

GENOME-WIDE ASSOCIATION MAPPING OF HOST GENETIC POLYMORPHISMS ON VACCINE-INDUCED SCUTICOCILIATOSIS DISEASE RESISTANCE IN OLIVE FLOUNDER

Paralichthys olivaceus

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Background

Scuticociliatosis, a catastrophic parasitic disease instigated by the scuticociliate, *Miamiensis avidus*, in olive flounder aquaculture leads to significant morbidity and mortality. Vaccination stands as a pivotal and reliable strategy in disease management, supplanting conventional therapeutic methods fraught with limitations. Concurrently, efforts in selective breeding to bolster disease resistance in olive flounder stocks are ongoing, contingent upon challenge tests with unvaccinated cohorts. However, the genetic predisposition to the infection may be influenced by the vaccination status, prompting an exploration into the genetic diversity underlying resistance. This study pioneers in scrutinizing the genetic basis of resistance to scuticociliatosis post-vaccination in olive flounder.

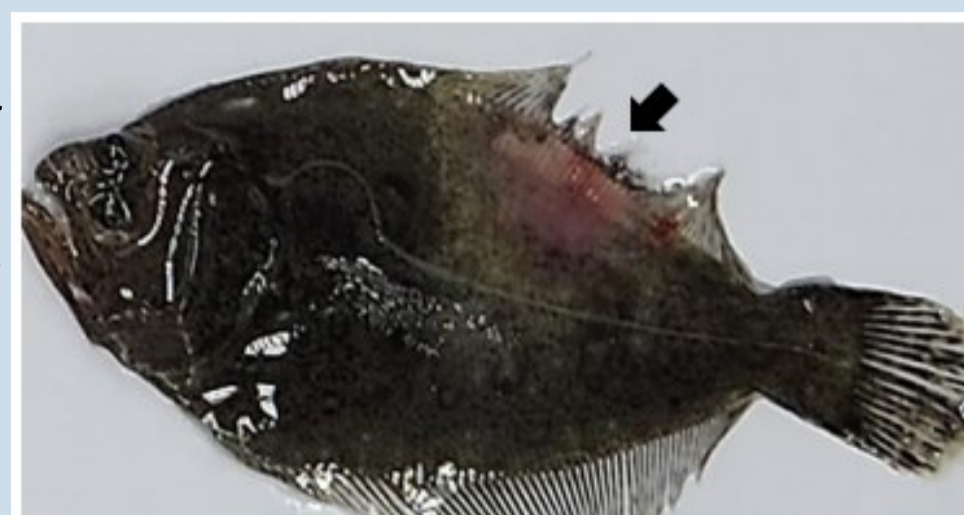


Figure: Skin lesions in infected olive flounder juvenile

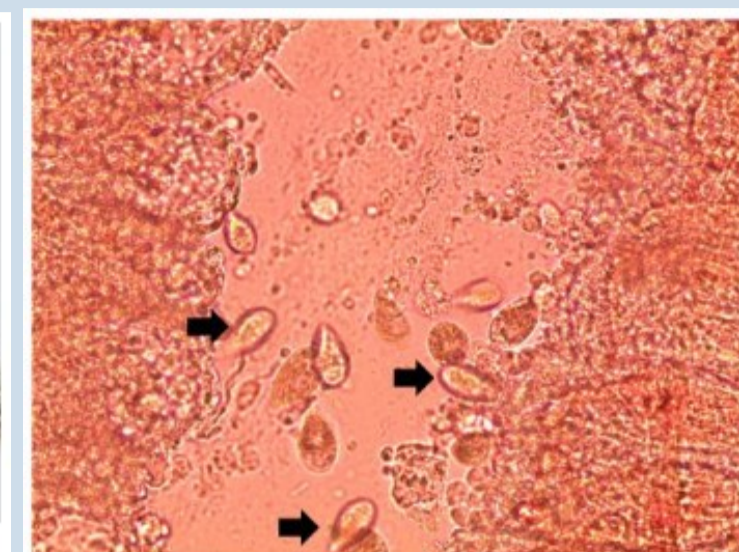
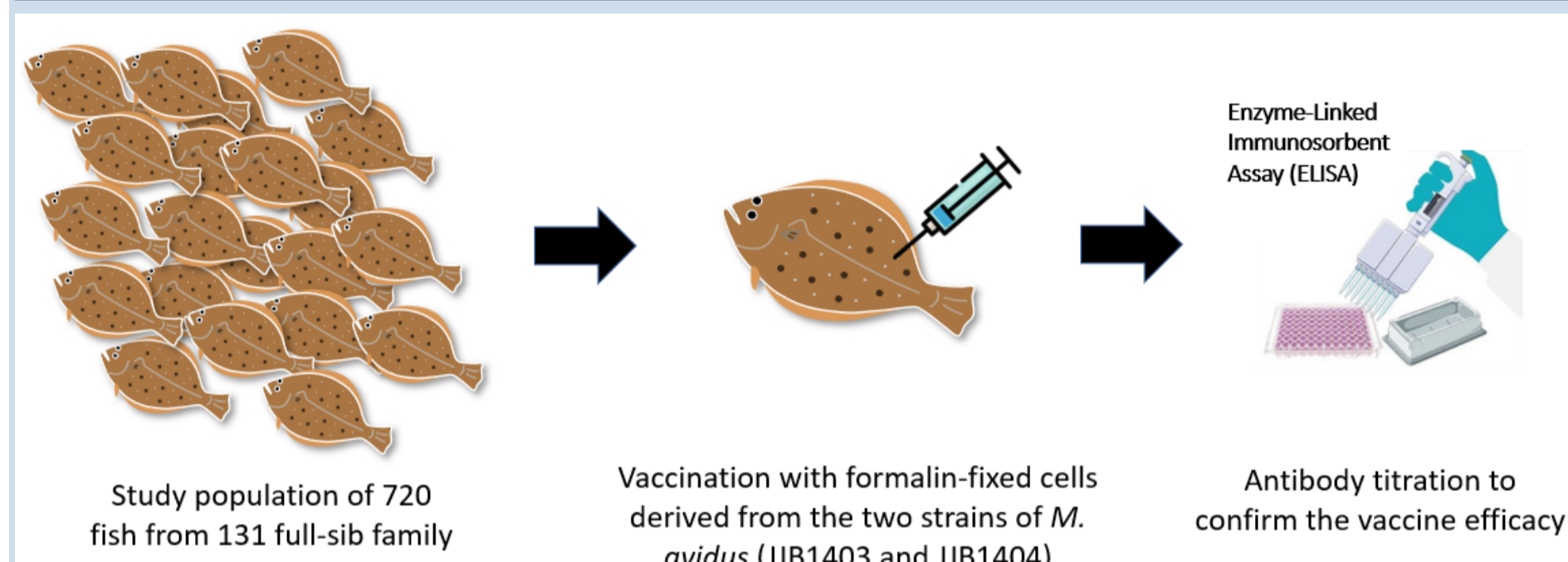


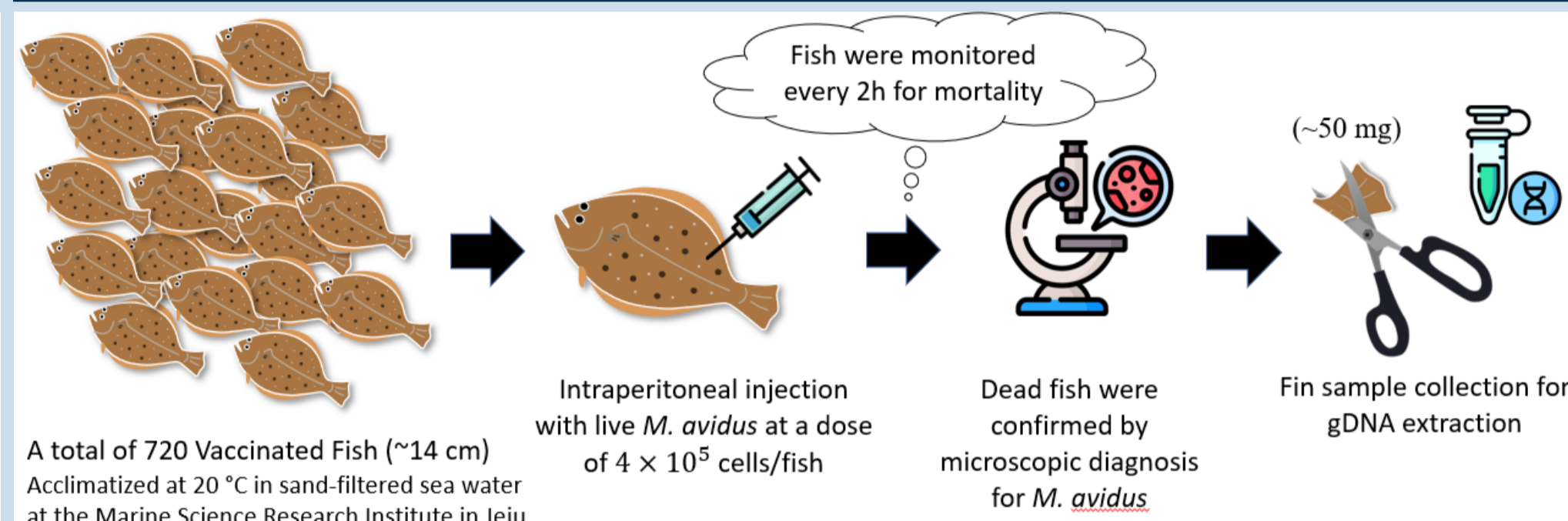
Figure: *Miamiensis avidus* in infected skin of olive flounder (x400)

