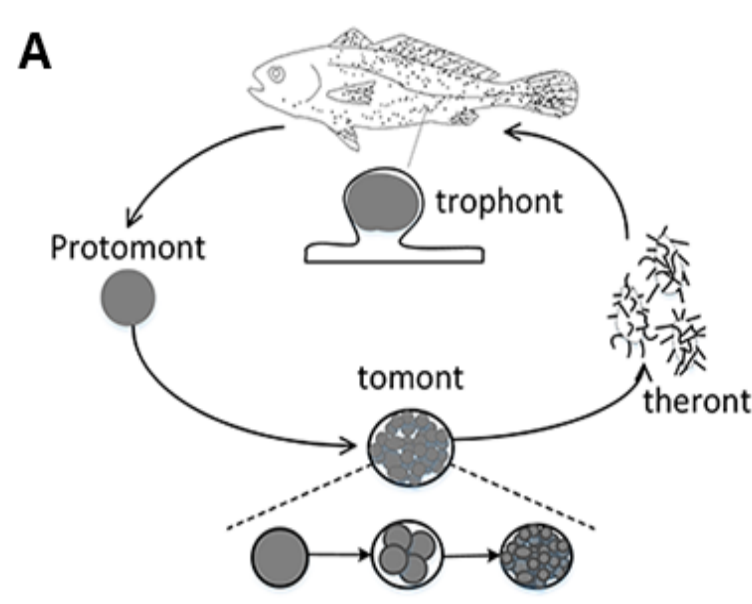


# ACHIEVEMENTS OF GENOMIC SELECTION FOR PARASITE RESISTANCE IN LARGE YELLOW CROAKER

Ning Li\*, Tao Zhou, Ji Zhao, Qiaozhen Ke, Jiaying Wang, Peng Xu

State Key Laboratory of Mariculture Breeding, College of Ocean and Earth Sciences, Xiamen University, Xiamen, 361102, China

## 1. Background



Life cycle of *C. irritans*



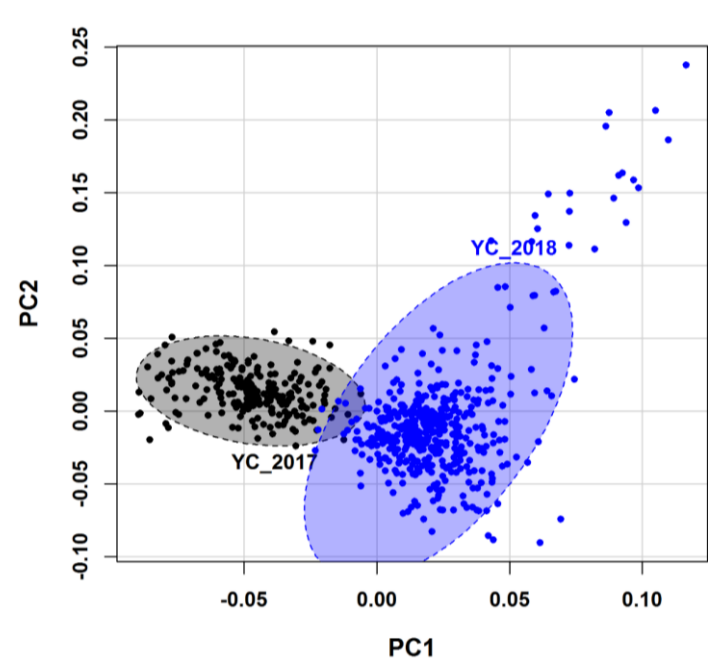
*C. irritans* infection on host

The large yellow croaker (*Larimichthys crocea*) is one of the most economically important marine aquaculture species in China, with an annual production exceeding 258,000 tons. The white spot disease caused by *Cryptocaryon irritans* has caused serious economic losses to the large yellow croaker industry, and unfortunately, there is still no effective treatment to this parasite infection. From the perspective of genetic selection, breeding new resistant strains may be a solution to treating the white spot disease.

