

Estimating dispersal rates in Skagerrak coastal cod from both genetic differentiation and population dynamics using an individual based model

Ingrid Spies^{1,2,4}, Lorenz Hauser³,
Per Erik Jorde^{4,5}, Halvor Knutsen^{4,5},
André E. Punt³, Lauren Rogers⁴,
Nils Chr. Stenseth^{4,5,6}

Main question: Skagerrak cod have different growth rates and maturity-at-age. Are they distinct populations from North Sea cod – how many migrants are there?

Abstract

Estimates of dispersal rate are important for managing exploited marine and terrestrial species. Genetic data are commonly used to draw conclusions about dispersal. However, even significant genetic differentiation cannot be directly translated into a dispersal rate. Here, a genetic individual-based, age structured population dynamics model was used to estimate the relationship between dispersal, genetic differentiation and demographic independence. The method was used to estimate the number of migrants between North Sea Atlantic cod (*Gadus morhua*), and two Norwegian Skagerrak populations, a fjord (Søndeled) and the adjacent coastal population (Risør). Results suggest that significant genetic differentiation observed between the North Sea and the fjord population was most consistent with 55-80 age-0 immigrants into the fjord each year from the North Sea. Observed genetic differentiation between the North Sea and the Risør coastal population was small and not significant; consequently, dispersal estimates were fairly high (1,300-6,000 larval migrants per year). The estimated number of migrants necessary to match empirical levels of genetic differentiation was sensitive to fishing mortality, fishery selectivity, maturity-at-age and Skagerrak population size, depending on the level of genetic differentiation.

Conclusions

- Greater than 10% of the outer fjord spawning population originates in the North Sea; therefore, migration is likely to have a demographic influence on the outer fjord. Genetic differentiation between these two populations is not statistically significant ($F_{ST}=0.0001-0.0003$).
- Only 1-2% of the inner fjord age-0 cohort appears to be from the North Sea. ($F_{ST}=0.0039-0.0051$). Statistically significant levels of genetic differentiation between the North Sea and the inner fjord support this result.

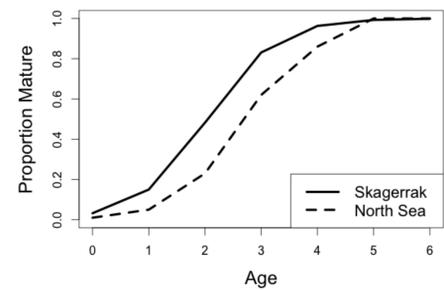
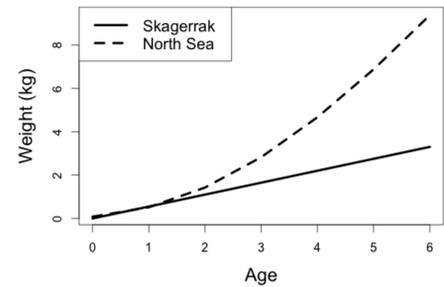


Figure 1: Skagerrak cod mature earlier (upper panel) and grow more slowly (lower panel) than North Sea cod.



The Model

An individual-based model, in which each fish was assigned a multilocus microsatellite genotype, projected the population dynamics for 100 years. Migration was estimated by varying the number of migrants from the North Sea to two Skagerrak spawning populations until F_{ST} in the model matched empirical results.

