

**MENU****Aquaculture Europe 2017
Dubrovnik, Croatia****GENETICS STRUCTURE OF GILTHEAD SEA BREAM
Sparus aurata IN THE ADRIATIC SEA INFERRED
WITH MICROSATELLITE MARKERS**

I. Žužul*, T. Šegvić-Bubić, I. Talijančić, I. Mandić, L. Grubišić, I. Katavić and J. Maršić-Lučić

Institute of Oceanography and Fisheries, PO Box 500, Šetalište Ivana Meštrovića 63, 21000 Split, Croatia

E-mail: zuzul@izor.hr

Introduction

The two new standardised panel of microsatellite multiplex (SMsa1 and SMsa2, Lee-Montero et al. 2013) have been applied to detect genetic structure of the gilthead sea bream in the Adriatic Sea. Together with the European sea bass, gilthead sea bream is the leading mariculture species in the Mediterranean as well as in Adriatic, with important economic value. The aim of the study was to assess genetic differentiation among wild and farmed, sea bream assemblages in the eastern Adriatic Sea as well as to detect potential impact of aquaculture on the wild sea bream populations. Within wild fish populations, special attention was devoted to the aggregated seabream populations around tuna fish farms and juveniles of F₀ wild generation, aiming to identify potential introgressive hybridization.

Materials and methods

In order to investigate gilthead sea bream population structure of the different origins (i.e. wild, farm, farm associated and juveniles) a total of 1760 samples were collected along the Croatian coast. DNA obtained from fin-clips was used as a template in PCR reaction for two microsatellite multiplex. Allelic richness (A_r) and inbreeding coefficient (F_{IS}) were calculated using FSTAT v.2.9.3, number of alleles (A) and mean effective number of alleles across loci (A_e) were calculated using POPGENE v.132. The global F_{ST} value was calculated using ARLEQUIN version 3.5 (Excoffier & Lischer 2010). The software STRUCTURE v 2.3.4. was used for determining the optimal number of genetic clusters.

Results

The average number of alleles per loci (A) was the highest in the wild populations (13.0 ± 6.6), while for the farmed populations A ranged from 7.2 ± 2.8 to 12.2 ± 6.7 . The inbreeding coefficient (F_{IS}) was the highest in farmed population (0.11). Overall allelic richness (A_r) was 6.2 ± 2.0 while the effective number of alleles across loci (A_e) was 4.8 ± 4.5 . The

global F_{ST} value between all populations was 0.023, while among wild populations F_{ST} was 0.001. Bayesian clustering analysis and after application of the ΔK procedure (Evanno et al. 2005) suggested 7 clusters as the most likely number of populations (Figure 1).

Farm populations (F) were assigned to four different clusters (Cluster 1; Cluster 2; Cluster 4; Cluster 5) depending of the origin. Wild populations (W1 to W7) along the eastern Adriatic Sea showed to be genetically homogenous and were assigned to Cluster 6 with proportions of membership from 0.45 to 0.70. Populations of sea bream aggregated around tuna fish farms (A2; A3; A5) and juveniles (J1; J2; J3; J5; J6) showed similar assignment pattern and were composed by the mixture of two main clusters (Cluster 3 and 7).

Discussion and conclusion

The global F_{ST} value among all populations was relatively small (0.0234) and it was in line with already reported values for the Adriatic Sea (Šegvić-Bubić et al. 2011) where only few wild populations were analyzed in comparison to the present study. Moderate variations of global gene flow were observed in other studies from Mediterranean where Alarcón et al. (2004) and De Innocentiis et al. (2004) found values of $F_{ST} = 0.036$ and $F_{ST} = 0.01$. The overall F_{ST} value of wild populations from the present study was low (0.001) and below average for a group of marine fishes (0.062, Ward, 2006), suggesting populations homogeneity. In addition, wild populations aggregated around tuna fish farms formed separated clustering system, implying reduced gene flow toward the others wild populations. It seems that permanent food supply from tuna feed waste and more complex environment due to farm installations (FAD effect) can provide a new ecological niches for wild seabream populations.

