Journal of Fisheries of China
ISSN 1000-0615,CN 31-1283/S

2021-10-09
2022-01-11

[J/OL] .
https://kns.cnki.net/kcms/detail/31.1283.S.20220110.1726.002.html

[redacted]

---

1 1 1 1 1,2✉

1. 266003

2. 266237

* E-mail qili66@ouc.edu.cn

3 1 G_1 48 863 REML 863 851 a^*( ) b^*( ) ΔE( ) 0.47±0.23 0.42±0.21 0.56±0.29 4 -0.79~0.86 -0.45~0.48 -0.33~0.17 -0.04~0.11

DOI: 10.11964/jfc.20211013102

Estimates of genetic parameters for orange shell color and correlation with growth traits in the improved orange shell line of Pacific oyster (*Crassostrea gigas*)

CHEN Yulu[1], XU Chengxun[1], LIU Shikai[1], KONG Lingfeng[1], LI Qi[1,2]✉

(1. Key Laboratory of Mariculture of Ministry of Education, Ocean University of China, Qingdao 266003, China; 2. Laboratory for Marine Fisheries Science and Food Production Processes, Pilot National Laboratory for Marine Science and Technology (Qingdao), Qingdao 266237, China)
*LI Qi. E-mail: qili66@ouc.edu.cn

Abstract The Pacific oyster (*Crassostrea gigas*) is one of the most widely farmed shellfish species in the world. With the rise of within-shell oyster market, shell color trait is increasingly of interest to the breeding industry and has been a target trait for selection. In our previous breeding process, an improved orange shell line of *C. gigas* with a unique shell color was established by the means of hybridization and mass selection. However, the genetic parameter of shell color trait and correlation with growth traits for the improved orange-shell line remains undocumented. This study aimed to estimate genetic parameters (heritability and correlations) for *C. gigas* at 10 months of age by applying mixed-family approach combined with a nested mating design and CVS imaging system. In this study, heritability for shell color-related traits was estimated in the improved orange shell line of *C. gigas* by fostering a single cohort of 48 families consisting of 16 sires and 48 dams. A total of 863 offspring were harvested at 10 mouth age. Pedigree was reconstructed with 12 microsatellite markers. The shell color parameters of selected oysters were measured based on the computer vision system and Lab colorimetric system. REML based on the animal model was used to estimate the genetic parameters of orange shell color traits and correlation with growth traits

---

2021-10-09

(2020LZGC016) (20-3-4-16-nsh)

E-mail chenyulu9712@126.com

Fund Agriculture Seed Improvement Project of Shandong Province (2020LZGC016); Science and Technology Benefiting People Demonstration Project of Qingdao City (20-3-4-16-nsh)

of *C. gigas*. The results of parentage assignment showed that 98.61% of the oysters were unambiguously assigned to single parent pairs. Unbalanced contributions of parents were found among families and parents. Coefficients of variation of the progeny were 16.51%-39.62% for growth traits, and 3.70%–43.32% for shell color parameters, suggesting that there was great genetic variation among growth traits. Heritabilities of L^*, a^*, b^*, and ΔE were 0.17±0.07, 0.47±0.23, 0.42±0.21, 0.56±0.29, respectively. The phenotypic correlations and genetic correlations of L^*, a^*, b^* and ΔE were with the ranges of -0.4-0.48 and -0.79-0.86, respectively. The phenotypic correlations and genetic correlations between the growth traits and shell color traits were low, ranging from -0.04-0.11 and -0.33-0.17 respectively. These results indicated that the breeding population had considerable additive genetic variation in orange shell color traits, and the ongoing selective breeding program should produce considerable genetic improvement in the orange shell color traits of *C. gigas*. However, indirect selection of growth traits using the shell color trait is infeasible due to their low correlations. Only both the shell color traits and growth traits were selected as the targets of selective breeding, the traits could be improved. Furthermore, our studies further confirmed the feasibility of the posteriori family reconstruction based on molecular markers in a communal rearing environment. The present study provides important information for future selective breeding programs for *C. gigas* with orange shell color trait.

