Basin-linked population genetic structure of turbot (*Psetta maxima*)

Vandamme S. G.[1,2], Maes G. E.[2], Moreau K. [1], Hoffman S. [1], Parmentier K. [1], Torreele E. [1], Delbare D. [1], Cooreman K. [1], Robbens J. [1] and Volckaert F.A.M.[2]

1 Institute for Agricultural and Fisheries Research (ILVO), Animal Sciences – Fisheries, Ankerstraat 1, B-8400 Ostend, Belgium

[2] Katholieke Universiteit Leuven, Laboratory of Animal Diversity and Systematics, Ch. Deberiotstraat 32, B-3000 Leuven, Belgium

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Introduction

The sea lacks clear physical barriers and fish have a large potential dispersal capacity
→ Weak or no population structure

A good understanding of the connectivity between fish populations is crucial for management of the stock & the evaluation of potential marine protected areas (MPA)

Genetic sampling includes collecting biological traits like length, weight, sex and tissue samples (fin clip and otoliths)

Turbot facts

➢ By-catch species
➢ Caught with bottom trawl, gill and trammel nets, longlines
➢ High commercial value
➢ No analytical assessment
➢ EC request analytical advise

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Aims & Methods

➢ Investigate connectivity among turbot (*Psetta maxima*) populations
➢ Evaluate the level of discreteness between the isolated Black Sea populations and other Mediterranean populations

Using a panel of 18 microsatellite markers (as well Type I as type II), we evaluated genetic diversity, differentiation and the relationship between populations
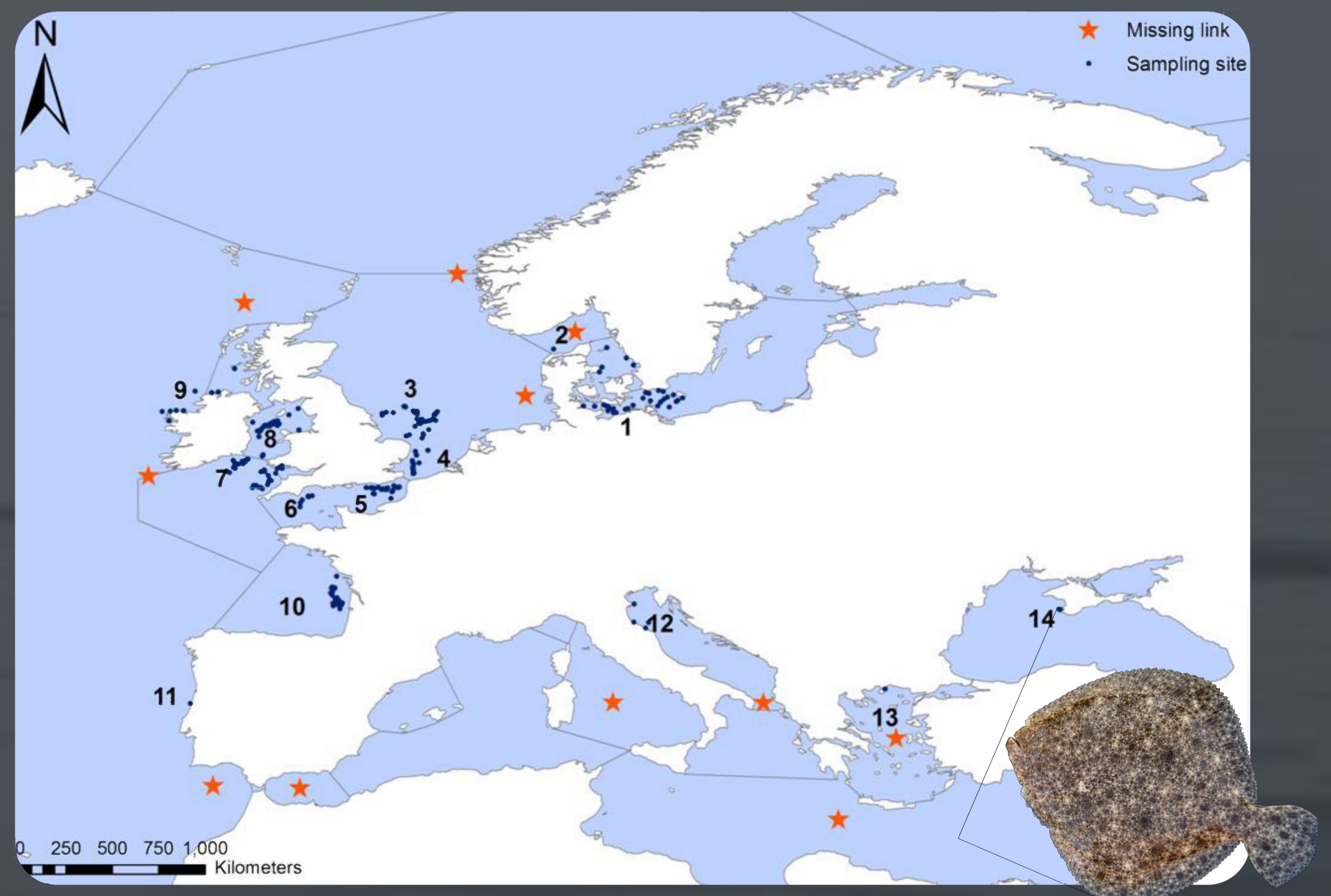
Geographical locations of all genotyped turbot samples, 1: Arkona Sea (n=54), 2: Skagerrak (n=12), 3: Central North Sea (n=137), 4: Southern North Sea (n=57), 5: Eastern English Channel (n=87), 6: Western English Channel (n=33), 7: Celtic Sea (n=136), 8: Irish Sea (n=161), 9: North & West Ireland (n=26), 10: Bay of Biscay (n=96), 11: Figueira da Foz (n=3), 12: Adriatic Sea (n=4), 13: Aegean Sea (n=2) and 10: Black Sea (n=47)

