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A Bayesian hierarchical model to unravel the spatial covariations in the response of Atlantic salmon populations to climate change in the North Atlantic Ocean.

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Analysing the spatial synchrony in the dynamics of several populations allows for separating out the factors susceptible to synchronize the dynamics of large groups of populations from those that affect populations more locally.

We investigate the drivers and mechanisms that could explain the widespread decline in abundance of Atlantic salmon (*Salmo salar*) populations observed in the North Atlantic Ocean over the last four decades. Specifically, we investigate the mechanisms that can affect A. salmon populations during their marine migrations and susceptible to synchronize large groups of populations over a wide spatial scale.

We developed a hierarchical Bayesian life cycle model for the collective analysis of the dynamics of all 13 A. salmon stock units (SU) from the North American (NA) and Southern European (SE) continental stock groupings (CSG) over the period 1971-2014. The model is designed for estimating time series of two key parameters associated with the marine phase of the life cycle: (i) the marine survival during the first summer-autumn spent at sea; and (ii) the proportion of fish maturing the first winter at sea. Those time series are estimated for each of the 13 SU within multivariate hierarchical structures that allow for quantifying the covariation in a hierarchy of spatial scales between the two CSG and between any pairs of SU within each CSG. We also test for the influence of marine environmental conditions to explain those variations. Specifically, we use hierarchical decomposition of time series to quantify how much variance is explained by the Sea Surface Temperature (SST) (i) considered on space-time domains supposedly shared by all populations within the same CSG during their sea-migrations (common feeding grounds); and (ii) on domains where different populations are supposedly separated during their migrations.

Results provide evidence of a decline in the marine survival together with an increase in the proportion of early maturing fish, common to all SU. The decomposition of the variance between spatial scales shows that the common trend shared by all SU of the two CSG explains 15% of the variance. When considered separately between the two CSG, common trends explains 50% of the variance, and residual specific trends for each SU explain the remaining 50% of the variability. Interestingly, variations in SST accounted for 40% of the time variations in survival for populations from the NA CSG, but only 1% for SE CSG.

Our findings support the hypothesis of a response of salmon populations to large scale bottom-up environmentally driven changes in the North Atlantic susceptible to simultaneously impact several populations reproducing in distant continental habitats. Results also suggest that drivers and/or mechanisms could be different between NA and SE populations in relation to partially different migration routes at sea.

Key words: Spatial covariation, hierarchical Bayesian model, stage-based life cycle model, marine survival, maturation probability, Atlantic salmon, environmentally driven changes, bottom-up, SST.