

Meta-analysis of QTL regions associated with pathogen resistance in rainbow trout

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INTRODUCTION & AIM

Rainbow trout (*Oncorhynchus mykiss*) is among the most widely farmed freshwater fish species, with a global production of about **900,000 tonnes annually** (FAO, 2024). Despite its economic importance, this species remains **highly susceptible to multiple infectious diseases**, posing major challenges to fish welfare and causing substantial production losses in aquaculture systems (Kania & Buchmann, 2025).

Genetic improvement through **quantitative trait loci (QTL) mapping** has proven effective in identifying genomic regions linked to disease resistance (Buchmann, 2022). Nevertheless, discrepancies among studies, together with variations in map quality and marker density, often hamper the detection of consistent QTLs across traits and experiments.

To overcome these limitations, **meta-analysis approaches**, supported by mathematical modelling, have emerged as a powerful means to integrate findings from multiple studies, thereby enhancing the **accuracy and robustness of QTL localization** (Kaur et al., 2023).

To our knowledge, this work presents the **first meta-analysis of pathogen resistance QTLs in rainbow trout**, addressing a key knowledge gap and providing novel insights relevant to the advancement of **disease-resistant breeding programs** in aquaculture.

MATERIAL AND METHODS

A thorough **review of studies** conducted over the past two decades that identified **QTLs** linked to pathogen resistance in rainbow trout.

The **consensus map** used for the meta-QTL analysis was generated with the **R package “LPmerge”**, integrating data from six genetic maps.

Projection of QTLs onto this consensus map. 95% of Confidence Intervals (CI) were calculated by:

- **F2 and BC** : CI (95%) = $530/(R^2 \times N)$
- **DH**: CI (95%) = $287/(R^2 \times N)$

where R^2 is the phenotypic variance explained by the individual QTL and N is the population size.

Meta-QTL analysis was conducted separately for each chromosome using **Biomeqator v4.2.3**, applying the **Goffinet & Gerber** method when **≤10 QTLs** were available and the **Veyrieras et al.** method when **>10 QTLs** were detected.

RESULTS

A total of **138 QTLs** related to pathogen resistance traits were compiled for the **meta-QTL analysis**. The number of QTLs per chromosome ranged from **1 to 21**, showing an uneven genomic distribution. Most of these QTLs originated from 32 studies on resistance to ***Flavobacterium psychrophilum***, although others were associated with **VHSV**, ***M. cerebralis***, **IPNV**, and **IHN** (Fig. 1A). The **phenotypic variance explained** by individual QTLs ranged from 2% to 72%, with an **average of 15.16%**, indicating the contribution of both major and minor loci to pathogen resistance (Fig. 1B).

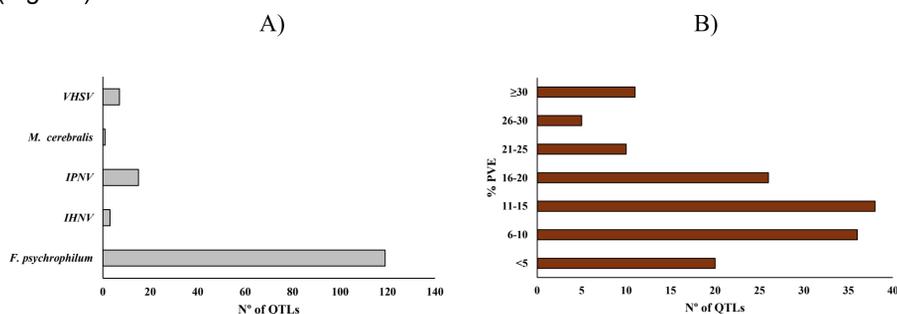


Fig. 1. Summary of QTLs associates with pathogen resistance. A) Distribution of initial QTL associated with pathogen resistance traits; B) % PVE of the initial QTLs

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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The high-density rainbow trout **consensus map** generated in this study, based on six genetic maps, achieved an average marker density of **2.84 markers per cM** across the genome. On average, **513 markers** were positioned per chromosome. Of the **138 QTLs collected**, 101 (73.19%) were successfully projected onto the newly constructed consensus map.

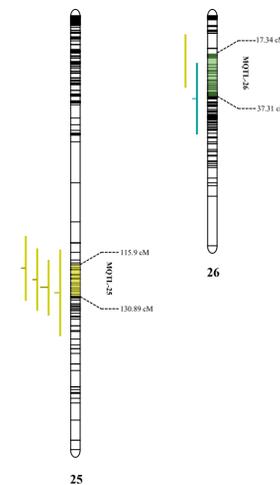


Fig. 2. Schematic representation of the distribution of projected QTLs and MQTLs on chromosomes 25 and 26, associated with pathogen resistance traits. Bars on the left side of each chromosome indicate QTLs related to BCWD resistance (green bars) and IPNV resistance (blue bars). Black bars within the chromosomes represent marker density. The chromosome map shows the MQTLs identified in this study and their co-location: light green indicates MQTLs formed by only one type of pathogen resistance QTL, while dark green indicates MQTLs formed by two different types of pathogen resistance QTLs.

The **Gerber and Goffinet** method was applied for the meta-analysis of QTLs on all chromosomes, except **chromosomes 3 and 8**, where the **Veyrieras** approach was implemented. In total, **26 meta-QTLs (MQTLs)** associated with pathogen-resistance traits were identified. Among them, **22 MQTLs** were exclusively linked to ***Flavobacterium psychrophilum***, while **four (MQTL 3.1, MQTL 12.1, MQTL 22, and MQTL 26)** were associated with both ***F. psychrophilum*** and **IPNV** (Fig. 2).

DISCUSSION

The **genetic basis of pathogen resistance** has been widely investigated, supported by the increasing availability of molecular markers, reduced genotyping costs, and significant progress in QTL mapping technologies (Huang et al., 2025). In this study, we examined QTLs associated with **disease resistance** in rainbow trout, focusing on key infections such as BCWD, IHN, and IPN. The **stability of QTLs** can vary depending on the genetic background, environmental conditions, and population structure. To **overcome** this variability, meta-QTL analysis enables the detection of consistent and robust QTLs by combining information from multiple independent studies (Kaur et al., 2023).

To our knowledge, this work represents the **first meta-analysis of pathogen-resistance QTLs in *O. mykiss***. Our findings highlight ***Flavobacterium psychrophilum*** as the most recurrent pathogen associated with QTLs for disease resistance. Moreover, **four MQTLs** were identified as **key genomic hotspots** potentially involved in resistance to multiple pathogens. These consensus regions consolidate evidence across studies and provide valuable targets for further investigation.

CONCLUSION

- This **meta-analysis** highlights the importance of **integrating** data from multiple studies to pinpoint genomic regions linked to pathogen resistance in **rainbow trout**.
- The identification of **26 MQTLs** offers a solid foundation for designing more precise and efficient selective **breeding strategies** in aquaculture.
- Flavobacterium psychrophilum*** was identified as the main **target** for genetic improvement in rainbow trout.
- The discovery of **genomic hotspots** for **disease resistance** enables for **functional genomics** research and the development of **disease-resistant** rainbow trout, advancing sustainability in aquaculture.

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