

# TRANSCRIPTOMIC ANALYSIS OF SKIN RESPONSE TO *Tenacibaculum maritimum* INFECTION IN EUROPEAN SEABASS FED DIETARY METHIONINE SUPPLEMENTATION

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## INTRODUCTION

The essential amino acid **methionine** plays pivotal roles in several physiological processes, from growth to immune function

Dietary methionine supplementation has been shown to **improve cell immunity and disease resistance in fish**

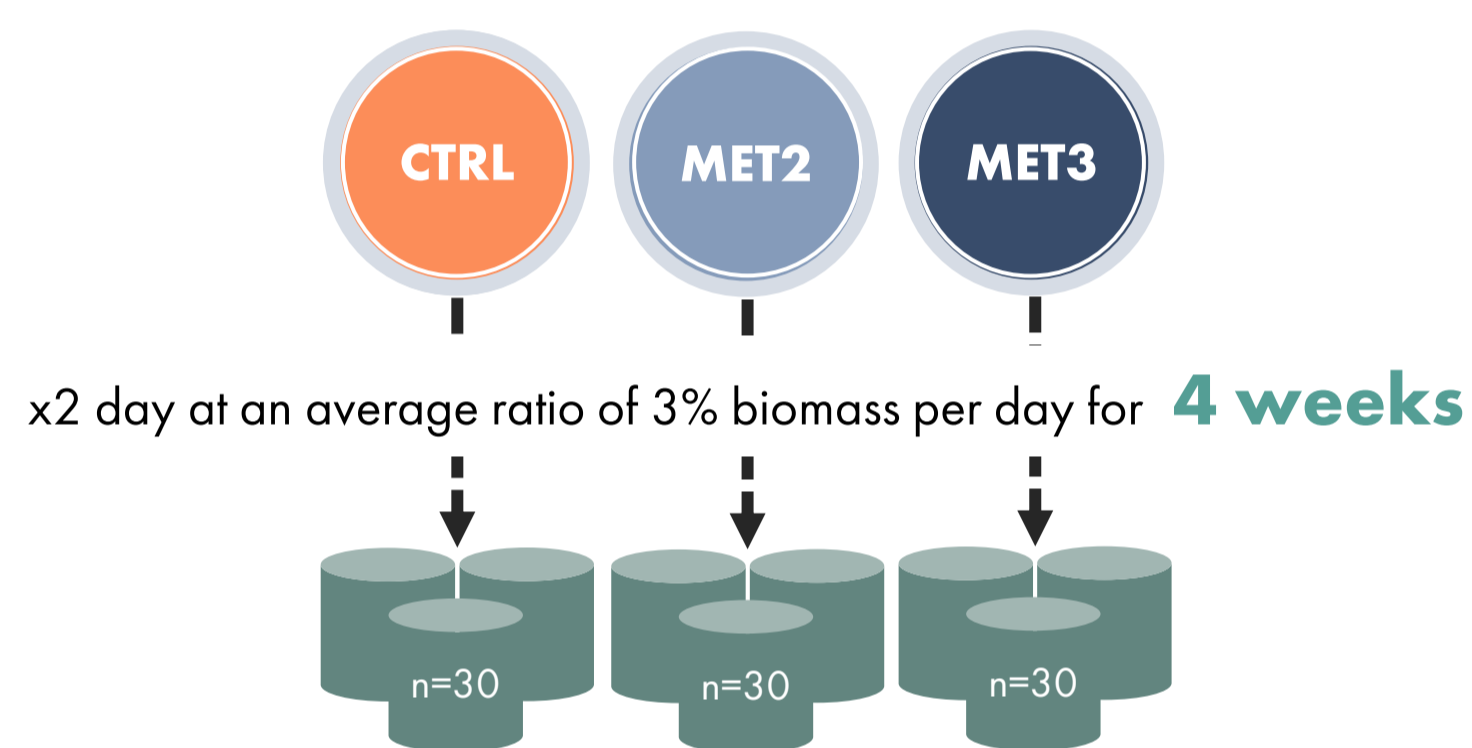
Its **impact on mucosal tissues**, particularly the skin, remains poorly explored

