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Estimation of genetic parameters for resistance to *Vibrio alginolyticus* infection in the Pacific oyster (*Crassostrea gigas*)

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ABSTRACT

The Pacific oyster (*Crassostrea gigas*) is one of the most important aquaculture species in the world, while its industry has been hampered by mass summer mortality caused by pathogenic factors including *Vibrio* bacteria. Selective breeding of oyster strains with high resistance to *Vibrio* bacteria would be an effective and sustainable approach to prevent massive economic loss. Estimation of genetic parameters for disease resistance is the critical step toward selective breeding. In this study, we constructed 52 full-sib families using the *C. gigas* with diverse genetic backgrounds, and performed an artificial infection experiment to assess disease resistance among families and estimate genetic parameters for resistance to *Vibrio alginolyticus* infection. The survival rate of the 52 families ranged from 0% to 56.25%, suggesting high levels of phenotypic variation in resistance to *V. alginolyticus* infection. Genetic parameters for resistance to *V. alginolyticus* infection estimated using six different models revealed low to moderate heritability, ranging from 0.133 to 0.257. The Pearson and Spearman correlation coefficients among family estimated breeding values (EBVs) were high (correlation coefficients $\geq$0.989), indicating that the predictive ability of different models for family EBVs was consistent. The genetic and phenotypic correlation between resistance to *V. alginolyticus* and growth traits were low, suggesting the feasibility of simultaneous genetic improvement of both growth and resistance traits. This work reported the first estimation of genetic parameters for resistance to *V. alginolyticus* and provided valuable information toward genetic improvement of resistance to *V. alginolyticus* using traditional selection or genomic selection breeding approach.

1. Introduction

The Pacific oyster (*Crassostrea gigas*) is one of the most important marine aquaculture species in the world, with the production of more than 643,000 tons in 2018 (FAO, 2020). It is naturally distributed in the estuaries and intertidal zones in the northwest Pacific, and has been introduced to many countries for aquaculture due to its high growth rate and strong adaptability to the environment (Orensanz et al., 2002; Miossec et al., 2009; Xu et al., 2019c; Zhang et al., 2019a, 2019b). In recent years, outbreaks of mass summer mortality have been reported worldwide, which caused great economic loss to the oyster industry (Wendling and Wegner, 2013; Alfaro et al., 2019). Many infectious pathogens, including viruses and bacteria, have been involved in mass summer mortality events (Friedman et al., 2005; Garnier et al., 2007; Malham et al., 2009; Barbosa Solomieu et al., 2015; King et al., 2019). In a recent work, we identified a highly virulent *V. alginolyticus* Cg5 strain as a causative pathogen associated with mass summer mortality of *C. gigas* in China (Yang et al., 2021). As a gram-negative pathogen, *V. alginolyticus* is widely distributed in marine environments of temperate and tropical waters (Zanetti et al., 2000), and has been reported to cause epidemic *Vibrio* disease in various marine animals (Go et al., 2017; Ye et al., 2016; Lee et al., 1996; Xie et al., 2016; Zhu et al., 2016; Castillo et al., 2015; Luo et al., 2016; Zavala-Norzagaray et al., 2015; Castillo et al., 2015; Kang et al., 2016). The *V. alginolyticus* has also been reported to be pathogenic to humans, leading to superficial wounds, otitis (Di Pinto et al., 2005; Reilly et al., 2011; Jacobs Slifka et al., 2017).

Oysters lack of adaptive immune systems and are cultured in open ocean environment, which makes it impossible to use vaccines or disinfectants to prevent and treat diseases (Prado-Alvarez et al., 2016; Alfaro et al., 2019). Therefore, genetic improvement of disease resistance of oyster would be the only effective method to solve the disease problem (Dégremont, 2013; Stear et al., 2001; Yáñez et al., 2013). The effectiveness of selective breeding depends on whether there is sufficient

