



B... (2015; L... (2013)). ... 480 ... *C. gigas* (H... (2000; ... (2003; ... L 2007, 2008; L... (2003; ... (2008 , ; ... (2008; ... (2005; ... (2009; ... (2009; L... (2009 , , 2011 ; B... (2011). H... M... (N) ... (AFL) ... *C. gigas*, ... (G... (2012), ... (H... (2011), ... (2010), ... (2014). ... I... MA ... A ... FAM-A ... FAM-B ... I ... FAM-A ... FAM-B ... (G... (2014). I ... (B... (2004; E... (2009). A ... (H... (2006; E... (2009; ... (2017), ... *C. gigas*, ... (M). ... (D...-C... (1996). M ... (2015). ... M ... *C. gigas*, ... *C. gigas*. I ... 480 ... L ... FAM-A ... FAM-B *C. gigas* ... FAM-A ... FAM-B ... *C. gigas*

Materials and Approaches

Mapping Population

F... *C. gigas* (F... 1). ... I M... 2012, FAM-A (♀ ♂) FAM-B (♀ ♂) ... 40 ... I J... 2013, 108 FAM-A 96 FAM-B

Trait Measurement

... (), ... (H), ... FAM-A FAM-B ... 16.0. ... ΔE ... (2004).

$$\Delta E = \sqrt{(L^* - L_0^*)^2 + (a^* - a_0^*)^2 + (b^* - b_0^*)^2}$$

$$L^* = \frac{L}{255} \times 100; a^* = \frac{240a}{255} - 120; b^* = \frac{240b}{255} - 120.$$

C 6 ... a ... b ... L ... L₀, a₀, b₀ ... (I A-M , A IAN, A)

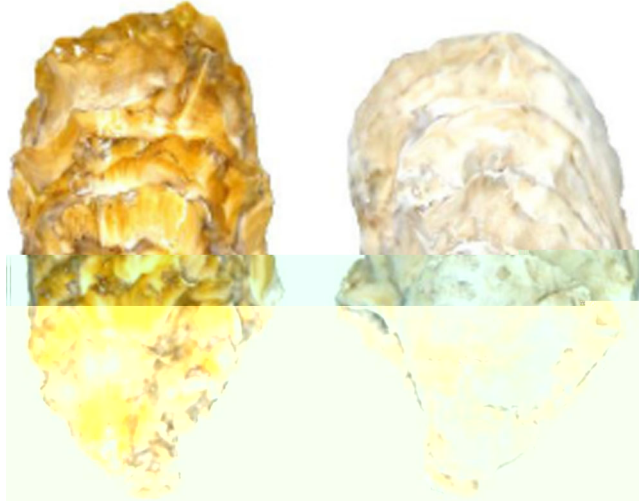


Fig. 1 ...

... M ... H ... (2015). ... /100 ...

SSR Markers

M ... (n=960) ... 480 ... (... 1). ... L ... (2009). An ... C ... ABI ... 96 ... C ... 10 μ ... 0.8 μ ... f ... N (2.5 ... /), 1 μ ... 10 ... ff ... 0.05 μ ... f ... Taq DNA ... (1 ... K ... J ...), 1 μ ... f ... (2.5 μ ... / ec), ... 5.15 μ ... p, c ... 1 μ ... e DNA (... 50 ...). ... C ... 95, C ... f ... 5 ... 35 c a ... f 95, ... 30 ... u ... e ... p ... f ... 30, 72, ... 0.5 ... , f ... 72, ... 5 ... C ... c ... p ... u ... 6% ... u ... f ...) ... p ...) ...

Construction of Genetic Maps and QTL Analysis

... J ... M ... 4.0 ... f ... (... 2006) ... c ... e ... p ... u ... f ... ec f ... u ... u ... u ... u ... u ... f ... 5 ... L ... (LG) ... L ... f ... 5.0 ... FAM-A ... 7.0 ... FAM-B, ... p ... p ... u ... a ... p ... P ... u ... u ... 0.03 ... p ... u ... p ... u ... u ... c ... f ... u ... u ... L ... f ... e ... 5 ... L ... f ... u ... f ... u ... M ... L ... p ... 6.0 (... 2009). I ... p ... (IM) ... u ... u ... u ... u ... f ... c ... e ... u ... u ... f ... u ... G ... c ... u ... u ... f ... u ... u ... p ... f ... u ... M ... C ... 2.2 (... 2002).