Key words *Crassostrea gigas*; shell color; growth traits; microsatellite; genetic parameter

(*Crassostrea gigas*)

2020 542 t[1]

[2-4]

(*Azumapecten farreri*) (*Ruditapes philippinarum*) (*Meretrix meretrix*) [5-8]

[9]

[10-14]

48

Lab

1

1.1

1

(G_1) 2020 4 1 (G_1)

2020 5

1 3 48 16

70%

1.2

100 L

20~40 /mL 24 22 h D
48 30~40 /mL 2 L 2 500 L
[15] 8~10 /mL
2~3 /mL 1 1/3 4
(*Isochrysis galbana*) (*Platymonas* sp.)
30%

Panel 3	*ucdCg*-152	F-TGTAAAACGACGGCCAGTTGGTTTTGGAGCTTGGCTTA VIC R-TCAAGCAAAGAAAGTCACCTCA	50	257
	*Crgi*39	F-TGTAAAACGACGGCCAGTTTCCAAGTCCGTTTTGTCATCGT VIC R-GTGCACAAACCCACCATCAGCTC	50	190~214
	*Crgi*45	F-TGTAAAACGACGGCCAGTGAGTCACCATGAAGAGTATCTGAA VIC R-ATGATTACATAACTCTGACCCAAT	50	158~164
Panel 4	*otgfa*0_0007_B07	F-TGTAAAACGACGGCCAGTTATCATCGCGGCAATTCGTG PET R-GCAACTTAGCTGGTCGTTCC	50	279~295
	*otgfa*0_0129_E11	F-TGTAAAACGACGGCCAGTTGACTGTTCTTCGTACCCATCA PET R-AGGTGGAACGAGATTGCCTTT	50	155
	*Crgi*4	F-TGTAAAACGACGGCCAGTCCAAAACACGATAAGATACACTTTC PET R-GATCAGTCCCTCACATCTTTCCTC	50	235

Notes: bold are the different fluorescent dyes used

1.5

SPSS 18.0 Excel

ASREML 3.0 REML

$$Y_{ijk}=\mu+\alpha_{ijk}+I_{ij}+e_{ijk}$$

i j k k Y_{ijk} μ

α_{ijk} I_{ij} e_{ijk}

ASREML 3.0

2

2.1

12 10.6 0.62 0.67 (PIC) 0.62 10 000 99.98% 95% 863 851 98.61% 48 (2) 6~48 2 4 48

2

Tab. 2 Number of progeny assigned to each of the 48 full-sib families based on microsatellite genotyping

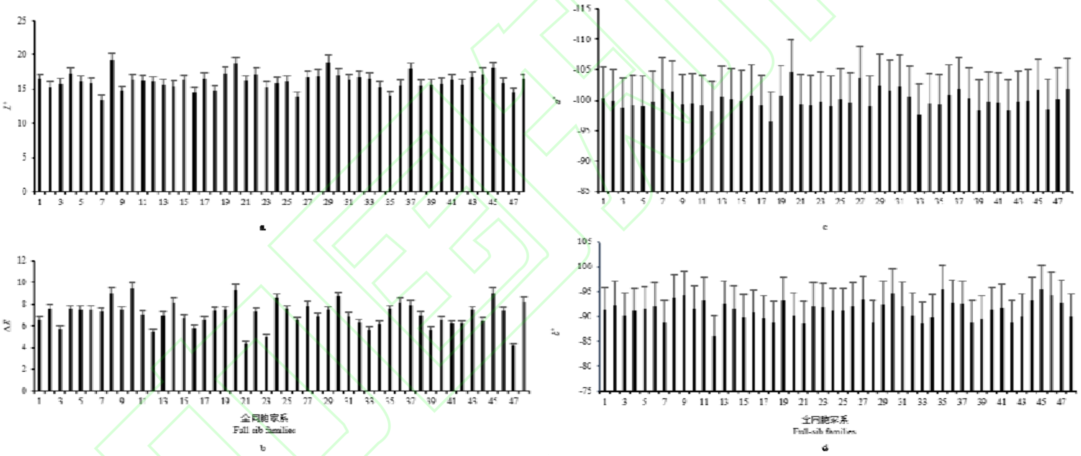
	sire number															
family number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	44/44/14															
2		48/39/44														
3			6/9/6													
4				12/10/7												
5					35/41/14											
6						7/14/14										
7																
14																

11											12/10/8					
12												24/7/38				
13													7/14/20			
14														26/28/36		
15															26/8/9	
16																8/6/7
total	102	131	21	29	90	35	24	47	43	35	30	69	41	90	43	21

-/-/-

Notes: each family is coded by its dam number. -/-/- means the number of progeny produced by sire and dam in each half-sibling families

48 L^* a^* b^* ΔE 12 4 b^* -85.93 47 16 ΔE 4.21(1) (3) 39.62% 16.51%~21.10% L^* ΔE L^* ΔE L^* ΔE a^* b^* 3.70%~5.70%



1

(a)~(d) L^* ΔE a^* b^* ±

Fig.1 Shell color-related trait performance in terms of L^*, a^*, b^*, and ΔE of *C. gigas*

