

Do juvenile sole belong to mixed spawning populations?

Tracing juvenile flatfish arriving at the Belgian nursery using genomics and otolith shape

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B-FishConnect

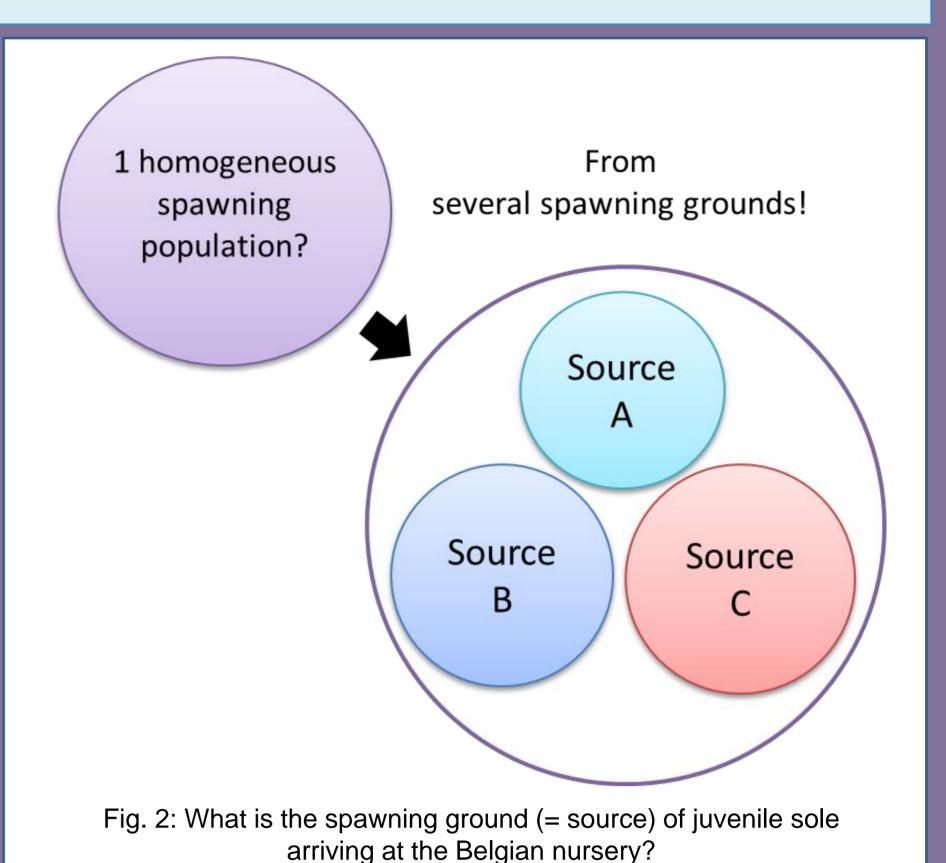
Belgians consume on average 10 kg fish/year/capita amounting to some 136,000 tonnes/year. Sole is a national food item, but its abundance in the North Sea is decreasing due to heavy fishing. Recruitment has varied a lot through time. Stock managers and decision makers need to differentiate populations to (1) better assess stock status, to (2) enforce fishing regulations and to (3) address mislabelling and illegal fishing.

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FINE SCALE SAMPLING of FLATFISH JUVENILES STAT16 Oostende Historical sample ICES sampling Fig. 1: Map of the sampling locations of sole samples to produce genetic baselines

