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The Editor,
G3: Genes|Genomes|Genetics

18th May 2018

Dear Editor,

Please consider our manuscript "Mapping and sequencing of a significant quantitative trait locus affecting resistance to Koi herpesvirus in common carp" for publication in G3. Carps are the most highly produced aquaculture fish globally. Koi herpes virus (KHV) can cause major economic losses due to high levels of mortality and is listed in the European Union as notifiable disease. In this study, we use RAD sequencing to generate genome-wide SNP genotype data from approximately 1,400 disease challenged individuals and their parents. We then use these data to examine the genetic architecture of host resistance. Pooled whole genome resequencing of a subset of resistant ($n = 60$) and susceptible animals ($n = 60$) was performed to characterize QTL regions, including identification of putative candidate genes and functional annotation of associated polymorphisms. The TRIM25 gene was identified as a promising positional and functional candidate within the QTL region of LG 44, and a putative premature stop mutation in this gene was discovered. Overall our results show that using genome wide polymorphism data could greatly benefit the carp industry towards selecting for KHV resistant carp. To our knowledge, this is the first study of large-scale application of genome wide association study in studying resistance of common carp against KHV. We hope this study is of interest both for basic research on disease resistance and for application in aquaculture, where use of genomic tools in selective breeding for disease resistance is of high economic interest for many species.

Yours sincerely,

Christos Palaikostas