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heritability of target traits (Taylor et al., 2009; Liang et al., 2017). Estimation of genetic parameters for target traits is the critical step toward selective breeding program (Sun et al., 2015; Wang and Ma, 2019). Currently, selective breeding of *C. gigas* have mainly focused on growth (Li et al., 2011; Wang et al., 2012; Zhang et al., 2019a, 2019b), shell color (Wan et al., 2017; Xu et al., 2019b; Han and Li, 2020), and meat composition (Wan et al., 2020). For disease resistance breeding, the genetic improvement of resistance to *Ostreid herpesvirus* 1 (OsHV-1) (Dégremont et al., 2015; Azéma et al., 2016; Camara et al., 2017; Azéma et al., 2017a; Azéma et al., 2017b; Dégremont et al., 2019) and *Vibrio aestuarianus* (Azéma et al., 2016; Azéma et al., 2017b; Dégremont et al., 2020) have been carried out in *C. gigas*. Although the pathogenic role of *V. alginolyticus* has drawn wide attention, genetic breeding toward resistance of this pathogen has not been conducted in *C. gigas*.

In this study, we constructed a total of 52 full-sib families using *C. gigas* with diverse genetic backgrounds, and performed artificial infection with the isolated virulent *V. alginolyticus* strain to assess the resistance levels among families and estimate genetic parameters for resistance to *V. alginolyticus*. This would provide valuable information toward genetic breeding of *C. gigas* strains with resistance to *V. alginolyticus*.

2. Material and methods

2.1. Generation of families

A total of 52 full-sib families were produced in 2019 spawning season, using 43 dams and 43 sires with diverse genetic backgrounds, in a hatchery farm located in Laizhou (Shandong, China). The detailed information of the families and broodstocks were provided in Supplementary Tables 1 and 2. Artificial fertilization and rearing management of families were carried out according to procedure described by Li et al. (2011). After about 40 days, all spats were placed on nylon ropes randomly when the shell height was reached 2–3 mm, which were transported to ocean for culture on suspended longlines in Rongcheng (Shandong, China) (Xu et al., 2019a; Xu et al., 2019b), which is one of the main areas for mariculture of *C. gigas* in China.

2.2. Artificial bacterial challenge experiment

A total of 1402 oysters randomly collected from 52 families were used for the artificial bacterial challenge experiment (Supplementary Table 1), which were randomly distributed in four communal experiment tanks (0.3 m^3) with each tank holding 13 families, and the treatment for each tank was same during acclimatization and experiment. The families were separated by small baskets, with each family in a single basket. Oysters were acclimated for 2 weeks at 22 °C and were fed with concentrated *Chlorella vulgaris*. The highly virulent *V. alginolyticus* Cg5 strain isolated previously (Yang et al., 2021) was used for artificial infection challenge. To ensure each oyster was infected with same quantity of pathogens, challenge experiment was conducted by injection. Pilot experiment by injection showed that the LD_{50} for 96 h was 5×10^7 CFU per oyster. During the injection process, the centrifuge tube was slowly reversed up and down to mix the bacterial suspension every 10 min. The oysters were anesthetized with a solution of magnesium chloride ($MgCl_2$, 50 g/L) before injection with bacteria. Each oyster was injected with a volume of 100 μL bacterial suspension into adductor muscle by microinjector (100 ± 0.5 μL). The injected *C. gigas* were cultured for mortality observation. Water quality was daily tested: water temperature was 22 ± 1 °C, pH at 8.1, dissolved oxygen at 8 mg/L, and salinity at 30–32‰. The seawater was changed every other day during the challenge experiment. Oysters were considered as dead when they lost muscle strength and were unable to close their shells after being out of water. Dead oysters were recorded and removed immediately from the tanks every 2 h during the experiment. Shell length (SL), shell height (SH) and shell width (SW) of all the dead *C. gigas* and survivors were measured.

2.3. Comparison of survival rates among families

One-way analysis of variance and multiple comparison in SPSS software (version 26) were used to analyze the differences in survival rate of families with diverse genetic backgrounds. The statistical significance was set as $P < 0.05$.

The Kaplan-Meier estimate of the survival function (Kaplan and Meier, 1958) was used to plot survival curves of families using GraphPad Prism software (version 8). The survival distribution function is:

$$\widehat{S}(t) = \Pi_{t_i<t}\left(1-\frac{d_i}{n_i}\right)$$

Where t_i is death time at day i, d_i is the number of oysters that die at t_i and n_i is the number of surviving oysters before t_i.

