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No anonymity for fish: tracing sole juveniles arriving at the Belgian nursery combining genomics, otolith microchemistry and otolith shape analysis.

To improve sustainability, fish stocks need to be monitored at an ecologically meaningful scale. Therefore fisheries management requires to understand population structure. However it is difficult to measure connectivity between populations especially because early-life stages cannot be tagged due to their small size. Success of larval dispersal is the key to connectivity between spawning grounds and nurseries. *Solea solea* is among the most economically valuable fish species in the North Sea, yet little is known about its population dynamics. In the present study, we investigate the geographical origin of young-of-the-year sole arriving at the Belgian nursery. Previous studies showed that genomic markers, otolith microchemistry and shape can reveal fine scale population structure for other fish species. We ran a sampling campaign and genotyped more than 400 juveniles of sole using the double digest Restriction Site-Associated sequencing (ddRAD) technique. Five hundred high quality Single Nucleotide Polymorphic sites were retained and used to define population structure at a fine spatial (<50 km) and temporal scale (2013-2014). Outlier tests were run to identify markers that could be used for traceability and might show signatures of local adaptation. In addition to the genomic approach, otolith microchemistry and shape were used to reveal small scale population structure. Combining the three different traceability measures increased our assignment power. Results show that southern North Sea populations of sole are highly connected, and that those caught off the Belgian coast are closely related to the Eastern English Channel populations. Improving the discrimination of subpopulations of fish would allow a better traceability and sustainable management of the resources.

Keywords: traceability, connectivity, small-scale, early-life stages, flatfish