Candidate Gene Identification

... f ... c ... u ... u ... u ... u ... e ... 5 ... L ... e ... p ... u ... u ... u ... NCBI ... (... // ... c ...) ... u ... u ... u ... e ... f ... C. gigas.

Quantitative RT-PCR Analysis

... NA ... f ... c ... u ... u ... u ... I ... f ... u ... (I ... u ... , K). E ... c ... u ... f ... u ... u ... u ... c ... u ... a ... u ... u ... EFI (E ... f ... c ... f ... I) ... p ... c ... f ... - C ... f ... u ... L ... C ... 480 ... B ... G ... u ... IM ... p ... K. (... G ...) ...

L ... C ... 480 ... u ... C ... f ... u ... - C ... f ... ce ... u ... u ... u ... f ... u ... u ... (F ... u ... 2015). ... f ... p ... f ... - C ... p ... u ... u ... 2. ... u ... - C ... c ... e ... u ... u ... e ... f ... u ... C ... u ... (ΔΔC).

Results

Phenotypes

A ... f ... f ... p ... u ... u ... u ... u ... u ... 3. ... - ... f ... u ... u ... u ... c ... e ... u ... u ... f ... M ... FAM-A ... H ... FAM-B ... u ... u ... f ... c ... f ... u ... u ... u ... (P < 0.05), ... u ... f ... u ... u ... u ... u ... u ... u ... (P > 0.05).

Microsatellite Genotyping

A ... 960- ... f ... u ... u ... f ... u ... u ... p ... , 289 ... p ... f ... u ... FAM-A ... 338 ... p ... p ... f ... u ... FAM-B. ... u ... u ... u ... p ... u ... u ... u ... f ... u ...

