

A PRELIMINARY LINKAGE AND QTL ANALYSIS FOR JAW DEFORMITIES IN GILTHEAD 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).

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 of maxillaries with pre-maxillaries (**FMaPm**) of the jaw, were 0.04 and 0.22, respectively.

In the present study a preliminary analysis was performed to Ibending (**bMa**) and Fusion (**FMaPm**) of the jaw.

Materials and Methods

- Genomic DNA from 498 offspring (53 dams and 45 sires) was extracted using a selective genotyping strategy based on the total length and /or their high phenotypic variation of the deformities.
- 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.
- Offspring at the age of 39 Days Post Hatching, were examined for b-Ma and f-MaPm deformations, as described by Fragkoulis et al. (2018).
- The phenotypes were analyzed as binary data due to low representation in each of the originally formed categories
 - 1: Absent of deformation
 - 2: Presents of deformation

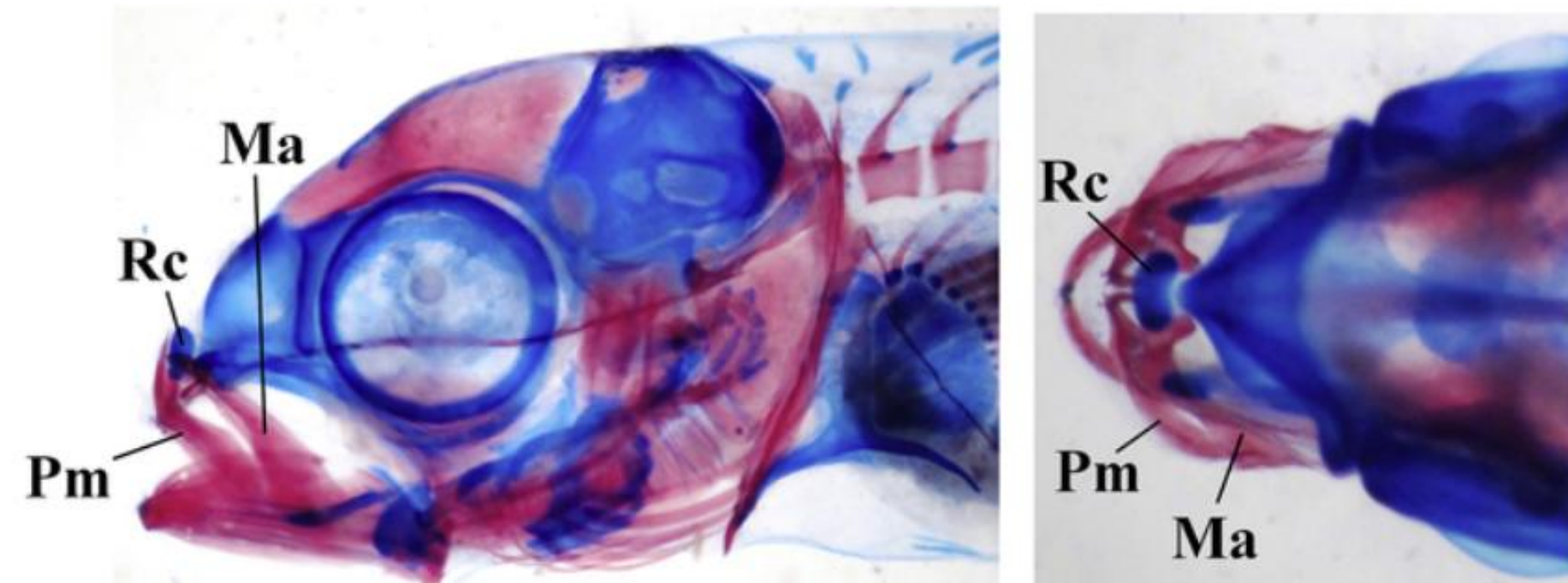


Fig 1 Position and normal anatomy of maxillaries (Ma), premaxillaries and rostral cartilage (Rc), on the left and top view in a seabream larva (9.5mm TL). Scale bars equal to 0.5mm

- 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.
- Quantitative Trait Loci (QTL) analysis was performed in QXPAK 5.0 software (Pérez-Enciso and Misztal, 2011), using a maximum likelihood Variance Component Analysis with the presence of a polygenic component (pedigree-based animal model) and the QTL effect.

Results and Discussion

For the **b-Ma** and **f-MaPm**, 28.7% and 26.31% of the offspring showed deformation, respectively.

