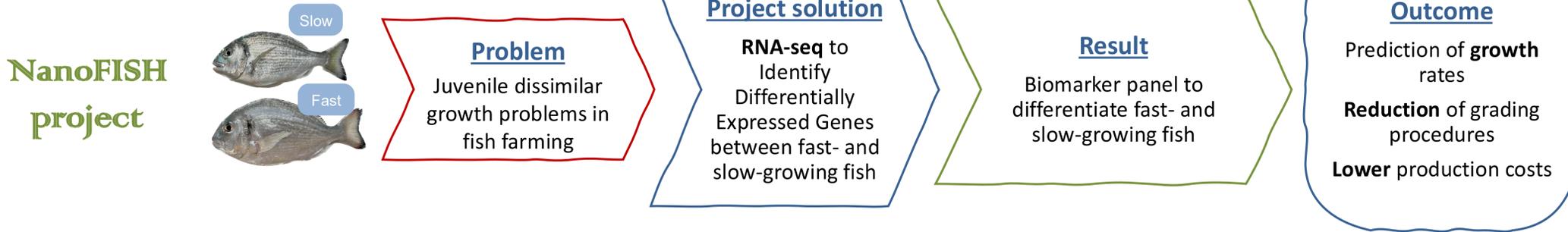# Uncovering Growth Variability in Gilthead Seabream (*Sparus aurata*) through Muscle Transcriptomic Profiling

Morgana Angelo[1]*, Marisa Barata[2], Mafalda Rocha[1], Pedro Pousão-Ferreira[1,2], Iris A.L. Silva[1#], Cátia Lourenço-Marques[1,2#]
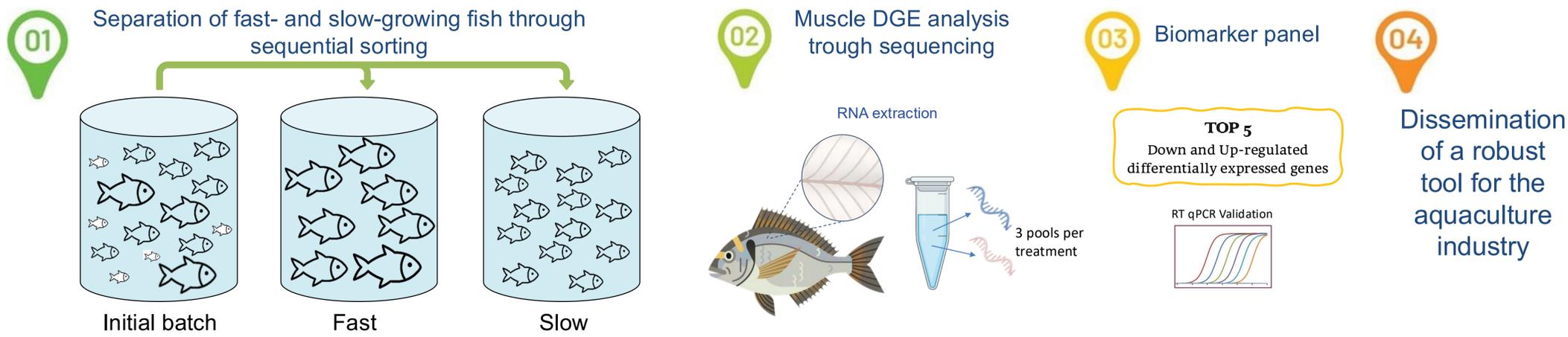
\# These authors contributed equally. * morgana.angelo@s2aquacolab.pt

