Using metabarcoding and « Diat.Barcode » database to perform molecular identification on marine biofilms

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Abstract

Marine benthic diatoms highly contribute to biofilms formation, playing a crucial role on both living and artificial surfaces colonization (Briand 2017, Salta 2013). However, their microscopic morphological identification is time consuming and requires a high expertise in taxonomy. We therefore decided to look toward molecular analyses and especially metabarcoding. In this study, we determine: (i) if the use of the “Diat.barcode” database, mostly developed for freshwater diatoms (Rimet 2019), is relevant to characterize marine biofilm communities, (ii) if the amplification of degenerated primers targeting the rbcL gene (Vasselon et al. 2017) could improve the diversity of marine diatom biofilms, and (iii) if molecular and morphological analyses could be correlated. A large majority of OTUs (>95%) was affiliated using the “Diat.barcode” database and the pipeline FROGS, with coverage and affinity values above 80%. OTUs tables contained 75% of diatom species already reported from marine environment, with 82% belonging to the pennates group. The use of degenerated primers significantly improved richness and diversity. Moreover, it allowed us to identify taxa that were not present before, as *Iconella*, *Sellaphora* and *Coronia*. Finally, we showed higher richness and diversity, but also a higher repeatability (replicates closeness) leading to a better clustering with metabarcoding. We found differences in terms of biomarkers, but more broadly, we were able to correlate significantly (*r* = 0.404; *p*<0.0001) diatom assemblages. While the latest version of “Diat.barcode”
The database contains only 12.4% species referenced as marine, it appears to be a powerful tool, even on biofilm samples from the Mediterranean, Baltic seas and Indian Ocean. Furthermore, we confirmed the relevance of degenerated primers to amplify a higher diversity of diatoms. Finally, beta-diversity similarity using molecular and microscopic analysis appeared positive, leading to the conclusion that the two methods should be used in a complementary way.

**Keywords**

Metabarcoding, "Diat.barcode" database, Marine biofilms, Diatoms, Biofouling

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**References**