

## **ASSESSMENT OF THE MYOGLOBIN VARIATION IN THE PERIWINKLE *LITTORINA LITTOREA* ALONG THE SCHELDT ESTUARY**

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The Scheldt Estuary (The Netherlands) consists of two tributaries, of which the western part is heavily polluted (i.e. domestic and industrial pollutants, including heavy metals) and the eastern is relatively clean. Pollutants generally follow downstream decreasing concentration gradients, thus opposing a natural occurring salinity gradient, which decreases upstream. Hence, the Scheldt Estuary forms an interesting setting to investigate the effects of both anthropogenic and natural kind.

The population genetic structure of the periwinkle, *Littorina littorea*, has already been studied in this estuary using esterases and RAPD markers. Both studies revealed an estuary based genetic structuring. This genetic patterning is unexpected since *L. littorea* has a planktonic larval development and thus little genetic differentiation is expected. However, radular myoglobin studies have shown intraspecific variation in *L. littorea* on a macrogeographical scale. In this contribution, myoglobin profiles of the radular muscle were phenotypically analysed along the Scheldt Estuary, using isoelectric focusing.

A total of 395 periwinkles, descending from four eastern estuarine, five western estuarine and one marine sampling site were collected and morphometrically characterized after which their individual Mb profile was determined. Four Mb bands could be identified and the distribution of each of these bands differed significantly between the western and eastern Scheldt Estuary. In addition, eight different Mb phenotypes were detected of which the distribution differed between both estuaries as well, yielding a significantly higher phenotypic variability in the Western Scheldt. A Dice similarity distance based multidimensional scaling minimum spanning tree (MDS-MST) analysis revealed no clear differentiation between both estuaries. Likewise the MDS-MST analysis failed to detect phenotypic structuring along the pollution-salinity gradient of the Western Scheldt sampling sites. However, the only marine sampling site was clearly separated from the nine remaining estuarine locations in the MDS-MST plot. These preliminary data suggest, in the presence of intense gene flow, (1) a high level of phenotypic Mb variability and (2) a marine versus estuarine phenotypic Mb structuring.