To classify families into resistant or susceptible to *V. alginolyticus,* a Cox proportional hazard regression analysis (Cox, 1972) was used to measure the survival time of each family. The risk of death for families was compared based on a hazard ratio HR = $h_i(t)/h_r(t)$, where $h_i(t)$ denotes the mortality risk in family i, $h_r(t)$ denotes the mortality risk in the reference family, and the survival rate in the reference family is 0%. Families with hazard ratio value <1 were classified as resistant to *V. alginolyticus*, while families with hazard ratio > 1 were classified as susceptible to *V. alginolyticus*.

2.4. Estimation of genetic parameters for resistance to V. alginolyticus

The genetic parameters for resistance to *V. alginolyticus* were estimated by linear models and threshold models. The resistance to *V. alginolyticus* was defined as a binary trait, which was scored 0 if the oyster died before the end of the experiment and scored 1 if the oyster survived at the end of the experiment.

Survival data was analyzed with six different models, of which, linear animal model was also used to analyze growth traits (SL, SH and SW), and the models are summarized as follows:

(1) Linear animal model (LAM)

$$y_{ij} = \mu + a_i + e_{ij}$$

where y_{ij} is the phenotypic trait for oyster i, μ is the fixed effect of the population mean, a_i is the additive genetic effect of oyster i as a random effect, e_{ij} is the residual effect.

(2) Linear sire-dam model (LSM)

$$y_{ijk} = \mu + S_j + D_k + e_{ijk}$$

where y_{ijk} is the death/survival state (1 = survivor, 0 = dead) for oyster i, s_j is the random additive genetic effect of sire j; d_k is the random additive genetic effect of dam k; and the other parameters are as described above.

(3) Threshold (logit) animal model (TAMl)

$$Pr(Y_{ij} = 1) = exp(\mu + a_i)/[1 + exp(\mu + a_i)]$$

where all parameters are same as described in LAM above.

(4) Threshold (logit) sire-dam model (TSMl)

$$Pr(Y_{ijk} = 1) = exp(\mu + S_j + D_k)/[1 + exp(\mu + S_j + D_k)]$$

where all parameters are same as described in LSM above.

(5) Threshold (probit) animal model (TAMp)

$$Pr(Y_{ij} = 1) = \Phi(\mu + a_i)$$

where Φ represents the standard cumulative normal distribution function and all parameters are same as described in LAM above.

(6) Threshold (probit) sire-dam model (TSMp)

$$Pr(Y_{ijk} = 1) = \Phi(\mu + S_j + D_k)$$

where all parameters are described above.

The ASReml-R3.0 software package was used to analyze all the models used in this study, which was based on restricted maximum likelihood (REML) (Butler et al., 2009). Wald F was used to test the significance of fixed effect (Tank), which was not included in the model because it was not significant ($P > 0.05$). The variance component of environmental effect was near the boundary, therefore, environmental effect was excluded from the model. For the six models, the random animal genetic effect was assumed to be ~N (0, $A\sigma_a^2$). The sire effects and dam effects were assumed to be ~N (0, $I\sigma_s^2$) and ~N (0, $I\sigma_d^2$), respectively. The residuals were assumed to be ~N (0, $I\sigma_e^2$). where A is the additive genetic relationship matrix for all animals including the parent, and I is an identity matrix.

2.5. Estimation of heritability

For the cross-sectional animal models (LAM, TAML, TAMP), heritability calculation formula is:

$$h^2 = \sigma_a{}^2 / (\sigma_a{}^2 + \sigma_e{}^2)$$

where σ_a^2 is additive genetic variance, σ_e^2 is the residual variance (The residual variance of the threshold logit model is $\pi^2/3$, and the residual variance of the threshold Probit is 1).

For the cross-sectional sire-dam models (LSM, TSML, TSMP), heritability calculation formula is:

$$h^2 = (2\sigma_s{}^2 + 2\sigma_d{}^2) / (\sigma_s{}^2 + \sigma_d{}^2 + \sigma_e{}^2),$$

where σ_s^2 is sire genetic variance component and σ_d^2 is dam genetic variance component, the other parameters are described above.

