



SUMMARY

This output describes the first successful parentage assignment in meagre at an industrial scale production system - over 90% on average. The results support the development of novel genetic approaches for meagre, to identify genomic regions associated with differential growth. This could lead to a more sustainable breeding programme with less variability in size and growth in farmed meagre.

KNOWLEDGE NEED

Meagre (*Argyrosomus regius*) is a relatively newly farmed species with great potential in large-scale European aquaculture. One of the major hurdles in successfully establishing a fish industry is variability in growth of farmed fish of the same age. Reducing variables such as these has thus become a highly desirable objective in fish breeding programmes.



POTENTIAL IMPACT

The aquaculture industry is expected to benefit from this first description of parentage in meagre production, particularly in the following ways:

- A genetic tool (a ten-microsatellite loci multiplex) is described, and can be used to assess the genetic variability and parentage assignment in the species.
- Less variability in size and growth leading to a more profitable meagre farming sector.
- Assistance with the identification of genomic regions associated with differential growth in the species, which will provide the necessary tools for marker-assisted and genomic selection.
- Development of a successful breeding programme for meagre to produce same-sized fish.

EATiP - Strategic Research and Innovation Agenda (SRIA) Thematic Area 3 - Managing the Biological Lifecycle; Goal 2. To see the full list and descriptions of the thematic areas and goals, please visit: eatip.eu/?page_id=46

UNDERLYING SCIENCE

A total of 800 meagre fish were sampled from two large cages in January and May 2016, both part of a commercial farm site in Valencia, Spain. All fish originated from the same spawning event obtained from a broodstock of 6 females and 13 males. However, due to differential growth during the juvenile stage, the fish were graded into two groups. A group of larger juveniles was transferred to one cage (batch 1) and a group of smaller juveniles was transferred to a second cage (batch 2). Heritability estimates for body weight and total body length were calculated, as well as the genetic correlation estimates for these two traits.

RESULTS

- Successful parentage assignment using the multiplex tool was 91 % for both batches analysed.
- Female and male broodstock do not contribute equally to offspring; this is also the same for fish injected with gonadotropin-releasing hormone agonists (GnRHA) and those that weren't.
- It was established that heritability estimates for body weight and total body length were different in the offspring of the different families that were analysed. Batch 1 showed higher heritability estimates than batch 2. Genetic correlation estimates were almost the same for both batches.
- Results indicate that, among the fifteen shared families in the two batches, there is some substantial, statistically significant, variation within families, with three families showing variation for weight and two for length.

END-USERS & POTENTIAL APPLICATIONS

END-USER 1: Aquaculture geneticists

APPLICATION: The results of this research will provide useful indications of novel future approaches concerning Quantitative Trait Locus (QTL) research for growth-related traits in meagre.

END-USER 2: Meagre farmers

APPLICATION: In the future, the identification of genomic regions associated with differential growth in the species will provide the necessary tools for marker assisted and genomic selection. Farmers can then produce same-age meagre with less variability in size.

STATUS

Technology Readiness Level (TRL) 2 – technology concept formulated

- A genetic linkage map for the species will soon be available, resulting from the application of the ddRAD (double-digest Random Amplified DNA) methodology on fish from selected families reported in the corresponding published paper (details below). The construction of a high-quality linkage map and future mapping of trait-related quantitative trait loci (QTL) is required as a foundation for implementation of Marker Assisted Selection (MAS) in any species.

AT A GLANCE

TITLE: Parentage assignment in meagre

KNOWLEDGE TYPE: Scientific publication

WHERE TO FIND IT: Nousias, *et al.* (2020). Parentage assignment, estimates of heritability and genetic correlation for growth-related traits in meagre *Argyrosomus regius*. *Aquaculture* 518;734663. DOI: 10.1016/j.aquaculture.2019.734663

STATUS: Published. More research in this area is required.

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PATENTS OR OTHER IPR EXPLOITATIONS: No