OBJECTIVES

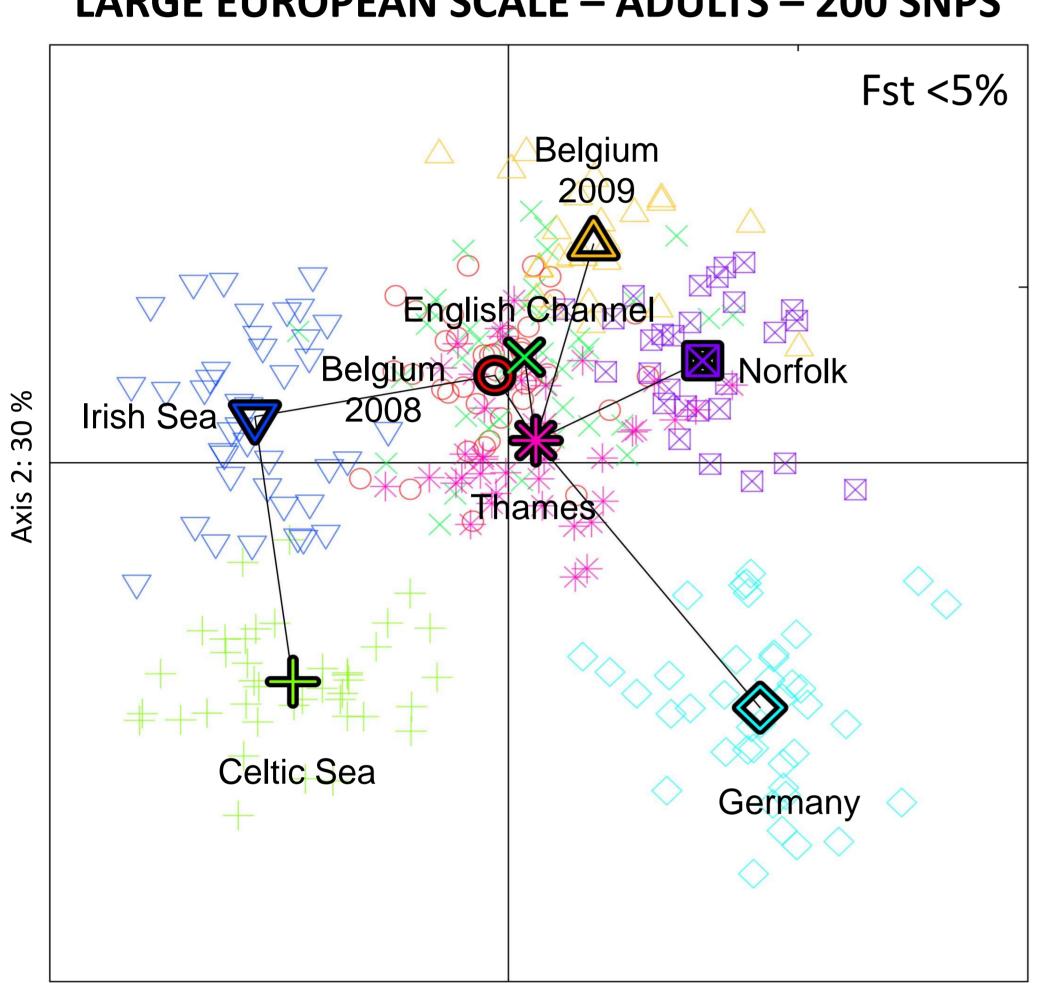
- 1. Compare population structure at large and small-scales using:
 - (1) Genomics
 - (2) Otolith shape
- 2. Determine the spawning population of origin of juveniles arriving on the Belgian nursery grounds



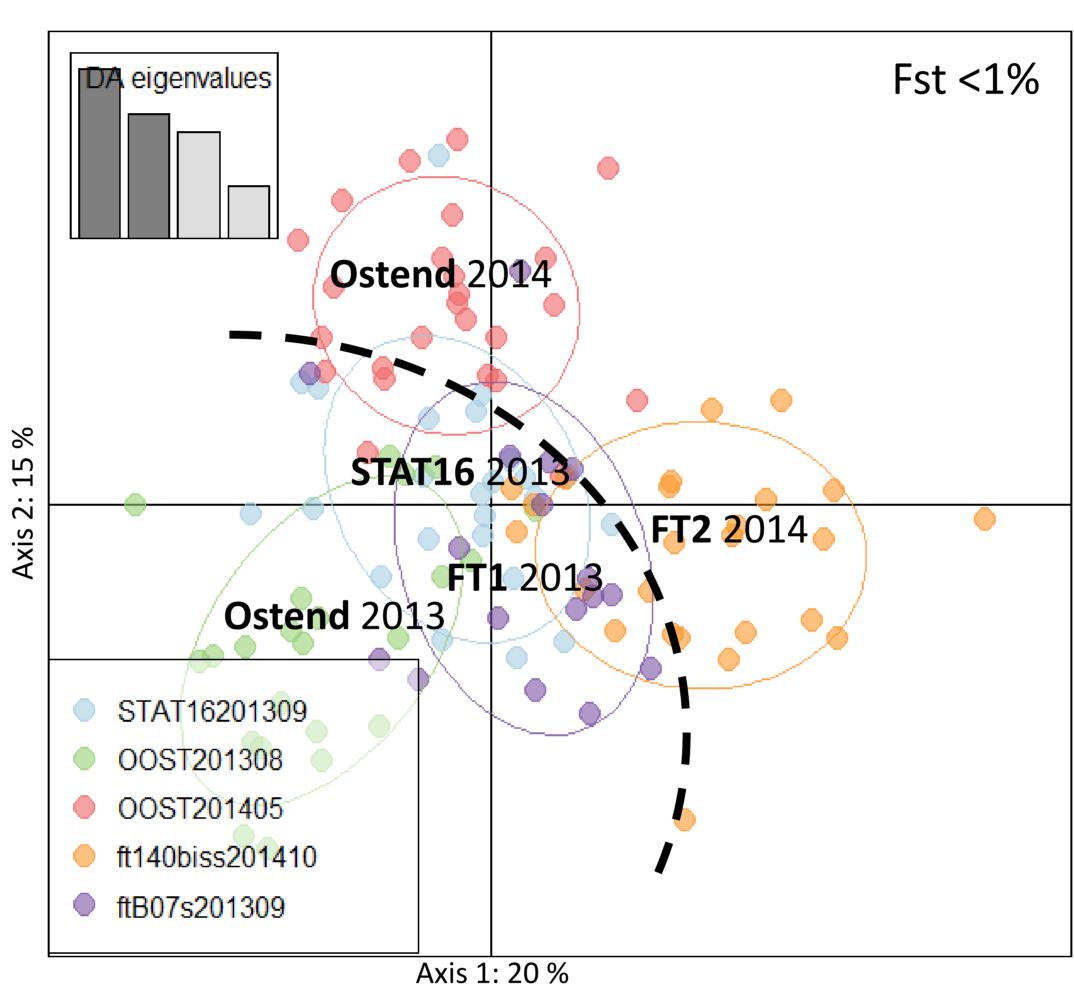
CONNECTIVITY MEASURES THROUGH (1) GENOMICS