2.6. Model comparison

Comparisons of the models were conducted based on their ability to predict estimated breeding values of resistance to *V. alginolyticus*. The Pearson and Spearman correlation coefficients between family EBVs in all models were calculated using SPSS software (version 26). Formula of family EBVs is $1/2(u_s + u_d)$, where u_s is the sire EBVs of each family, and u_d is the dam EBVs of each family.

2.7. Correlation of resistance and growth trait

The genetic correlation (r_g) between the trait of resistance to *V. alginolyticus* and growth traits (SL, SH and SW) were calculated, and bivariate analysis was performed based on LAM. The genetic correlation formula is:

$$r_{g(m,n)} = \frac{Cov_g(m,n)}{\sqrt{Var_g m \times Var_g n}}$$

where $Cov_g(m,n)$ is the genetic covariance between survival and growth traits, $Var_g m$ and $Var_g n$ is the additive genetic variance of trait m and trait n, respectively.

The phenotypic correlation (r_p) formula is:

$$r_{p(m,n)} = \frac{Cov_p(m,n)}{\sqrt{Var_p m \times Var_p n}}$$

where $Cov_p(m,n)$ is the phenotypic covariance between survival and growth traits, $Var_p m$ and $Var_p n$ is the phenotypic variance of trait m and trait n, respectively.

The correlations were calculated using ASReml-R3.0 software package.

3. Results

3.1. Comparison of survival rate among families

The dead oysters caused by *V. alginolyticus* infection showed no obvious lesions in the shell or soft tissue, but with a pungent odor. Additionally, the adductor muscle of infected oysters contracted slowly and the shells were not able to close completely. The bacteria load of the dead oysters was determined by bacteria culture in plate, which was significantly higher than that of healthy oysters as controls. The bacteria isolated from dead oysters were identified as *V. alginolyticus* by PCR and 16S rRNA sequencing. The artificial infection experiment of *V. alginolyticus* was carried out in 52 families for 12 days (Table 1). The daily mortality and survival curve for all 52 families during 12 days of infection with *V. alginolyticus* were shown in Fig. 1. It's apparent that the daily mortality was first increased, then decreased. The daily mortality rate peaked on the 4th day after *V. alginolyticus* infection. There was a distinct peak period from day 3 to 5. The challenge test was terminated when the daily mortality rate of day 10 to 12 was <1%. A total of 982 oysters from 52 families died at the end of the challenge experiment, with cumulative mortality rate of 70.04% for all families.

The survival rate varied widely among families, suggesting a significant phenotypic variation associated with resistance to *V. alginolyticus*. The survival rate was 0% in 3 families (0524–20, 0421–22 and 0421–11), and the family with the highest survival rate was 0609–10 (56.25%) (Fig. 2). The Kaplan-Meier curves of 20 families, the top ten families and the last ten families in terms of survival rate in the experiment, indicating significant differences in mortality among families (Fig. 3). Hazard ratio value of each family based on Cox proportional regression analysis was shown in Fig. 4. In this experiment, 13 families with hazard ratio less than 1 ($P < 0.05$) were regarded as resistant families (0430–3, 0609–5, 0524–4, 0609–11, 0421–9, 0609–8, 0524–30, 0626–6, 0421–10, 0421–24, 0609–6, 0609–9, and 0609–10), and two families with hazard ratio greater than 1 ($P < 0.05$) were regarded as susceptible families (0524–20 and 0421–22) (Fig. 4).

3.2. Estimation of genetic parameters

The estimated variance components and heritability estimated using different models were presented in Table 2. The results showed that heritability of resistance to *V. alginolyticus* in *C. gigas* was low to moderate, ranging from 0.133 to 0.257. The values of estimated heritability varied among different models. The heritability estimated from the TSMp model was the highest (0.257 ± 0.071), while the lowest estimated heritability (0.133 ± 0.040) was calculated from LAM model. The estimated heritability from other models, including LSM, TAMl, TSMl

Table 1
Summary of artificial bacterial challenge with *V. alginolyticus* in *C. gigas*.

