

Historical DNA barcoding library of Polychaete worms

Natural science collections are a rich source of foundational biodiversity information that is primarily related to spatial, habitat and bathymetric parameters. They form the baseline for studies such as biogeography, conservation biology, ecology and the evolutionary history of species. While specimens in natural science collections are known to have DNA degradation and contamination due to preservation methods, modern molecular techniques have enabled the successful amplification of DNA sequences thereby unlocking historical information which can subsequently be used to validate and assign correct taxonomic identities to cryptic species complexes, among other research questions. Although our knowledge of polychaetes in southern Africa is reasonably good, recent molecular evidence has shown that diversity has been significantly underestimated, and that our understanding of the taxonomy and biogeography of many species remains incomplete. By developing a historical DNA reference barcoding library of polychaete worms for the first time from natural history collections, we would be able to validate taxonomically confusing (cryptic) species from type and non-type material of representative specimens. Not only will this enhance our local and global understanding of biodiversity and biogeography of polychaete worms, but such a dataset will form the baseline for subsequent complex research hypotheses such as investigating phylogenetic relationships between species and the historical population connectivity of species. The subsequent molecular techniques used and developed during this project to extract DNA from preserved material can be transferred to other important groups of marine taxa.