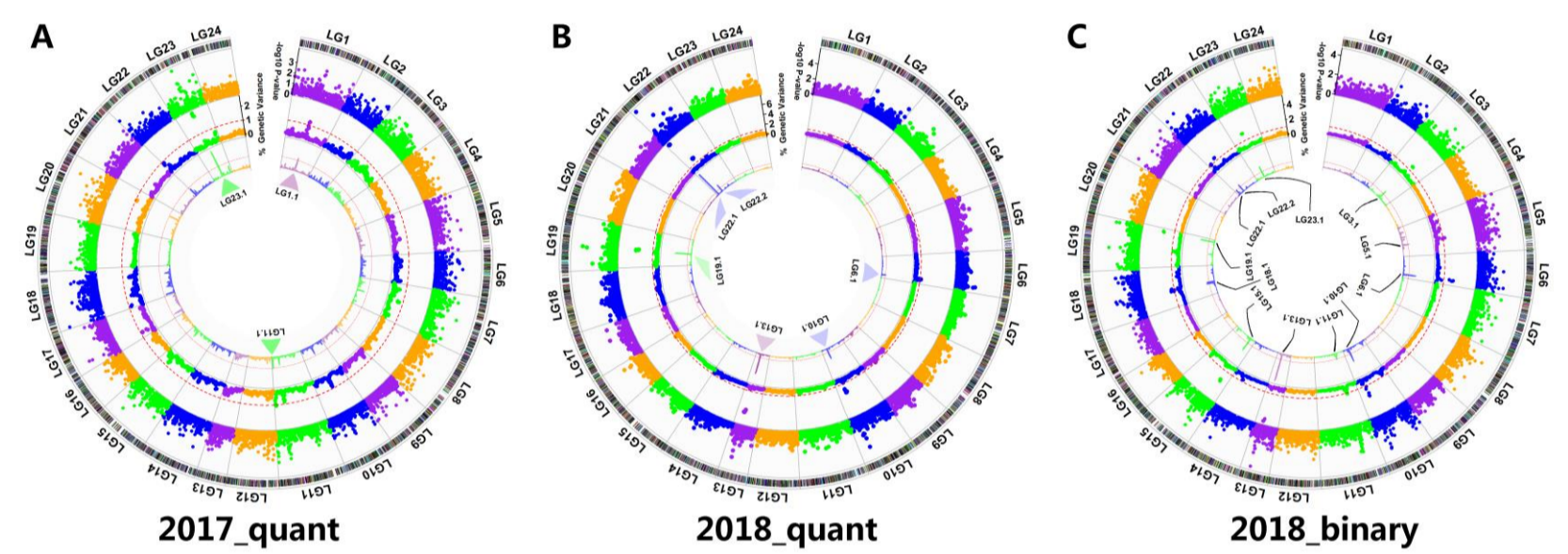
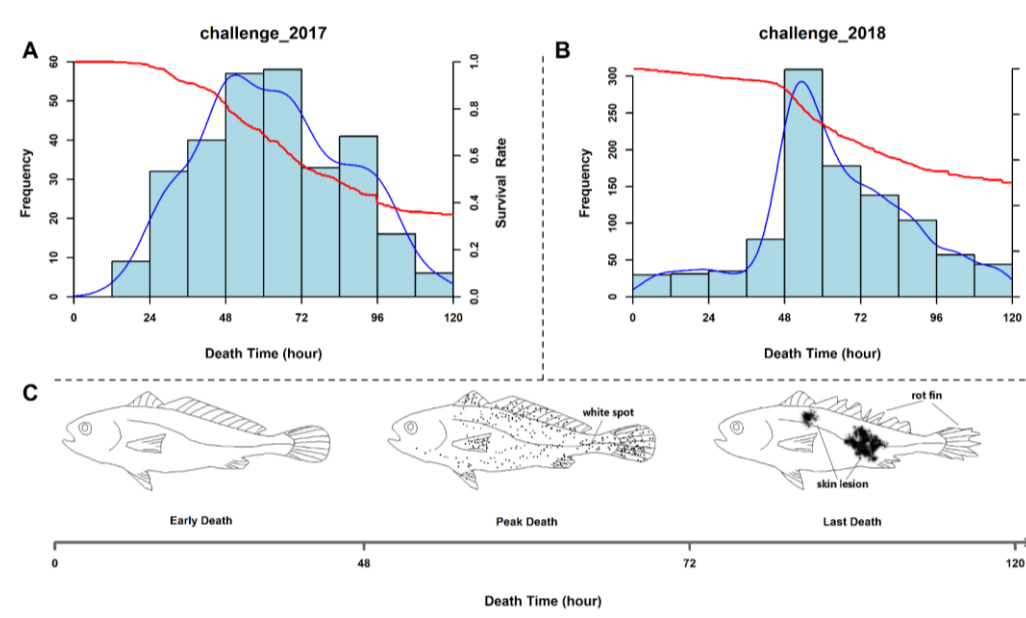
## 2. GWAS for the resistance trait of large yellow croaker against *C. irritans*