Individual-Based Linkage Maps

C ... u ... p ... 9 ... (...)-39(...)-382(94)89(.0)-(6)-388(93-7(...))-6 ... 82

Table 1 N. f. r. p. u. f. C. gigas

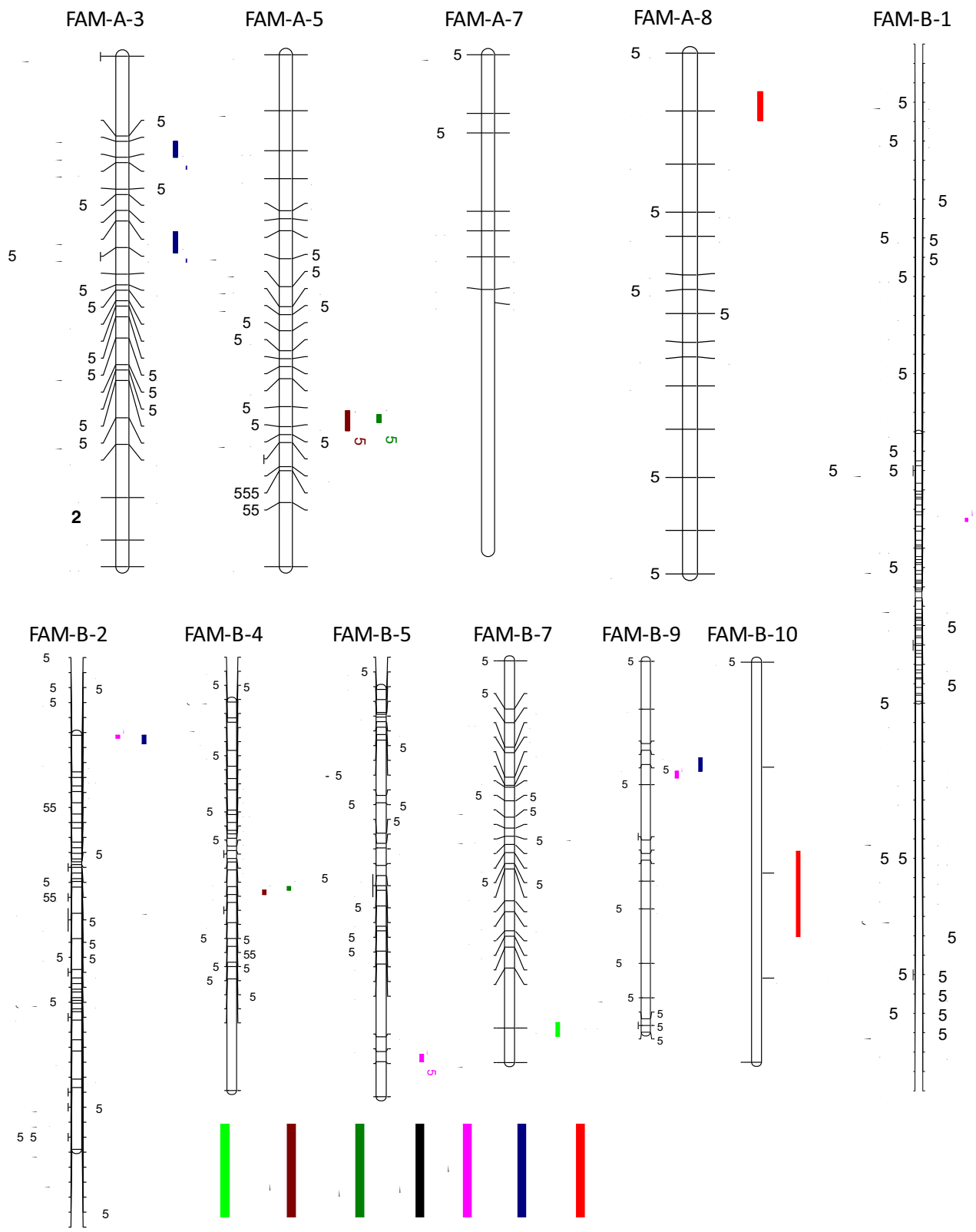
LG	FAM-A			FAM-B		
	N. f. r. p. u. f. (c)	A. p. u. c. (c)		N. f. r. p. u. f. (c)	A. p. u. c. (c)	
1	31	142.9	4.8	58	168.3	2.7
2	34	169.3	5.1	49	147.7	3.2
3	27	96.4	3.7	42	88.8	2.2
4	25	109.3	4.4	30	97.2	3.3
5	25	128.1	5.3	29	161.9	5.8
6	22	114.4	5.4	27	124.8	5.0
7	16	75.7	5.0	24	149.2	6.5
8	15	108.4	7.7	14	86.7	6.7
9	7	119.9	19.99	18	54.3	3.2
10	5	40.3	10.08	2	37.9	37.9
	207	1104.8	5.6	293	1116.9	3.9
G. u. c. p. u.	89.6%			90.6%		

PVE, u. c. r. c. u. u. u.

I FAM-A, L p. u. f. u. LG3 (5.31), 22.9% f. u. u. c. r. u. u. M B9 (A3-1 A3-2). L (2.95), c. e. u. u. u. M B2 f 17.9 34.4%, u. r. N L c. u. u. M M B9 p. u. f. u. f. L c. u. u. u. FAM-A. H u. p. f. u. f. L c. u. u. (F. 2), c. c. u. f. 26.7 14.2% f. u. u. u. FAM-B. LG1 (M B1), LG2 (M B2), LG5 (M B5), LG9 (M B9). A u. u. u. M B2 u. u. u. u. L. u. u. FAM-A LG10 FAM-B (CA8 CB10). I

