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### (G×E)

1 1,2\* 1

(1. 266003 266200)

2. (G×E)

G×E REML 11 (BLUP ) L\*

(0.14±0.08)~(0.62±0.18) (0.01±0.03)~(0.78±0.19)

(0.02±0.02)~(0.51±0.09)

/ (-0.47±0.40)~(0.75±0.18) 0.8

G1 G21 20 G4 G22 G5

G2

: (G×E)

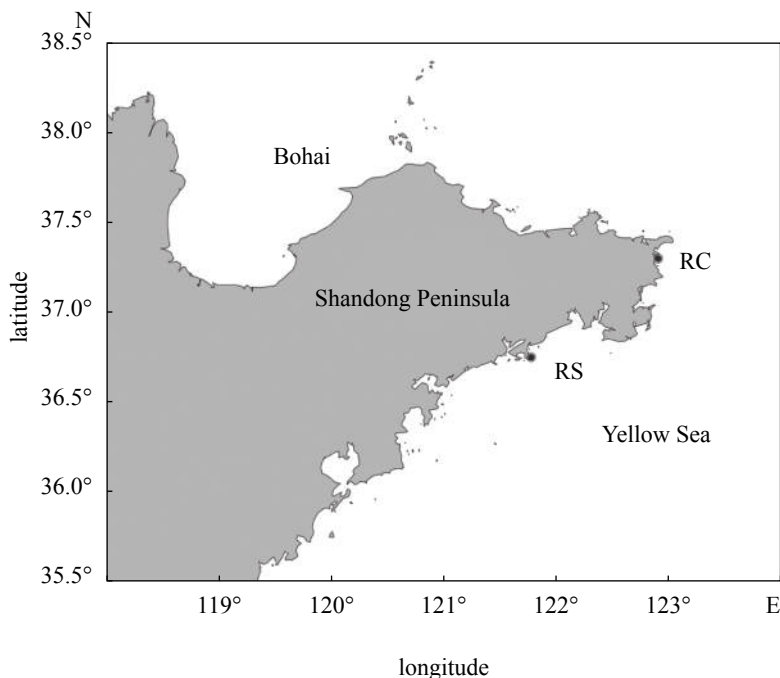
: Q 346 S 968.3 : A

(*Crassostrea gigas*)

( ) ( ) <sup>[1]</sup> (genotype by environ-  
ment interactions, G×E) G×E

4 <sup>[1]</sup> <sup>[2]</sup> 2010 <sup>[3]</sup>

Evans <sup>[8]</sup> 24 G×E 4 <sup>[4-7]</sup> 1 1/2  
 (Platymonas sp.) (Isochrysis galbana)  
 5 G×E Swan <sup>[9]</sup> 2 2 10 d  
<sup>[10]</sup> 5 2017  
 G×E (BLUP ) 2  
 (36.75°N 121.65°E)  
 (37.30°N 122.59°E)( 1)  
<sup>[11]</sup> BLUP 14.2 °C  
<sup>[12-14]</sup> 30 pH 8.0<sup>[17]</sup> 0.5 m<sup>[18]</sup>  
 2.4 m<sup>[19]</sup>  
 BLUP G×E 12.95 °C 32.2 pH 8.15<sup>[20]</sup>  
 0.3 m 0.7 m<sup>[19]</sup>  
**1.4**  
 1 18  
**1.1** <sup>[21]</sup> 11  
 2016 6 (%)= / ×100  
 6 Brake <sup>[22]</sup> A  
 (ISA, %)= / ×100 B (ISB, %)=  
 / ×100  
 Comstock <sup>[15]</sup> 6%  
 3  
 10 30 2 h  
<sup>[2]</sup> (computer vision  
**1.2** system, CVS)  
 100 L 2 D<sub>65</sub>(6 500 K)  
 20~30 /mL 23~24 °C 45° 5  
 22 h  
 D 10 /mL  
<sup>[16]</sup> D 5~6  
 /mL 1~2 /mL



1 (RS) (RC)  
**Fig. 1** Locations of growout environments in Rushan (RS) and Rongcheng (RC)

$L^*$   $a^*$   $b^*$

[24]

$$L^* = \frac{\text{lightness}}{255} \times 100 \quad (1)$$

$$a^* = \frac{240a}{255} - 120 \quad (2)$$

$$b^* = \frac{240b}{255} - 120 \quad (3)$$

$L^*$  100

0  $a^*$

$b^*$

[25]

