

ESTIMATION OF GENETIC PARAMETERS AND GENOME WIDE ASSOCIATION ANALYSIS (GWAS) FOR HEAD SIZE IN MEAGRE *Argyrosomus regius*

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Introduction

Meagre is a relatively new species in Mediterranean aquaculture industry, and it is considered a fast-growing sciaenid with an increasing commercial importance.

Recently, the genome of the meagre became available (Papadogiannis et al., 2023), therefore methods which have been utilized in other Mediterranean species, such as GWAS, are becoming achievable and are expected to advance selective breeding in the species.

The aim of the present study is to investigate the inheritance and genetic architecture of the head size as well as its relationship with the body weight in meagre.

Materials and Methods

762 fish at the age of 770 days-post-hatching (DPH) were weighed and a digital picture for each fish was taken.

The images were used to analyze body shape, head centroid size (HCS, as a ratio to the overall centroid size) by means of geometric morphometrics.

Apart from the phenotype, fin-clips were collected for each fish.

Samples were genotyped using the double-digest random amplified DNA (ddRAD) methodology.

After quality control and use of the available genome information, 4,573 SNPs remained.

The genomic heritability of the HCS and the genomic correlation with the body weight were estimated using maximum likelihood methods with the AIREMLF90.

To analyze the body weight at 770 DPH, the body weight at 394 DPH was used as a covariate in the analyses.

Furthermore, a univariate GWAS for the HCS was performed to identify associated QTL using the GEMMA.

An alternative Bonferroni correction was performed in which the 0.05 and 0.01 were divided with the independent SNPs only and the haplotype blocks instead of the total number of SNPs (Nyholt, 2004).

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References

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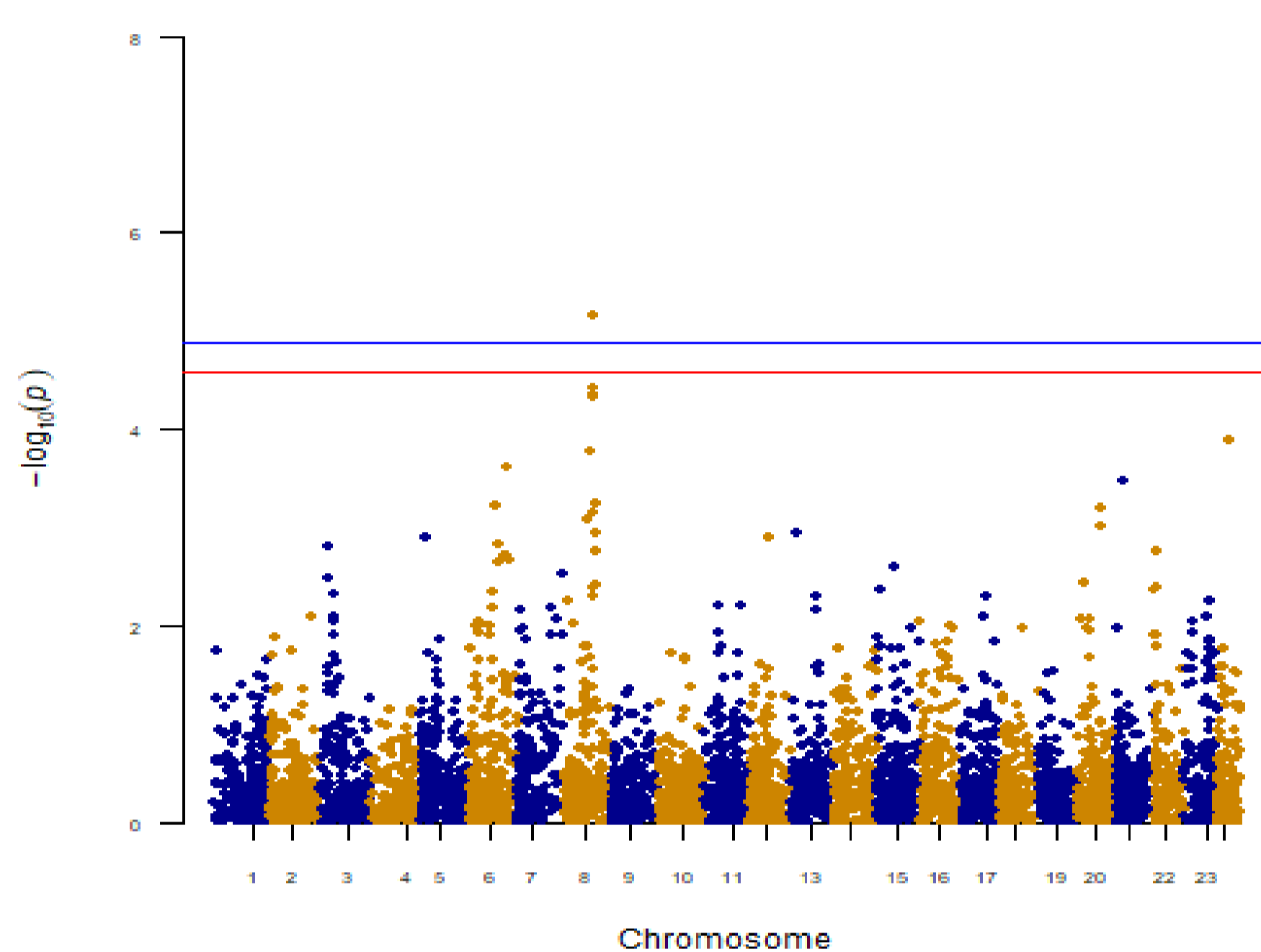


Fig 1. Manhattan plot for head size (HCS). The blue (initial value 0.05) and the red line (initial value 0.1) illustrate the threshold after the alternative Bonferroni correction (at the genomic level).

Results

- A high genomic heritability of the head size [0.49 ± 0.06]
- A high genomic correlation [0.86 ± 0.04] with the body weight were found.
- A QTL on chromosome 8 was detected, which explains approximately 2.62% of the total phenotypic variance of the HCS (Fig. 1).

Discussion

The present findings suggest that the head size (HCS) is a heritable trait but given its high positive genetic correlation with the body weight, any potential selection towards the reduction of the head size is expected to negatively influence its body weight.

Therefore, given the verification of the reported QTL a Marker Assisted Selection scheme might be very beneficial in a future breeding program for meagre.