

# How can molecular phylogenies help to improve the use of benthic foraminifers as proxies?

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Benthic foraminifers are widely used as proxies for paleoenvironmental reconstructions. However there are some limitations in their use as proxy. Despite an increase of the number of studies, their ecology is still not well known and their taxonomy is not as well constrained as the one of planktic foraminifers.

Here the aim is to show that studies based on foraminiferal DNA (e.g. molecular systematics, molecular phylogeny) can help untangling benthic foraminiferal taxonomy. With a method based on the DNA extraction of one single specimen, after SEM imaging, it is possible to connect the DNA sequence to the morphology and study the molecular phylogeny and the fossil record in parallel.

This method allows to answer different questions such as what is the most logical generic name for *Anomalina/Cibicides/Cibicidoides/Fontbotia/Planulina wuellerstorfi*, is *Cibicidoides kullenbergi* the same species for all researchers, are there cosmopolitan or (pseudo)cryptic species in benthic foraminifers, etc. We will focus here on two groups of benthic foraminifers which are widely used as proxies: the cibicidids and the uvigerinids.