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1 1,2 1 1

(1. , 266003; 2. , 266200)

: 7 , 12

29 , ,

3.65%—14.58% 1.11%—19.26%; ($P<0.05$), G11 G15

G35 , 19 ,

11.87% 17.03% 30.32%, 38.35% 33.41% 51.07%; ,

34.09% 28.18% 49.31%, 65.00% 59.11% 80.18%

0.88, ; 0.28—0.81 0.42—

0.35—0.81 0.57—0.85

: ; ; ; ;

: Q344⁺.5 : A : 1000-3207(2019)02-0315-07

(*Crassostrea gigas* Thunberg) , ,

, [3]

, (*Argopecten irradians*)^[4, 5] , (*Ruditapes philippinarum*)^[6, 7]

, 2016 , (*Pinctada martensii*)^[8] (*Cyclina sinensis*)^[9] ,

34.03%^[11] ,

[2] , ,

[10]

, Dégremont

, [11, 12] Langdon [13] Evans [14]

[15, 16]

: 2018-04-11; : 2018-09-25

: (2016ZDJS06A06); (2017LZGC009) [Supported by Taishan Scholar Seed Industry Experts Project; Shandong Key Research and Development Project (2016ZDJS06A06); Agriculture for Project Funding of Shandong Province (2017LZGC009)]

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[17]

(ANOVA) Tukey
 $P < 0.05$

7

29

$$(\%) = \frac{\quad - \quad}{\quad} \times 100$$

$$(\%) = \frac{\quad - \quad}{\quad} \times 100$$

ASReml 3.0 (REML)
[17]

1

1.1

2017 5 4 3
7 (F7)

$$Y_{ijk} = \mu + a_{ijk} + f_{ijk} + e_{ijk}$$

Y_{ijk} , μ , a_{ijk} , f_{ijk} () , e_{ijk}

2017 6 ,
5 L , 12
, 36 3

e_{ijk}

2

2.1

3 ,
($P > 0.05$);

1.2

100 L , 3
1 100 L ,
20—40 /mL 22h ,
D , 300 ,
300 240 L ,
[15],
10—12 /
mL , 1 ,
1/3;

7 11

1.11%—19.26% , G7 G9 G13 3
, 19
13.88% 12.29% 13.64%;
G1 G3 G4 G11 G15 G28 G32 G35
, 19 ,
54.17% 31.58% 42.86% 33.33%
32.14% 30.77% 59.15% 36.40%,
($P < 0.05$, 1)

(*Isochrysis galbana*) (*Platymonas* sp.);
230 160

(ANOVA) ,

; 2 1 ,
23—25 ,

F ($P < 0.01$);

1.3

D , 3 7
11 15 19 ,
3 , ; ,
30 , ,

Tukey , (1)

3.65%—14.58% , 3
7 11 15 19

1.4

Excel 2016 SPSS 20.0

G4 G21

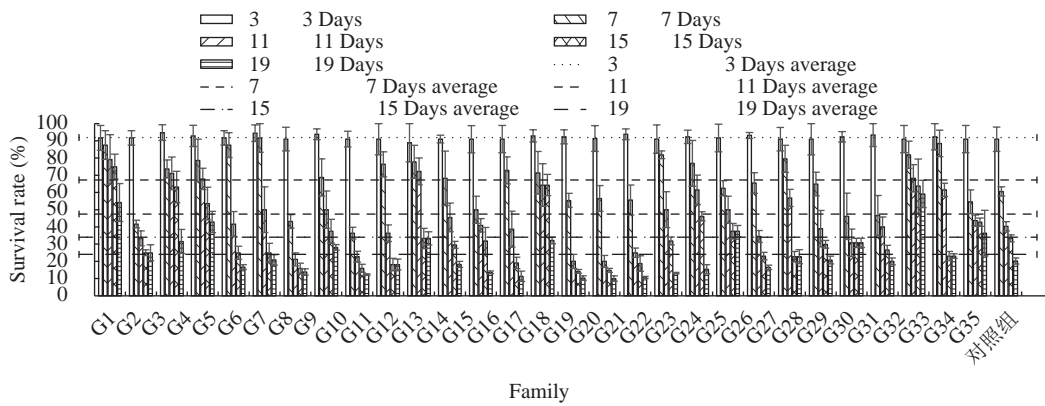
pin
 , G9 G10 G11 G15 G16 , 3 7 11 15 19 ,
 G35 19 , 33.37% 0.35—0.81 0.57—
 22.35% 17.03% 11.87% 23.09% 40.80%, 0.85, (4)
 52.81% 40.18% 34.09% 28.18%
 41.03% 61.32%(2) **3**

