

Molecular diversity and population structure of three different marine benthic taxa in relation to their means of dispersal

Remerie T., A. Vanreusel, and J. Vanfleteren

¹ Ghent University, Marine Biology Section
K.L. Ledeganckstraat 35, B-9000 Gent, Belgium
E-mail : thomas.remerie@rug.ac.be

Biodiversity can be studied at several levels from ecosystem-, species-, to population-level. At the population level genetic variation can appear within a species due to mutation, genetic drift, recombination, gene migration and selection, which can cause differences between populations. Gene flow is an important determinant in population genetic structuring and is closely associated with the dispersal capacities of a species, the presence of barriers and historical phenomena. The objective of this research project is a study of the genetic diversity and structuring of some dominant species-populations of different invertebrate taxa from the North Sea, adjacent North East Atlantic coast and estuaries. Three benthic taxa with different means of mobility were selected for this research: hyperbenthic Mysidacea, meiobenthic Harpacticoida and meiobenthic Nematoda. This research will focus on the link between the gene flow and the different means of dispersal of these three benthic taxa. Within each taxon two species are selected from different habitat types. Different populations will be analysed in order to get insight on the effect of habitat fragmentation on the degree of genetic diversity and structuring.

Within the taxon of the Mysidacea populations of the species *Neomysis integer*, which inhabits discrete estuarine habitats, and *Mesopodopsis slabberi*, which has a more continuous habitat will be investigated and compared. So far the genetic diversity and population genetic structure are analysed by sequencing two different molecular markers: the Internal Transcribed Spacer (ITS), which is a region in the ribosomal DNA between the more conservative 18S and 28S genes, and the cytochrome *b* gene, which is a mitochondrial gene. Four different estuaries (the Wista, Weser, Westerschelde and Gironde) are analysed for the mitochondrial cytochrome *b* gene of *Neomysis integer*. This molecular marker with a length of 419 bp shows a small degree of differentiation between the four estuaries. Especially the Gironde estuary seems to be quite distinct from the 'northern' estuaries (Westerschelde, Weser and Wista). The analysis of the ribosomal ITS1 region of *Neomysis integer* shows more problems than the cytochrome *b* gene. Almost no variation is detected in the preliminary sequence data from six estuaries (Wista, Lake Ferring, Weser, Westerschelde, La Canche, Gironde). This suggests that the ITS1 region of Mysidacea is not so useful in detecting population subdivision and analysing molecular diversity.