Items	Number
Number of families	52
Number of oysters	1402
Age (months)	14
Number of Sires	43
Number of Dams	43
Final mortality (%)	70.04
Challenge test time (days)	12
Average shell length (mm)	29.76
Average shell height (mm)	40.23
Average shell width (mm)	13.35

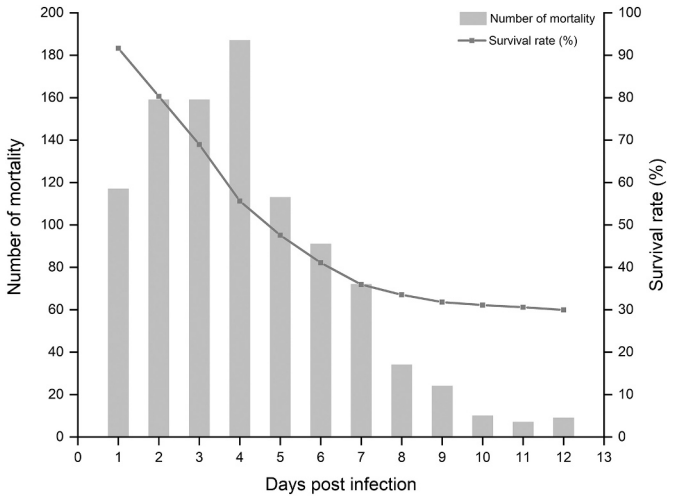

Fig. 1. The daily mortality and survival curve for all 52 families ($n = 1402$) during 12 days of challenge with *V. alginolyticus*.

and TAMp, was 0.135 ± 0.041, 0.138 ± 0.036, 0.213 ± 0.062 and 0.162 ± 0.040, respectively.

3.3. Model comparison

The Pearson and Spearman correlation coefficients between family EBVs estimated by six different models were shown in Table 3. The Pearson and Spearman correlation coefficients among the six different models were highly positive correlation, and all the correlation coefficients were greater than 0.989, indicating a near identical ranking of families in all six models.

3.4. Correlation of resistance with growth

The estimated heritability of SH, SL and SW using linear animal model was 0.254 ± 0.060, 0.169 ± 0.047, 0.055 ± 0.026, respectively. The genetic and phenotypic correlation coefficients between resistance trait and growth traits (SL, SH and SW) were provided in Table 4. The phenotypic correlations between resistance to *V. alginolyticus* and SL, SH and SW were 0.016 ± 0.030, 0.029 ± 0.031, 0.044 ± 0.028, and genetic correlations were 0.379 ± 0.199, 0.231 ± 0.200, −0.039 ± 0.276, respectively. All the genetic and phenotypic correlations between growth traits and resistance were not statistically significant ($P > 0.05$). The estimated genetic correlation between resistance to *V. alginolyticus* and two growth traits (SL and SH) was low and positive, 0.379 and 0.231, respectively. The correlation value between resistance to *V. alginolyticus* and SW was at a low negative correlation level (−0.039). The phenotypic correlation between these traits was low positive correlation, with value of 0.016 between resistance to *V. alginolyticus* and SL, 0.029 between resistance to *V. alginolyticus* and SH, and 0.044 between resistance to *V. alginolyticus* and SW, respectively.

4. Discussion

The Pacific oyster is one of the most important aquaculture species in China and around the world. Disease outbreaks associated with virus and bacterial pathogens during summer cause mass mortality, which have become a serious problem of the oyster industry worldwide (Friedman et al., 2005; Garnier et al., 2007; Malham et al., 2009; Wendling and Wegner, 2013; Barbosa Solomieu et al., 2015; Alfaro et al., 2019; King et al., 2019). Selective breeding of strains with resistance to disease pathogens will be an effective and sustainable approach (Li et al., 2019; Sukhavachana et al., 2019; Dégremont et al., 2020; Noble et al., 2020). Toward genetic breeding for disease resistance, we performed a pathogen screening of oysters undergone summer mass mortality and identified *V. alginolyticus* as a potential causative pathogen (Yang et al., 2021). In this work, we move forward to perform artificial infection challenge experiment to estimate the genetic parameters that are critical information for the genetic improvement of resistance using traditional selection or genomic selection breeding approach. We found that phenotypic variation of the resistance to *V. alginolyticus* was high based on observation with a total of 1402 oysters from 52 families. The estimated heritability of resistance was at a low to moderate level. Genetic and phenotypic correlation between resistance to *V. alginolyticus* and growth traits were low. These suggested that the resistance to *V. alginolyticus* could be improved by selective breeding, and both growth and resistance trait can be considered simultaneously.