**To investigate the effects of graded levels of methionine surplus on the skin tissue transcriptomes of European seabass (*Dicentrarchus labrax*) upon infection with *Tenacibaculum maritimum***

## MATERIAL & METHODS

European seabass juveniles ( $5.19 \pm 0.65$  g) were fed:

- Commercial diet (**CTRL**)
- CTRL supplemented with 1.9% methionine (**MET2**)
- CTRL supplemented with 2.9% methionine (**MET3**)



**T0 h** (after the 4 weeks feeding trial)  
**T. Maritimum** (strain ACC13.1) **bath infection**  
 (2 hours, 24 °C, strong aeration)

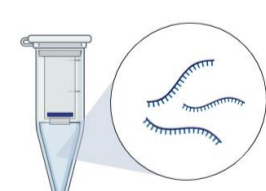
**T24 hpi\*** **Time-course trial**  
 3 fish per tank (n=9)  
**T48 hpi\***

**Mortality**  
 recorded daily for 1 week

\* hpi hours post-infection

**Skin tissue** samples were collected from 3 fish per tank and pooled within each tank

① RNA extraction



n=3

② RNA sequencing



Illumina PE150

③ Differential expression analysis

Infected dietary groups were compared with the CTRL group before infection using R/DESeq2 package v1.28.1

( $p$ -value < 0.01, |Log2 Fold Change|  $\geq$  2)

Gene Ontology (GO) enrichment analysis was performed on g:Profiler

(Benjamini-Hochberg False Discovery Rate (FDR)-corrected  $p$ -value < 0.05)

