Biodiversity and genetic patterns in marine invertebrates

Emma Thuróczy Vodoti, 2010

UNIVERSITY OF GOTHENBURG

Faculty of Science, Department of Zoology

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Department of Zoology, University of Gothenburg, Box 463, SE-405 30
Göteborg, Sweden

Abstract:

Systematics based on genetic data has both confirmed and contradicted earlier, morphologically defined species and their relatedness. Morphology does not always correspond to genetic lineages, and this will inevitably affect both traditional systematics as well as biodiversity assessments. My thesis aims to investigate genetic biodiversity in some marine invertebrates, dealing with both species and population (intraspecific) relationships. I discuss gene lineage relatedness in correlation to species morphs and geographical species distribution, which has bearing upon the species recognition problem, the barcoding approach and the meaning of phylogeographic patterns.

Results show that morphology does not generally reflect gene lineage relationships in the considered species and that cryptic species are common, mainly in the nemertean groups studied (*Oerstedia dorsalis*; *Cerebratulus* spp). Despite having a relatively established status as a species, the horse mussel (*Modiolus modiolus*) is also found to hold cryptic lineages. Further, the difficulties in species delimitation become apparent, as an almost continuous range of genetic divergence prevails between most of the found clades. The Antarctic krill (*Euphausia superba*) is the only study species lacking cryptisism, at least in the samples and geographical region studied. The intraspecific genealogies were in this case used to estimate population parameters by means of the coalescent. Despite being an abundant species of modest size, results suggest a low effective population size and a population with common ancestry, most likely capable of migrating over relatively great distances. This stresses that factors such as demography and genetics can provide a preliminary, general base for management issues.

I conclude that cryptic species are common, and therefore taxonomic work cannot be isolated from the barcoding quest of summoning genetic data for species identification. Since genetic relationships and morphological traits do not always go hand in hand, a barcoding approach could in some cases be misleading. Further, it is probably impossible to find a universal way of defining, identifying and delimiting species. This thesis illustrates some practical examples of these problems, and suggests that a case-to-case evaluation is likely needed in future taxonomic and phylogenetic efforts.

Keywords: *biodiversity, molecular genetics, intraspecific patterns, morpho-species, genealogy, marine invertebrates, phylogeography, haplotype network*

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