(Zhao *et al.*, 2021. Marine Biotechnology)

Through multiple large-scale experiments on *C. irritans* infection in large yellow croaker, we established a resistance phenotypic evaluation scheme, and used GWAS to preliminarily investigate the genetic architecture of the resistance trait.



Two populations of large yellow croaker (Left) were used to conduct *C. irritans* challenge tests. It was found that the distribution of death time was close to a normal distribution (Right, Panels A and B), and the death feature of experimental fish showed various patterns at different times after challenge (Right, Panel C).

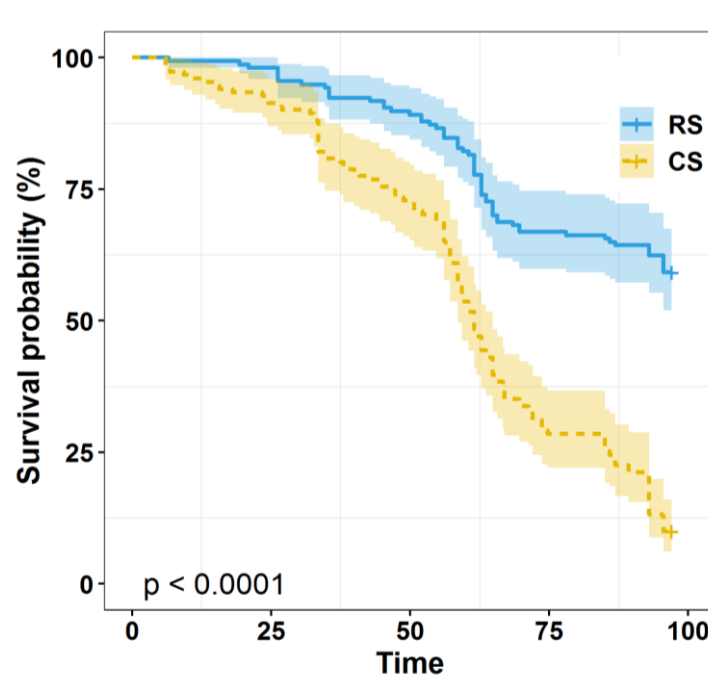


Based on the quantitative and binary resistance trait (death time and survive status), GWAS results revealed that the resistance trait has a medium heritability (0.36 in quantitative trait; 0.59 in binary trait), and is controlled by several QTL ( $n = 15$ ) with small-effect and a lot of genetic loci with micro-effect. In conclusion, the resistance trait has a relatively complex genetic architecture.

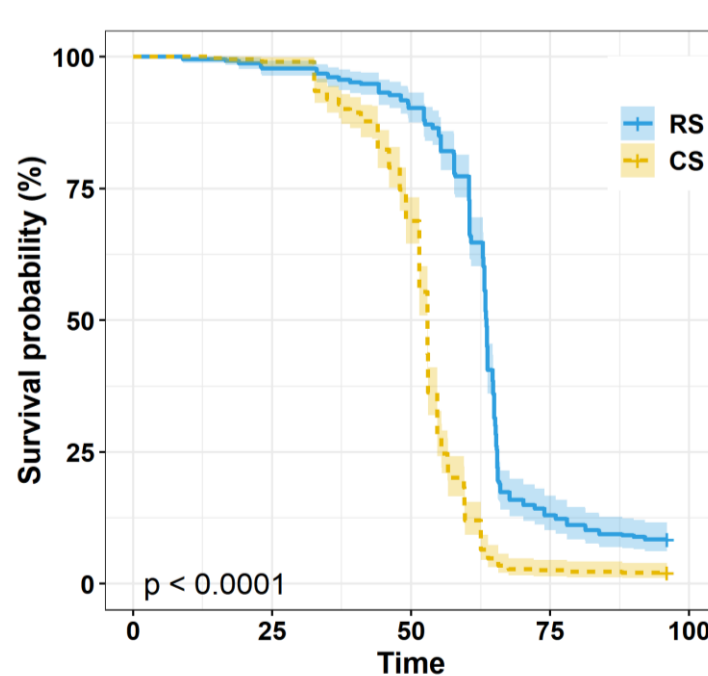
## 3. Genomic selection in the breeding of resistance trait against *C. irritans*

