

Genetic Stock Assessment of *Merluccius capensis* and *Merluccius paradoxus*

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Abstract

Sampling for an adequate hake stocks structure analysis using genetics is difficult because of logistic limitations over a very large area, necessity to sample same sites simultaneously in any given year, and repetitive sampling for several years (minimum 3). After a number of attempts, good sampling was achieved for 2012 and 2013 (with 2014 sampling planned). However, these results are as yet not available. Previous limited results were difficult to interpret: some weak structure was discovered between Namibia and SA in *Merluccius paradoxus*, but no structure was present in *M. capensis* when using mitochondrial DNA. This early result was repeated later on the much larger material, but then pairwise comparisons between regions (using Φ_{ST} stats) were not significant. Opposite results were obtained using microsatellite DNA.