over the past 10 years. Isobath every 10 meters.

LARGE EUROPEAN SCALE – ADULTS – 200 SNPS



BELGIAN SCALE – JUVENILES – 450 SNPs



between populations is 70% at the European scale (Fig. 3) and much lower at the local scale (35%, Fig. 4).

assignment

power

statistical

Overall

Populations remote from the Southern Bight are genetically distinct. Locally, 114 juveniles have been ananlyzed using ddRAD sequencing. We obtain a low pairwise Fst between neighboring fish populations (<1%). The strongest structure suggests inter-annual variability which is supported by the model of Lacroix et al. 2013.

> More markers and more individuals needed!

To improve resolution, combine genomic measures with otolith shape and microchemistry. Different time scale of connectivity.

Fig. 3 and 4: Discriminant Analysis of the Principal Components (DAPC) on the genetic data based on 200 SNPs markers in 10 adult sole sampled at the European scale (left) and 450 SNPs in 114 juveniles sampled at the Belgian scale (right)

CONNECTIVITY MEASURES THROUGH (2) OTOLITH SHAPE

Axis 1: 40 %

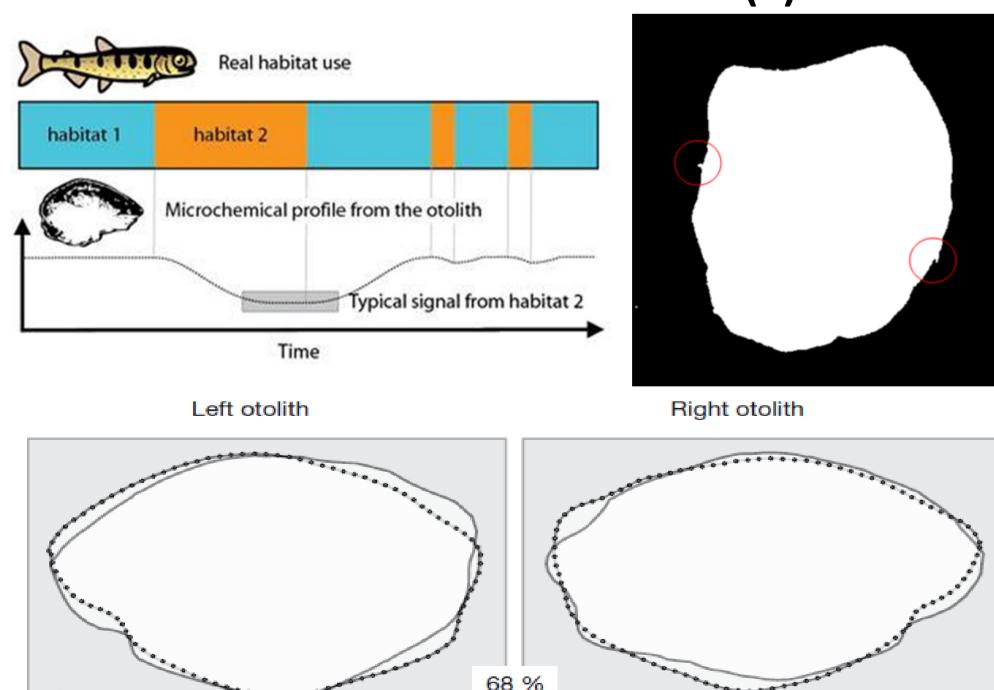


Fig. 5: Otolith shape and microchemistry concept and example of shape asymmetry between left and right otolith in Solea solea (figures from Vignon and Morat 2010)

