking action to protect water resources for meeting human and socio-economic needs and, in 1977, the United Nations Water Conference approved the Mar del Plata Action Plan which stated several goals on water management before the end of the 20th century, namely, the assessment of water resources status based on a national and international standardization of methodologies and instruments for comprehensive analysis, the improvement of new available data on water quantity and quality in order to safeguard its adequate supply and the increment on water use efficiency (Biswas, 2004).

Later, in 1992, the International Conference on Water and the Environment took place in Dublin representing an important marker but this time on freshwater policy (Gleick, 1993). The necessity of developing and implementing a holistic and interdisciplinary approach on a global scale for water protection was reinforced by the international community and set as urgent, following Agenda 21 (Rio de Janeiro, 1992) which proposes a list of activities undertaken by all States from the United Nations including the establishment of “appropriate policy frameworks and national priorities” for water assessment. Following this, other meetings occurred worldwide with environmental sustainability in view: the Convention of Biological Diversity in 1992, Earth Summits in 1995 (New York) and 2002 (Johannesburg) (Hering et al., 2010).

1.1. Biomonitoring in Europe and Portugal

1.1.1. Background

In Europe, an EU Directive based on the Ecological Quality of Surface Waters was drafted to implement several measures, monitoring schemes and water quality standards in the European countries. From here, the European Water Framework Directive (WFD) (Directive 2000/60/EC) was adopted in 2000 sharing some ecological objectives and approaches with the US CWA from 1972.

The WFD became an important political instrument which, by definition, provides economic, social and environmental approaches on sustainable exploitation of water bodies based on the improvement and prevention of its chemical and biological quality at a local, regional, national and European levels (INAG, 2008; Cruz et al., 2009). It requires that European Member States achieve the “good status” of all their water bodies, including estuaries,

coastal waters, rivers and streams, lakes and groundwater (Hering et al., 2018). After its publication, started the identification and characterization of river basins, the establishment of monitoring networks, the execution of the operational programmes of measures until the meeting of environmental objectives in 2015. At the end of that year, the first management cycle ended, however, the objectives were not fully accomplished by the Member States. Due to this default, a second and a third (final deadline) management cycles were established for 2021 and 2027, respectively (Directive 2000/60/EC).

In Portugal, political initiatives concerning water management go back to 1919, when Portuguese government approved the Water Law, which exclusively safeguarded the economic interests on water resources (Costa et al., 2011). Until the 1970's, many attempts to reform water legislation were made, by introducing legal provisions for the preservation of water quality. The first came in the late 1940's, with the creation of a commission to "study and codify measures to avoid pollution of the country's waterways" (Pato, 2007). Since 2000, the legislation concerning to water resources management and protection has been following the norms of the WFD.

1.1.2. Technical Procedures

The assessment of water bodies' ecological quality in lotic systems defined by the WFD strategy is based on biological elements and support physical-chemical and hydromorphological parameters. The biological parameters include organisms such as phytoplankton, phytobenthos, macrophytes, benthic invertebrates and fish fauna and their characterization must contain information of communities' composition and abundance data. The physical-chemical parameters include temperature, pH, dissolved oxygen, conductivity, water flow, transparency, total phosphorus, total nitrogen, Chemical Oxygen Demand (COD), among others (European Commission, 2009).

In order to assess their status, the sampling of biological communities must respond to specific standards and protocols. Table 1 shows a brief description of the major aspects to be considered in the sampling routine established by the Institute of Water (INAG, 2008) for the assessment of biological quality (using phytobenthos) of Portuguese rivers under the WFD norms.

The final ecological quality classification is expressed in 5 quality classes according to the level of alteration of natural conditions (low to high disturbance): High, Good, Moderate, Poor and Bad (INAG, 2009). This approach is based on preliminary establishment of reference conditions for each river type, which should correspond to the absence of human disturbance (including industrial, urban and agricultural influences) (Feio et al., 2014).

Table 1. Methodological norms for the correct sampling and analysis of phytobenthos contemplated in the monitoring program adopted for river systems at a national level.

	Sampling Routine
Time of the year	Spring (recommended)
Location	A section with approximately 50m which include coarse substratum, turbulent flow with current velocity between 10-50 cm/s, no overshadow and similar luminosity
Sampling procedure	Random selection of 5 stones with biofilm and scraped into a tray using a toothbrush and water from the river. In the absence of stones, biofilm is collected from macrophytes
Preservation	The biofilm fixation is made using lugol, stored in 250 mL flasks and kept at 4°C until analysis
Slides preparation	First, the fixative is removed. Then, cellular organic matter is oxidized, and finally, the definitive slides are mounted for microscopic observation
Identification	Count and identification of at least 400 valves to species level, under light microscope

1.1.3. Biological Element Phytobenthos (Diatoms)

The biological element phytobenthos is usually restricted to benthic diatoms in the majority of the member states of the European Union (INAG, 2008). The diatoms are photoautotrophic microalgae abundant in almost all aquatic systems (Smol and Stoermer, 2010) with life strategies including benthic species that adhere to different substrates (e.g. stones, plants, sand, animals, mud) (Zimmermann et al., 2015). Their structure consists of two valves and siliceous bands forming the frustule (Smol and Stoermer, 2010). They are responsible for 20 to 25% of all organic carbon fixation on the planet representing an important food resource for marine and freshwater organisms (Round et al., 1990). Diatoms are considered good water quality bioindicators due to the easy preservation of the frustules and its sensitivity to several stress factors, which is a consequence of their short generation time (fast response to environmental changes) (Smol and Stoermer, 2010; Keck et al., 2018).

1.1.4. Diatom Indices

Among many algal bioindicator groups, diatoms are the most used due to their sensitivity to contamination, easy sampling, handling and preservation, vast diversity and ubiquity of the species (Martín et al., 2010). The assessment of freshwater resources (rivers and streams) using the entire aquatic community, including diatoms, was firstly approached by Kolkwitz and Marsson (1902, 1908), who published the theoretical foundation of the relations between aquatic organisms and water degradation (organic contamination). Later, several other

ecologists (Butcher, 1947; Patrick, 1949; Zelinka & Marvan, 1961; Lange-Bertalot, 1979) contributed to the development of diatom biotic indices. Many other assessment methods were also developed for other BQEs used in biomonitoring, such as the BQI (Benthic Quality Index), BMWP (Biological Monitoring Working Party Index), FBI (Family Biotic Index) and the IPTI (Índice Português de Invertebrados) used for benthic macroinvertebrates (Wiederholm, 1980; Armitage et al., 1983; Hilsenhoff, 1988; Ferreira et al., 2008); Damage rating, River Trophic Status Indicator (RTSI), River Macrophyte Nutrient Index (RMNI) used for macrophytes from rivers (Haslam, 1982; Ali et al., 1999, Willby et al., 2012) or, more recently, HeLM (Hellenic Lake Macrophyte) method developed for Greek lakes (Zervas et al., 2018); and the IBI (Index of Biological Integrity) which was adapted for fish, algae, macroinvertebrates and macrophytes, among others (Karr, 1981).

The construction of biological indices comprises years of sampling to collect enough data for evaluation of long-term trends as well as to define the origin of those trends (anthropogenic pressures or natural variation) (Wallace, 1996). They incorporate biological diversity and integrity concepts, providing useful information on the assessment of ecosystems' health (Karr, 1993). The majority of the diatom indices are based on relative abundance combined with a level of sensitivity or tolerance of selected taxa (usually at the species level). Some of those indices are the IPS (*Indice de Polluosensibilité Spécifique*; Cemagref, 1982), the TDI (Trophic Diatom Index; Kelly, 1998), the IBD (*Indice Biologique Diatomées*; Prygiel & Coste, 1998) or the EPI-D (Diatom-Based Eutrophication/Pollution Index; Dell'Uomo et al. 1999). Portugal adopted the IPS method for biomonitoring using diatoms, which addresses specific pressures such as acidification, salinity, eutrophication and organic matter (Almeida et al., 2014). This index is based on the relative abundance of all the taxa present in a set of samples, their indicator values (1 to 3 scale) and their sensitivity values to pollution (1 to 5 scale) (Descy & Coste, 1991). The following Equation (1), describes the IPS, where $IPSV_i$ is indicator value, a_i is the relative abundance of species i in the sample, and $IPSS_i$ is the pollution sensitivity.

$$IPS = \frac{\sum_{i=1}^n a_i \times IPSV_i \times IPSS_i}{\sum_{i=1}^n a_i \times IPSV_i} \quad (1)$$

In the case of ecological assessment under the WFD strategy, these indices are then converted to Ecological Quality Ratios (EQR). The EQR is calculated by dividing the index value of each sampling site by the median of that index pre-established for the reference sites of the same typology, which results in a value between 0 and 1 (INAG, 2009). According to the watercourse typology, EQR value of 1 represents the reference conditions and values close to 0 indicates bad ecological status (Bund & Solimini, 2006).

2. Morphological *versus* DNA-based Monitoring Tools

To estimate diatom indices, it is required to identify the taxa at species level (as shown in Table 1) and elaborate an accurate taxonomic inventory of the community. The current method used in most countries (morphological approach) requires identifying the taxa by observation of their morphological features. This demand has some limitations/disadvantages, namely:

- 1) Phenotypic plasticity and genetic variability of organisms (Hebert et al., 2003) leading to misidentifications, nomenclatural divergences and incorrect biodiversity estimation (Belton et al., 2014), although, according to Will and Rubinoff (2004), the bigger problem regarding this topic is the definition of species (or another taxonomic group) which remains in debate among scientists;
- 2) Cryptic taxa, which is problematic due to the lack of conspicuous differences in external appearance (Pfenninger and Schwenk, 2007). The sympatric coexistence of cryptic species might have considerable consequences not only for bioassessment but also for other areas of study, such as conservation, biogeography or macroecology (Muangmai et al., 2016);
- 3) Specificity of morphological keys (Hebert et al., 2003): only single “semaphoronts” (*sensu* Hennig, 1965) translated as “an individual during a very small temporal duration of its life” (Havstad et al., 2015) are possible to identify;
- 4) The personal concept and perception of specific characteristics of a given organism is different between taxonomists which is aggravated by the aspects above mentioned;
- 5) It is a time-consuming task (Belton et al., 2014; Taberlet et al., 2012; Zimmermann et al., 2014), taking months of work in some cases;
- 6) It is financially expensive. Ex.: Identification of a small group of known species can cost about \$2 per specimen, and when it comes to a larger group of species, identifying a single specimen can cost \$50 to \$100 (all costs assumed) in North America, according to Hebert and Gregory (2005).

These disadvantages also limit the identification process of diatoms. They are a very diverse group and the morphological features analysed using traditional approach are, among others, the frustule’s symmetry [radial (*Centrales*) or bilateral (*Pennates*)], the presence or absence of raphe (in pennate diatoms) and its position, striae pattern, the length and width of

cells and the patterns of pores distributed in a species-specific way (Smol & Stoermer, 2010; De Tommasi, Gielis & Rogato, 2017). It is difficult to identify diatoms beyond the genus level for reasons 1) and 2) and also because there are considerable variations in morphology within a population (Babanazaroya et al., 1996). Besides all the limitations mentioned above, morphological approach also entails expensive equipment (in many cases it is necessary to resort to electron microscopy) for diatom identification.

2.1. The Advent of DNA-Based Approach in Biomonitoring

2.1.1. DNA Barcoding and Metabarcoding (eDNA)

DNA barcoding, as a standardised alternative method for taxonomic identification, was first introduced by Hebert et al. (2003) who demonstrated the reliable assignment of organisms to higher taxonomic categories based on the differences in cytochrome *c* oxidase subunit I (COI) amino-acid. By definition, the DNA barcode is a short sequence of DNA (400-800 bp) easily sequenced in one read (in principle), which unambiguously identifies a given taxon (Kress & Erikson, 2008; Zimmermann et al, 2015). This technique can either be used for assignment of unknown individuals to species, or improvement of new species discovery by using large-scale screening of one or few reference genes (Moritz & Cicero, 2004).

«DNA barcoding is a novel system designed to provide rapid, accurate, and automatable species identifications by using short, standardized gene regions as internal species tags.»

Hebert and Gregory, (2005)

This approach brought solution to the identification of cryptic species (Hebert et al., 2004), but it also can be useful in other fields such as, forensics science to analyse biological samples of crime scenes or in environmental and ecological genomic studies (Li et al., 2014). COI sequence has been used as one of the universal barcodes for animals' sequencing (including macroinvertebrates). For plants, it has been more difficult to find a universal marker due to the lack of correct variation within single loci (Li et al., 2014), however, four plant DNA barcodes have been developed and widely used in systematics: *rbcL*, *matK*, *trnH-psbA* and ITS (Kress, 2017). For protists, Table 2 shows DNA markers used in some studies for identification purposes (Pawlowski et al., 2012, 2016).

Table 2. Alternative protistan DNA barcodes proposed and used for identification.