Table 2 L. u. f. u. f. u. f. C. gigas

F. u. u. L. u. LG	R. u. p. C. f. u. c. u. p. (c)	L. u. u. M. L. u. E (%)
FAM-A H HA7-1 G7 E549-C 329	20.7–29.8	3.1 3.6 16.8
HA7-2 G7 E367-L70	37.8–38.8	3.7 16
A5 G5 51- 13	89.3–93.6	3.2 5.94 36.7
A5 G5 51- 45	90.3–92.3	3.8 4.88 31.3
A3-1 G3 CDCG192- CDCG162	16.2–18.9	3.1 3.93 17.9
A3-2 G3 CDCG164-E10	33.1–37.4	4.57 34.4
ΔE CA8 G8 E523-G221	8–14.2	3.1 3.23 20.2
FAM-B B7 G7 E53- CDCG 148	133.7–138.9	3.2 3.6 14.6
B4 G4 CGE211-H34	47.3–47.9	3.3 3.67 15.8
B4 G4 CGE211-H34	46.3–47.3	3.4 3.57 15.5
M M B1 G1 E563-G46	52.9–54.9	4.3 4.37 19.3
M B2 G2 E531-G118	0–1	4.4 5.31 22.9
M B5 G5 G130- CDCG194	144.6–147.6	3.2 3.52 15.8
M B9 G9 CGE32-H153	16.1–17.1	2.8 2.95 13.5
B2 G2 E531-G118	0–3	3.5 6.35 26.7
B9 G9 CGE9-H153	14.1–16.1	2.9 3.13 14.2
ΔE CB10 G10 E324-H104	18–26	2.3 2.36 10.5



FAM-A, CA8 $\chi^2 = 10.5$, $P < 0.01$, LOD (3.23), $r = 0.85$, $c = 10.5\%$
 FAM-B, CB10 $\chi^2 = 10.5$, $P < 0.01$, LOD (2.36), $r = 0.85$, $c = 20.2\%$

Candidate Genes of Traits

In total, 35 candidate genes were identified. The genes include *FAM-A* (H), *FAM-B* (M), *FAM-C* (M), *FAM-D* (M), *FAM-E* (M), *FAM-F* (M), *FAM-G* (M), *FAM-H* (M), *FAM-I* (M), *FAM-J* (M), *FAM-K* (M), *FAM-L* (M), *FAM-M* (M), *FAM-N* (M), *FAM-O* (M), *FAM-P* (M), *FAM-Q* (M), *FAM-R* (M), *FAM-S* (M), *FAM-T* (M), *FAM-U* (M), *FAM-V* (M), *FAM-W* (M), *FAM-X* (M), *FAM-Y* (M), and *FAM-Z* (M).

... (132.9–152.4 /, $P < 0.05$). A... M... NA... M1... M... (P < 0.05; F...). ... C... (C1)... (C2)... *PTPPK*... *KMT2D*... (P < 0.05; F...).

The mRNA Expression of Candidate Genes

The mRNA expression of candidate genes was analyzed. The genes include *ACTA1*, *USP15*, *ARRB1*, *LIG1*, *FBLN1*, *PHXR5*, *AFTPH*, *PTPRK*, *RBP1*, *CDO1*, *SMARCC1*, *NMT2*, *HSPA*, and *KMT2D*. The expression levels were measured in various tissues and developmental stages.