The cross-sectional model is widely used to estimate disease resistance traits (Wang and Ma, 2019). In the cross-sectional model, the survival trait of challenge test is analyzed as a binary trait (1 = survival, 0 = dead) (Ødegård et al., 2011). In aquaculture species, linear model and threshold model are widely used to fit binary trait data (Ødegård et al., 2011; Xiong et al., 2017). Among them, binary data is regarded as normally distributed data when using linear model for genetic analysis

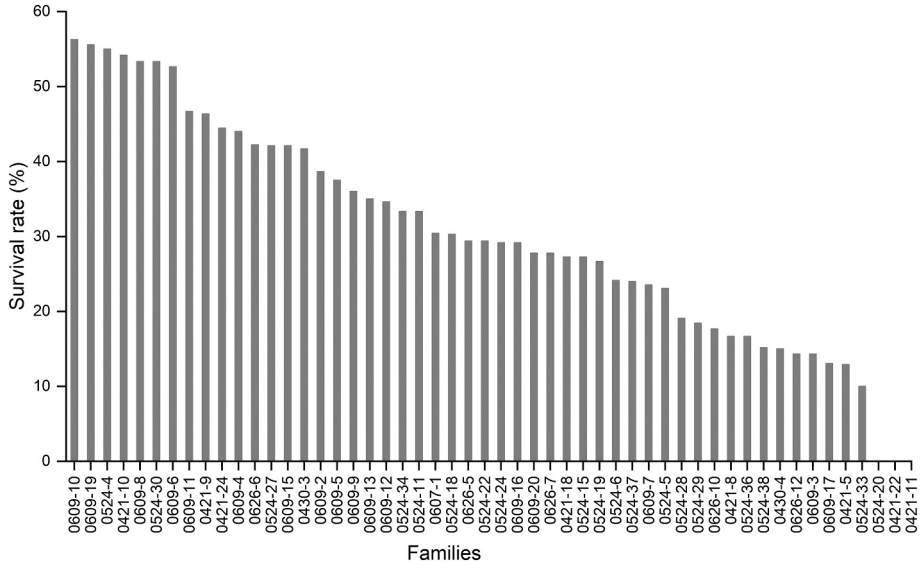

Fig. 2. The survival rate of 52 families at day 12 after challenge with *V. alginolyticus*.

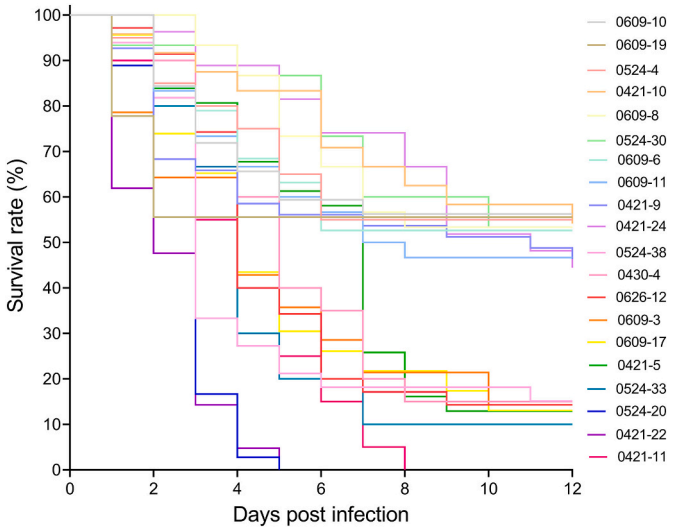

Fig. 3. Kaplan-Meier curves of 20 families (the top ten families and the last ten families in terms of survival rate) infected with *V. alginolyticus* during the 12-day challenge experiment.

of challenge test, and the threshold model apply to the evaluation of disease resistance traits could reflect the phenotypic classification characteristics of traits (Liang et al., 2017). Therefore, in this study, the disease resistance was recorded as a binary trait, and the linear model and threshold model were used to estimate the resistance of *C. gigas* to *V. alginolyticus*. High level of phenotypic variation for resistance to *V. alginolyticus* was observed, with the cumulative survival rate ranging from 56.25% of the resistant families to 0% of the susceptible families, suggesting a great potential to improve the resistance to *V. alginolyticus* using selective breeding. The correlation coefficients between family EBVs estimated by six different models suggested high consistency among the predicted EBVs with the different models. These results were consistent with observations from previous studies (Liang et al., 2017; Wang and Ma, 2019; Li et al., 2019; Hu et al., 2020).