**1.5**

Excel 2010 SPSS

20.0

$L^*$   $a^*$   $b^*$

$t$  2

ASReml

$$Y_{hijk} = \mu + Env_h + a_i + d_j + I_{ik} + a_i(Env_h) + e_{hijk} \quad (4)$$

$Y_{hijk}$   $\mu$

$Env_h$   $h$   $a_i$   $I_{ik}$

$d_j$   $a_i(Env_h)$   $e_{hijk}$

(likelihood ratio tests)

[26] (4)  $d_j$   $I_{ik}$

$Y_{hi} = \mu + Env_h + a_i + a_i(Env_h) + e_{hi} \quad (5)$

(5)

2

$G \times E$  (5)  $Env_h$

$a_i(Env_h)$

$Y_i = \mu + a_i + e_i \quad (6)$

(6) 2

(6) [27] 2

$L^*$

2

$L^*$

[12]

(0.14±0.08)~(0.62±0.18)

$L^*$  (0.01±0.03)~(0.78±0.19)

$$A_i = W_1 a_{1i} + W_2 a_{2i} \quad (7)$$

ISA

0.5U  $a_{1i}$   $a^*$

ISA ISB  $L^*$   $a^*$   $b^*$

0.5U  $a_{2i}$   $i$   $L^*$  ISB  $L^*$   $b^*$

2

2.1

2

(P<0.05)( 1)

L\*  $a^*$  ( 2)

(P<0.01)

ISA ISB  $b^*$  (P<

0.05)

2.2 G×E

G×E ( 2)

1

**Tab. 1 Phenotypic parameters of growth and shell color related traits in strains of the white shell *C. gigas* in two environments**

trait	RS						RC					
	no.	minimum	maximum	mean	SD	CV	no.	minimum	maximum	mean	SD	CV
shell height /mm	446	29.43	74.95	53.05	8.25	15.56	487	23.85	65.94	39.61	6.91	17.44
shell length /mm	446	12.11	57.08	33.39	5.92	17.73	487	13.19	43.26	27.81	5.49	19.76
shell width /mm	446	7.88	69.43	16.58	4.47	26.99	487	1.12	28.48	13.47	3.07	22.78
total weight /g	446	5.31	36.25	14.49	4.99	34.46	487	1.73	20.08	7.53	3.36	44.58
shell weight /g	444	3.44	29.93	10.65	3.85	36.15	485	1.17	13.49	5.16	2.28	44.25
meat weight /g	438	0.33	13.12	3.91	1.80	46.06	485	0.24	6.94	2.38	1.27	53.21
meat ratio /%	438	1.79	71.02	26.83	7.22	26.91	485	6.96	67.73	31.03	7.65	24.66
ISA A/%	446	0.12	1.36	0.32	0.09	28.33	487	0.03	0.68	0.35	0.08	22.19
ISA B/%	446	0.21	1.08	0.64	0.13	20.44	487	0.37	1.05	0.71	0.11	15.98
ISB $L^*$	429	45.35	73.02	63.63	3.60	5.66	438	34.44	76.70	60.50	4.87	8.05
$a^*$	429	-3.23	0.87	-2.26	0.47	-20.92	438	-4.90	-1.35	-2.86	0.53	-18.56
$b^*$	429	-12.01	11.54	-4.67	3.31	-70.87	438	-15.88	11.65	-4.06	3.71	-91.46

**Tab. 2 Genetic parameters of growth and she**  
**the white shell *C. gigas* in two**

	heritabilities	
	RS	RC
l height	0.55±0.16	0.57±0.16
ell length	0.24±0.11	0.48±0.15
hell width	0.23±0.10	0.39±0.13
al weight	0.53±0.16	0.75±0.18
ell weight	0.46±0.15	0.66±0.17
neat weight	0.50±0.16	0.76±0.18
o meat ratio	0.30±0.12	0.52±0.16
A/% ISA	0.14±0.08	0.08±0.05
B/% ISB	0.40±0.14	0.01±0.03
	0.21±0.39	0.18±0.09
	0.62±0.18	0.78±0.19
	0.56±0.17	0.43±0.15