Methods

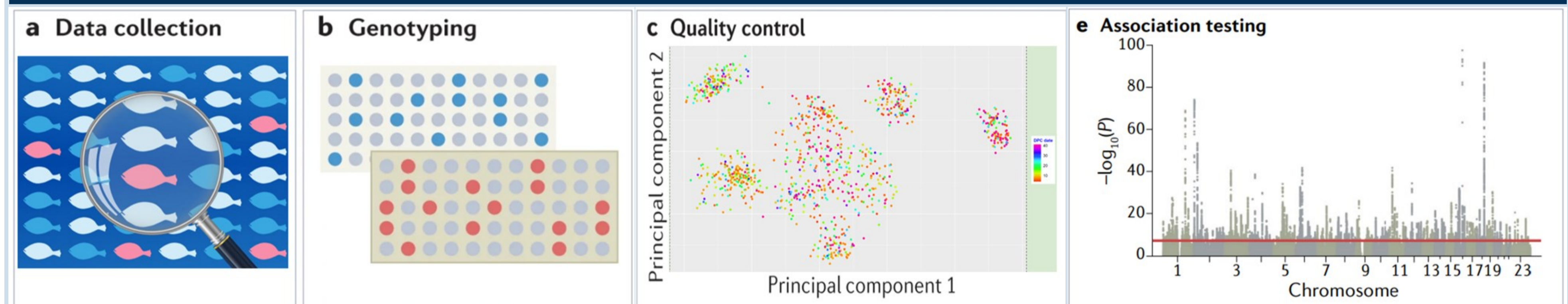
1. Study Population & Vaccination



2. Challenge Experiment



3. Quality control & Genome-wide association study



A cohort of 474 fish from 141 full-sib families underwent formalin-killed vaccination followed by an intraperitoneal challenge with *M. avidus*. Genotyping of 474 fish was performed using a custom-made high-density 70K single nucleotide polymorphism (SNP) array designed for olive flounder. Substantial genetic variation in resistance to scuticociliatosis post-vaccination was observed, with an estimated heritability of around 0.10.

Results

Genome-wide Association (GWAS) analysis revealed sixteen significantly associated SNP variants across chromosomes 1, 7, 11, 12, and 13, explaining a considerable phenotypic variance. Sixteen candidate genes linked to scuticociliatosis resistance post-vaccination were discerned and enriched with gene ontology terms concerning cell migration, morphogenesis, extracellular and cell membrane, cell adhesion, and innate immune response.