Gene	Organism	Reference in literature
D1-D2/D2-D3 regions at 5' end of 28S rDNA	Ciliates	Gentekaki and Lynn, 2009
	Haptophytes	Liu et al., 2009
	Acantharians	Decelle et al., 2012
	Diatoms	Rimet et al., 2014
ITS1/ITS2 rDNA	Chlorarachniophytes	Gile et al., 2010
	Dinoflagellates	Litaker et al., 2007; Stern et al., 2012
COI	Euglyphida	Heger et al., 2011
	Dinoflagellates	Stern et al., 2010
	Coccolithophorid haptophytes	Hagino et al., 2011
	Ciliates	Barth et al., 2006
ITS	Diatoms	Evans et al., 2009
<i>rbcL</i>		Kermarrec et al., 2013; Zimmermann et al., 2014
<i>Cox1</i>		Evans et al., 2009; Rimet et al., 2014
4V 18S		Rimet et al., 2014

The number of DNA barcodes for protists' diversity evaluation has greatly increased in the last decade. Reference databases have received up to tenfold more sequences of some eukaryotic supergroups than in the years before 2000 (Pawlowski et al., 2016). The application of high-throughput sequencing (HTS) technologies contributed to the constant emergency of new unidentified eukaryotic sequences which shows that reference databases for protists barcoding still needs more curation compared to the ones for animal or plant species.

Environmental DNA (eDNA) barcoding – metabarcoding – derive from DNA barcoding, however, instead of linking a specimen to a unique sequence, it identifies multiple taxa from mixed samples identifying the community composition of a given environment, using HTS techniques (Zimmermann et al., 2015). Early studies using metabarcoding approach were focused on the discovery of protists' diversity (Pawlowski et al., 2016), resorting to group-specific primers for a given DNA barcode. In the case of diatoms, different DNA barcodes are suitable for different purposes. *Cox1*, ITS and 28S genes are considered suitable for taxonomic

studies, while *rbcL* and 18S genes are recommended for biomonitoring (Pawlowski et al., 2016) (Table 2).

The first works on diatom identification using eDNA barcoding were based on Sanger sequencing of clones (Jahn et al., 2007), however, some years later, Next-Generation Sequencing (NGS) was introduced as a high speed and large-scale approach which revealed interesting results for DNA sequencing (Kermarrec et al., 2014). This HTS technique allowed scientists to improve the DNA metabarcoding method for bioassessment. Calculation of taxa abundances using HTS data derives from the number of DNA sequences (i.e. reads) assigned to each taxon (species) (Vasselon et al., 2018). Each read is clustered into Operational Taxonomic Units (OTU), which will then be assigned to a Linnaean taxon using a reference library (Keck et al., 2018). Afterwards, OTUs list is converted to a taxonomic list and the traditional indices based on the ecological species preferences can be calculated. Figure 1 shows a scheme of the metabarcoding standard steps including eDNA sample processing (1), PCR amplification (2), high-throughput sequencing (3), filtering of the sequence data (4), clustering into OTUs (5) and assignment to morphospecies (6).

2.1.2. Pros and Cons on Using DNA Metabarcoding for Biomonitoring

Species detection using DNA metabarcoding is subjected to some biases, which have been reported in many studies and summarized by Pawlowski et al. (2016):

1. Incompleteness of reference libraries;
2. The choice of DNA barcode (marker);
3. The selection and efficacy of PCR primers.

The incompleteness of reference databases (1) is considered the primary reason for high levels of “unassigned” reads/OTUs (i.e. those which have no Linnaean taxon correspondence in the reference library) resulting from HTS data (Vasselon et al., 2017; Rivera et al., 2018; Pawlowski et al., 2016). Presently, in order to calculate biological indices (specially diatom indices) it is necessary to associate autoecological values and other factors to morphospecies. Thus, the more unassigned reads to species in a dataset, the less accurate the calculation of the indices will be for a certain sample site. Visco et al. (2015) reported this gap in the reference database when compared the results of DI-CH calculations based on eDNA and rDNA data from diatoms and verified that only a small fraction (30%) of the sequences matched a species in the library. This represents a problem if we intend to use the metabarcoding approach alone in bioassessment. For example, the COI gene barcode is present in the database of numerous species. A study using benthic macroinvertebrates performed by Emilson et al. (2017) and based

on the comparison between morphological and DNA metabarcoding metrics across streams (i.e. % chironomid, richness, % EPT) benefited from the well-developed COI reference sequence database to support their results on the effectiveness of metabarcoding, which provided higher richness values than morphological approach. According to Valentini et al., (2016), 90% of the fish species have been sequenced (in Western European continental waters). However other markers need to be sequenced to provide also intraspecific and geographic variation data.

Besides diatoms, prokaryotes and eukaryotes in general, require a specific set of eDNA markers (2) for each in order to cover the majority of the phyla. The most sequenced eDNA barcode is the 16S, highly represented in reference databases and because of that, it is an obvious choice for prokaryotes. On the other hand, eukaryotes have not yet an ideal marker. Its choice mostly depends on the taxonomic resolution and groups of interest (Drummond et al., 2015). Table 2 shows the DNA markers most applied for the different organisms.

Primer specificity (3) or recent divergence are two factors controlling detection limits on genetic identification of taxa. They also reduce species number and alter its composition in molecular inventories (Pawlowski et al., 2018). The PCR is the main step in samples' processing which contributes to these events. Elbrecht et al. (2017), for example, identified primer biases as the primary source of variation, while Vivien et al. (2016) points out the existence of false negatives. PCR reaction generates a number of amplicons which will highly influence the number of sequences attributed to a given taxon resulting in the quantitative ambiguities reported in some metabarcoding studies (Kermarrec et al., 2013; Elbrecht et al., 2017). Sequences of some species are easily amplified than others, which lead to a preferential amplification of those species (that sometimes may be a few) compared to others, contributing to more biases (Pawlowski et al., 2018).

The problematic of abundance biases has tried to be overcome, for example by applying correction factors. Vasselon et al. (2018) tested the efficiency of a correction factor for biovolume on 8 diatom species from pure cultures by comparing the copy number of *rbcL* gene and cells biovolume. Their results showed a reduction of 47% on the differences between morphological and metabarcoding-based water quality indices. Because cells with high biomass can comprise a higher number of copies of the marker compared with small cells (therefore, lower copy number), this correction factor brought both molecular and morphological approaches together.

Because DNA metabarcoding associated with HTS techniques is a relatively recent approach, it still presents obstacles to the correct and accurate identification of species. Optimization and standardization of protocols are necessary. However, it is evident that this method carries great advantages if we intend to apply it in bioassessment. Some of the most denoted benefits are their precision compared with morphological methods, especially for microorganisms, certain life stages (for example, juveniles and pupae) and cryptic taxa (Hering

et al., 2018). The reduction of costs inherent to technical procedures using DNA-based approach compared with morphological one is overly defended, and indeed, NGS technologies have similar costs (in some cases slightly lower, depending on the indicator and number of specimens treated) to traditional method (Stein et al., 2014). In the future, with the advance of technology and competitiveness of the market, the prices will decrease and possibly there will be a burst in the application of DNA metabarcoding in bioassessment. Also, the results of NGS techniques may proportionate easier and faster identifications compared with those under the microscope.

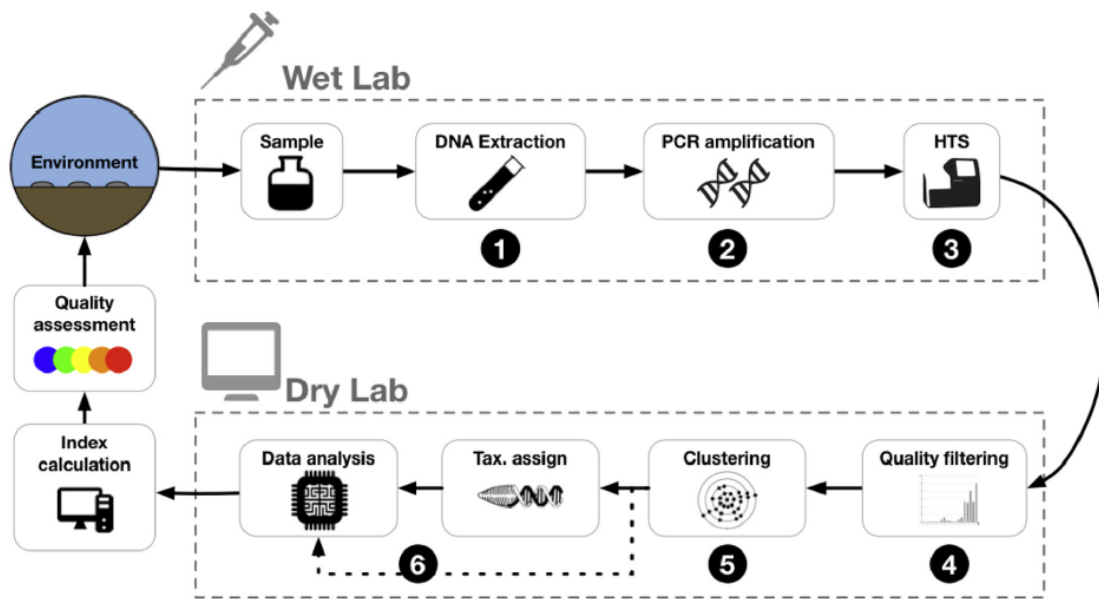


Fig. 1. Scheme of the main steps carried out in DNA metabarcoding procedure for biomonitoring (Pawlowski et al., 2016).

OBJECTIVES & HYPOTHESES

DNA-based methodologies associated with advanced technologies have opened the door to an easier and more resolute approach for water bioassessment. Worldwide, ecologists and taxonomists are studying and debating the efficacy of this new method applied to aquatic ecosystems. For now, in Europe, DNA metabarcoding can be included in biomonitoring under the WFD goals for ecological assessment only for complementing the traditional approaches (Hering et al., 2018). A realistic option would be to replace the process of identification of organisms by molecular procedures for more cost-efficiency and speed of process (Pawlowski et al., 2016) without the need of restructuring the whole framework which would take time and more investigation. However, this is a gradual transition (if it happens) and will take more optimization and standardization of the protocols. For now, and to our knowledge, no studies on this subject have been made in Portuguese rivers.

For those reasons, the major aim of our study is to evaluate the applicability of DNA metabarcoding associated with HTS techniques for biomonitoring on Portuguese rivers based on diatom samples collected from the central region of Portugal, in parallel with the WFD strategy. For that we focused on two main questions:

- I) Do indices based on molecular and morphological data provide similar classifications of study sites in Portuguese rivers with different disturbance levels?
- II) What is the best approach to obtain realistic abundance data from molecular analyses in Portugal?

To answer these questions, we compared the diatom community structure and ecological quality classifications based on IPS values obtained from the traditional (morphological identification) and more recent approach (eDNA metabarcoding).

And because many authors already pointed out limiting factors on DNA metabarcoding procedures (some of them are explored above), we also considered in this study the application of a correction factor (CF) for cell biovolume already proposed by Vasselon et al. (2018). Their work revealed an evident success on diminishing the discrepancies between molecular and morphological inventories (underestimating the big taxa) by applying an equation to the resulting number of reads from HTS data.

Summarizing, we compared three main aspects between two methodologies (molecular-DNA metabarcoding - and morphological-based approach): abundance, index values and resulting quality classifications, and the response of indices to stressors (given by physical-chemical parameters). Within the molecular approach, we also analysed the effect of a correction factor for biovolume (based on the work of Vasselon et al., 2018) on those three aspects.

MATERIAL & METHODS

Under the WFD norms, Portuguese entities responsible for elaborating the River Basin Management Plans (RBMP) have established 8 hydrographic regions in continental Portugal considered in the water monitoring actions for the 2nd cycle of the management plans in force from 2016 to 2021. These hydrographic regions comprise their main river basins as well as the catchment areas of coastal streams, groundwater and adjacent coastal waters. The river basins which defined the 8 regions are (Agência Portuguesa do Ambiente, 2015):

1. Minho and Lima
2. Cávado, Ave and Leça
3. Douro
4. **Vouga, Mondego and Lis**
5. Tejo and western streams
6. Sado and Mira
7. Guadiana
8. Algarve streams

1. Study Area

The study region is located in central Portugal (Fig. 2) and covers a total area of approximately 11,215 km² (Mendes et al., 2014) which comprises three hydrographic basins: **Vouga, Mondego and Lis**. This region belongs to the western part of the Iberian Peninsula, between important paleogeographic and tectonic units and consists of two geomorphological components: the Hesperian Massif and the Western Mesocenozoic Orla (Lisboa et al., 2015; Agência Portuguesa do Ambiente, 2015).

The source of river Vouga lies in Serra da Lapa at 930 m of altitude and runs 148 km until it drains into Ria de Aveiro, a lagoon connected to the Atlantic Ocean. River Vouga basin has a surface area of 3,685 km² and is separated from Mondego river basin to the south by Serra do Buçaco (Agência Portuguesa do Ambiente, 2015).

The Mondego catchment region is the second largest basin in national territory covering an area of 6,659 km². It lies between Vouga basin (to the East) and Tagus and Lis basins (to the South). The source of Mondego river is in Serra da Estrela at 1,537 m of altitude. It runs approximately 300 km until it flows into the Atlantic Ocean near Figueira da Foz (Agência Portuguesa do Ambiente, 2015).