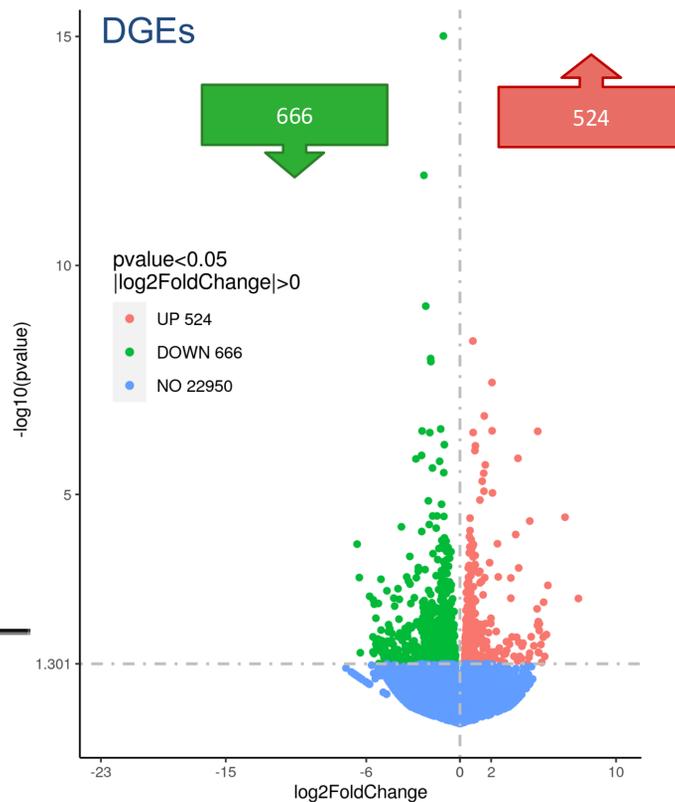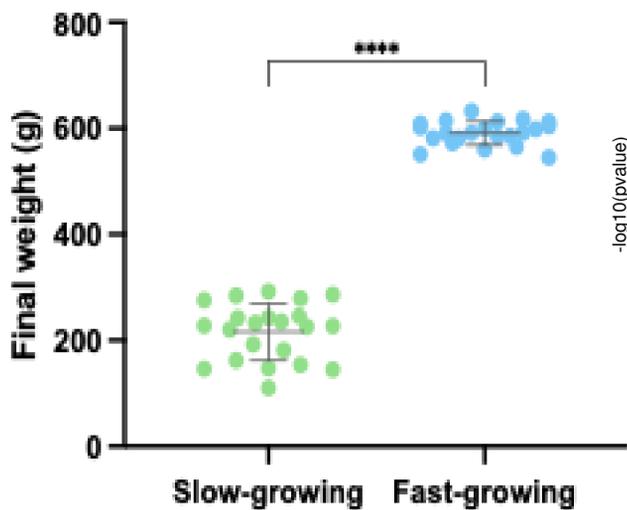1 S²AQUA — Laboratório Colaborativo Sustainable and Smart Aquaculture

2 IPMA — Instituto Português do Mar e da Atmosfera

Overview

NanoFISH project

Slow / Fast

Problem — Juvenile dissimilar growth problems in fish farming

Project solution — RNA-seq to Identify Differentially Expressed Genes between fast- and slow-growing fish

Result — Biomarker panel to differentiate fast- and slow-growing fish

Outcome — Prediction of **growth rates**. **Reduction** of grading procedures. **Lower** production costs

Methodology

01 Separation of fast- and slow-growing fish through sequential sorting

Initial batch / Fast / Slow

02 Muscle DGE analysis trough sequencing

RNA extraction — 3 pools per treatment

03 Biomarker panel

TOP 5 Down and Up-regulated differentially expressed genes

RT qPCR Validation

04 Dissemination of a robust tool for the aquaculture industry

Results

Growth

DGEs

666 (DOWN) 524 (UP)

pvalue<0.05
|log2FoldChange|>0

- UP 524
- DOWN 666
- NO 22950

TOP 5

tmprss9	Muscle tissue remodelling	Reduced ECM stiffness	*mfap4*
nlrp12	Suppress excessive inflammation	Protein synthesis	*dhys*
dpy30	Marker of active transcription	Protein synthesis	*mdn1*
ctxn3	High metabolic efficiency	ECM interactions, immune responses	*lgals3*
znf608	High metabolic efficiency	Metabolic signalling	*gpr12*

Final remarks

→Key genes and regulatory networks linked to **growth performance** were identified

→**Potential** biomarkers for predicting growth rate in aquaculture

https://sciforum.net/event/IOCAN2026