2.3

3.1

3 7 11 15
 19 , [18]

0.28—0.81,
 0.42—0.88,
 3 15 ,
 0.81±0.15 0.88±0.15; 7
 3 , 0.28±0.09 0.42±0.11(3) ,



1
 Fig. 1 The survival rate of different families at larval stage of *C. gigas*

1
 Tab. 1 Components of phenotypic variation of white shell families of *C. gigas* larvae at different stages

Age (d)	Traits	Source of variance								
		Sires			Sams			Progenies		Total
		df	MS	F	df	MS	F	df	MS	df
3	SH	11	1565.60	25.03**	28	1063.26	21.75**	869	81.57	908
	SL	11	1446.85	19.19**	28	826.37	12.09**	869	92.75	908
7	SH	11	2886.64	21.80**	28	1612.30	11.46**	869	235.54	908
	SL	11	1116.13	8.41**	28	1081.55	9.48**	869	145.16	908
11	SH	11	11012.26	26.68**	28	6424.59	16.53**	869	635.10	908
	SL	11	4859.49	13.65**	28	4462.36	16.03**	869	413.07	908
15	SH	11	24820.53	33.39**	28	13989.00	21.32**	869	1143.15	908
	SL	11	14728.30	34.90**	28	9059.20	28.17**	869	603.07	908
19	SH	11	49985.33	26.56**	28	29505.72	17.27**	869	2757.61	908
	SL	11	34683.49	35.74**	28	18004.78	21.32**	869	1397.25	908

: SH , SL ; ** ($P<0.01$),
 Note: SH means shell height, SL means shell length; **means very significant difference ($P<0.01$), the same applies below

[19] , 10.0%,
 12%, 14.2% Dégremont
 [20] , [11] 43 ,
 2 , [22] 25 ,
 Langdon [13] ,
 2.27%—16.67% 1.72%—9.40%
 9.5%; Taris [21] 30 ,
 2