The Lis basin covers an area of 837 km² and has its source in the district of Leiria (Ramos, 2008). It is limited to the north by Mondego's basin, to the south by Alcoa's basin and to the east by Tagus river basin (Vieira et al., 2012). The majority of its area is below 200 m of altitude, with the exception of Estremadura Limestone Massif where it can reach altitudes above 400 m (Agência Portuguesa do Ambiente, 2015).

These three basins include rivers classified into 4 typologies based on their geological and hydrological similarity: mountain (M), littoral (L), medium-large and small northern river types ($N1 > 100 \text{ km}^2$ and $N1 \leq 100 \text{ km}^2$, respectively). The definition of each river typology results from the selection of several factors such as geology and size of the drainage area or biological information of diatom communities, invertebrates, macrophytes and ichthyofauna (Agência Portuguesa do Ambiente, 2015).

According to the WFD, surface water bodies can be grouped into 6 categories: rivers, lakes, transitional waters, coastal waters, artificial water body and heavily modified body of water. Vouga, Mondego and Lis basins comprise all of them except lakes. This study is focused on rivers.

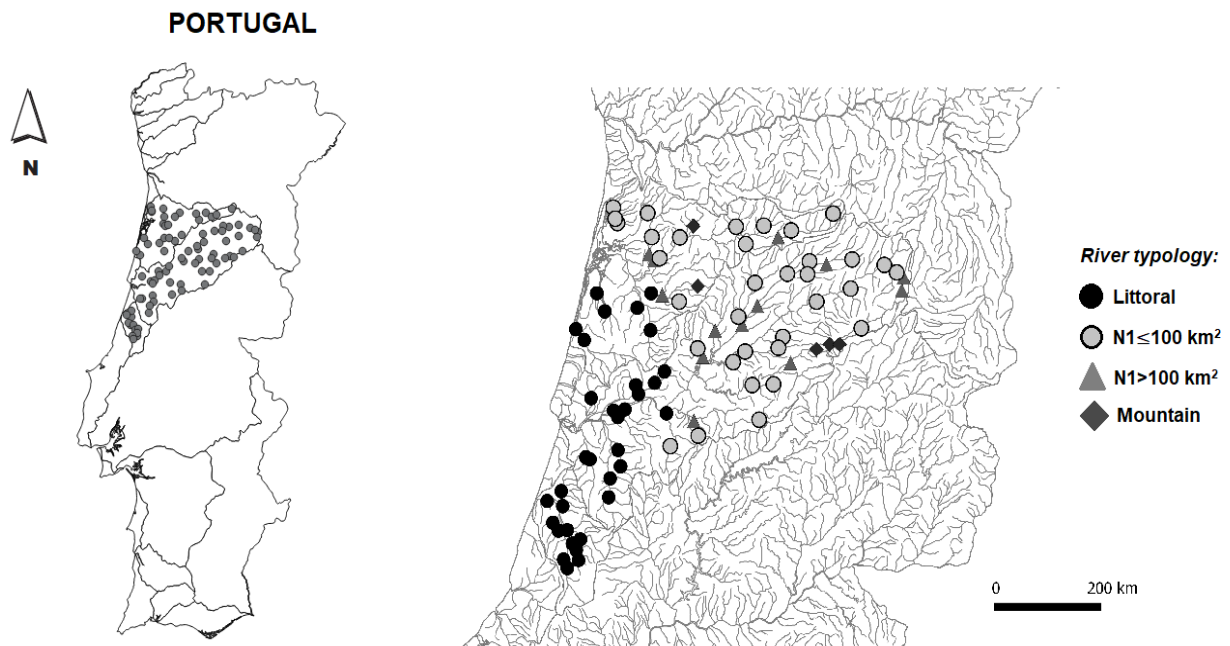


Fig. 2. Localization of the study area in central Portugal. The river sites sampled are indicated with dots (on the left map) and symbols corresponding to different river typologies properly identified on the right map.

2. Sample Collection

In the spring of 2017, a total of 88 river sites (Fig. 3) were selected and sampled following the WFD protocols for collection of phytobenthic organisms in lotic systems (INAG, 2008) and resumed in Table 2 (*Introduction*). For each sampling site, at least 5 randomly selected stones from turbulent flow areas were scraped into a tray using a toothbrush and water from the river. When stones were not the dominant substrate available or were absent, we collected biofilm attached to macrophytes or sediment. In those cases, we obtained samples from more than one substrate when possible:

- Four of the 88 samples were from sand and stone
- Three were from macrophytes and sand
- One was from macrophytes and stone
- Four were from sand only

In the analysis, when there was more than one sample per site, we always preferred the ones extracted from stones, than macrophytes and only in the last case, we used samples from sand. For morphological analysis, the biofilm was stored using formaldehyde in 50 mL glass flasks and kept in a dark and dry environment until treatment. For DNA metabarcoding analysis, 96% ethanol was used for biofilm removal and immediate fixation. About 15 mL of biofilm and 35 mL of ethanol filled 50 mL falcons (Vasselon et al., 2017). These flasks were kept at 4 °C until analysis (for approximately 5 months).



Fig. 3. Example of two of the 88 sites sampled showing different features: 09I_06 (a) and 09F_06 (b).

3. Laboratory Procedures

3.1. Microscopic Analysis

After collection of samples from river sites, these were prepared for morphological analysis of diatoms using the light microscope (LM) and according to WFD standards for phytobenthos (INAG, 2008). The first step was oxidation of the biofilm (Fig. 4) adding 5 mL of nitric acid and about 0.25g of potassium dichromate and left to react for 24 hours at room temperature. After that, oxidation by-products were removed with distilled water by centrifugation (5', 2000 rpm). Centrifugation was repeated at least 3 times. The oxidized pellet was resuspended in water and a drop was left to dry on a coverslip. The slides were then mounted using Naphrax® (Fig. 5) and the diatoms identified to the lowest taxonomic rank possible, usually to species level but also to infra-specific levels using Krammer and Lange-Bertalot (1986, 1988, 1991a and 1991b), Krammer (2000, 2001 and 2009) and Prygiel and Coste (2000). Relative abundance of diatoms was determined by enumeration of at least 400 valves per sample under the light microscope (Leitz Biomed 20 EB) using an immersion objective of 100× (numerical aperture: 1.32).



Fig. 4. Oxidation of samples using nitric acid and potassium dichromate.

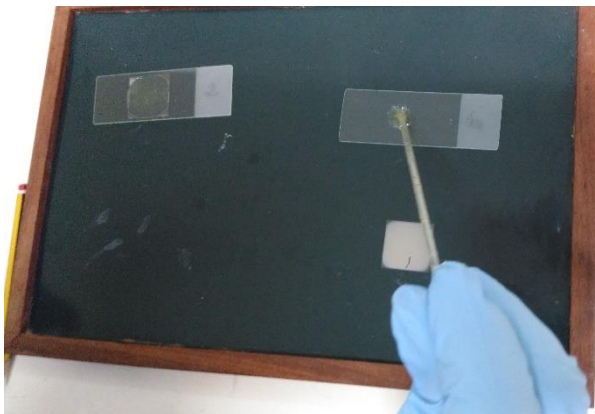


Fig. 5. Mounting of the permanent slides using Naphrax® for further observation under the light microscope.

3.2. Environmental DNA Metabarcoding

3.2.1. DNA Extraction

For DNA extraction, a volume of 2 mL of each sample was centrifuged for 20 min at 4°C and 12000 rpm. The supernatant (ethanol) was removed and the DNA contained in the pellet was isolated with commercial kit NucleoSpin® Soil, following the manufacture's recommended protocol (NucleoSpin® Soil User Manual, MACHEREY-NAGEL GmbH & Co. KG, November 2017 / Rev. 07). This protocol includes a first step of diatom cells' mechanical lysis and a second step of enzymatic lysis. First, the sample was resuspended in Lysis Buffer SL1 and 2 (supplemented with the Enhancer SX), and ceramic beads mechanically contributed to its disruption. These reagents along with lysis buffer SL3 precipitated proteins and PCR inhibitors. A centrifugation step followed for 2' and 11000g. The tube containing the pellet and reagents was refrigerated at 0-4°C for 5 minutes, and centrifuged again (1', 11000g). The supernatant was removed and added to a first NucleoSpin® Inhibitor Removal Column in order to filter the lysate by centrifugation (Fig.6). A binding buffer was added to the column to remove residual humic substances and other PCR inhibitors. A new volume of the binding buffer and three wash buffers passed through a second Inhibitor Removal Column by successive centrifugation (30'', 11000g) and vortex (2'') in the last two steps. This was necessary to



Fig. 6. Removal of the supernatant before centrifugation for filtering of the lysate.

remove the diatoms' silica wall. Then, the membrane was dried by centrifugation (2', 11000g). Finally, the elution buffer SE was added to the column and left to rest for 1 minute, followed by the last centrifugation (30'', 11000g). The eluted DNA was ready to amplify.

3.2.2. PCR Amplification

For PCR, the ideal amount of DNA in each sample should be 25 ng/μL. In order to quantify the DNA extracted, a NanoDrop™ 1000 Spectrophotometer was used. PCR was

performed by amplification of *rbcL* plastid gene focusing on a 312 bp barcode. *rbcL* was chosen because there is already public information available about it and it is more resolute than other DNA barcodes (Frigerio et al., 2016). The 312 bp was selected for its suitability in size for NGS sequencing requirements which are limited to <500bp long. The primer pair used to amplify the 312 bp region was Diat_rbcL_708F (forward) and R3 (reverse), with some modifications (Frigerio et al., 2016).

For PCR, three replicates were generated from each sample. Two forward primers and 3 reverse primers of 100 μ M each were mixed separately and diluted in molecular biology grade water until a final volume of 150 μ L. 15.4 μ L of water was mixed with 2.5 μ L of 10X Buffer, 2 μ L of 2.5 mM of dNTP, 1.25 μ L of 10 mg/mL of BSA and the same volume of 10 pmol/ μ L of forward and reverse primers, and finally, 0.15 μ L of 4U of Takara LA Taq $\text{\textcircled{R}}$ polymerase. From this mixture, 24 μ L were added to 1 μ L of DNA extracted. PCR reactions were performed in PTC-100 $\text{\textcircled{R}}$ Thermal Cycler featuring 33 cycles of 1 min of denaturation at 95°C, 1 min of annealing at 54°C and 1 min of extension at 72°C. At the end of this process, the PCR products from each sample ran in electrophoresis gel (Fig. 7) and the results were analysed in order to verify the success of extraction and the relative amount of DNA available.

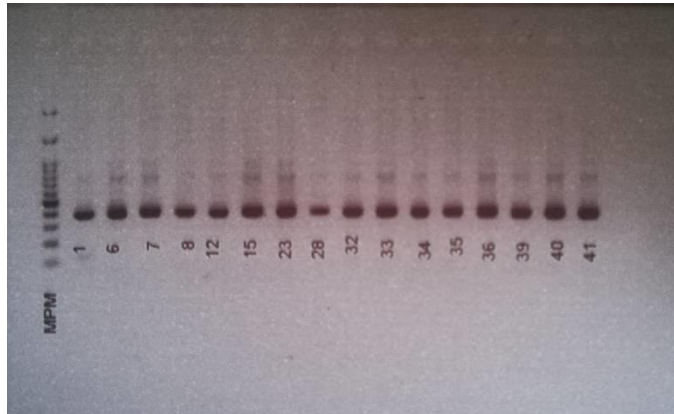


Fig. 7. Example of a DNA run through the electrophoresis gel.

3.2.3. High-Throughput Sequencing

The 3 replicates of DNA per sample resulting from PCR amplification were placed in a 96 well microplate and sent to *Plateforme Génome-Transcriptome* of Bordeaux, France, for sequencing with Illumina MiSeq System.

4. Analysis

4.1. Bioinformatic Analysis

The sequencing platform in Bordeaux, performed the first step of demultiplexing resulting a *fasta* and quality file for each of the total libraries. Paired-end reads were assembled into a contiguous sequence and only reads with an overlap region > 140bp and a maximum of 1 mismatch were kept. Then, only reads with length > 300 bp, Phred quality score > 23 over a moving window of 25 bp, > 1 mismatch in the primer sequence, homopolymer > 8 bp, or with ambiguous base (N) were excluded. All the samples were analysed together using the Mothur software (version 1.39.5, Schloss et al. 2009) following the bioinformatics process described in Vasselon et al. (2017) and outlined in Table 3. Briefly, data was dereplicated in order to work with Individual Sequence Unit (ISU), Chimera were removed using the “chimera.vsearch” command with default parameters, and ISU with 1 read were removed. Selected DNA reads were clustered in OTUs using a distance similarity threshold of 95 % using the Opticlust method with default parameters (Schloss et al., 2009). Finally, all samples were normalized to the same read number (using the smallest read abundance obtained for 1 sample) in order to allow inter-sample comparison. Diatom molecular inventories were obtained using the method described previously in Vasselon et al. (2017) with the R-Syst::diatom library (Rimet et al. 2016, version 17-05-2017, <http://www.rsyst.inra.fr/en>) for taxonomic assignment of OTUs. Briefly, taxonomy of each DNA read was obtained with the “classify.seqs” command (method=wang, confidence score threshold=60%) and used to determine the consensus taxonomy of OTU with the “classify.otu” command (confidence threshold=80%). From the set of normalised samples, a correction factor was applied to the number of reads in each sample, for each species, based on the biovolume of cells indicated in OMNIDIA version 5.5 (Lecointe et al., 1993) and following the instructions from Vasselon et al. (2018). This was only performed for molecular data.