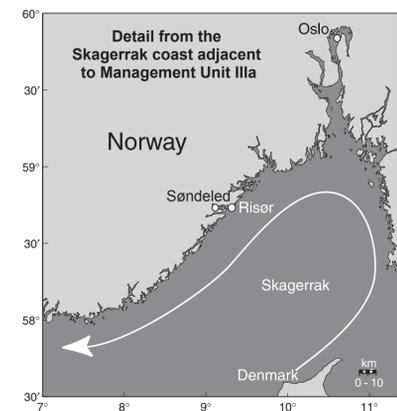
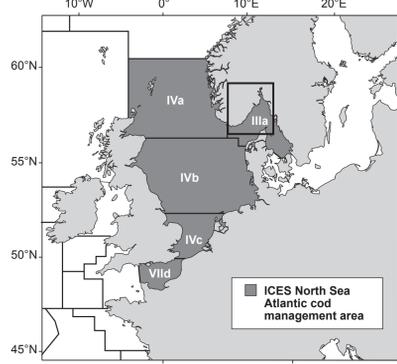
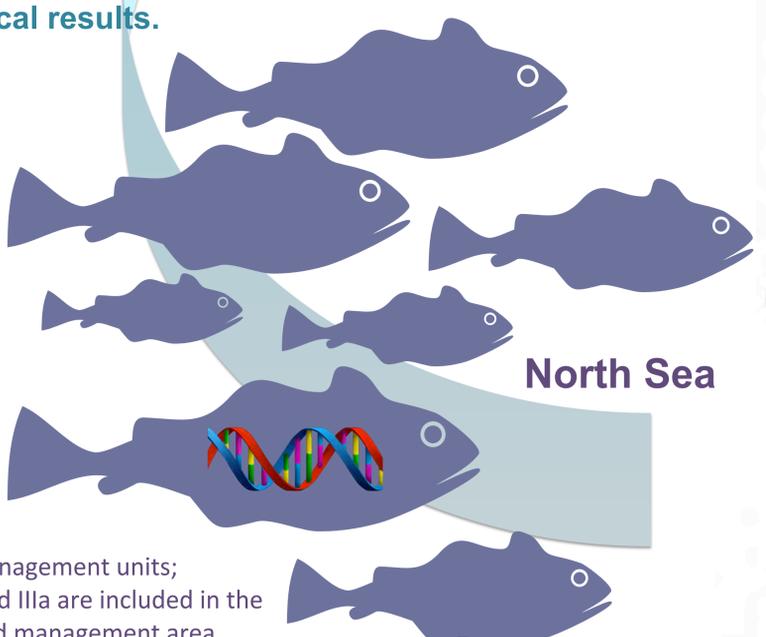
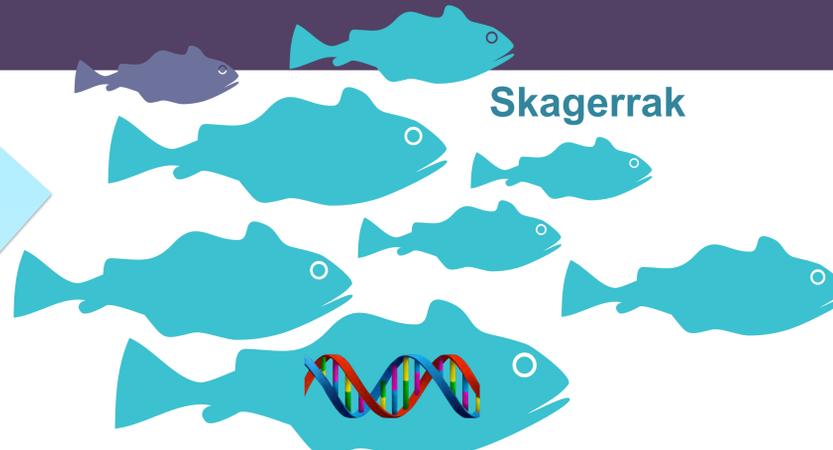


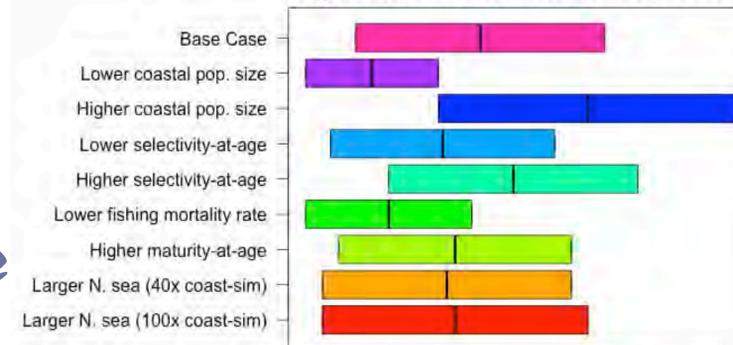
Figure 2: Upper panel: ICES management units; areas IVa,b,c, VIIId, and IIIa are included in the North Sea Atlantic cod management area (Figure adapted from Reiss et al. 2009). Lower panel: map of the Skagerrak coast.

¹ Alaska Fisheries Science Center, NMFS/NOAA, Seattle Washington U.S.A.
² Quantitative Ecology and Resource Management, University of Washington Seattle, Washington, U.S.A.
³ School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA, U.S.A. ⁴Centre for Ecological and Evolutionary Synthesis, Oslo, Norway.
⁵ Institute of Marine Research, Flødevigen, Norway. ⁶University of Agder, Kristiansand, Norway.



Results

Migration between North Sea and outer coast



Migration between North Sea and fjord