## RESULTS & DISCUSSION

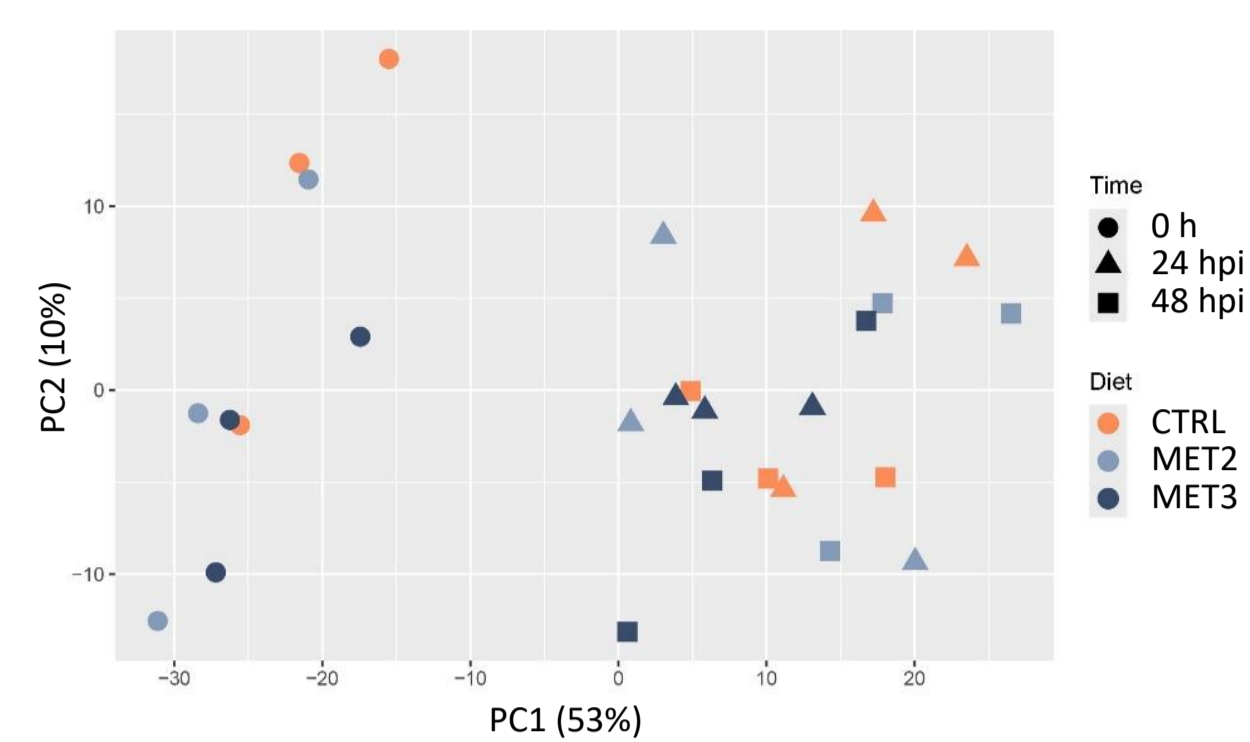


Fig.1 Principal component analysis showing the clustering of RNA-seq data

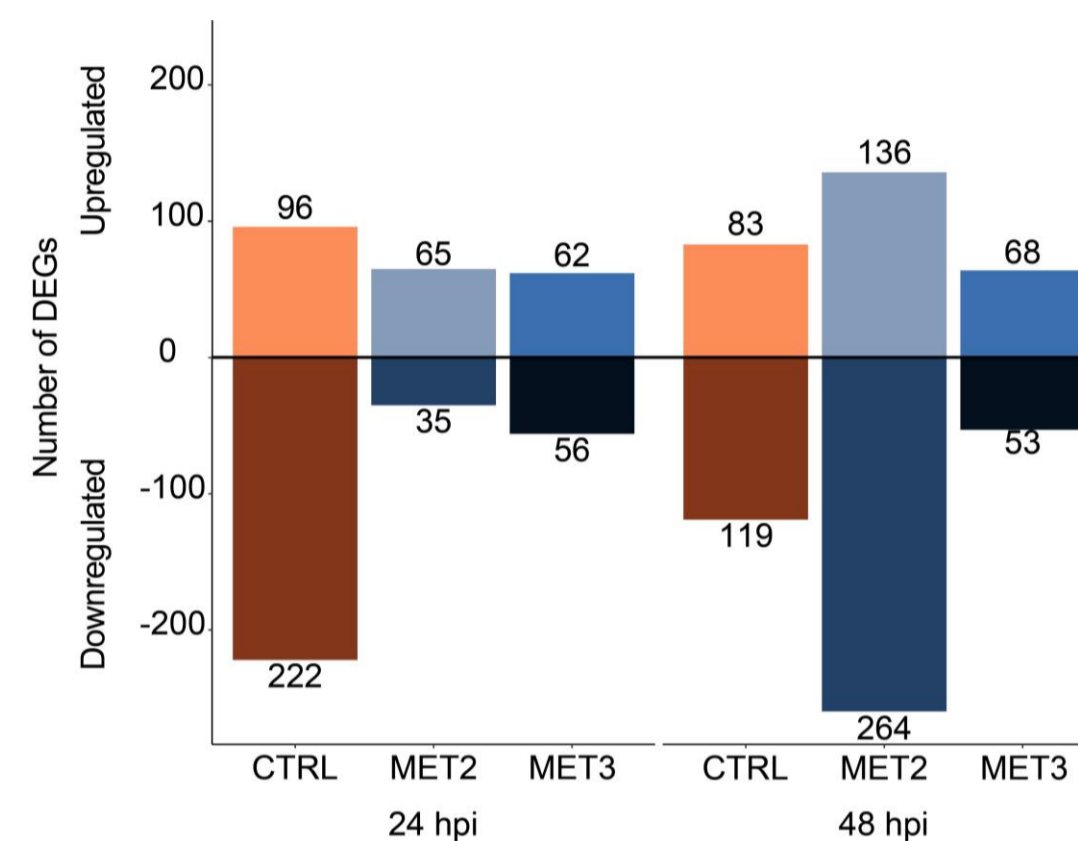


Fig.2 Diverted stacked bar chart of the number of differentially expressed genes (DEGs)