(Zhao *et al.*, 2020. Aquaculture)

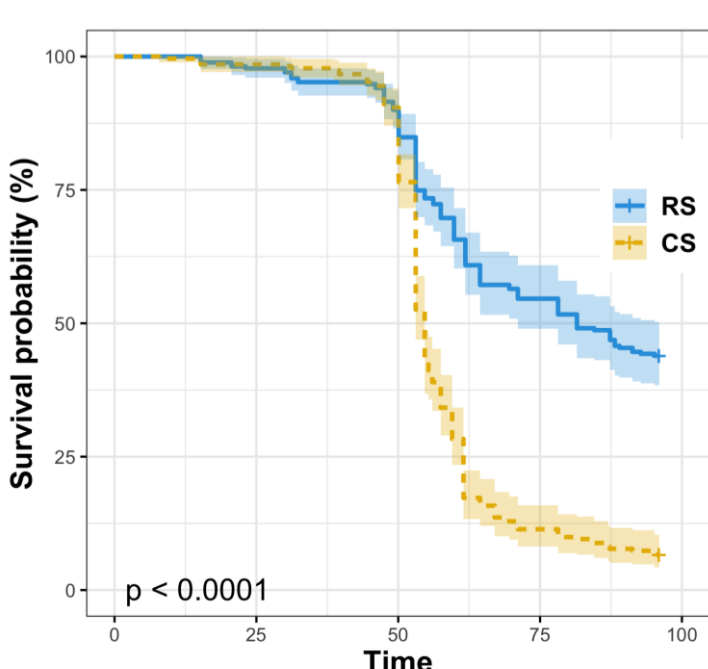
Considering that the resistance trait of large yellow croaker against *C. irritans* has a complex genetic architecture, a cutting-edge technology of genetic selection, genomic selection (GS), is used to cultivate new resistant lines. At present, we have bred two independent resistant strains (GS3 and GS3R), and the selection of both strains have reached F4 generation.



