

Depth-differentiation *versus* depth-refugia hypotheses: a case study in two Southern Ocean sea stars

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The depth-differentiation hypothesis proposes that deep areas represent areas of genetic divergence. In the Southern Ocean, this was suggested for several taxa (bryozoans, polychaetes, molluscs) and some species that were assumed to be a single eurybathic species were found to be in fact composed of several stenobathic species. However, the deep-refugia hypothesis suggests that deep areas can serve as refugia for shallower zones during disturbance periods like glacial maxima. Associated to this hypothesis, there should be some level of present connectivity between shelf and deeper populations. During the last decade, the depth-differentiation hypothesis gained in popularity, but the number of taxa investigated remains limited and it is still unclear if the depth-differentiation hypothesis can be considered as a general rule for benthic communities of the Southern Ocean. The current project will test the depth-differentiation/refugia hypotheses in two close sea stars species (Astropectinidae family): *Bathybiaster loripes* and *Psilaster charcoti*. If the depth-differentiation hypothesis is correct, a genetic differentiation between shallow and deep waters as well as a bigger differentiation along vertical rather than horizontal distances could be expected. If depth-refugia hypothesis is valid, gene flow between shallow and deep waters as well as equal (or lower) differentiation along vertical and horizontal distances could be expected. In this study, the main region of interest is the Antarctic Peninsula for which significant quantities of samples have been collected for a population genetics approach. Other locations will be added to the analysis (South Georgia, South Sandwich, South Orkney, Weddell Sea, Adélie Land, Ross Sea, Amundsen Sea, Subantarctic New Zealand). A total of 268 specimens for *B. loripes* (86 deep samples) and 236 specimens for *P. charcoti* (101 deep samples) will be analysed. Molecular markers will include one mitochondrial gene (cytochrome oxidase I, COI) as well as nuclear markers (SNP or microsatellites).

Keywords: Antarctica; population genetics; asteroidea; COI; RAD sequencing; microsatellites