Results

➢ **Genetic variation of each populations**

| Population	N	H exp	H obs	MAR	FIS
Baltic Sea	54	0.5657	0.5698	4.51	0.00494
Cen North Sea	136	0.6011	0.6042	4.90	-0.00095
S North Sea	57	0.6003	0.5726	5.10	0.05584*
E English Channel	87	0.6126	0.6011	5.16	0.02542
W English Channel	33	0.6109	0.6278	5.02	-0.01084
Celtic Sea	135	0.6069	0.6154	5.03	-0.00988
Irish Sea	161	0.6121	0.6180	5.08	-0.00614
NW Ireland	26	0.6066	0.6452	5.09	-0.04373
Bay of Biscay	96	0.6019	0.5879	5.00	0.02927*
N Black Sea	47	0.4671	0.4702	3.66	0.00498

Number of individual per population (N), expected heterozygosity (Hexp), observed heterozygosity (Hobs), Mean allelic richness (MAR), mean FIS (inbreeding coefficient) per population, significant value are marked with * ($\alpha=0.05$)

Turbot has typical genetic profile: high genetic variation & low differentiation between population

➢ **Genetic differentiation between populations**
Global FST (fixation index) = 0.0242
→ based on pairwise FST
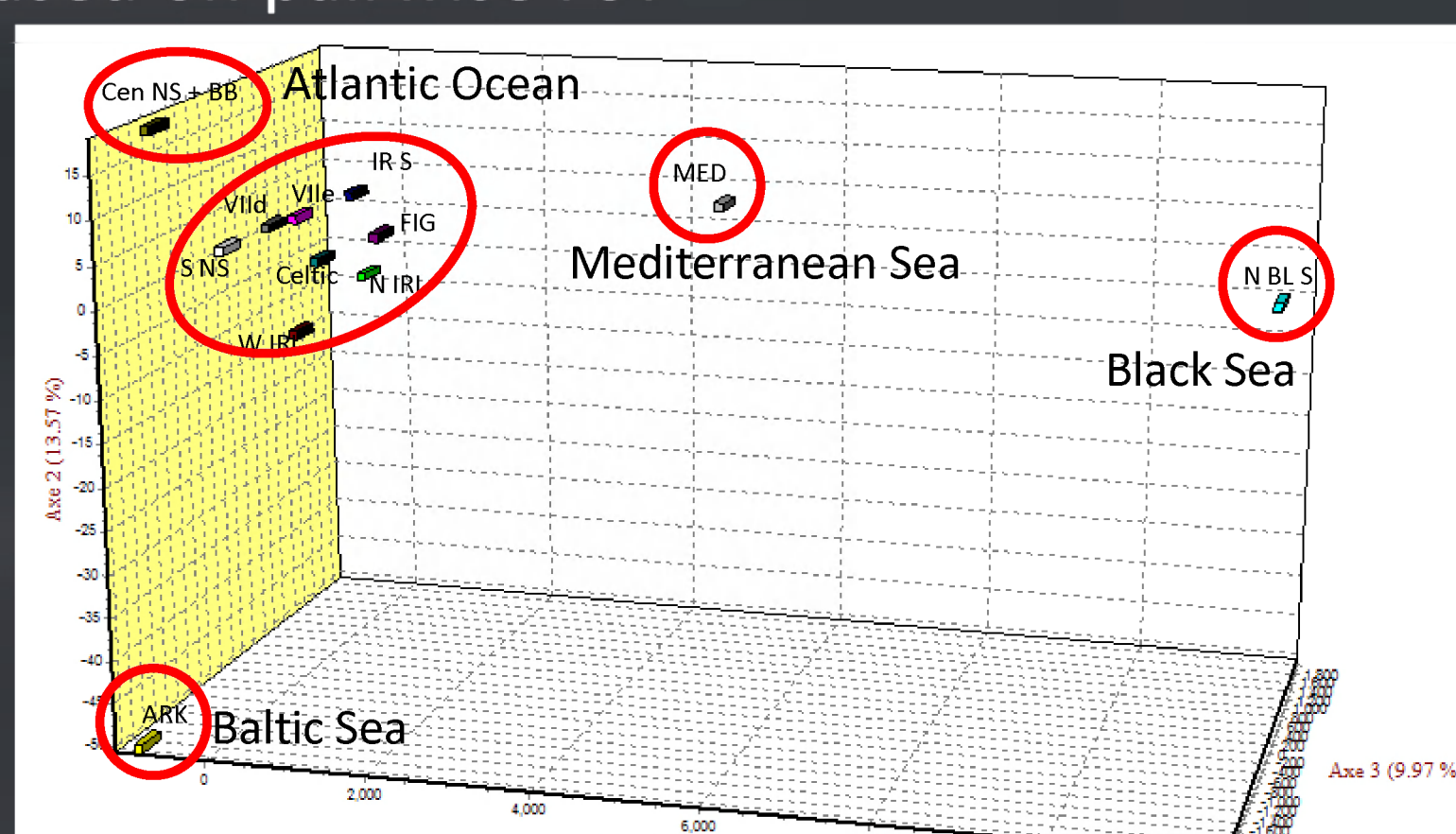
FCA-plot based on microsatellite analyses of 18 markers
50.87% of the variation is explained by the axes

Discussion & Conclusion

The Hobs and allelic richness are similar over all populations with exception of the Black Sea.
➢ Possible biological reasons inbreeding, bottleneck or overfishing

Pairwise FST reveals clear population differentiation:
➢ large scale differentiation:
• Atlantic vs Mediterranean
• Baltic & Black Sea populations differ from all the rest, most likely due to strong ecological & physical separation from neighboring populations
➢ Subtle small scale differentiation:
• Northeast Atlantic vs Central North Sea & Bay of Biscay
• vs Irish Sea (graph not shown)

Management

The historical demarcation of the ICES areas implies gross simplifications and assumptions on fish biology. The spatial organization of the true population structure, connectivity and life-history traits are not taken into account.

Combination with genetic & ecological data will allow to set up a management plan.

Future plans

➢ Increase the number of sampling sites & individuals
➢ Analyze the historical population structure
➢ Correlate with environmental factors
➢ Adaptive variation with gene-linked microsatellites
➢ Comparative study with other flatfish
➢ Proposal for sustainable management

Institute for Agricultural and Fisheries Research (ILVO), Animal Sciences – Fisheries

Corresponding author: ☎ +32(0)59/569896 📠 Sara.Vandamme@ilvo.vlaanderen.be

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