

POPULATION GENETIC STRUCTURE OF TWO BACTERIVOROUS NEMATODES ALONG THE NORTH SEA AND ADJACENT ESTUARIES

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Pellioiditis marina and *Geomonhystera disjuncta* are two nematode species living on decaying brown algae and are abundant in the marine and estuarine environment. They can reach very high densities and are important in decomposing processes.

The population genetic structure will be analysed using molecular information and experimental approaches. By integrating different spatial scales and tidal vs nontidal systems, the observed population genetic structure with respect to passive dispersal capacities will be examined. The genetic structure using the mitochondrial cytochrome oxidase c subunit 1-gene and a nuclear gene will give information on intraspecific variation.

Furthermore, (a) the assessment of the role of stochastic factors in allowing 'confunctional' species to coexist in space and time, and (b) the evaluation of the importance of intraspecific variation in a species' resilience to major environmental stresses is investigated. A litterbag experiment to follow the colonization pattern of *Fucus* sp. in the field will be carried out. By analysing the population genetic structure of the colonizing *Pellioiditis marina*, we will be able to see if the nematodes are recruited from populations nearby or from more distant populations. Furthermore, it will be possible to evaluate if this colonization consists of mass recruitment or founder events. Results from this ongoing experiment will be discussed.