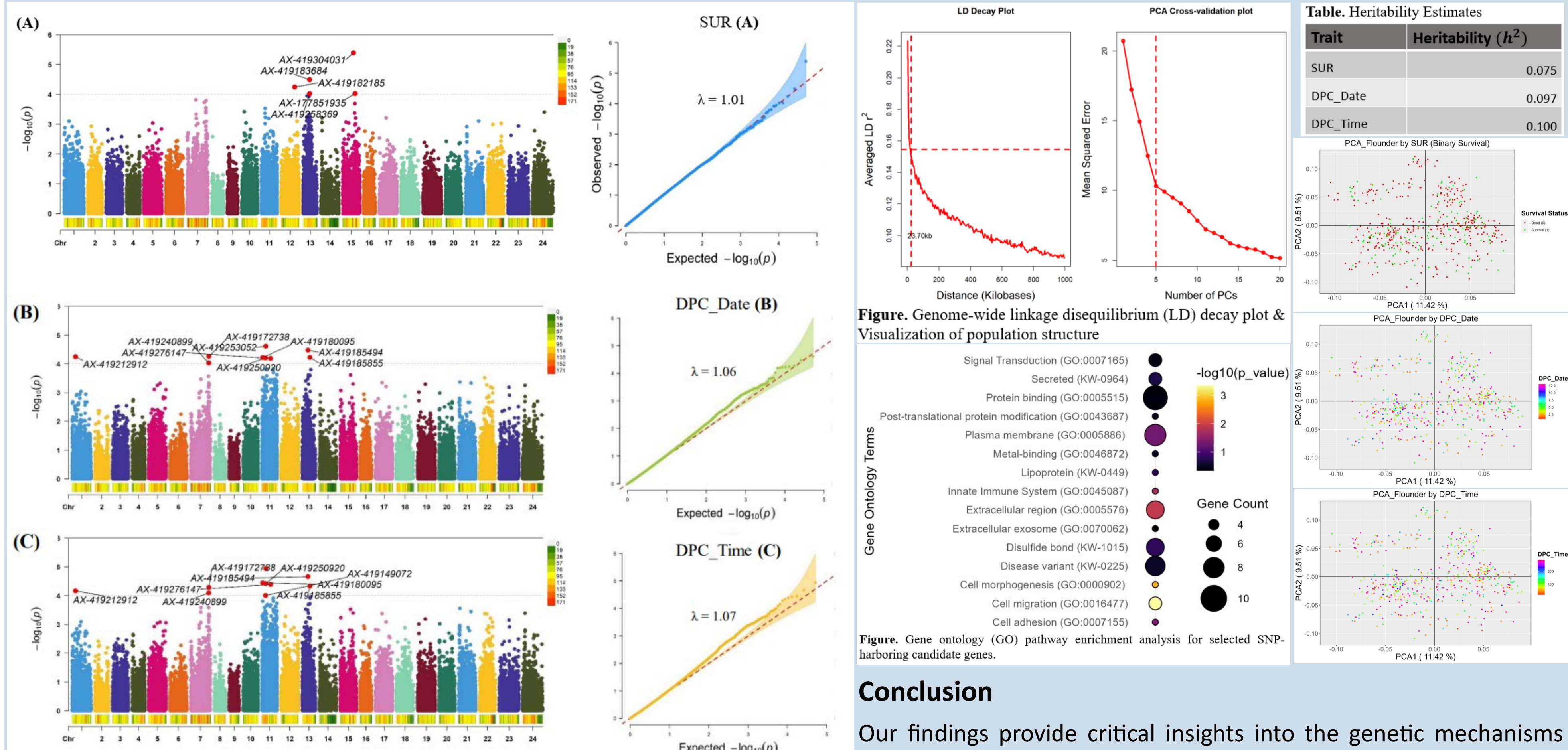
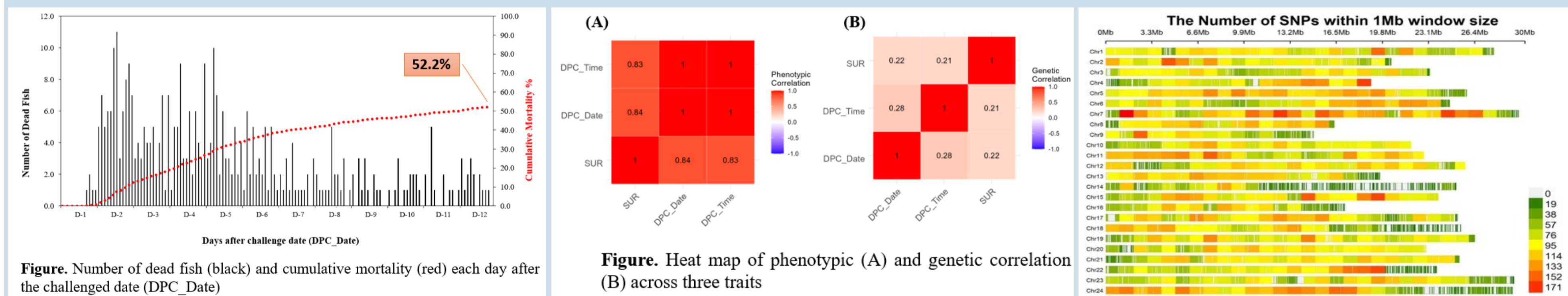


Figure. Manhattan plot of GWAS with p-values distributed across different chromosomes in olive flounder for SUR (A), DPC_Date (B) and DPC_Time (C) phenotypes. Genome-wide and suggestive threshold levels are indicated in solid and dotted lines respectively. Markers crossing the suggestive thresholds are indicated by red color dots.

Conclusion

Our findings provide critical insights into the genetic mechanisms underpinning vaccine-induced resistance to scuticociliatosis, with implications for enhancing selective breeding initiatives in flounder.