BLUP  
L\* 20  
20

34~0.63

2

0.28~

## 3

Tab. 3 Ranks of comprehensive breeding values of the white shell *C. gigas* in two environments

rank	RS			RC		
	ID	EBV	family	ID	EBV	family
1	RS_133	6.28	G2	RC_494	6.88	G22
2	RS_115	6.15	G1	RC_122	5.36	G2
3	RS_113	6.00	G1	RC_204	5.01	G5
4	RS_137	5.98	G2	RC_177	4.92	G4
5	RS_108	5.67	G1	RC_190	4.71	G4
6	RS_118	5.64	G1	RC_178	4.71	G4
7	RS_474	5.48	G21	RC_114	4.47	G2
8	RS_152	5.45	G3	RC_535	4.39	G25
9	RS_112	5.42	G1	RC_219	4.39	G5
10	RS_150	5.39	G3	RC_196	4.09	G4
11	RS_103	5.32	G1	RC_112	4.03	G2
12	RS_132	5.28	G2	RC_488	3.93	G22
13	RS_470	5.28	G21	RC_109	3.78	G1
14	RS_465	5.26	G21	RC_174	3.73	G4
15	RS_135	5.11	G2	RC_517	3.73	G25
16	RS_146	5.10	G2	RC_193	3.70	G4
17	RS_129	4.97	G1	RC_508	3.67	G22
18	RS_130	4.97	G1	RC_181	3.65	G4
19	RS_476	4.94	G21	RC_116	3.61	G2
20	RS_128	4.94	G1	RC_212	3.60	G5

Evans <sup>[8]</sup>	0.81~0.97			G×E	<sup>[36]</sup>
	4				
		G×E			
Langdon <sup>[33]</sup>	2%	5%		G×E	
			G×E		
<sup>[10]</sup>			—		
	—			L*	
37%					
	(-0.47±0.40)~(0.75±0.18)				
0.8					20
	<sup>[34]</sup>		90%	G1(45%)	G2(25%)
			G21(20%)		85%
			G4(35%)	G2(20%)	G22(15%)
<sup>[35]</sup>					G5(15%)
					25%

- G2(20%) G1(5%) 75%
- G1 G21
- G4 G22
- G5 G2
- G×E
- G1 G21
- G4 G22 G5
- G2
- [ 1 ] , , , . 4  
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## Genotype by environment (G×E) interaction for growth and shell color traits in the white-shell strain of Pacific oyster (*Crassostrea gigas*)

XING De<sup>1</sup>, LI Qi<sup>1,2\*</sup>, ZHANG Jingxiao<sup>1</sup>

(1. Key Laboratory of Mariculture, Ministry of Education, Ocean University of China, Qingdao 266003, China;

2. Laboratory for Marine Fisheries Science and Food Production Processes, Qingdao National Laboratory for Marine Science and Technology, Qingdao 266200, China)

**Abstract:** The purpose of the present study is to reveal the genotype by environment (G×E) interactions on growth and shell color traits in the white-shell strain of Pacific oyster (*Crassostrea gigas*). The specimens of the white shell strain of *C. gigas* under six-generation of selection as parents were used to construct full-sib families following the method of nested design. All families were divided into two batches and grown in two environments, Rushan and Rongcheng. Linear mixed model and REML method based on an animal model were applied to estimate genetic parameters of white shell *C. gigas* at the age of 11 months. The best linear unbiased prediction (BLUP) method was used to estimate breeding values for shell height and  $L^*$ , and superior families were selected based on comprehensive estimated breeding values. The results showed that heritabilities for growth and shell color traits in Rushan ranged from  $0.14 \pm 0.08$  to  $0.62 \pm 0.18$ , while these were different in Rongcheng, varying from  $0.01 \pm 0.03$  to  $0.78 \pm 0.19$ , which indicated that G×E interactions might be present as scale effects. After integrating the data in two different environments, heritabilities for growth and shell color traits ranged from  $0.02 \pm 0.02$  to  $0.51 \pm 0.09$ . However, the estimates of heritabilities might be over-estimated because maternal/common environmental effects and dominance effects were included in the estimation model due to absence of some families and convergence problem. Genetic correlations for all growth and shell color traits between two environments, ranging from  $-0.47 \pm 0.40$  to  $0.75 \pm 0.18$ , were less than 0.8. This suggested that G×E interactions in the form of re-ranking of families across environments was apparent. It will be necessary to select lines that are suited to particular sites. The top 20 offspring in the rank of comprehensive estimated breeding values derived from different families in two different environments, indicating that the different families performed differently across the different rearing sites. The families G1 and G21 performed better in Rushan area, while the G4, G22 and G5 were most excellent families in Rongcheng area, and family G2 had high adaptability to both sites. The information obtained in this study will benefit genetic improvement of the white shell strain of *C. gigas*.

**Key words:** *Crassostrea gigas*; white-shell ; growth traits; shell color traits; genotype by environment (G×E) interaction; breeding value

**Corresponding author:** LI Qi. E-mail: qili66@ouc.edu.cn

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