Tab. 2 The shell height of different families at larval stage of *C. gigas*

Family	Age (d)				
	3	7	11	15	19
G1	86.71±5.25 ^{a-e}	110.54±9.96 ^{de}	130.9±21.51 ^{e-i}	144.23±11.12 ^{a-f}	162.74±31.8 ^{ab}
G2	82.03±4.83 ^a	101.46±25.76 ^{a-e}	118.89±26.01 ^{a-f}	152.1±35.35 ^{c-g}	190.8±32.62 ^{a-f}
G3	84.92±4.93 ^{a-d}	100.77±16.05 ^{a-e}	115.4±9.33 ^{a-f}	135.2±28.3 ^{a-d}	150.23±34.06 ^a
G4	82.51±6.21 ^a	101.67±13.48 ^{a-e}	116.17±25.28 ^{a-f}	121.14±13.83 ^a	149.07±30.01 ^a
G5	84.93±5.83 ^{a-d}	96.24±11.04 ^a	122.76±29.23 ^{b-g}	158.07±32.71 ^{d-g}	173.16±18.25 ^{abc}
G6	88.65±8.18 ^{a-f}	102.92±21.03 ^{a-e}	134.27±35.69 ^{f-i}	146.07±34.59 ^{a-f}	160.11±17.6 ^{ab}
G7	86.44±9.26 ^{a-e}	94.47±9.94 ^a	127.4±19.08 ^{c-g}	157.2±34.26 ^{d-g}	227.85±48.7 ^{gh}
G8	87.45±6.65 ^{a-e}	106.05±11.52 ^{a-e}	131.54±33.09 ^{e-i}	165.77±20.61 ^{fgh}	185.75±26.29 ^{a-e}
G9	89.71±5.35 ^{b-f}	103.54±8.97 ^{a-e}	141.97±22.79 ^{ghi}	185.95±26.77 ^{hij}	254.34±41.78 ^h
G10	88.34±9.74 ^{a-f}	110.03±21.4 ^{b-e}	151.09±18.14 ^{ij}	195.02±30.61 ^{ij}	233.32±51.2 ^{gh}
G11	82.17±7.05 ^a	104.59±10.1 ^{a-e}	148.03±22.85 ^{hij}	193.55±54.35 ^{ij}	223.17±54.4 ^{c-h}
G12	92.66±10.03 ^{e-h}	99.26±15.66 ^{a-d}	119.95±35.64 ^{a-f}	147.68±26.38 ^{b-f}	182.46±28.3 ^{a-e}
G13	103.48±9.98 ^{ij}	113.29±27.71 ^c	120.11±25.24 ^{a-f}	150.89±47.18 ^{c-f}	152.63±19.07 ^a
G14	89.91±8.42 ^{c-g}	95.73±10.76 ^a	108.52±16.16 ^{abc}	135.81±17.61 ^{a-d}	231.54±64.03 ^{fgh}
G15	90.78±8.55 ^{d-g}	106.39±10.91 ^{a-e}	130.18±15.04 ^{e-h}	162.89±24.28 ^{e-h}	213.33±92.67 ^{c-h}
G16	98.22±6.85 ^{hi}	103.43±6.47 ^{a-e}	131.53±11.61 ^{e-i}	177.72±21.33 ^{ghi}	234.72±51.56 ^{gh}
G17	83.05±5.58 ^{ab}	94.43±4.96 ^a	115.01±6.15 ^{a-f}	149.01±5.43 ^{b-f}	201.49±44.38 ^{b-g}
G18	84.95±5.28 ^{a-d}	100.51±10.57 ^{a-e}	116.49±27.44 ^{a-f}	159.15±23.08 ^{d-g}	217.11±57.15 ^{c-h}
G19	90.62±5.73 ^{d-g}	94.93±7.45 ^a	105.8±9.14 ^{ab}	127.92±10.32 ^{abc}	182.39±48.85 ^{a-e}
G21	90.74±5.21 ^{d-g}	95.96±5.71 ^a	109.6±5.89 ^{a-d}	136.19±4.65 ^{a-d}	175.49±51.06 ^{a-d}
G22	94.64±5.49 ^{fgh}	98.88±14.62 ^{a-d}	107.18±3.38 ^{abc}	137.01±17.97 ^{a-d}	167.15±35.6 ^{ab}
G23	91.41±3.73 ^{d-g}	106.13±4.17 ^{a-e}	121.83±20.63 ^{a-g}	143.53±6.47 ^{a-f}	174.02±22.29 ^{abc}
G26	92.65±5.33 ^{e-h}	97.83±7.05 ^{a-d}	111.22±24.72 ^{a-e}	146.72±9.68 ^{a-f}	168.21±27.34 ^{ab}
G27	92.39±6.09 ^{e-h}	99.52±10.93 ^{a-d}	131.09±13.81 ^{e-i}	134.7±19.75 ^{a-d}	181.75±32.32 ^{a-e}
G28	96.64±4.18 ^{gh}	110.22±8.81 ^{cde}	129.07±14.89 ^{d-h}	138.61±13.42 ^{a-e}	168.77±43.14 ^{ab}
G31	94.73±8.28 ^{fgh}	98.88±7.91 ^{a-d}	121.98±14.32 ^{a-g}	123.61±9.52 ^{ab}	158.18±59.5 ^a
G32	92.88±1.9 ^{e-h}	97.01±8.88 ^{abc}	103.43±8.05 ^{ab}	147.92±14.77 ^{b-f}	170.72±32.59 ^{ab}
G33	83.7±7.18 ^{abc}	96.83±2.34 ^{ab}	102.42±6.86 ^a	137.74±20.8 ^{a-e}	171.1±10.25 ^{ab}
G35	105.6±11.78 ^j	129.09±26.9 ^f	162.98±28.07 ^j	206.46±56.35 ^j	248.5±45.98 ^h
	90.1±9.03	102.43±15.35	123.68±25.20	152.34±33.81	190.00±52.51
	85.71±5.86	99.16±14.15	115.15±11.31	140.23±29.07	166.43±41.55