Table 3. Main data processing steps in Mothur software.

Process	Description of the step	Mothur command	Working file
Trimming	Input (one fastq file per library (1 to n))	-	Pre-treated data (fastq files)
	Checking of file consistency	fastq.info()	fastq files
	Trimming by sample (quality, length,...)	trims.seqs()	fastq files
	Merging all samples data	merge.file	fasta libraries (1 to n)
	Selecting representative unique reads	unique.seqs()	fasta All
	Performing alignment (<i>rbcL</i> barcode)	align.seqs()	"unique reads"/Read number per "unique reads"
		screen.seqs()	
		filter.seqs()	
	Removing chimeras	pre.cluster()	Curated reads alignment
		shimera.uchime() remove.seqs()	
Affiliating taxonomy to reads	classify.seqs()	Filtered reads	
Removing "non-diatom" reads	remove.lineage()	Filtered reads	
Clustering	Clustering reads into OTU	dist.seqs()	"Diatom" reads
		cluster()	
	Removing singleton	split.abund()	OTU list
		remove.seqs()	
	Homogeneizing read number per sample	make.shared()	OTU list
sub.sample()			
Affiliating taxonomy to OTU	classify.otu()	Reads taxonomy/OTU list	
Analysis	OTU level	-	Final OTU list per sample
	Taxonomic level	-	Final taxonomy list per sample

4.2. Morphological and Molecular IPS

The molecular method was separated in two approaches according to the application or not of a correction factor for biovolume to the matrix of reads' relative abundances per sample. The equation of the correction factor (CF), where b is the biovolume of a given species follows:

$$CF = 10^{[0.0703 \times (\log b^{2.4908})]} \quad (2)$$

Annexes I, II and III show morphological, molecular without and with correction factor inventories (based on relative species abundance and DNA reads, respectively) from which the

IPS, *Indice de Polluosensibilité Spécifique* (Cemagref, 1982), was calculated for each river site using OMNIDIA version 5.5 software (Lecointe et al., 1993). Quality classes were obtained based on IPS values and the following boundaries: IPS ≥ 17 - “High”, IPS [13-17[- “Good”, IPS [9-13[- “Moderate”, IPS [5-9[- “Poor” and IPS [1-5[- “Bad”.

4.3. Statistical Analysis

The number of families, genera and species were determined for each methodology (morphological, molecular with and without CF) as well as relative abundances of individuals per species and the 5 most abundant species. The numbers of species per method were compared performing pair-wise *T*-tests (univariate - PERMANOVA, Primer 7; Clarke et al., 2014), and boxplots for graphical inspection.

Means and respective standard-deviations of the IPS values for each site and method were determined. The correlation between IPS values from all approaches was determined using the Pearson’s coefficient (SigmaStat version 4.0; Systat Software, Inc., San Jose California USA) and visualised using linear regression.

To compare the ecological quality classes attributed to each site, a NMDS (non-metric Multidimensional Scaling) based on Bray-Curtis similarity matrices of abundances was performed for the three methodologies (Primer 7; Clarke et al., 2014).

Principal COordinate analysis (PCO) based on Bray-Curtis similarity was performed based on data from 8 physical-chemical parameters [dissolved oxygen, Habitat Quality Assessment (HQA), conductivity, total nitrogen, total phosphorus, water temperature, Chemical Oxygen Demand (COD) and pH] for quality classes based on species abundances per method. The HQA is derived from the River Habitat Survey (RHS) data and consists of 3 key indicators scored and summed all together: site condition, site context and species habitat index. This parameter indicates the overall habitat diversity deduced by the physical features of the channel or river corridor and it is only comparable between rivers with similar typologies (Raven et al., 1998).

The relative contribution of each parameter to the differences between sites from each class was evaluated using the correlation coefficient. The parameters with correlation coefficients >0.2 between the abiotic factors and ecological quality classes attributed to biological elements on the principal coordinate axes were plotted.

RESULTS

1. Taxonomic Composition and Diversity

Inventories of diatom communities based on morphological identification revealed a total number of 8 families, 71 genera and 306 species. Within 88 samples identified (one per site), the minimum number of species per sample was 7 and the maximum was 64, with an average of 24 species per sample. The most abundant species were *Achnantheidium minutissimum*, *Karayevia oblongella*, *Eolimna minima*, *Cocconeis placentula* and *Cocconeis euglypta*, respectively (Table 4; Fig. 8a, b, c, d; Fig. 9a).

The approach using environmental DNA (eDNA) metabarcoding for all the samples sequenced resulted in a total number of 6,952,790 DNA reads with an average of 63,207 reads per sample. After the quality filtering step, 1,017,833 reads were retained and clustered into 1285 Operational Taxonomic Units - OTUs (95 % similarity threshold) with an average of 63,207 OTUs per sample. At this point and from the 88 samples, the total percentage of successfully assigned OTUs to the reference library was 32%, with an average of 47.5% (Standard-Deviation, SD=0.07%) per sample, while the average percentage of unassigned reads from the converted OTUs to taxa list was 52.5% (SD=0.07%) and varied between 2 and 95%, among all samples. From the 1285 OTUs obtained in the clustering step, 863 corresponded to those unassigned species. As mentioned above, to allow inter-sample comparison, 3 samples characterized with less than 2500 reads were removed, and the remaining samples were rarefied to 2776 reads (lowest read abundance obtained for one sample) for a total of 297,032 reads corresponding to 846 OTUs.

We obtained between 20 and 68 species, per sample, and an average of 39 species in the whole dataset and a total of 125 species using molecular approach after removing low reads and without the correction for biovolume (CF). The most abundant diatom taxa in this case were *Cocconeis sp.*, *Ulnaria ulna*, *Gomphonema rhombicum*, *Achnantheidium minutissimum* and *Melosira varians* (Fig. 8a, e, f, g). When applying the correction factor, we obtained between 13 and 58 species with an average of 33 species in the whole dataset and a total of 111 species. The most abundant taxa were *Cocconeis sp.*, *Achnantheidium minutissimum*, *Achnantheidium sp.*, *Eolimna minima* and *Navicula sp.* (Table 4; Fig. 8a, c; Fig. 9b, c).

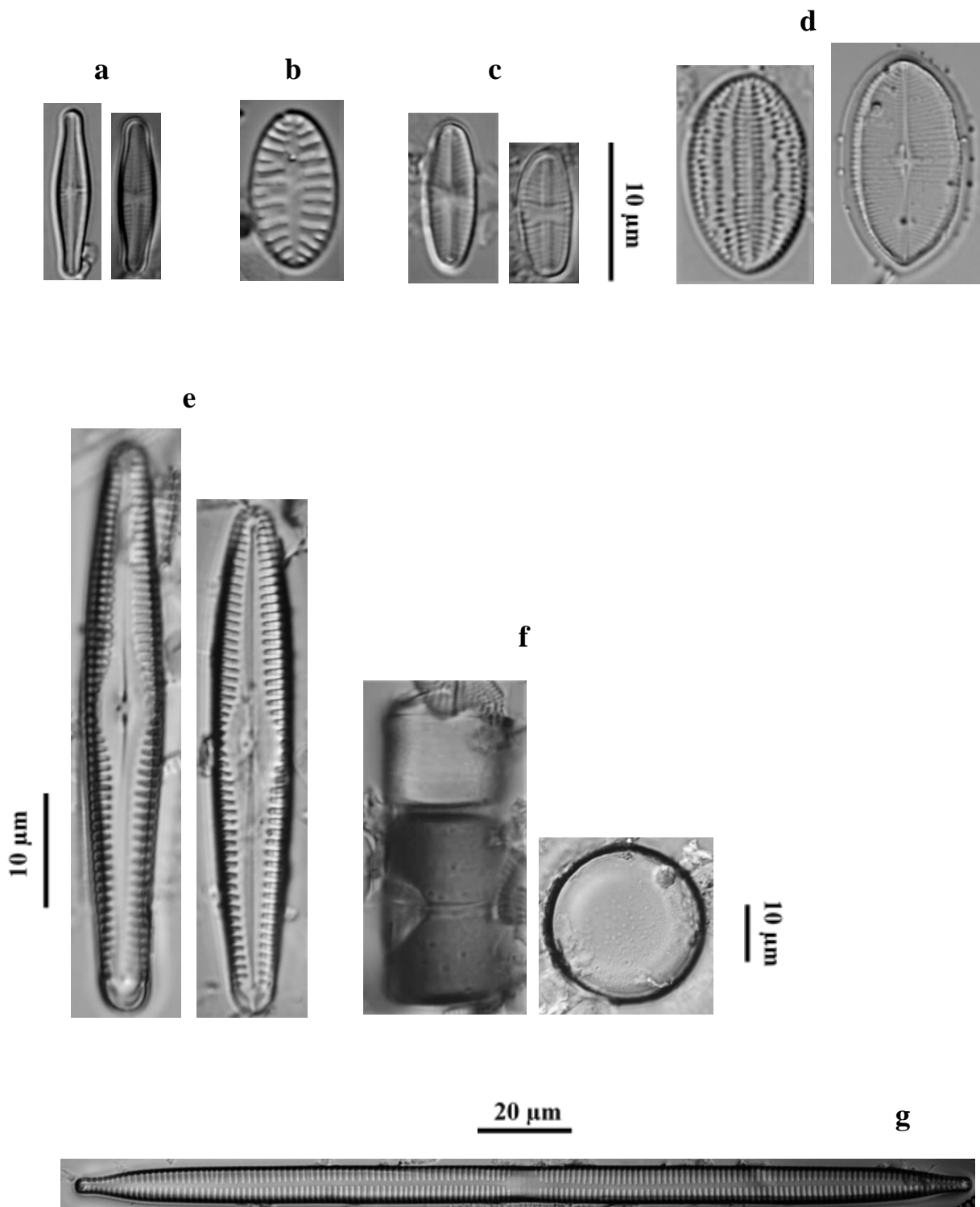


Fig. 8. LM micrographs of *Achnantheidium minutissimum* (a), *Karayevia oblongella* (b), *Eolimna minima* (c), *Cocconeis placentula* (d), *Gomphonema rhombicum* (e), *Ulnaria ulna* (f) and *Melosira varians* (g).

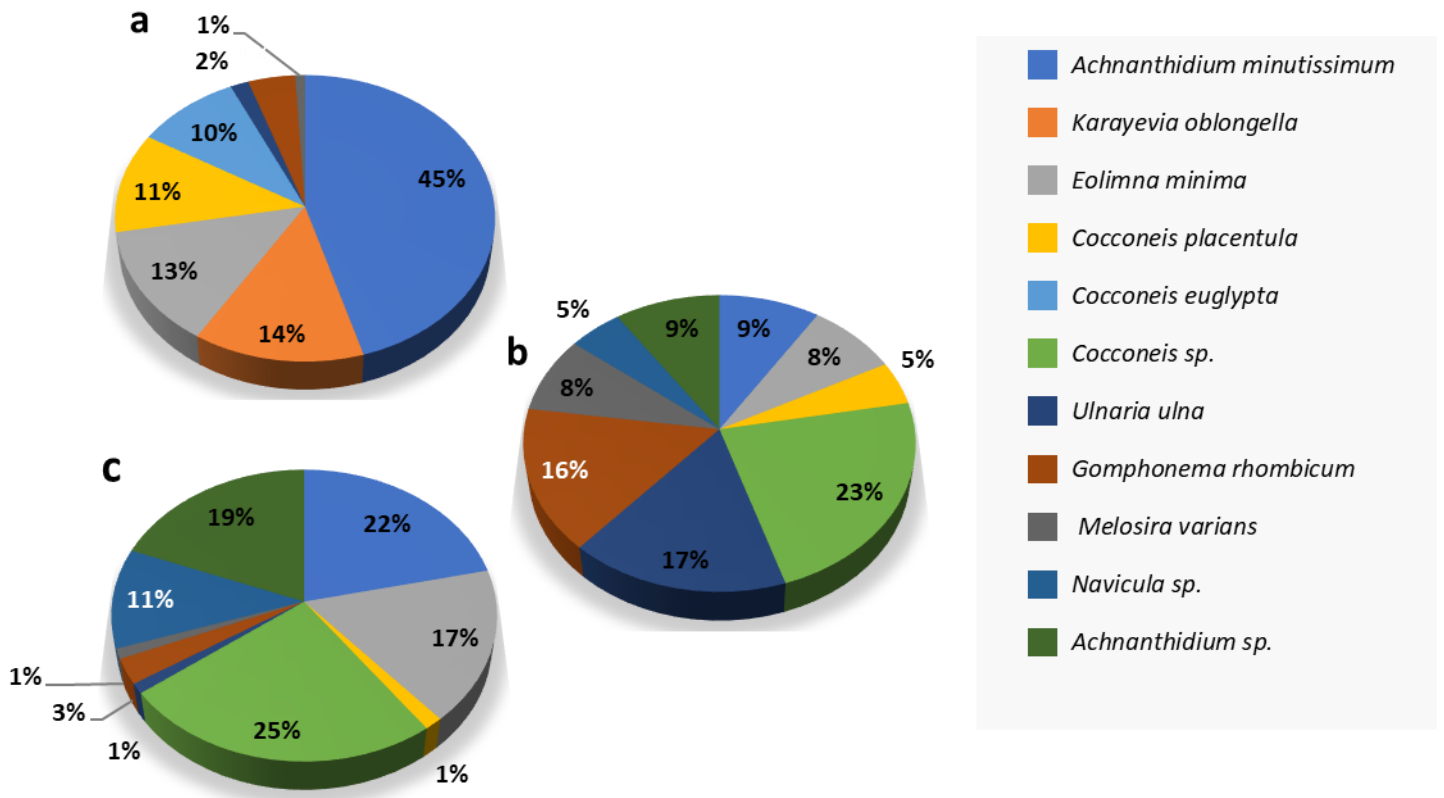


Fig. 9. Dominant species for the morphological (a) and molecular approaches (without biovolume correction – CF (b); and with this correction (c)). The three approaches only share one species within the 5 most abundant: *Achnantheidium minutissimum*.