Heritability reflects the genetic ability of traits, which is an important parameter for selective breeding of aquaculture animals (Visscher

Table 2
Estimation of variance components and heritability for resistance to *V. alginolyticus* in *C. gigas* using six different models.

Model	σ_a^2	σ_s^2	σ_d^2	σ_e^2	h^2
LAM	0.028 ± 0.009			0.182 ± 0.009	0.133 ± 0.040
LSM		0.010 ± 0.005	0.004 ± 0.004	0.196 ± 0.008	0.135 ± 0.041
TAMl	0.527 ± 0.159			3.2897	0.138 ± 0.036
TSMl		0.297 ± 0.153	0.095 ± 0.110	3.2897	0.213 ± 0.062
TAMp	0.193 ± 0.057			1	0.162 ± 0.040
TSMp		0.111 ± 0.057	0.036 ± 0.041	1	0.257 ± 0.071

Table 3
The Pearson rank correlation coefficients (above diagonal) and Spearman rank correlation coefficients (below diagonal) of EBVs of families between the different models.

Model	LAM	LSM	TAMl	TSMl	TAMp	TSMp
LAM		0.997**	0.997**	0.991**	0.996**	0.989**
LSM	0.995**		0.994**	0.995**	0.994**	0.993**
TAMl	0.998**	0.994**		0.995**	1.000**	0.994**
TSMl	0.993**	0.999**	0.993**		0.995**	1.000**
TAMp	0.998**	0.994**	1.000**	0.993**		0.994**
TSMp	0.993**	0.999**	0.992**	1.000**	0.992**	

** $P < 0.01$.

Table 4
The genetic and phenotypic correlations between survival and growth traits.

Traits	Survival (r_g)	Survival (r_p)
SL	0.379 ± 0.199	0.016 ± 0.030
SH	0.231 ± 0.200	0.029 ± 0.031
SW	−0.039 ± 0.276	0.044 ± 0.028

r_g for genetic correlation, r_p for phenotypic correlation.

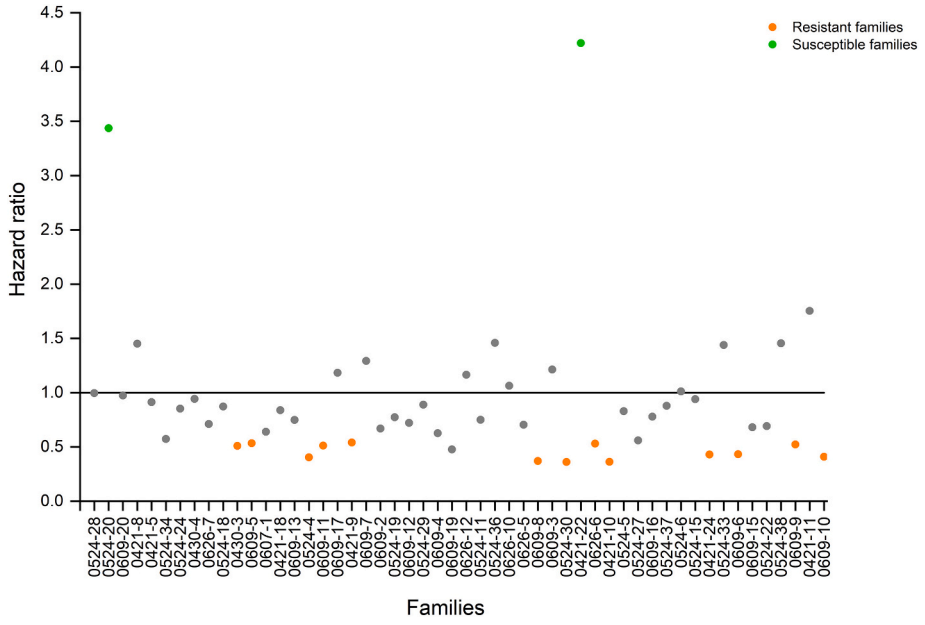

Fig. 4. Hazard ratio plot based on Cox regression analysis for resistance to *V. alginolyticus* in *C. gigas*. Families with hazard ratio values <1 ($P < 0.05$) were classified as resistant, and families with hazard ratio values >1 ($P < 0.05$) were classified as susceptible.