Note: The ‘—’ indicates continuous strings of letters which omitted between the first and the last letter. Values with different superscripts letters in the same column mean significant differences at $P < 0.05$

3

Tab. 3 Heritabilities of growth traits in white shell *C. gigas* larvae at different stages

Trait	Age (d)				
	3	7	11	15	19
SH	0.81±0.15	0.28±0.09	0.53±0.12	0.63±0.13	0.59±0.13
SL	0.42±0.11	0.56±0.13	0.81±0.15	0.88±0.15	0.62±0.13

4

Tab. 4 Genetic and phenotypic correlations of growth traits in white shell *C. gigas* larvae at different stages

Correlation	Age (d)				
	3	7	11	15	19
Genetic correlation	0.81±0.05	0.67±0.01	0.48±0.01	0.47±0.01	0.35±0.01
Phenotypic correlation	0.57±0.04	0.71±0.02	0.76±0.03	0.83±0.02	0.85±0.02

G10 G11 G15 G16 G35

G1 G3 G4 G11 G15 G28 G32 G35

7 G11 G15 G35

3.2

29 3 7 11 15 19
0.28—0.81 0.42—0.88,^[15]
Hedgecock^[23] 0.20; Lannan^[24] 11—15
18
0.15 0.33 0.32 0.37; Dégremont^[11]
43 6—8
0.47—1.08; Kong^[25]
, 12

0.45±0.23 0.35±0.17;^[16] 0.49±0.25 0.36±0.19
24 36 , 360

[10] Losee^[26]
(*Crossostrea virginica*)
; Newkirk Haley^[27]
(*Ostrea edulis*) 1
; Collet^[28]
; Ernande^[29]

4

G11 G15
G35 , 19
11.87%—30.32%, 28.18%—
49.31%;
30% , G11 G15 G35

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GENETIC PARAMETERS AND GROWTH TRAITS IN WHITE SHELL FAMILIES OF PACIFIC OYSTER (*CRASSOSTREA GIGAS*)

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Abstract: Pacific oysters (*Crassostrea gigas*), the most widely cultivated shellfish over the world with advantages of fast growth and strong environmental adaption, are suitable materials for selective breeding due to the characters of high fertility, short reproductive cycle and large genetic variation. Broodstocks from white shell strain of *C. gigas* that had undergone four-generation family selection and three-generation mass selection were used to establish 29 full-sib families and 12 half-sib families by nested design. Random selected individuals were utilized as parents to generate the control families. Phenotypic traits such as growth and survival rate of different periods in larval stage were analyzed. Results showed that the growth performance and average survival rates of white shell families were significantly higher than those of control group with the augmentation of 3.65% to 14.58% and 1.11% to 19.26% in a family dependent pattern, respectively. The G11, G15 and G35 families represented remarkable superiorities in shell height and survival rates. At the age of 19 days, the increased shell heights of G11, G15 and G35 families were bigger than the average values of white shell families by 11.87%, 17.03%, and 30.32%, respectively, and were greater than the average values of the control by 34.09%, 28.18%, and 49.31%, respectively. Besides, the survival rates of G11, G15 and G35 families at 19d were higher than the average values of both white shell by 38.35%, 33.41%, 51.07%, and control families by 65.00%, 59.11%, and 80.18% (G35), respectively. Results of genetic parameters of larvae shell height and shell length of white shell strain indicated that the variation of heritability was ranged from 0.28 to 0.81 in shell height and from 0.42 to 0.88 in shell length, representing the heritability at medium to high level. The genetic and phenotypic correlations were positive between the two growth traits with the correlation coefficients ranging from 0.35 to 0.81 and from 0.57 to 0.85, respectively. This study provides optimum breeding strategy for white shell strains of *C. gigas* to improve performance in growth and survival.

Key words: *Crassostrea gigas*; White shell families; Larval; Growth traits; Genetic parameters