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Emilie Delpuech, Marc Vandeputte, Florence Phocas, Anastasia Bestin,
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WHOLE GENOME SEQUENCING TO REFINE THE DETECTION OF QTL FOR VIRAL NERVOUS NECROSIS IN EUROPEAN SEA BASS (DICENTRARCHUS LABRAX)

Delpuech, E.^{1,2}, Vandeputte, M.^{2,3}, Phocas, F.³, Bestin, A.¹, Besson, M.¹, Bajek, A.⁴, Brunier, J.⁴, Imarazene, B.⁵, Sourdioux, M.¹, Haffray, P.¹, Morvezen, R.¹ and Allal, F.²

¹ SYSAAF, Station LPGP/INRAE, Campus de Beaulieu, 35042 Rennes, France

² MARBEC, Univ. Montpellier, Ifremer, CNRS, IRD, INRAE, 34250 Palavas-les-Flots, France

³ Université Paris-Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy-en-Josas, France

⁴ Ecloserie Marine de Gravelines-Ichtus, 59273 Gravelines, France

⁵ Ferme Marine Du Douhet, 17840 La Brée Les Bains, France

SUMMARY

Viral Nervous Necrosis (VNN) is considered the most impacting disease for the European sea bass industry, leading to mortality up to 90%. Selective breeding is a promising strategy to reduce the frequency and severity of the outbreaks. Several genomic regions for VNN resistance have been identified with SNP arrays (Palaikostas et al., 2018, Griot et al., 2021, Faggion et al., 2022). This work presents a next level of the genome-wide association studies (GWAS) using whole genome sequencing and imputation in order to refine the genetic architecture of VNN resistance in European seabass.

Four full-sib backcross families were produced by mating four resistant x susceptible hybrid sires from different geographic backgrounds (western, north-eastern and south-eastern Mediterranean Sea) to four susceptible females from the western Mediterranean Sea. All sires and females used in these backcrosses were sequenced on a NovaSeq sequencer. Moreover, offspring were challenged to nervous necrosis virus and genotyped on the ThermoFisher 57K DlabCHIP SNP array (Griot et al., 2021). We analysed sequences with a home-made pipeline. In a first step, the variant calling was processed according to the DeepVariant best practice and 2,390,971 SNPs were identified. In a second step, FImpute v2.2 software was used to obtain an imputed sequence for each of the 1,334 offspring. Then, GWAS were performed to detect association between 2,4 million imputed SNPs and the VNN resistance trait, using GEMMA software.

A high association was detected on LG12 in three of the four backcross families. In two of them, an additional QTL was located on LGx. We thus validate the strong effect QTL on LG12 and refine its position compared to previous studies with lower density genotypes.

Palaikostas, C., Cariou, S., Bestin, A., Bruant, J.-S. et al., 2018. *Genet. Sel. Evol.* 50, 30. <https://doi.org/10.1186/s12711-018-0401-2>

Griot, R., Allal, F., Phocas, F., Brard-Fudulea, S. et al., 2021. *Aquaculture* 530. <https://doi.org/10.1016/j.aquaculture.2020.735930>

Faggion S., Bertotto D., Bonfatti V., Freguglia M et al., 2022. *Animals* 12, 367. <https://doi.org/10.3390/ani12030367>