Discussion

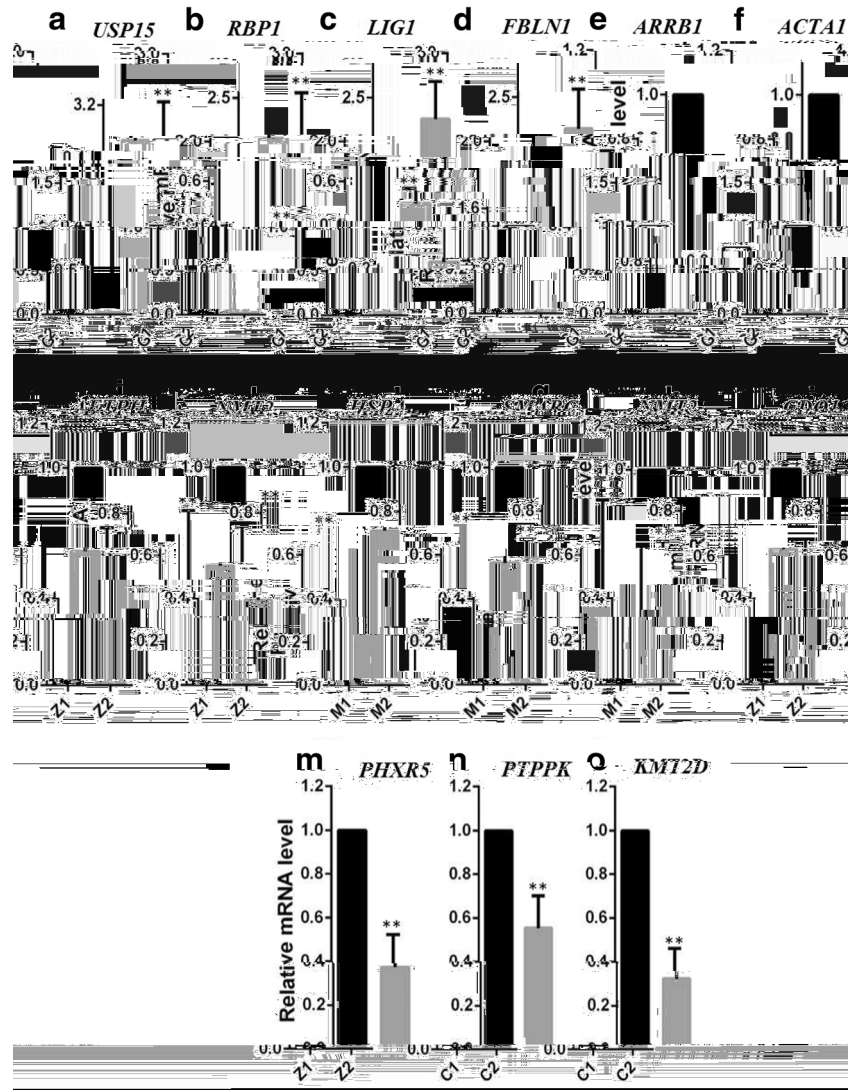
Linkage Mapping

The linkage mapping results showed that the candidate genes were located on chromosomes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, and 30. The genes were mapped to specific genomic regions.

Table 3 Candidate genes of traits in *C. gigas*

Family	Gene	Linkage Group	Marker	Gene	Gene	
FAM-A	H	HA7-1	G7	E549	<i>ACTA1</i>	
			G7	E82	<i>USP15</i>	
		A5	G5	CGE329	<i>ARRB1</i>	
			G5	L70	<i>LIG1</i>	
			G5	45	<i>FBLN1</i>	
	ΔE	3-2	G3	CGE164	<i>FBLN1</i>	
			G3	CGE199	<i>PHXR5</i>	
		A 3-2	G3	CGE199	<i>AFTPH</i>	
			G8	E523	<i>PTPRK</i>	
			G4	CGE211	<i>RBP1</i>	
FAM-B	M	M B1	G1	E563	<i>RBP1</i>	
			G1	G46	<i>CDO1</i>	
	M B9	G9	H153	CGI10000944/1/NF1	<i>SMARCC1</i>	
			CGE9	H153	<i>NMT2</i>	
	ΔE	CB10	G10	H104	<i>HSPA</i>	
			G10	H104	<i>NMT2</i>	
						<i>KMT2D</i>

Fig. 3 NA
 14
 C.E
 EF I
 (D). * $P < 0.05$; ** $P < 0.01$



(10–20 c f L (M . 2008).
 Lf C. gigas.

Mapping Growth Traits

Lf C. gigas (. 2014; G. . 2013).
 H . I .
 Lf LG5 LG7 FAM-A LG4 LG7 FAM-B, c c . 14.6–36.7% f . C. gigas . L .

G. . (2013) .
 f . c . I .
 () .
 H . 2009).

I .
 M, f Lf (Cyprinus carpio L.), A (Lates calcarifer), A (Salmo salar), c . (Chlamys farreri) (J . 2012; B, . 2010; . 2013; J . 2014), .
 L (J . 2012). I .
 L . MA, .

... H... 5 L
f... C. gigas.
...
... ACTA1, LIG1, ... FBLN1. ACTA1
... f... c... c... p...

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Compliance with Ethical Standards

Conflict of Interest The authors declare that they have no conflict of interest.

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