et al., 2008; Wang and Ma, 2019; Tang et al., 2020). Previous studies have shown that heritability can be divided into four levels: low (0.05–0.15), moderate (0.20–0.40), high (0.45–0.60) and very high (> 0.65) (Xu et al., 2015; Ma et al., 2018; Wang and Ma, 2019). In this study, six different statistical models were used to estimate heritability of resistance to *V. alginolyticus,* the results showed that the heritability was at a low to moderate level. The level of heritability estimated in this study was consistent with observations in other studies (Mahapatra et al., 2008; Yáñez et al., 2013; Li et al., 2019; Li et al., 2020; Hu et al., 2020; Ariede et al., 2020). The moderate heritability of resistance to *V. aestuarianus* was reported in the juvenile stage *C. gigas* (Azéma et al., 2017b). The estimate of genetic parameters in this study was based on a relatively small number of families, but heritability estimates were statistically reliable because these values had the low standard deviation (Ariede et al., 2020). The heritability values estimated by threshold model were higher than that by linear model, which were consistent with previous studies (Yáñez et al., 2013; Xiong et al., 2017; Barría et al., 2020). Some studies had suggested that it was more appropriate to choose threshold model to estimate heritability when the experimental data were recorded as cross-sectional binary data (Moreno et al., 1997; Xiong et al., 2017; Liang et al., 2017). For the low to moderate level of heritability as estimated in this study, previous studies had shown that breeding methods used in genetic improvement can be flexible except that breeding strategies should be carefully considered for traits with low levels of heritability (Xu et al., 2015; Ma et al., 2018; Wang and Ma, 2019). Traits with low levels of heritability were suitable for breeding by family selection if the common environmental effects remain at a low level (Rye et al., 1990; Wang et al., 2010; Ma et al., 2018; Wang and Ma, 2019). Therefore, family selection would be the preferred breeding approach for genetic improvement of resistance to *V. alginolyticus* in the Pacific oyster.

The phenotypic and genetic correlations between different traits are an important basis for designing breeding programs for multiple traits (Zhang et al., 2014; Ma et al., 2018). Level of correlations are caused by the different traits and the pleiotropy between genes and the linkage between genes (Falconer and Mackay, 1996; Xu et al., 2015; Bassini et al., 2019). In this study, all the genetic and phenotypic correlations between growth traits and resistance were not statistically significant ($P > 0.05$). Previous studies had shown that absolute value of correlations can be classified as low (0–0.40), medium (0.45–0.55), and high (0.60–1) (Cardellino and Rovira, 1987; Xu et al., 2015; Ma et al., 2018). Therefore, the genetic and phenotypic correlations between growth traits (SL, SH, SW) and resistance to *V. alginolyticus* were at a low level. Similar results had been reported in Chinese tongue sole and rainbow trout (Li et al., 2020; Silverstein et al., 2009). The results showed that growth (SL, SH, SW) and resistance to *V. alginolyticus* were two relatively independent traits that could be improved respectively, that was, selective breeding of resistance to *V. alginolyticus* would not have negative effects on the growth traits (SL, SH, SW) in *C. gigas*, or vice versa.

5. Conclusion

This study reported the first estimation of genetic parameters for resistance to *V. alginolyticus* in *C. gigas*. There was significant genetic variation for resistance to *V. alginolyticus*. The heritability of resistance to *V. alginolyticus* estimated based on six models was at a low to moderate level, suggesting that the resistance to *V. alginolyticus* could be improved by selective breeding. Furthermore, the genetic and phenotypic correlation between resistance to *V. alginolyticus* and growth traits were low, indicating the feasibility of simultaneous genetic improvement of both growth and resistance to *V. alginolyticus*.

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Declaration of Competing Interest

The authors declare no conflict of interest.

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