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The power of integrating genetic and otolith microchemistry data to investigate population connectivity in common sole

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Many marine species are characterized by high fecundity, pelagic larvae, and high dispersal potential, resulting in high gene flow and weak genetic structure. It therefore remains a challenge to measure connectivity and reliably define management units in the open marine environment, which is lacking obvious physical barriers to dispersal. Although genetic assignment methods are limited by high gene flow and low genetic structure, otolith techniques are in turn dependent on distinct environmental differences. The combined use of otolith microchemistry and genetic markers, however, can provide valuable, powerful, and complementary information on population structure. In this study, estimates of stock composition based on genetic data and otolith microchemistry were compared for the common sole (*Solea solea*) in northern Europe. The degree of genetic differentiation between samples caught at several geographic locations, from Skagerrak and Kattegat in the north to the Bay of Biscay in the south, was analysed with 12 microsatellite markers and a mitochondrial marker (cytochrome *b*). The elemental composition of otoliths from 244 adult sole was measured using laser-ablation inductively coupled plasma mass spectrometry (LA-ICPMS). In all 13 elements were measured at the core and the outer edge of the otoliths, corresponding to different life-history stages. In general, there was a lack of genetic differentiation, suggesting high levels of gene flow at the spatial scale studied. On the other hand, elemental concentrations did differ significantly between the "core" and "edge", suggesting that the adult sole were caught in very different environments than their birth location. The integration of results of both techniques is discussed in the light of an optimal strategy to assess the level of connectivity in sole and other flatfish.

Keywords: common sole, connectivity, microsatellite markers, otolith microchemistry.

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