Table 4. List of the 5 most abundant species per approach.

	Morphology	Molecular Without CF	Molecular With CF
5 most abundant species	<i>Achnantheidium minutissimum</i> (Kützing) Czarnecki	<i>Cocconeis sp.</i> Ehrenberg	<i>Cocconeis sp.</i> Ehrenberg
	<i>Karayevia oblongella</i> (Østrup) M. Aboal	<i>Ulnaria ulna</i> (Nitzsch) Compère	<i>Achnantheidium minutissimum</i> (Kützing) Czarnecki
	<i>Eolimna minima</i> (Grunow) Lange-Bertalot	<i>Gomphonema rhombicum</i> M. Schmidt	<i>Achnantheidium sp.</i> Kützing
	<i>Cocconeis placentula</i> Ehrenberg	<i>Achnantheidium minutissimum</i> (Kützing) Czarnecki	<i>Eolimna minima</i> (Grunow) Lange-Bertalot
	<i>Cocconeis euglypta</i> Ehrenberg	<i>Melosira varians</i> Agardh	<i>Navicula sp.</i> Bory

Although the values seem close, PERMANOVA analysis showed significant differences between all methodologies. Morphology *versus* molecular method with and without CF ($t=5.76$ and $t=8.59$, $p<0.05$, respectively); Molecular with and without CF ($t=3.49$ and $p<0.05$) (Fig. 10).

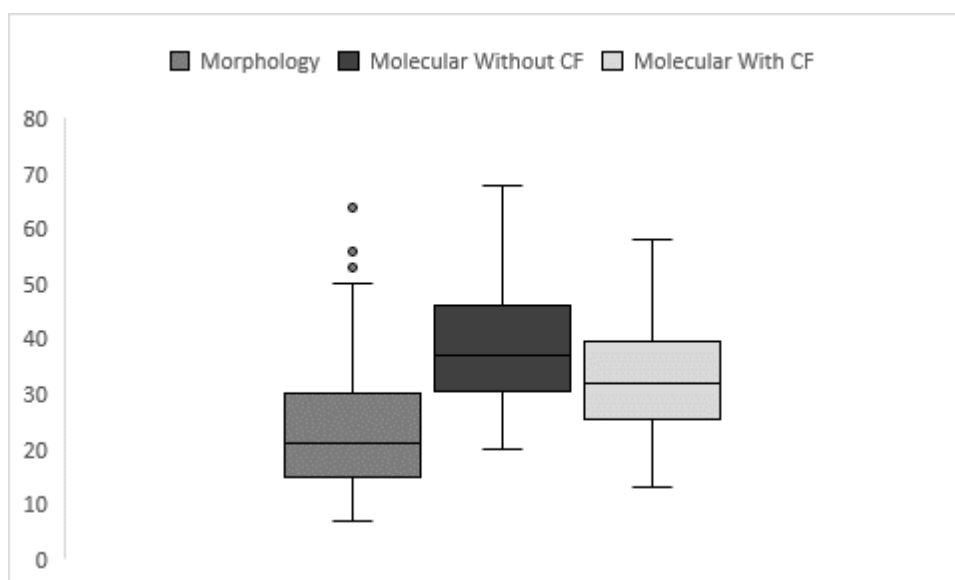


Fig. 10. Boxplot showing the average number of species from all samples (central dash) for the three methodologies. The limits of the boxes indicate the minimum and the maximum of the variances, vertical lines represent the quartiles (the 1st are the lower ones and the 3rd are the upper ones) and the dots are outliers. All methods show significant differences between each other (T -test, $p<0.05$).

2. Comparison Between the IPS Values for Morphological and Molecular Approaches

The comparison of IPS values from the morphological and molecular methods was made with the application of a biovolume correction factor (CF) and without the correction factor. The IPS values varied between 6.8 and 19.9, 4.9 and 19.7, 7.5 and 19.9 and the average IPS values were 14.9 (SD=3.16), 14.7 (SD=2.78) and 13.9 (SD=3.4) for the morphological approach, the molecular without CF and the molecular with CF, respectively.

According to Pearson's Correlation performed for the linear regressions shown in Fig. 11, the coefficients R describe a high correlation between the variables for both the molecular method with CF and morphology ($R=0.64$) (Fig. 11a) and molecular without CF and the morphological approach ($R=0.60$) (Fig. 11b). As expected, there is a stronger correlation

between both molecular approaches ($R=0.88$) (Fig. 11c), although the p -values are lower than 0.05, which indicates significant differences between all the three combinations of methods.

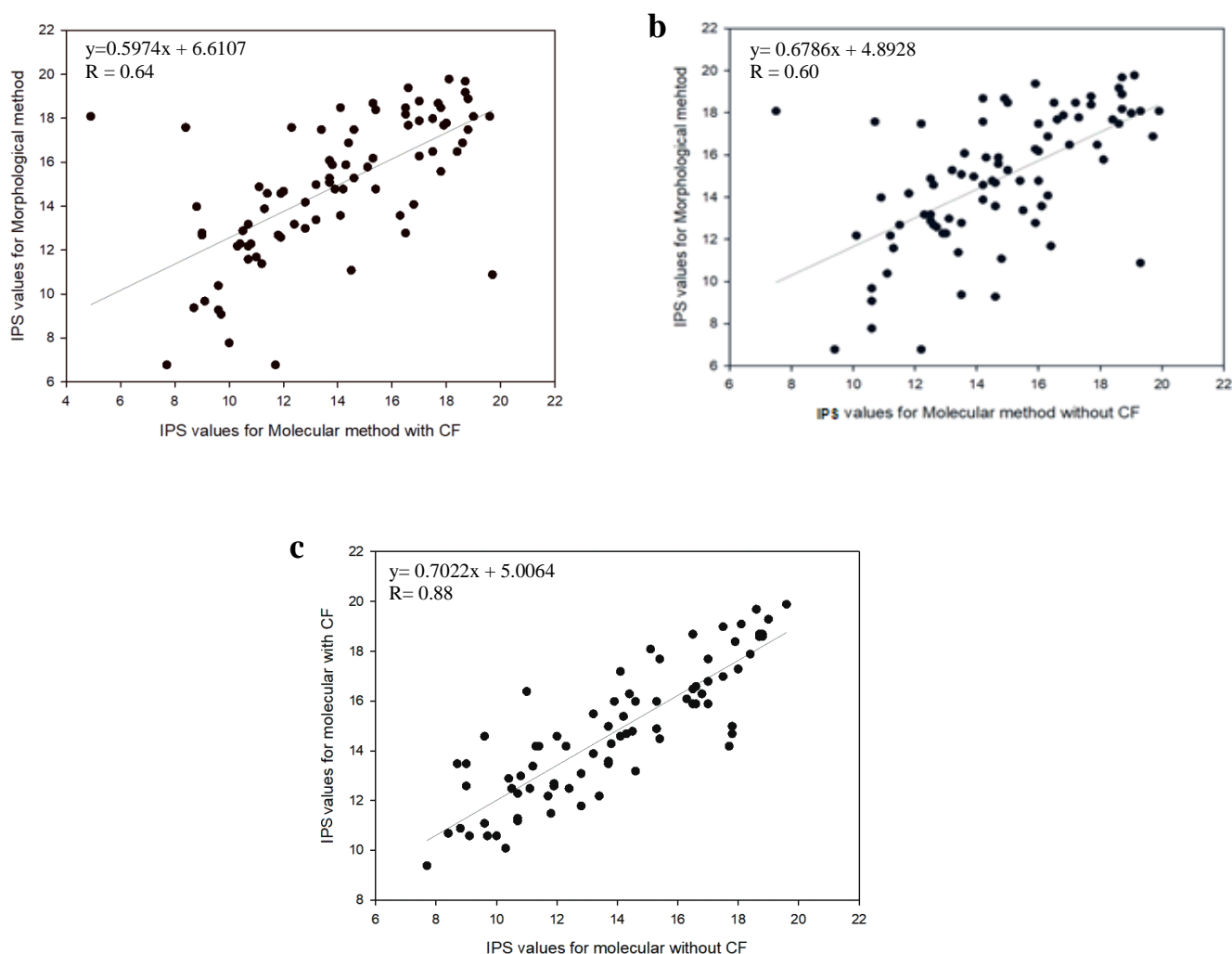


Fig. 11. Linear regression of IPS values from morphological and molecular approaches with CF (a) and without CF methods (b) and both molecular approaches (c). Significant differences between all combinations of methods (p -value<0.05).

The great majority of sites were classified in “Good” quality status for all approaches. The molecular method without CF resulted in the highest percentage of samples with class “Good” followed by the morphological approach, as presented in Table 5. The methodology showing the highest percentage of quality classes below “Good” (including 1 sample site with “Bad” status) was the molecular with CF, while the morphological approach resulted in the highest percentage of samples with classifications above “Good”.

More than half of the samples had the same quality class from all the methodologies applied. The methodologies sharing more sites with the same quality class were the molecular with and without the correction factor (Table 6). Molecular method with CF is closer to the

morphological approach sharing 57% of samples with the same classification and 6% of samples with 2 or more classes of difference.

Table 5. Percentage of sites by quality class and approach.

	High	Good	Moderate	Poor	Bad
Morphology	32%	42%	22%	4%	0%
Molecular with CF	25%	35%	35%	5%	1%
Molecular without CF	23%	48%	27%	1%	0%

Table 6. Percentage of sites which share the same ecological quality class and have 1 and 2 classes of difference between approach.

		Molecular with CF	Molecular without CF
Share the same class	Morphology	57%	56%
	Molecular without CF	69%	-
1 class of difference	Morphology	37%	40%
	Molecular without CF	30%	-
≥2 classes of difference	Morphology	6%	5%
	Molecular without CF	1%	-

The NMDS (Fig. 12) shows a visible and similar gradient of quality for all approaches, “High” and “Good” classes concentrated on the left side and worst quality classes (“Moderate”, “Poor” and “Bad”) on the right side of the diagram, for all approaches. Yet, there are some cases where the same site has contrasting classifications. For example, site 14D_53 (in the dark circles) was classified as “Poor” by the molecular method without CF and as “High” by morphology. Another contrasting result occurred for site 09F_06 (in the dotted circles) (Fig. 3b), which was classified as “High” by both molecular methodologies and as “moderate” by the morphological approach.