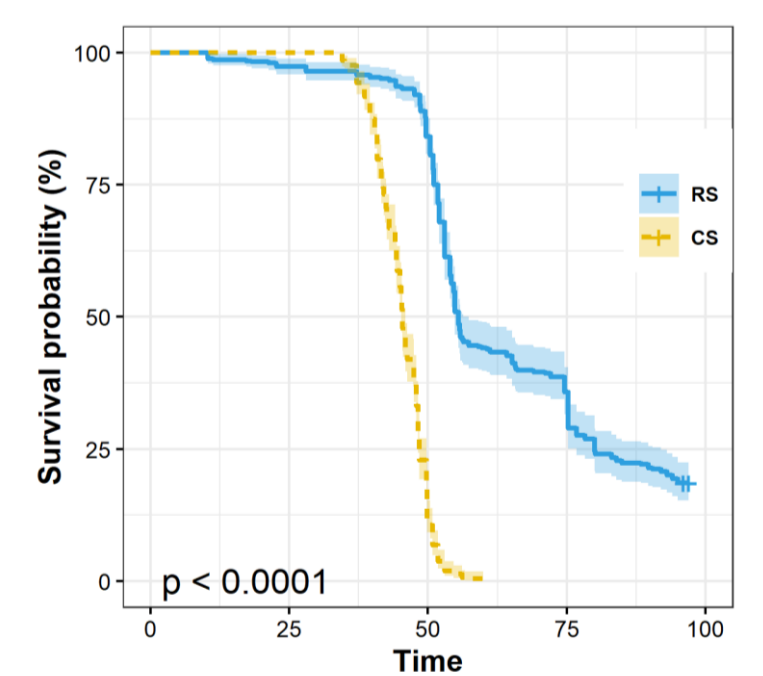
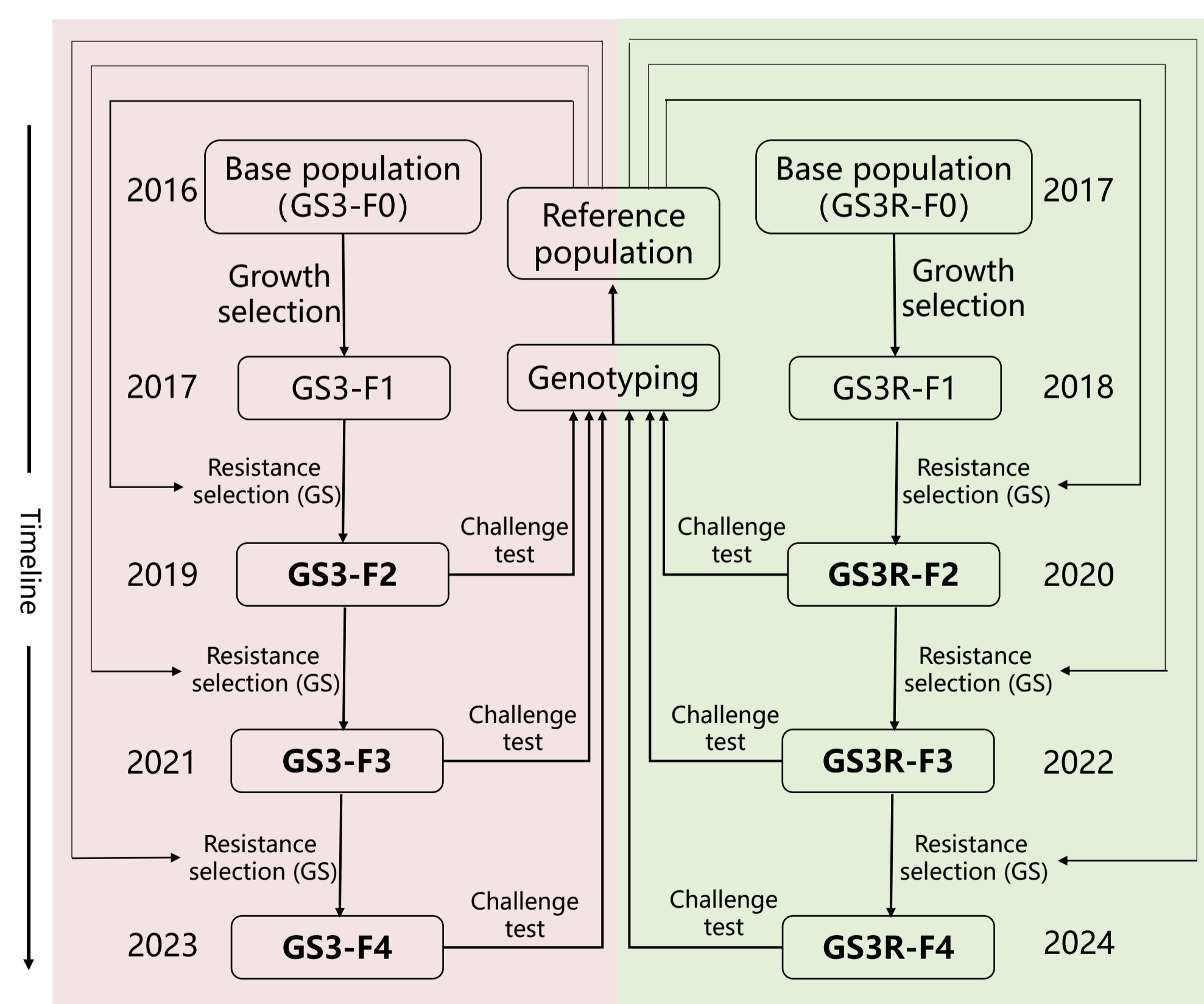
Survival curve for **GS3-F2**