Acknowledgments

This work has been fully supported by the Croatian Science Foundation under project number IP-2014-09-9050

References

- Alarcón J.A., A. Magoulas, T. Georgakopoulos, E. Zouros, and M.C. Alvarez. 2004. Genetic comparison of wild and cultivated European populations of gilthead sea bream (*Sparus aurata*). *Aquaculture* 230:65-80.
- De Innocentiis S., A. Lesti, S. Livi, A.R. Rossi, D. Crosetti, and L. Sola. 2004. Microsatellite markers reveal population structure in gilthead sea breams (*Sparus auratus*) from Atlantic Ocean and Mediterranean Sea. *Fisheries Science* 70:852-859.
- Dempster T., P. Sanchez-Jerez, J.T. Bayle-Sempere, F. Giménez-Casalduero, and C. Valle. 2002. Attraction of wild fish to sea-cage fish farms in the south-western Mediterranean Sea: spatial and short-term temporal variability. *Marine Ecology Progress Series* 242: 237-252.
- Evanno, G., S. Regnaut, and J. Goudet. 2005. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology* 14: 2611-2620.
- Excoffier L. and H.E. Lischer. 2010. Arlequin suite, version 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. *Molecular Ecology Resources* 10: 564-567.
- Lee-Montero I., A. Navarro, Y. Borrell, M. Garcia-Celdran, N. Martín, D. Negrin-Baez, G. Blanco, E. Armero, C. Berbel, M.J. Zamorano, J.J. Sanchez, A. Estevez, G. Ramis, M. Manchado, and J.M. Afonso. 2013. Development of the first standardised panel of two new microsatellite multiplex PCRs for gilthead seabream (*Sparus aurata* L.). *Animal genetics* 44:533-546.
- Šegvić-Bubić <<http://www.sciencedirect.com/science/article/pii/S004484861100487X>> T., I. Lepen <<http://www.sciencedirect.com/science/article/pii/S004484861100487X>>, Ž. Trumbić <<http://www.sciencedirect.com/science/article/pii/S004484861100487X>>, J. Ljubković <<http://www.sciencedirect.com/science/article/pii/S004484861100487X>>, D. Sutlović <<http://www.sciencedirect.com/science/article/pii/S004484861100487X>>, S. Matić-Skoko <<http://www.sciencedirect.com/science/article/pii/S004484861100487X>>, L. Grubišić <<http://www.sciencedirect.com/science/article/pii/S004484861100487X>>, B. Glamuzina

<<http://www.sciencedirect.com/science/article/pii/S004484861100487X>>, I. Mladineo
<<http://www.sciencedirect.com/science/article/pii/S004484861100487X>>. 2011. Population genetic structure of reared and wild gilthead sea bream (*Sparus aurata*) in the Adriatic Sea inferred with microsatellite loci. *Aquaculture* 318: 309-315.

Ward R.D. 2006. The importance of identifying spatial population structure in restocking and stock enhancement programmers. *Fish Resources* 80: 9-18.

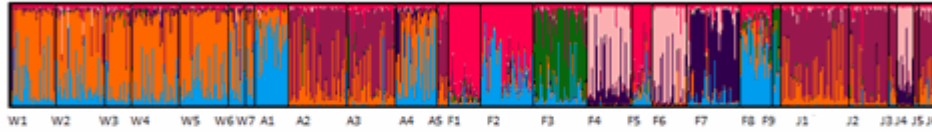


Fig. 1. Proportional membership of each individual of gilthead sea bream in 7 clusters identified by STRUCTURE.

<< Abstract Session
([SessionAbstracts.aspx?Session=102](#))

<< All Sessions
([Sessions.aspx](#))

Copyright © 2006 - 2018 EAS Online. All Rights Reserved.