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 **f-MaPm** was found on neither of the linkage groups studied, even though, Fragoulis et al. (2018) estimated a heritability of the trait equal to 0.22 using an animal model.

On the other hand, a QTL related to b-Ma was detected on LG1 linked to *Cdn14p0004o13* and its heritability was 0.11. For the b-Ma 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.

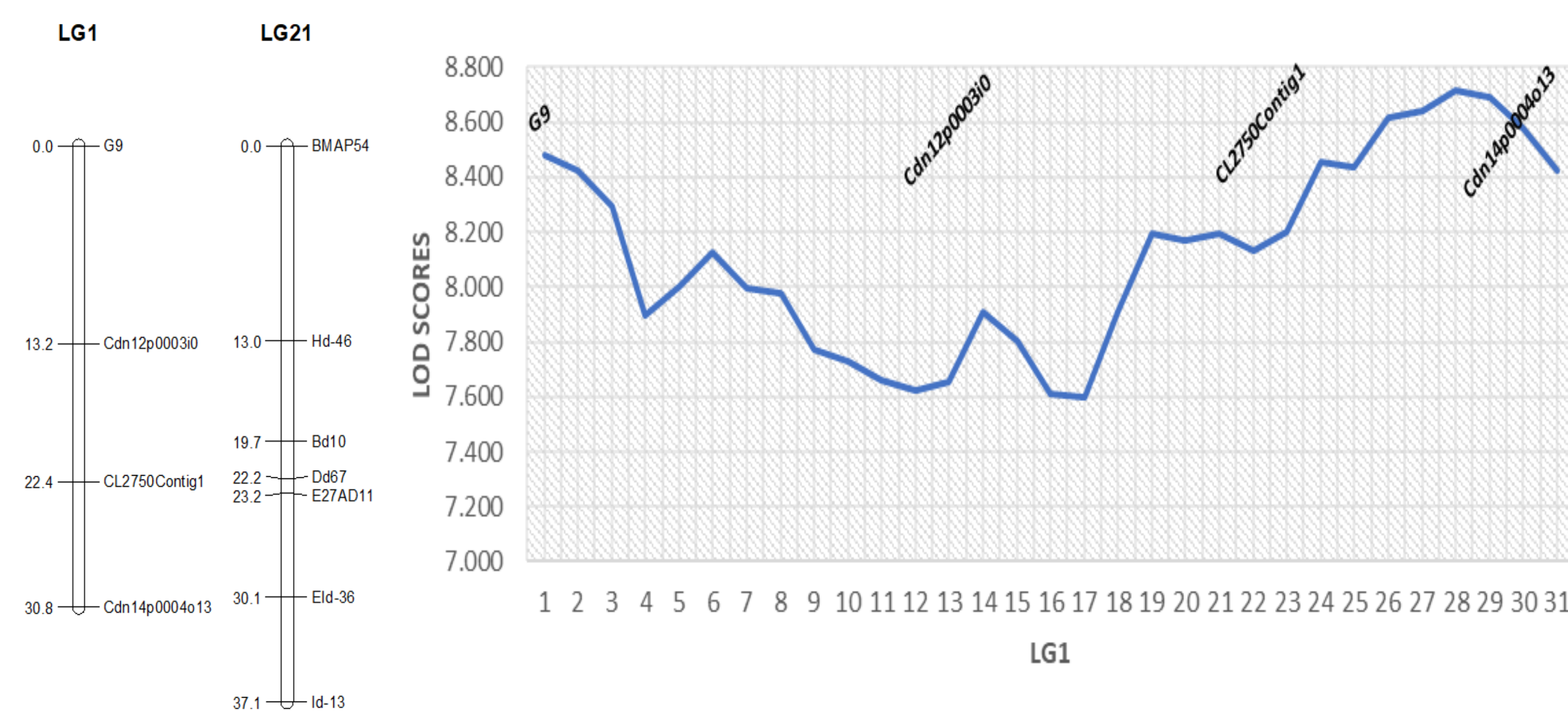


Fig 2 (a) Linkage groups 1 and 21 named according to Loukovitis et al. 2016 (b) Quantitative trait loci (QTL) analysis of bMa in LG1

Conclusions

Studying seabream larvae at the age of 39DPH, a QTL related to inbending was detected on LG1 and further research is conducted by increasing the sample size, in order to evaluate the present findings.

Acknowledgments

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