- The exposure to *T. maritimum* elicited a local response in the skin of all dietary groups

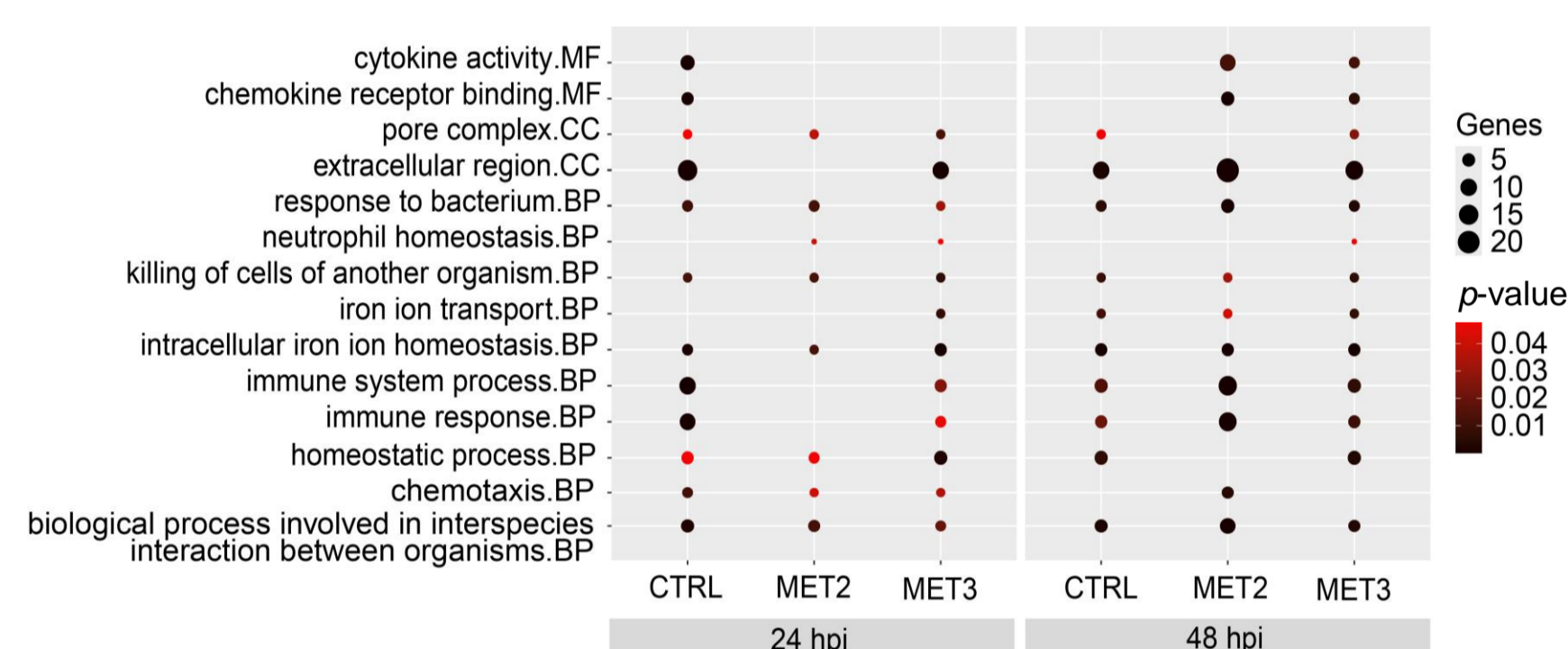


Fig.3 Bubble chart of the gene ontology enrichment analysis in up-regulated DEGs

- The CTRL group exhibited the strongest pro-inflammatory response at 24 hpi
- The initially attenuated immune response in the MET2 group was replaced by the most intense one at 48 hpi