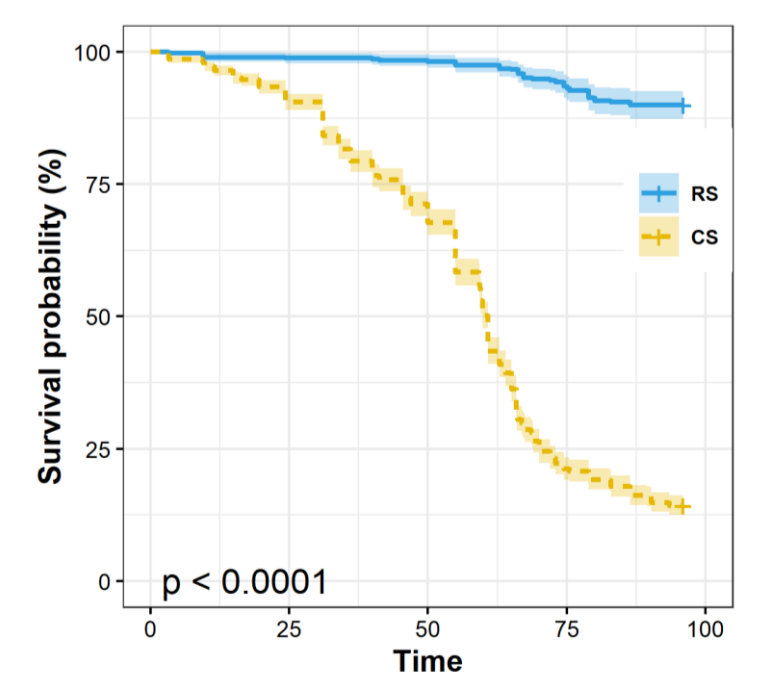
Survival curve for **GS3-F3**



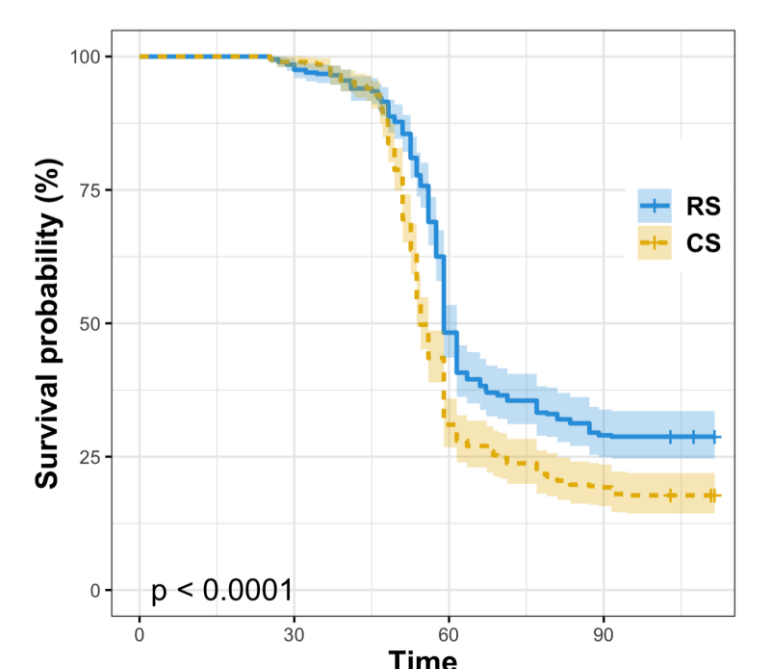
Survival curve for **GS3-F4**



Survival curve for **GS3R-F2**



Survival curve for **GS3R-F3**



Survival curve for **GS3R-F4**

The two resistant strains started with different base populations but shared the same reference population in the GS applications. Both strains have gone through one round of growth selection and three of resistance selection. After each resistance selection, challenge test was carried out for four-month-old offspring ( $n = 150$  individuals $\times 3$  replicates). The survival curves have consistently exhibited superior resistance performance of both resistant strains against *C. irritans*. Our promising GS applications of resistance trait against *C. irritans* in large yellow croaker highlights the potential of genetic improvement and selective breeding for parasite resistance in aquaculture.