



Conference Abstract

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"

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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