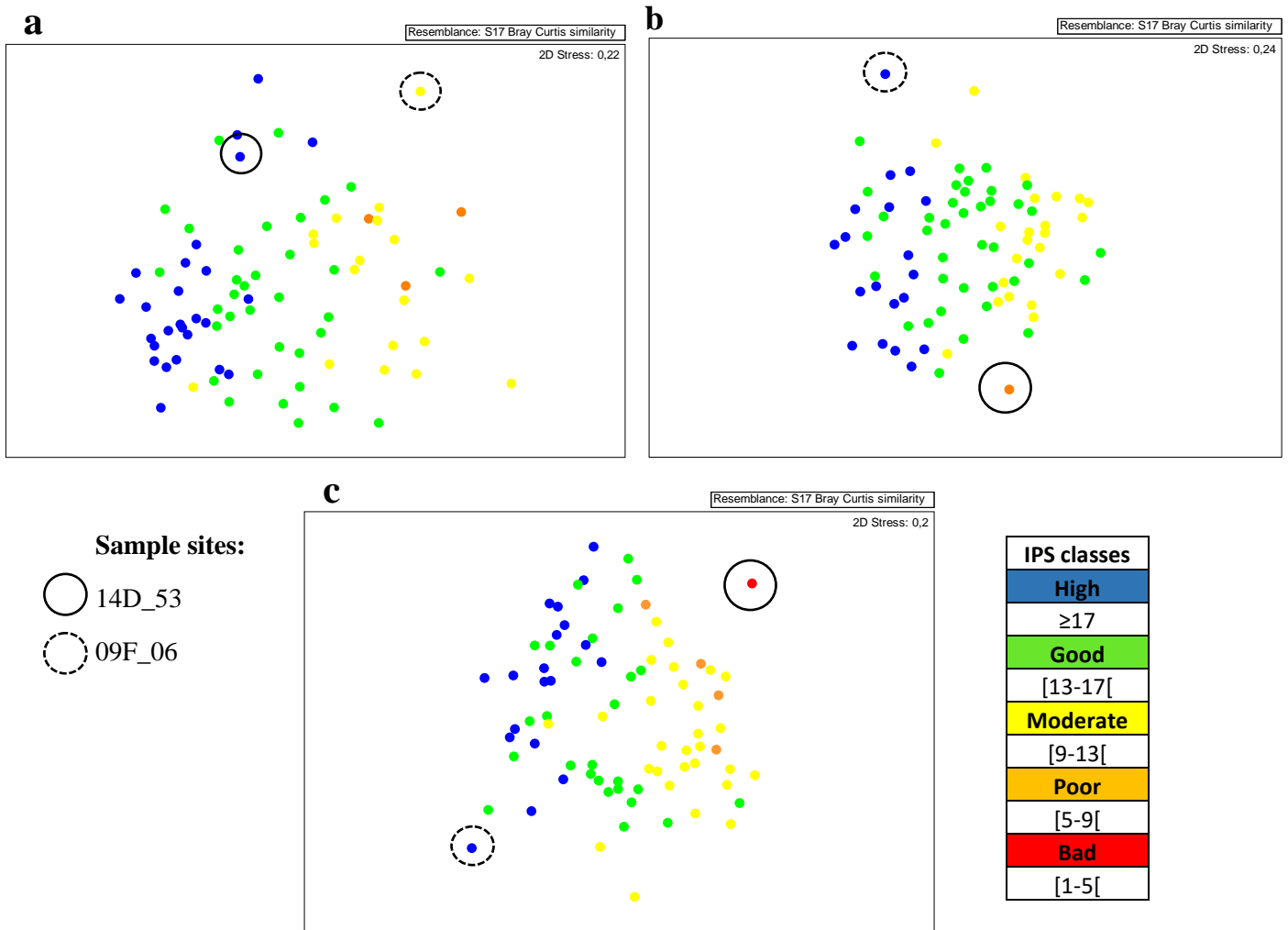


Fig. 12. NMDS plots based on the diatom communities and correspondent ecological quality classes based on IPS values obtained from morphological data (a), molecular data without (b) and with CF (c). The intervals of IPS and respective classes and colours are indicated on the figure, as well as the highlighted sample sites 14D_53 and 09F_06.

The PCO ordination (Fig. 13) shows that 30 to 40% of the variation among methodologies is explained by axes 1 and 2 (31.1 - 41%). The distribution of samples is similar to that obtained with NMDSs (Fig. 12). A higher dissolved O₂ and Habitat Quality Assessment (HQA) scores were associated with better quality classes in the 3 cases. Higher conductivity, nutrients (phosphorus and nitrogen) concentration and Chemical Oxygen Demand (COD) are associated to the worst quality classes of all methods.

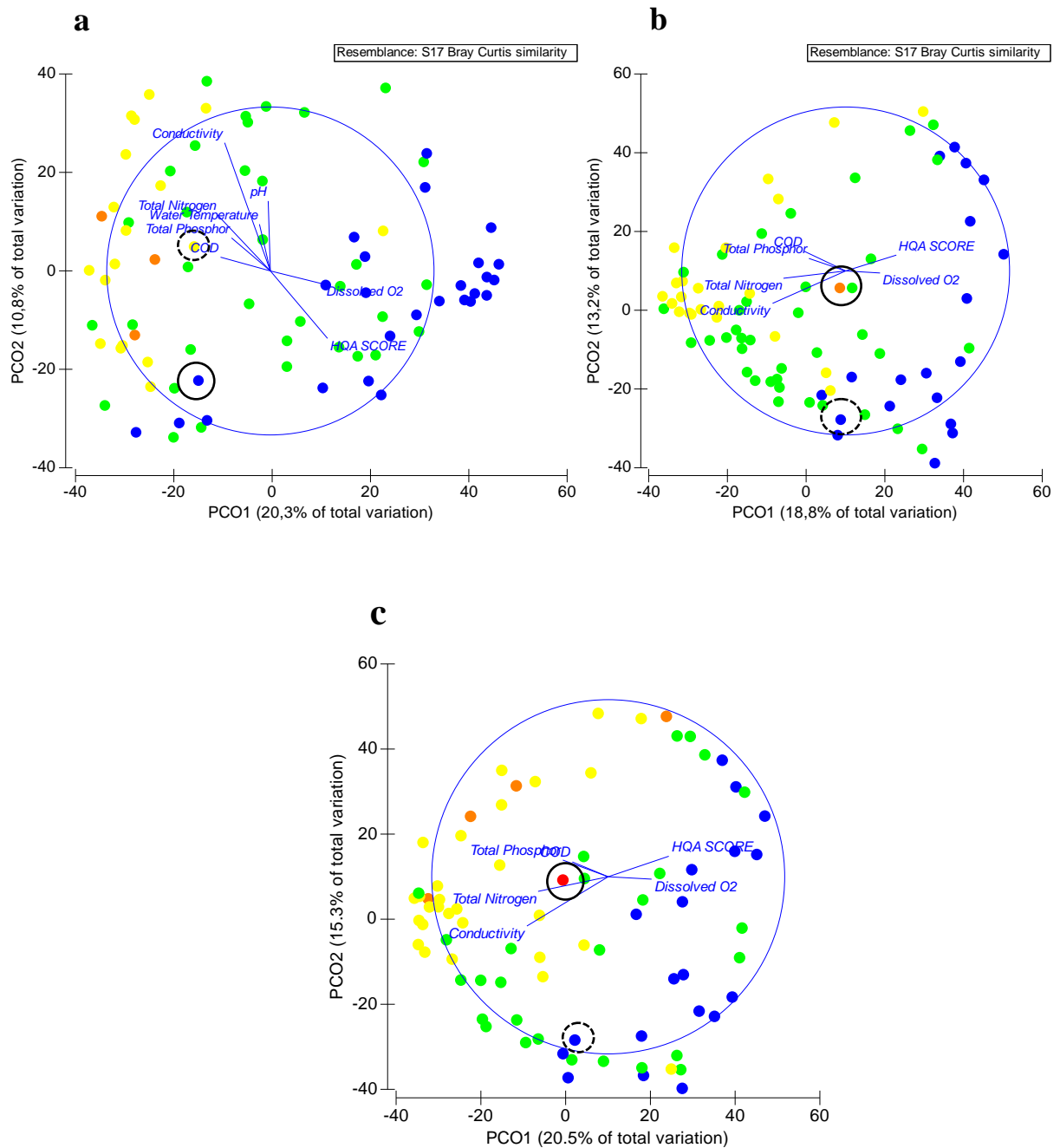


Fig. 13. Principal Coordinates Analysis (PCO) for sites using Bray-Curtis similarity based on diatom communities and corresponding ecological quality classes attributed by IPS index for data obtained with the morphological approach (a), molecular method without (b) and with CF (c). Vectors representing physical-chemical parameters [conductivity, pH, total nitrogen, water temperature, total phosphorus, Chemical Oxygen Demand (COD), dissolved O₂ and Habitat Quality Assessment (HQA)] which present Pearson coefficient > 0.2. The quality classes and respective colours are indicated on Fig. 12, as well as the dark and dotted circles representing 14D_53 and 09F_06 sample sites, respectively.

DISCUSSION

Recent studies demonstrated the effectiveness of DNA-based approaches for water quality assessment using diatom assemblages for different European regions and types of water bodies (Zimmerman et al., 2014; Visco et al., 2015; Vasselon et al., 2017; Rivera et al., 2018). In our study, we compared the eDNA and conventional (based on morphological determination using the light microscope) approaches in terms of community structure and ecological status classifications applied to Portuguese rivers and found similarities but also differences between morphological and molecular approaches.

1. Composition of Diatom Communities

The total number of species identified by both methods varied between 306 with the morphological approach (204, 120 and 534 in Vasselon et al., 2017; Rivera et al., 2018 and Keck et al., 2018, respectively) and 125-111 in DNA metabarcoding (66, 102 and 61 in Vasselon et al., 2017; Rivera et al., 2018 and Keck et al., 2018, respectively). The higher number of species identified in the traditional manner compared with the molecular method reveals a discrepancy between species diversity as was also demonstrated in other studies referred in the former sentence. However, other studies using diatoms (Zimmermann et al., 2014) and fish (Valentini et al., 2016) showed the opposite. Zimmermann et al. (2014) obtained 263 *versus* 102 taxa detected by eDNA and traditional approaches, respectively, while, in the second (Valentini et al., 2016), in 89% of the sites, eDNA-based approach detected a higher or identical number of taxa when compared to the traditional method. The differences between species diversity in the first studies may lay in the high percentage of unassigned reads. In our work, a total of 32% of OTUs were successfully assigned to species level which is congruent with other results (35.7% by Vasselon et al., 2017; 41% by Rivera et al., 2018; 30% by Keck et al., 2018), while 67% of OTUs corresponded to unassigned species.

In our study we also concluded that applying a correction factor (CF) to molecular data approximated it to the morphological results. The correction factor used approximates the two approaches by down weighting the largest taxa which are overestimated with the molecular approach compared to the traditional one which ignores size of diatoms and only regards the number of individuals. Regarding the community structure, this approximation is reflected on the similarity of the dominant taxa as well as their proportion, and consequently the ecological classifications inferred. Other authors obtained similar results when using correction factors for organisms such as bacteria (Angly et al., 2014), oligochaete (Vivien, Lejzerowicz & Pawlowski (2016), arthropods (Krehenwinkel et al., 2017) or fishes (Thomas et al., 2016). Those

corrections reduced bias in reads' abundances increasing correlation between morphological and molecular inventories. Based on their work, Krehenwinkel et al. (2017) suggest that a deeper focus on developing correction factors for groups of larger and more complex taxa may be of great use for comparative studies of invasive species' abundances in different sites. Regarding diatom cells and according to Vasselon et al. (2018), the correction factor based on biovolume differences between individuals brought together the molecular and morphological approaches. These results are built upon the correlation between *rbcL* gene copy number and genome size (linked to biovolume) in diatoms. *rbcL* copy number varies depending on several aspects such as the number of chloroplasts per cell, the number of genomes per chloroplast and/or the number of copies of *rbcL* gene per chloroplast genome (Ersland, Aldrich & Cattolico, 1981; Treusch et al., 2012). In the first case, it is known that there is a great stability in chloroplasts' number within a single genus varying from 1 to approximately 8 chloroplasts per cell between genera. In the second case, unicellular algae show a number of copies of chloroplast genome varying from hundreds to dozens, such as the example of *Olisthodiscus luteus* and *Thalassiosira pseudonana* with 650 and 55 genome copies per cell, respectively, contrarily to higher plants which can display thousands of copies of chloroplast genome per cell. At last, there is only one copy of *rbcL* gene per chloroplast genome (Vasselon et al., 2018). In their study, Vasselon and colleagues assumed that if there is an increase in cells' biovolume, the chloroplasts' biovolume also increases, as well as the genome copies per chloroplast, consequently the DNA quantity and thus, the *rbcL* gene copy number. However, this is not so linear and other factors which were not considered can affect the gene copy number, such as cells' life cycle stage, cells' physiological status, chloroplasts' physiology and DNA integrity (Eberhard, Drapier & Wollman, 2002). Iron limitation, for example, can reduce the number of chloroplasts per cell. Given all those variations and influences, it is important to perform a deeper evaluation of the correction factor for a more realistic and correct metabarcoding quantification.

The variations in the number of species detected by both molecular methodologies (with and without (CF)) were partially due to the removal of species with no biovolume correction factor already established. Therefore, it is important to improve biovolume data as well as other metrics. Also, as mentioned by Weber and Pawlowski (2013), one of the causes of discrepancies in abundances between molecular and morphological approaches may be due to biological biases such as biovolume variation. In this case, although the proximity of abundances with the application of a correction factor for biovolume is significant, this difference still exists. In view of this, some authors (e.g., Zaiko et al. 2015) opted to use only presence-absence molecular data of plankton communities for analysis.

Although 50% of the species recorded in molecular inventories are also present in morphological inventories, only one of the 5 most abundant species is shared by the three

approaches: *Achnanthydium minutissimum*, occurring in 90% of the samples and showing a higher abundance in the morphological method. As it is widely known (Martín et al., 2010; Kermarrec et al., 2014; Rivera et al., 2018; Sun et al., 2018; Keck et al., 2018), *Achnanthydium minutissimum* is a widespread species, identified as one of the most abundant species in morphological inventories for biomonitoring worldwide and also in Portugal (Luís et al., 2009; Almeida and Feio, 2012). *A. minutissimum* has a lower biovolume ($76 \mu\text{m}^3$, on average) when compared with other species such as *Ulnaria Ulna* and *Melosira varians* (present in both molecular and morphological inventories), with an average of $467 \mu\text{m}^3$ and $3267 \mu\text{m}^3$ (obtained from OMNIDIA version 5.5), respectively. Based on the correlation between *rbcL* gene copy number and diatom cell biovolume (Vasselon et al., 2018), the correction factor (CF) affected the abundance of the number of reads per sample by underestimating the big cells without interfering significantly with the small cells. This justifies the removal of the two big taxa above mentioned from the list of 5 most abundant species using the molecular method with CF. Additionally to *A. minutissimum*, the presence of *Eolimna minima* in both morphological and molecular with CF approaches of the 5 most abundant species supports the remaining results which shows a positive effect of the correction factor towards the morphological approach. *Eolimna minima* is often found among the most abundant benthic species in freshwaters (Wetzel et al., 2015) and recorded in another study (Keck et al., 2018) as one of the most abundant species in morphological analysis. This naviculoid diatom is similar to *A. minutissimum* in biovolume ($88 \mu\text{m}^3$) and is also considered a cryptic taxon, suggesting that future changes in nomenclature and insertion of other species in this complex may occur (currently in discussion).

