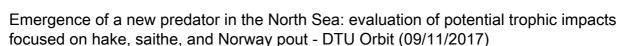
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Emergence of a new predator in the North Sea: evaluation of potential trophic impacts focused on hake, saithe, and Norway pout

During the last 15 years, northern European hake (Merluccius merluccius) has increased in abundance, and its spatial distribution has expanded in the North Sea region in correlation with temperature. In a context of global warming, this spatial shift could impact local trophic interactions: direct impacts may affect forage fish through modified predator-prey interactions, and indirect impactsmay materialize through competition with other resident predators. For instance, North Sea saithe (Pollachius virens) spatial overlap with hake has increased while saithe spawning-stock biomass has decreased recently notwithstanding a sustainable exploitation. In this context, we investigated the range of potential impacts resulting from most recent hake emergence in the North Sea, with a particular focus on saithe. We carried out a multispecies assessment of North Sea saithe, using the Stochastic MultiSpecies (SMS) model. In addition to top-down processes already implemented in SMS, we built in the model bottom-up processes, relating Norway pout (Trisopterus esmarkii) abundance and saithe weight-at-age. We simulated the effects, on all North Sea species being considered but focusing on Norway pout and saithe, of combining different hake abundance trends scenarios with the inclusion of bottomup processes in SMS. North Sea saithe F-MSY was then evaluated in a multispecies context and contrasted with singlespecies value. The different scenarios tested revealed a negative impact of hake emergence on saithe biomass, resulting from an increase of predation pressure on Norway pout. These results confirm the competition assumption between saithe and hake in the North Sea and might partially explain the most recent decrease of saithe biomass. This study also highlighted that taking into account bottom-up processes in the stock assessment had a limited effect on the estimation of saithe FMSY which was consistent with single-species value.

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