Parameter values of L^*, ΔE, a^* and b^* are showed in figure (a)-(d), respectively; The shell color-related trait performances are represented by mean±SD. Each family is coded by its dam number

3

Tab. 3 Descriptive statistic of the orange shell color-related parameters (L^*, a^*, b^* and ΔE) and the growth-related traits of *C. gigas*

trait	mean	SD	CV /%
L^*	16.08	3.19	19.84
a^*	-99.75	3.69	3.70
b^*	-91.15	5.20	5.70
ΔE	7.11	3.08	43.32
/mm SH	53.92	8.93	16.51
/mm SL	34.60	7.19	20.78
/mm SW	18.24	3.85	21.10
/g TW	16.91	6.70	39.62

2.2

4

L^* 0.17±0.07 a^* b^* ΔE
0.47±0.23 0.42±0.21 0.56±0.29(4)
L^* ΔE
0.51±0.30 0.08±0.04 b^* L^* a^* ΔE
-0.79±0.24 -0.64±0.31 -0.68±0.52

4 L^* a^* b^* ΔE

Tab.4 Heritabilities (in the diagonal), genetic correlations (above the diagonal) and phenotypic correlation (below the diagonal) of shell color parameters of *C. gigas*

parameter	L^*	a^*	b^*	ΔE
L^*	0.17±0.07	0.86±0.45	-0.79±0.24	0.51±0.30
a^*	-0.09±0.04	0.47±0.23	-0.64±0.31	0.66±0.33
b^*	0.16±0.04	0.48±0.03	0.42±0.21	-0.68±0.52
ΔE	0.08±0.04	-0.31±0.03	-0.45± 0.03	0.56±0.29

2.3

5 ΔE
-0.29~-0.23
L^* a^* L^*
L^* -0.33±0.25 a^*
0.11±0.04 b^* 0.01±0.03

5 (r_p) (r_g)

Tab.5 Phenotypic and genetic correlation between the shell color and growth traits of the improved orange shell line *C. gigas*

trait	L^*		a^*		b^*		ΔE	
	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p
/mm SH	-0.02±0.04	0.03±0.07	0.02±0.04	0.04±0.03	0.17±0.12	0.09±0.04	-0.29±0.23	-0.02±0.09
/mm SL	-0.07±0.02	0.05±0.04	0.03±0.09	0.04±0.03	0.03±0.02	0.04±0.03	-0.23±0.05	-0.02±0.13
/mm SW	0.02±0.05	-0.04±0.03	-0.24±0.18	0.11±0.04	0.07±0.08	0.08±0.04	-0.14±0.04	-0.03±0.14
/g TW	-0.33±0.25	0.06±0.04	0.12±0.13	0.04±0.03	-0.19±0.18	0.01±0.03	-0.05±0.08	-0.03±0.03

3

3.1

(*Lates calcarifer*) (*Hypophthalmichthys molitrix*) (*Cyprinus carpio*) [21-23] [16] (*Haliotis asinine*) [24]

[25] 12 G_1 863 851 98.61% [26] 8 [13] 11

3.2

[27] QTL [28-29]

10 L^* a^* b^* ΔE 0.17 0.47 0.42 0.56 $h^2 < 0.15$ $0.15 < h^2 < 0.3$ $h^2 > 0.3$ [30] L^* a^* b^* ΔE^*

Xu [14] Evans [4] [30] 1 L^* a^* b^* ΔE^*

3.3

[9]

[13] L^* 0.49~0.91 Wan [16] -0.04~0.26 -0.10~0.13 [31]

-0.33~0.17

[32]

4

10

References

[1] [M] 2021 45
Bureau of Fisheries, Ministry of Agriculture and Rural Affairs, National Fisheries Technology Extension Center, China Society of Fisheries. China Fishery Statistical Yearbook[M]. Beijing: China Agriculture Press, 2021: 45 (in Chinese).

[2] Nell J A. The history of oyster farming in Australia[J]. Marine Fisheries Review, 2001, 63(3): 14-25.

[3] Brake J, Evans F, Langdon C. Evidence for genetic control of pigmentation of shell and mantle edge in selected families of Pacific oysters, *Crassostrea gigas*[J]. Aquaculture, 2004, 229(1-4): 89-98.

[4] Evans S, Camara M D, Langdon C J. Heritability of shell pigmentation in the Pacific oyster, *Crassostrea gigas*[J]. Aquaculture, 2009, 286(3-4): 211-216.

[5] Han Z Q, Li Q, Liu S K, *et al*. Genetic variability of an orange-shell line of the Pacific oyster *Crassostrea gigas* during artificial selection inferred from microsatellites and mitochondrial COI sequences[J]. Aquaculture, 2019, 508: 159-166.

