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Conference Abstract

Stones in the road prevents effective implementation of eDNA-based freshwater quality monitoring in the Iberian Peninsula

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Abstract

The Water Framework Directive (WFD) monitoring requires the use of stressor-specific Multimetric Indices, intercalibrated and validated at river basin level, such as the IBMWP, which is one of the most widely used indices for the biomonitoring of rivers in the Iberian Peninsula. This qualitative index is based on the identification mainly at family level of 125 groups of macroinvertebrates. Currently, molecular biomonitoring systems (biomonitoring 2.0) is widely considered as a good alternative to conduct water quality assessments. The problem comes with the requirement of having complete DNA sequences databases for the targeted species within the indicator groups. In order to know the percentage of sequence coverage of the different taxonomic groups, is needed to know the number of freshwater species in each group. The fact that currently it is only necessary to identify them morphologically at family level to calculate the index means that there are no exhaustive lists of lower taxonomic ranges. In this study, we have studied the available taxonomic databases at species level for river macroinvertebrates in the Iberian Peninsula. For this purpose, species geographically referred to the Iberian Peninsula were extracted from three sources: two European (Freshwaterecology.info database and Weigand et al. (2019)) and one Iberian database/list (Múrria et al. 2020). The resultant species list was compared with GBIF (Global Biodiversity Information Facility) using its tool “Species Matching” to find synonyms and fuzzy names. The similarities and differences between databases were studied (considering the synonyms but not the fuzzy names) and a new list of 3586 species was constructed. Our analysis revealed that from 125 taxonomic groups covered by the IBMWP, there are no species collected for 11 of them (9%) and for another 34 groups (27%) there are less than 5 species collected in the databases. Then, using the BAGS software, all sequences of the mitochondrial gene COX1 were mined from BOLD database. From the 3586 species in the list, only 1900 (53%) have at least one sequence in BOLD. Therefore, conducting biomonitoring 2.0 in Iberian freshwater ecosystems is far from effective today. We need to overcome two big obstacles to reach the goal of using molecular biomonitoring in the Iberian Peninsula: a complete taxonomic list of quality indicators species by groups, and to sequence DNA barcodes from all relevant species.

Keywords

Macroinvertebrates, Iberian Peninsula, IBMWP, Biomonitoring 2.0, BOLD, COX1.

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