

APRELIMINARY LINKAGE AND QTL ANALYSIS FOR JAW DEFORMITIES IN GILT HEAD SEABREAM

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Introduction

Morpho-anatomical abnormalities is a critical issue in terms of unpredictability, product quality and animal welfare that requires continuous awareness in fish production (Koumoundouros 2010). Anomalies could be developed due to unfavorable abiotic conditions, inappropriate nutrition, and genetic factors (Boglione et al., 2013). Hence, their early detection is long ago considered of immense importance and selective breeding is widely recognized as a key factor for the development of resource efficient, sustainable, and economically profitable aquaculture productions (FAO 1995). Recently, Fragkoulis et al. (2018) studied the genetic parameters of the upper-jaw abnormalities in gilthead seabream and showed a low range of heritability (0.01-0.22), especially the heritability of the Inwards bending (bMa) and Fusion (FMaPm) of the jaw, were 0.04 and 0.22, respectively. In the present study a preliminary analysis was performed to identify microsatellite markers, from two linkage groups, affecting the Inwards bending (bMa) and Fusion (FMaPm) of the jaw.

Materials and methods

Genomic DNA from 498 offspring was extracted using a selective genotyping strategy based on the total length and /or their high phenotypic variation of the deformities. The selected offspring belonged to 153 full sib families, from 53 dams and 45 sires. All fish were genotyped using the microsatellite loci in LG1 and LG21 which were described by Loukovitis et al. (2016). Alleles were sized and individuals were genotyped using the software STRand 2.4.110 (<http://www.vgl.ucdavis.edu/informatics/STRand>). Offspring at the age of 39 Days Post Hatching, were examined for Inwards bending (bMa) and Fusion (FMaPm) deformations, as described by Fragkoulis et al. (2018). The phenotypes were analyzed as binary data (1: Absent of deformation, 2: Presents of Deformation). For the Inwards bending (bMa) and Fusion (FMaPm), 28.7% and 26.31% of the offspring showed deformation, respectively. A de novo linkage analysis was performed using the options “prepare”, “build” and finally the “flipsn” of CRI-MAP v3.0 software (Green et al., 1990). The linkage distances were estimated assuming the Kosambi’s mapping function. Furthermore, Quantitative Trait Loci (QTL) analysis was performed in QXPAK 5.0 software (Pérez-Enciso and Miszta, 2011), using a maximum likelihood Variance Component Analysis with the presence of a polygenic component (pedigree-based animal model) and the QTL effect.

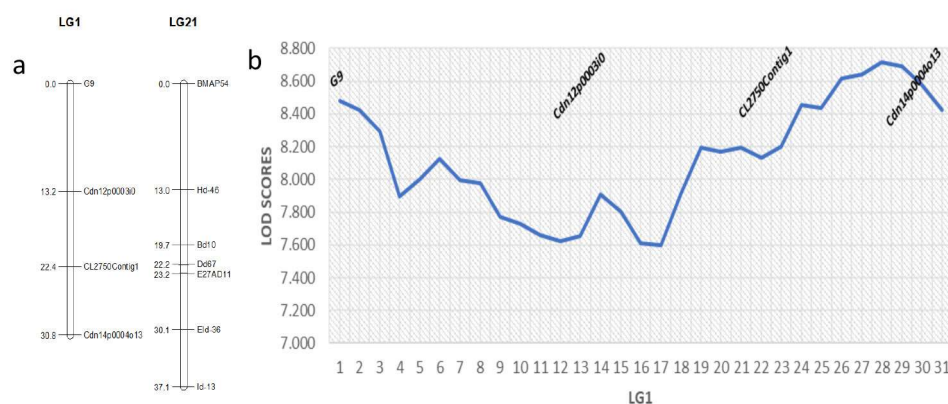


Fig 1 (a) Linkage groups 1 and 21 named according to Loukovitis et al. 2016 (b) Quantitative trait loci (QTL) analysis of bMa in LG1

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Results and Discussion

The markers were distributed into two linkage groups (LG1, LG21) named according to Loukovitis et al. (2016). The constructed map showed small differences between Loukovitis et al. (2016) and Tsigenopoulos et al. (2014). In our study, the length of the LG1 and LG21 were 30.8cM and 37.1cM while in Loukovitis et al. (2016) were 23.5cM and 17.2cM respectively. Focusing on QTL analysis, no QTL related to the Fusion (FMaPm) was found on neither of the linkage groups studied, even though, Fragoulis et al. (2018) estimated an inheritance of the trait equal to 0.22 using an animal model. On the other hand, a QTL related to Inwards bending (bMa) was detected on LG1 linked to *Cdn14p0004o13* and its heritability was 0.11. For the Inwards bending (bMa) the related QTL must be investigated deeply, in order to examine its presence and clarify its effect, using a higher sample size before it can be used in Marker Assisted Selection.

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