2. Comparison of IPS values and Ecological Status Classifications

Despite the differences, the IPS values obtained from molecular data were well correlated with those obtained with morphological data ($R=0.64$ and 0.60 , with molecular data with and without CF, respectively). More than half of the samples shared the same class either between molecular with CF and morphological approaches (57%), and between molecular method without CF and morphology (56%). A low percentage of the samples showed 2 or more classes of difference between the 3 combinations of methodologies. The morphological approach revealed the most optimistic ecological quality classifications summing up to 74% of the sites with “High” and “Good” status, followed by molecular method without the correction factor (71%) and molecular method with CF (60%).

The NMDS and PCO showed a similar global gradient of quality with the sites with better quality classifications associated to higher dissolved oxygen and higher habitat quality (HQA), independently of the approach used (morphological/molecular). Higher values of the HQA index in streams are also normally associated with sites less affected by anthropogenic

pressure (Raven et al., 1998). Higher nutrient concentration and conductivity is related to sources of pollution/eutrophication (Morrison et al., 2001), supporting the PCO results, which show an association between the worst quality classified sites by the IPS (diatoms) and higher concentrations of phosphorus and nitrogen. In general, the more common species in sites with “moderate” or “poor” quality classifications were *Nitzschia palea* in morphological list and *Eolimna minima* in both inventories. The two species were already reported as tolerant to high nutrient concentration and, organic pollution (Takamura et al., 1990; Thi et al., 2006). Thus, we verified that the molecular approach also responded well to anthropogenic degradation in rivers.

Yet, it is worthwhile to attend to the differences found between methods. In one site the IPSs varied between 18.1 (class “High”) with morphological data and 7.5 (“Poor”) and 4.9 (“Bad”) with molecular data without and with CF, respectively. In this sample, the most abundant species found with the molecular approach was *Sellaphora seminulum*, a tolerant species (sensitivity value of 1.5 in the IPS), while the morphological inventory showed high abundance of the sensitive species *Eunotia incisa* (sensitivity value of 5 in the IPS). In fact, *Eunotia incisa* was absent from the reference library used and occurred in the inventory as unassigned, which was probably the main reason for the different results. In another sample the opposite situation occurred: the classification of “High” ecological quality (IPS= 19) with molecular data while with morphological data the classification was “Moderate” (IPS= 10.9). This sample showed high abundance of *Achnanthydium minutissimum* (sensitivity = 5) in molecular methods, while *Achnanthydium saprophilum* (sensitivity = 3) was the most abundant species in the taxonomic list. In this case, there might be a problem of correspondence in molecular databases between species and barcodes or a misidentification under the light microscope in the traditional approach. As it is known, *Achnanthydium* taxa have been clustered into “species complexes” due to difficulties in its identification. The small cell size makes it hard to recognise specific morphological features under the light microscope (Wojtal et al., 2011). Additionally, the constant change of *Achnanthydium* genus concept over time becomes a barrier for taxonomists to name uniformly and correctly these organisms (Ponader et al., 2006). For these reasons, taxa lists based on species’ morphology are also subjected to errors and misidentifications which can compromise the accuracy of bioassessment. However, the degradation observed in the river and high conductivity and low dissolved oxygen values support the morphological results, with a higher abundance of *Achnanthydium saprophilum* (more tolerant) than *Achnanthydium minutissimum* (more sensitive). Thus, a meticulous curation of reference libraries is also essential in the process of developing molecular-based methods for ecological assessment of streams.

The effort and time needed were lower for metabarcoding than for the traditional approach. Taxonomic inventories based on the counting of valves per sample took some months and a great taxonomic expertise effort, while the eDNA approach associated with HTS

technique allowed a reduction of the effort and time consumed by standardizing the laboratory protocols and automating the handling of samples (larger spatio-temporal sampling possible), as also verified in other studies (Zimmermann et al., 2014; Vasselon et al., 2017, Hering et al., 2018).

Summarizing, the major problem which molecular ecologists face regarding DNA metabarcoding in biomonitoring is the low accuracy of the taxonomic assignment to HTS data (consequence of the high number of unassigned reads), especially due to incompleteness of reference libraries. Two possible solutions have been proposed to solve this problem (Hering et al. 2018): i) data generation for improvement of barcode reference database by collecting diatom cells from biofilm samples and selecting monoclonal strains for further sequencing (Vasselon et al., 2017), or ii) data generation of ecological preferences of unassigned OTUs. For now, the ideal solution is to continue adding more information to reference libraries since current indices (including IPS) depend on species identification and abundances.

CONCLUSIONS & FUTURE PERSPECTIVES

Our results confirm previous studies (Visco et al., 2015; Vasselon et al., 2017; Rivera et al., 2017) on the contribution of DNA metabarcoding to the traditional approach for ecological quality assessment of freshwaters using diatoms. Although there is a good correlation between DNA and morphological-based methodologies in terms of ecological classifications, the incompleteness of reference libraries along with the need for standardization and harmonization of laboratory and field procedures, must be improved before replacing the traditional methods by molecular approaches. Currently, the major focus is on completing the reference databases, although a full coverage of all diatom species is not expected in the near future due to the difficulties in isolation and cultivation of some taxa. However, it is possible to explore alternative approaches to overcome this issue, especially because the understanding of species concept continues to evolve (Mann, 2010).

New-generation sequencing (NGS) techniques applied in biomonitoring should become very advantageous due to their promising future lower costs, rapid processing of samples and identification accuracy. The majority of studies have been focusing on measuring biodiversity by determining the species richness of a specific ecological niche. According to this new perspective and the fact that, currently, the end-point of bioassessment is to attribute ecological classifications to the water bodies, the taxonomic correspondence of OTUs to morphospecies could be indeed discarded. Therefore, the direct assignment of HTS data to ecological values already proposed by Keck et al. (2018) for diatom communities can be a way to overcome the problems inherent to taxonomic identification. However, with the target of 2027 in view, it is not feasible to completely replace the current water bioassessment strategies set out in the WFD by a DNA-based approach which would require the establishment of a whole new framework including indices recalculation and adaptation of laboratory protocols. Instead, we recommend the use of molecular methods as a complement to the traditional approach for biomonitoring.

In Portugal, other studies have been made using DNA metabarcoding approach associated with HTS techniques in aquatic ecosystems. One of them, for biomonitoring of estuarine macrobenthic communities (Lobo et al., 2017) and the other, for assessment of crustacean trophic niches (Siegenthaler et al., 2018). Both agreed on the efficacy and potential of this method when compared to the morphology-based approach. On the other hand, and to our knowledge, the present study is the first one covering the ecological assessment with diatoms of Portuguese river types which constitutes an important basis for further application of metagenomics of microalgae in the country.

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ANNEX I

Table of the species and their relative abundances (%) per sample for morphological approach

Navicula vilaplani (Lange-Bert. & Sabater) Lange-Bertalot & Sabater in Rumrich & al.

Navicula viridula (Kützing) Ehrenberg

Naviculadicta absoluta (Hustedt) Lange-Bertalot in Lange-Bertalot & Moser

Neidium ampliatum (Ehrenberg) Krammer in Krammer & Lange-Bertalot

Neidium dubium (Ehrenberg) Cleve

Nitzschia acicularis (Kützing) W.M. Smith

Nitzschia acidoclinata Lange-Bertalot

Nitzschia agnita Hustedt

Nitzschia amphibia Grunow f. *amphibia*

Nitzschia archibaldii Lange-Bertalot

Nitzschia capitellata Hustedt in A. Schmidt & al.

Nitzschia costei Tudesque, Rimet & Ector

Nitzschia disputata Carter

Nitzschia dissipata (Kützing) Grunow ssp. *dissipata*

Nitzschia dubia W.M. Smith

Nitzschia epithemoides Grunow var. *disputata* (Carter) Lange-Bertalot

Nitzschia filiformis (W.M. Smith) Van Heurck var. *filiformis*

Nitzschia fonticola Grunow in Van Heurck

Nitzschia frequens Hustedt

Nitzschia gracilis Hantzsch

Nitzschia hantzschiana Rabenhorst

Nitzschia incognita Legler et Krasske

Nitzschia inconspicua Grunow

Nitzschia inconspicua Grunow f. *anormale*

Nitzschia intermedia Hantzsch ex Cleve & Grunow

Nitzschia lacuum Lange-Bertalot

Nitzschia linearis (Agardh) W.M. Smith var. *linearis*

Nitzschia linearis (Agardh) W.M. Smith var. *tenuis* (W. Smith) Grunow in Cleve & Grunow

Nitzschia media Hantzsch.

Nitzschia microcephala Grunow in Cleve & Moller

Nitzschia nano Grunow in Van Heurck

Nitzschia palea (Kützing) W. Smith var. *debilis* (Kützing) Grunow in Cl. & Grunow

Nitzschia palea (Kützing) W. Smith var. *palea*

Nitzschia paleacea (Grunow) Grunow in van Heurck

Nitzschia parvula W. M. Smith

Nitzschia perminuta (Grunow) M.Peragallo

Nitzschia pusilla (Kützing) Grunow emend Lange-Bertalot

Nitzschia recta Hantzsch in Rabenhorst

Nitzschia rosenstockii Lange-Bertalot

Nitzschia soratensis Morales & Vis

Nitzschia sigma (Kützing) W.M. Smith

Nitzschia sociabilis Hustedt

Nitzschia solgensis Clave-Euler

Nitzschia A. H. Hassall

Nitzschia subacicularis Hustedt in A. Schmidt et al.

Nitzschia supralitoria Lange-Bertalot

Nitzschia umbonata (Ehrenberg) Lange-Bertalot

Nitzschia valdestrata Aleem & Hustedt

Nitzschia vermicularis (Kützing) Hantzsch in Rabenhorst

Nupela lapidosa (Lange-Bertalot) Lange-Bertalot var. *lapidosa*

Parlibellus protractus (Grunow) Witkowski Lange-Bertalot & Metzeltin

Pinnularia lundii Hustedt var. *lundii*

Pinnularia microstauron (Ehr.) Cleve var. *microstauron*

Pinnularia parvulissima Krammer

Pinnularia C. G. Ehrenberg

Pinnularia subcapitata Gregory var. *elongata* Krammer

Pinnularia subgibba Krammer var. *subgibba*

Pinnularia viridis (Nitzsch) Ehrenberg var. *viridis*

Placoneis clementis (Grunow) Cox

Placoneis clementoides (Hustedt) Cox

Placoneis pseudanglica (Lange-Bertalot) Cox

Placoneis C. Mereschkowsky

Planothidium dau (Foged) Lange-Bertalot

Planothidium delicatulum (Kützing) Round & Bukhtiyarova

Planothidium frequentissimum (Lange-Bertalot) Lange-Bertalot

Planothidium granum (Hohn & Hellerman) Lange-Bertalot

Planothidium hauckianum (Grun.) Round & Bukhtiyarova

Planothidium haynaldii (Schaarschmidt) Lange-Bertalot

Planothidium lanceolatum (Brébisson ex Kützing) Lange-Bertalot

Planothidium minutissimum (Krasske) Morales

Planothidium robustius (Hustedt) Lange-Bertalot

Planothidium rostratum (Østrup) Lange-Bertalot

Platessa conspicua (A.Mayer) Lange-Bertalot

Platessa hustedtii (Krasske) Lange-Bertalot

Pleurosira laevis (Ehrenberg) Compere f. *laevis* Ehrenberg

Prestauroneis integra (W. Smith) Bruder in Bruder & Medin

Psammothidium sacculum (Carter) Bukhtiyarova et Round

Pseudofallacia monoculata (Hustedt)

