Outlier SNP markers reveal fine-scale genetic structuring across European hake populations (Merluccius merluccius)

Shallow population structure is generally reported for most marine fish and explained as a consequence of high dispersal, connectivity and large population size. Targeted gene analyses and more recently genome-wide studies have challenged such view, suggesting that adaptive divergence might occur even when neutral markers provide genetic homogeneity across populations. Here, 381 SNPs located in transcribed regions were used to assess large and fine-scale population structure in the European hake (Merluccius merluccius), a widely distributed demersal species of high priority for the European fishery. Analysis of 850 individuals from 19 locations across the entire distribution range showed evidence for several outlier loci, with significantly higher resolving power. While 299 putatively neutral SNPs confirmed the genetic break between basins (FCT = 0.016) and weak differentiation within basins, outlier loci revealed a dramatic divergence between Atlantic and Mediterranean populations (FCT range 0.275–0.705) and fine-scale significant population structure. Outlier loci separated North Sea and Northern Portugal populations from all other Atlantic samples and revealed a strong differentiation among Western, Central and Eastern Mediterranean geographical samples. Significant correlation of allele frequencies at outlier loci with seawater surface temperature and salinity supported the hypothesis that populations might be adapted to local conditions. Such evidence highlights the importance of integrating information from neutral and adaptive evolutionary patterns towards a better assessment of genetic diversity. Accordingly, the generated outlier SNP data could be used for tackling illegal practices in hake fishing and commercialization as well as to develop explicit spatial models for defining management units and stock boundaries.
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 5.36 SJR 3.068 SNIP 1.684
Web of Science (2012): Impact factor 6.275
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 5.56 SJR 3.508 SNIP 1.834
Web of Science (2011): Impact factor 5.522
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.564 SNIP 1.919
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.489 SNIP 2.022
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.363 SNIP 2.075
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 3.508 SNIP 2.102
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.978 SNIP 1.908
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.98 SNIP 2.089
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.799 SNIP 2.092
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.582 SNIP 1.716
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 2.259 SNIP 1.445
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.165 SNIP 1.571
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.821 SNIP 1.67
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 2.483 SNIP 1.783

Original language: English

DOIs:
10.1111/mec.12568

Research output: Research - peer-review › Journal article – Annual report year: 2013