[6] “ ” [J] 2003 4 18-19
Sun J Z, Wang M X, Zhu C J. Experiment on "Peng Lai Hong" scallop culture[J]. Fishery Modernization, 2003(4): 18-19 (in Chinese).

[7] [J] 2010 34 8 1190-1197
Yan X W, Zhang Y H, Zhang G F, *et al*. Three way crosses between two-band red and white zebra strains of Manila clam, *Ruditapes*

[15] [J] 2009 16 5 736-743

Wang Q Z, Li Q, Liu S K, *et al*. Estimates of heritabilities and genetic correlations for growth in *Crassostrea gigas* larvae[J]. Journal of Fishery Sciences of China, 2009, 16(5): 736-743 (in Chinese).

[16] Wan S, Li Q, Liu T, *et al*. Heritability estimates for shell color-related traits in the golden shell strain of Pacific oyster (*Crassostrea gigas*) using a molecular pedigree[J]. Aquaculture, 2017, 476: 65-71.

[17] Hunter R S. Scales for the Measurements of Color Difference[M]. New York: John Willy & Sons, 1975: 133-140.

[18] Chakraborty S K, Singh D S, Kumbhar B K. Influence of extrusion conditions on the colour of millet-legume extrudates using digital imagery[J]. Irish Journal of Agricultural and Food Research, 2014, 53(1): 65-74.

[19] Li Q, Yu H, Yu R H. Genetic variability assessed by microsatellites in cultured populations of the Pacific oyster (*Crassostrea gigas*) in China[J]. Aquaculture, 2006, 259(1-4): 95-102.

[20] Kalinowski S T, Taper M L, Marshall T C. Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment[J]. Molecular Ecology, 2007, 16(5): 1099-1106.

[21] Wang C M, Lo L C, Zhu Z Y, *et al*. Estimating reproductive success of brooders and heritability of growth traits in Asian sea bass (*Lates calcarifer*) using microsatellites[J]. Aquaculture Research, 2008, 39(15): 1612-1619.

[22] Gheyas A A, Woolliams J A, Taggart J B, *et al*. Heritability estimation of silver carp (*Hypophthalmichthys molitrix*) harvest traits using microsatellite based parentage assignment[J]. Aquaculture, 2009, 294(3-4): 187-193.

[23] Vandeputte M, Kocour M, Mauger S, *et al*. Heritability estimates for growth-related traits using microsatellite parentage assignment in juvenile common carp (*Cyprinus carpio* L.)[J]. Aquaculture, 2004, 235(1-4): 223-236.

[24] Lucas T, Macbeth M, Degnan S M, *et al*. Heritability estimates for growth in the tropical abalone *Haliotis asinina* using microsatellites to assign parentage[J]. Aquaculture, 2006, 259(1-4): 146-152.

[25] Fu J J, Shen Y B, Xu X Y, *et al*. Genetic parameter estimates for growth of grass carp, *Ctenopharyngodon idella*, at 10 and 18 months of age[J]. Aquaculture, 2016, 450: 342-348.

[26] [J] 2019 6 83-89

Shi J G, Feng Y W, Zhao H F, *et al*. A comparison of growth traits and aanalysis of genetic parameters among green eggs families of *Haliotis discus hannai*[J]. Transactions of Oceanology and Limnology, 2019(6): 83-89 (in Chinese).

[27] Mizuta D D, Wikfors G H. Seeking the perfect oyster shell: A brief review of current knowledge[J]. Reviews in Aquaculture, 2019, 11(3): 586-602.

[28] Han Z Q, Li Q. Mendelian inheritance of orange shell color in the Pacific oyster *Crassostrea gigas*[J]. Aquaculture, 2020, 516: 734616.

[29] Han Z Q, Li Q, Xu C X, *et al*. QTL mapping for orange shell color and sex in the Pacific oyster (*Crassostrea gigas*)[J]. Aquaculture, 2021, 530: 735781.

[30] [M] 2001 37-38

Zhang Y. Animal Breeding[M]. Beijing: China Agriculture Press, 2001: 37-38 (in Chinese).

[31] 1 [J] 2014 38 5 644-650 Wang Z Q Han X K Bai Z Y *et al* Estimates of genetic parameters for inner shell color and growth straits during one year old stage in the purple strain of *Hyriopsis cumingii* using microsatellite based parentage assignment[J] Journal of Fisheries of China 2014 38 5 644-650 in Chinese

[32] Evans S, Langdon C. Effects of genotype×environment interactions on the selection of broadly adapted Pacific oysters (*Crassostrea gigas*)[J]. Aquaculture, 2006, 261(2): 522-534.