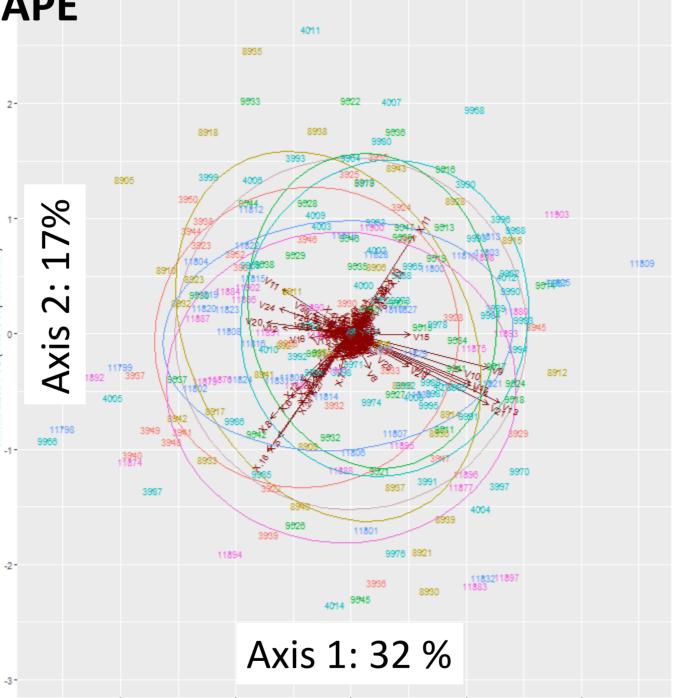
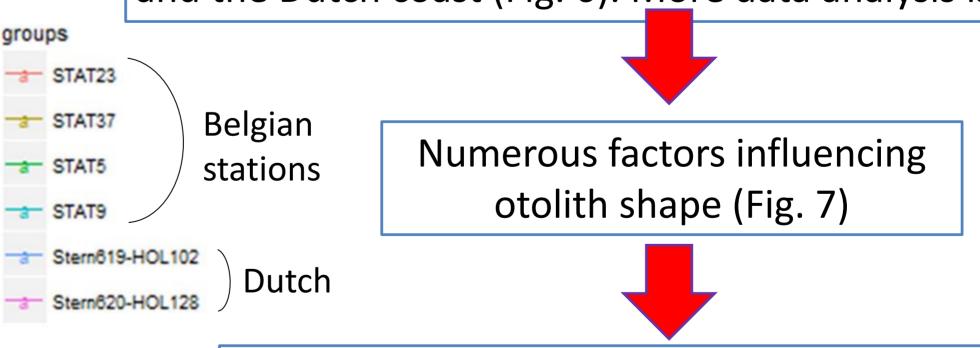


Fig. 6: Biplot of a Principal Component Analysis of otolith shape of juvenile sole described by 76 coefficients of Fourier series and each colour represents a sampling station

Otolith shape has became a common in fisheries to detect population structure. Fourier series are used to analyzed the outline of an otolith silhouette. Otolith shape of 300 juveniles from the Belgian and the Dutch coast is described by 76 coefficients of Fourier series. There are no significant differences in otolith shape of juvenile sole from the Belgian and the Dutch coast (Fig. 6). More data analysis is needed.



Combine several measures on the same individuals to increase assignment power.

GENETICS ONTOGENY

Fig. 7: Main factors influencing

otolith shape and otolith

microchemistry

There is no a priori knowledge on fish source population, so individual assignment to a spawning population requires Bayesian clustering.

Potential bias in otolith shape:

- Age of the fish => ontogeny
- Siblings => genetics

PERSPECTIVES



- Develop thousands of SNP markers using Next Generation Sequencing of part of the genome
- Select the markers that differentiate the spawning populations we want to trace the most

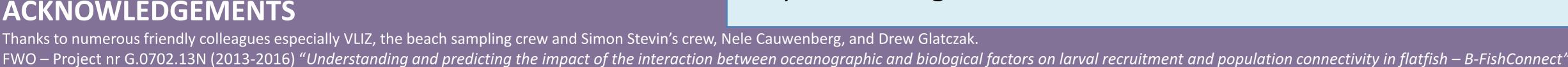
Trace fish movements with otolith microchemistry on the same populations

groups

- Age reading of larval and juvenile sole sagittae to determine dispersal pathways
- Select 15 chemical elements that differentiate the spawning populations we want to trace

OUTPUTS

- Spatial and temporal tracing of juvenile sole
- Increase enforcement capacity, detection of fraud and IUU fishing
- Improve management of stocks and certification of Marine labels to reward sustainable fishing







SEAFOOD

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