Pseudofallacia tenera (Hustedt) Liu Kociolek & Wang

Pseudostaurasira parasitica (W. Smith) Morales

Reimeria sinuata (Gregory) Kociolek & Stoermer

Reimeria uniseriata Sala Guerrero & Ferrario

Rhoicosphenia abbreviata (C. Agardh) Lange-Bertalot

Rossithidium linearis (W. Sm.) Round & Bukhtiyarova

Sellaphora pseudopupula (Krasske) Lange-Bertalot

Sellaphora pupula (Kützing) Mereschkowsky

Sellaphora seminulum (Grunow) D. G. Mann

Simonsenia delognei Lange-Bertalot

Stauroneis gracilis Ehrenberg

Stauroneis kriegeri Patrick

Stauroneis separanda Lange-Bertalot & Werum

Stauroneis smithii Grunow

Stauroneis thermicola (Petersen) Lund

Stausira binodis Lange-Bertalot in Hofmann Werum & Lange-Bertalot

Stausira brevistriata (Grunow) Grunow

Stausira construens Ehrenberg

Stausira elliptica (Schumann) Williams & Round

Stausira martyi (Heribaud) Lange-Bertalot

Stausira mutabilis (Wm Smith) Grunow

Stausira (C. G. Ehrenberg) D. M. Williams & F. E. Round

024

060

074

024

222

024

1796

045

024

086

272

075

025

147

049

024

148

024

166

125

538

048

071

261

071

060

145

296

048

100

088

119

024

024

071

025

125

048

049

047

047

400

049

074

122

474

075

072

048

057

048

047

049

219

060

025

623

125

088

189

048

024

084

048

024

100

071

060

024

220

074

025

049

048

049

166

049

049

150

024

049

073

048

046

024

060

125

060

073

099

025

963

1200

024

550

575

060

349

291

024

024

673

235

2325

1894

047

189

046

742

2024

049

325

1150

324

218

060

047

024

048

047

048

169

088

060

074

122

025

100

024

046

141

048

232

289

150

025

150

125

024

088

711

048

071

287

047

048

024

425

049

060

224

024

635

049

320

225

122

567

197

048

249

072

172

1798

024

356

302

602

025

525

060

048

047

047

047

071

072

894

047

088

310

<i>Pinnularia lundii</i> Hustedt var. <i>lundii</i>										
<i>Pinnularia microstauron</i> (Ehr.) Cleve var. <i>microstauron</i>										
<i>Pinnularia parvulissima</i> Krammer										
<i>Pinnularia</i> C. G. Ehrenberg										
<i>Pinnularia subcapitata</i> Gregory var. <i>elongata</i> Krammer						00				
<i>Pinnularia subgibba</i> Krammer var. <i>subgibba</i>										
<i>Pinnularia viridis</i> (Nitzsch) Ehrenberg var. <i>viridis</i>										
<i>Placoneis clementis</i> (Grunow) Cox								00		
<i>Placoneis clementoides</i> (Hustedt) Cox										
<i>Placoneis pseudanglica</i> (Lange-Bertalot) Cox										
<i>Placoneis</i> C. Mereschkowsky										
<i>Planothidium dau'i</i> (Foged) Lange-Bertalot			08							
<i>Planothidium delicatulum</i> (Kützing) Round & Bukhtiyarova	58	77	34	74	513	884	322	08	304	194
<i>Planothidium frequentissimum</i> (Lange-Bertalot) Lange-Bertalot										
<i>Planothidium granum</i> (Hohn & Hellerman) Lange-Bertalot										
<i>Planothidium hauckianum</i> (Grun.) Round & Bukhtiyarova										
<i>Planothidium haynaldii</i> (Schaarschmidt) Lange-Bertalot										
<i>Planothidium lanceolatum</i> (Brébisson ex Kützing) Lange-Bertalot		120	070	700		107	100	1634	06	187
<i>Planothidium minutissimum</i> (Krasske) Morales										
<i>Planothidium robustius</i> (Hustedt) Lange-Bertalot										
<i>Planothidium rostratum</i> (Østrup) Lange-Bertalot										
<i>Platessa conspicua</i> (A.Mayer) Lange-Bertalot										
<i>Platessa hustedii</i> (Krasske) Lange-Bertalot										
<i>Pleurosira laevis</i> (Ehrenberg) Compere f. <i>laevis</i> Ehrenberg										
<i>Prestauroneis integra</i> (W. Smith) Bruder in Bruder & Medin										
<i>Psammothidium sacculum</i> (Carter) Bukhtiyarova et Round										
<i>Pseudofallacia monoculata</i> (Hustedt)										
<i>Pseudofallacia tenera</i> (Hustedt) Liu Kociolek & Wang										
<i>Pseudostaurosira parasitica</i> (W. Smith) Morales										
<i>Reimeria sinuata</i> (Gregory) Kociolek & Stoermer		024	047	290	05	116	297		08	
<i>Reimeria uniseriata</i> Sala Guerrero & Ferrario										
<i>Rhoicosphenia abbreviata</i> (C. Agardh) Lange-Bertalot	38									
<i>Rosithidium linearis</i> (W. Sm.) Round & Bukhtiyarova										
<i>Sellaphora pseudopupula</i> (Krasske) Lange-Bertalot										
<i>Sellaphora pupula</i> (Kützing) Mereschkowsky								02		
<i>Sellaphora seminulum</i> (Grunow) D. G. Mann		08		08		367	674	297		514
<i>Simonsenia delagnei</i> Lange-Bertalot										
<i>Stauroneis gracilis</i> Ehrenberg										
<i>Stauroneis kriegei</i> Patrick						073				08
<i>Stauroneis separanda</i> Lange-Bertalot & Werum										
<i>Stauroneis smithii</i> Grunow										
<i>Stauroneis thermicola</i> (Petersen) Lund										
<i>Staurosira binadis</i> Lange-Bertalot in Hofmann Werum & Lange-Bertalot										
<i>Staurosira breviseriata</i> (Grunow) Grunow										
<i>Staurosira construens</i> Ehrenberg										
<i>Staurosira elliptica</i> (Schumann) Williams & Round										
<i>Staurosira martyi</i> (Heribaud) Lange-Bertalot										
<i>Staurosira mutabilis</i> (Wm Smith) Grunow										
<i>Staurosira</i> (C. G. Ehrenberg) D. M. Williams & F. E. Round										
<i>Staurosira venter</i> (Ehr.) Cleve & Moeller										
<i>Staurosirella pinnata</i> (Ehr.) Williams & Round										
<i>Surirella angusta</i> Kützing										
<i>Surirella brebissonii</i> Krammer & Lange-Bertalot var. <i>brebissonii</i>		09								
<i>Surirella brebissonii</i> var. <i>keutzingii</i> Krammer et Lange-Bertalot										
<i>Surirella linearis</i> W.M.Smith in Schmidt & al.	10			03						
<i>Surirella roba</i> Leclercq										
<i>Surirella robusta</i> Ehrenberg										
<i>Tabellaria fenestrata</i> (Lyngbye) Kützing										
<i>Tabellaria flocculosa</i> (Roth) Kützing										
<i>Tabellaria ventricosa</i> Kützing										
<i>Tabularia fasciculata</i> (Agardh) Williamset Round										
<i>Tabularia tabulata</i> (C. A. Agardh) Snoeijs										
<i>Thalassiosira pseudonana</i> Hasle et Heimdal										
<i>Tryblionella calida</i> (Grunow in Cl. & Grun.) D. G. Mann in Round Crawford & Mann										
<i>Tryblionella constricta</i> (Kützing) Poulin in Poulin & al.										
<i>Tryblionella debilis</i> Arnott ex O'Meara										
<i>Tryblionella hungarica</i> (Grunow) D.G. Mann										
<i>Ulnaria biceps</i> (Kützing) Compère		145		08						
<i>Ulnaria ulna</i> (Nitzsch.) Compère	05	03	177	072		047				024

ANNEX II

Table of the species and corresponding abundance in reads (total number of reads retained: 2500) per sample, in %, for molecular approach without the application of a correction factor (CF)

ANNEX III

Table of the species and corresponding abundance in reads (total number of reads retained: 2500) per sample, in %, for molecular approach with the application of a correction factor (CF)

<i>Craticula buderi</i>													
<i>Craticula cuspidata</i>			016										
<i>Craticula subminuscula</i>													
<i>Craticula sp.</i>													
<i>Ctenophora pulchella</i>	066		004	021									
<i>Cyclotella meneghiniana</i>													
<i>Cyclotella sp.</i>													
<i>Cymbella excisa</i>													
<i>Cymbella tumida</i>			000										
<i>Cymbella sp.</i>													
<i>Diploneis subovalis</i>													
<i>Diploneis sp.</i>													
<i>Discostella stelligera</i>													
<i>Ellerbeckia sp.</i>										000			
<i>Encyonema minutum</i>			000										
<i>Encyonema prostratum</i>			065	342	005	205	004	179	029	009	020	026	008
<i>Encyonema silesiacum</i>	015									004			
<i>Encyonema sp.</i>													
<i>Encyonopsis subminuta</i>													
<i>Eolimna minima</i>	188	1099	058	1810	048	666	169	4428	3668	1440	180	3547	573
<i>Epithemia sorex</i>													
<i>Eunotia bilunaris</i>		009	008										
<i>Eunotia glacialis</i>		001		002				004	004	002		002	004
<i>Eunotia minor</i>		2970		676		086	088	488	081	397	008	009	117
<i>Eunotia pectinalis</i>		005											
<i>Eunotia sp.</i>													
<i>Fallacia pygmaea</i>			001										
<i>Fallacia sp.</i>													
<i>Fistulifera saprophila</i>	040		281	596		510		064	089	048	010	212	279
<i>Fragilaria arcus</i>													
<i>Fragilaria capucina var. capucina</i>	513	622		1088	022	368	010	048	018		014	018	138
<i>Fragilaria sp.</i>		000											
<i>Frustulia erifuga</i>													
<i>Frustulia sp.</i>													
<i>Frustulia vulgaris</i>										001			001
<i>Geissleria decussis</i>													
<i>Geissleria sp.</i>						071							
<i>Gomphonema minuta</i>													
<i>Gomphonema affine</i>													
<i>Gomphonema bourbonense</i>													
<i>Gomphonema parvulum</i>											008		
<i>Gomphonema rhombicum</i>	154	001	138	012	888	280	018	012	061	011	002	018	018
<i>Gomphonema sp.</i>	457	334	1161	099		066	089	072	170	178	066	084	176
<i>Gyrosigma acuminatum</i>			000										
<i>Halamphora montana</i>													
<i>Halamphora veneta</i>													
<i>Hantzschia amphioxys var. major</i>													
<i>Iconella sp.</i>		002	007										
<i>Karayevia ploenensis var. gessneri</i>			356										
<i>Lemnicola hungarica</i>								081					
<i>Mayamaea perinitis</i>	147		228	248		125		651	080	220		667	756
<i>Mayamaea sp.</i>													
<i>Melosira sp.</i>													
<i>Melosira varians</i>	010	002	011	061	010	029		084	004	001	001	004	081
<i>Navicula capitatoradiata</i>	008							077	019	007	002	062	068
<i>Navicula cryptocephala</i>								008	020	005	070	017	
<i>Navicula cryptotenella</i>		008	041	144		046	004	006	020	044	005	068	008
<i>Navicula cryptotenelloides</i>	004		069	277		121	005	006	010			189	251
<i>Navicula gregaria</i>			112			026							
<i>Navicula lanceolata</i>										002		001	
<i>Navicula phyllepta</i>			002										
<i>Navicula rostellata</i>		004						016	010	001		008	007
<i>Navicula slesvicensis</i>													
<i>Navicula tripunctata</i>			002										
<i>Navicula sp.</i>	011		2082	455	022	146		076	208	064	006	1561	318
<i>Navicula veneta</i>												008	
<i>Neidium sp.</i>									012				
<i>Nitzschia acidoclinata</i>													
<i>Nitzschia amphibia</i>			029										
<i>Nitzschia capitellata</i>													
<i>Nitzschia cf. bulnheimiana</i>													
<i>Nitzschia cf. microcephala</i>													
<i>Nitzschia cf. pusilla</i>			018									008	006
<i>Nitzschia communis</i>													
<i>Nitzschia dissipata</i>													
<i>Nitzschia dissipata var. media</i>		244	097	138		016	001	105	020	008	008	048	117
<i>Nitzschia filiformis</i>													
<i>Nitzschia fonticola</i>			044										
<i>Nitzschia inconspicua</i>			009										
<i>Nitzschia lorenziana</i>													
<i>Nitzschia palea</i>	013	108	148	065		080		077	087	026	002	060	065
<i>Nitzschia sigmaidea</i>			000										
<i>Nitzschia supralittorea</i>			009										
<i>Nitzschia tubicola</i>													
<i>Nitzschia sp.</i>	120		352	011		528		660	028	010		062	215
<i>Pinnularia cf. marchica</i>													008
<i>Pinnularia isselana</i>													
<i>Pinnularia stomatophora</i>													
<i>Pinnularia subcommutata var. nonfasciata</i>													001
<i>Pinnularia subgibba</i>				001				006	008	001		001	002
<i>Pinnularia sp.</i>			008				002	006	011	005		002	007
<i>Pinnularia viridis</i>										000			
<i>Placoneis constans</i>									019				
<i>Placoneis sp.</i>									088				
<i>Planothidium frequentissimum</i>	042		029	886	028	022		1541	017	847	008	008	611
<i>Planothidium lanceolatum</i>	069		524	115		1611	088	192	359	651	023	748	152
<i>Planothidium sp.</i>						275	005					188	
<i>Pleurosira laevis</i>													
<i>Rhoicosphenia abbreviata</i>													
<i>Sellaphora pupula</i>			001						002				
<i>Sellaphora seminulum</i>	024	011	010	119		128		700	138	208	006	578	671
<i>Sellaphora sp.</i>			009					007	042				027