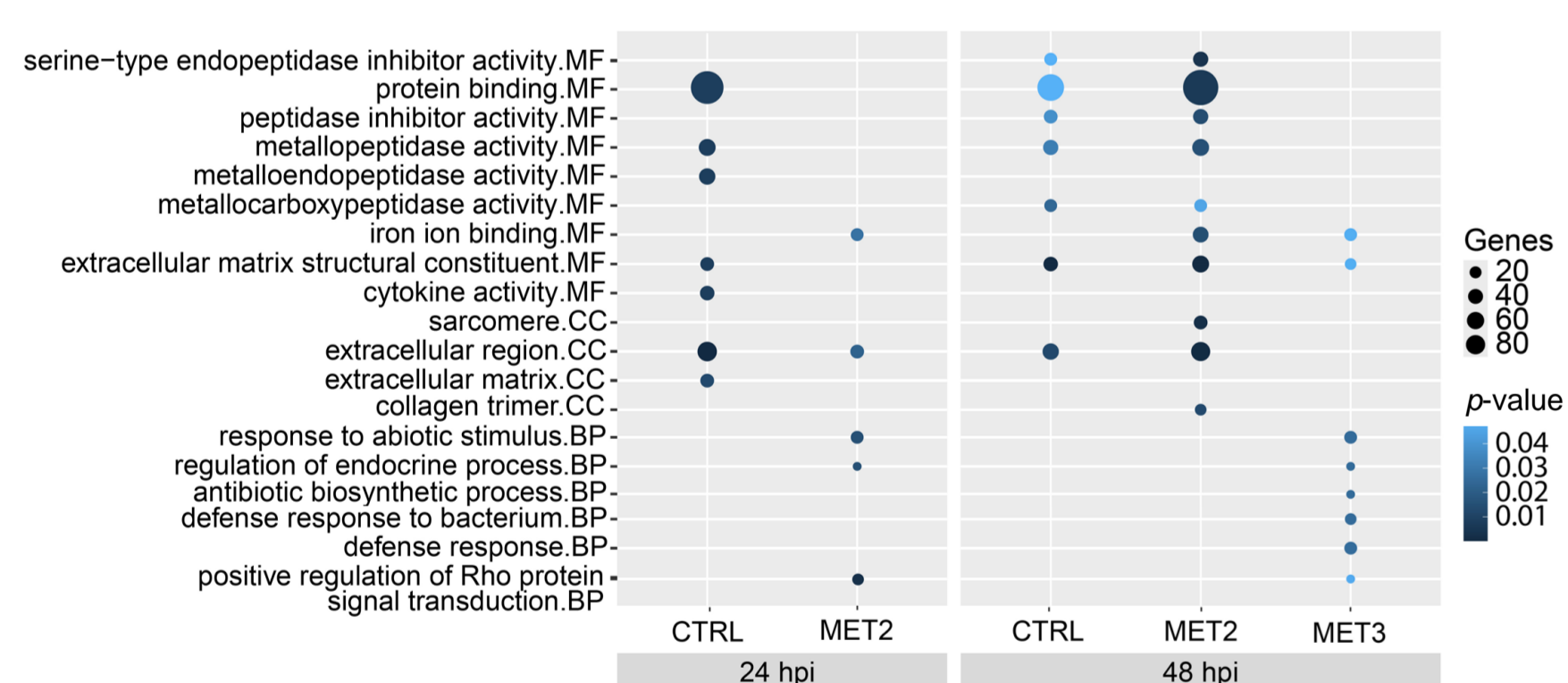


Fig.4 Bubble chart of the gene ontology enrichment analysis in down-regulated DEGs

- The down-regulation of transcripts associated with the immune response suggested an impaired response to infection in the MET3 group at 48 hpi
- Cumulative mortality was higher in the MET3 group (95%) compared to the other groups (85%) (statistically non-significant)

## CONCLUSION

The **delayed pro-inflammatory response of the MET2 group and the down-regulation of immune-related transcripts in the MET3 group, coupled with higher mortality, highlight the need for further investigation into potential adverse effects associated with elevated methionine intake**

## ACKNOWLEDGMENTS

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