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Abstract The present study was aimed at identifying the genetic diversity of *Crassostrea gigas* in the Pilya (Caspian Sea) region. DNA samples were collected from 2284 individuals in the Pilya region. The genetic diversity was analyzed using the PCR-RFLP method. The results showed that the genetic diversity of *C. gigas* in the Pilya region is high. The genetic diversity was analyzed using the PCR-RFLP method. The results showed that the genetic diversity of *C. gigas* in the Pilya region is high.

Keywords Genetic diversity, DNA, PCR-RFLP, *Crassostrea gigas*, Pilya region



The present study was aimed at identifying the genetic diversity of *Crassostrea gigas* in the Pilya (Caspian Sea) region. DNA samples were collected from 2284 individuals in the Pilya region. The genetic diversity was analyzed using the PCR-RFLP method. The results showed that the genetic diversity of *C. gigas* in the Pilya region is high. The genetic diversity was analyzed using the PCR-RFLP method. The results showed that the genetic diversity of *C. gigas* in the Pilya region is high.

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 m i l . 2010). An in in r m i

Gene	Primer	Sequence (5'-3')
C-D-1	EF	ACCACCC GG GAGA CAAG
	EF	ACGACGA CGCA C C
C-D-2	DM	CCA GGAG GG G CCGC
	DMA B	G GCC C GC A CAGGG
C-D-3	F 12 2	AA A CAGGGA GGGCACAA
	F 12A 1	G CC GGG GCAGGAAC A
C-D-4	E PCR 1	GCCA CAAGGAGAAAACGA
	E PCRA 1	G AAGAGC GG CCAGGA G
C-D-5	AG J/ n/A	l (BDC1.92799997 0)

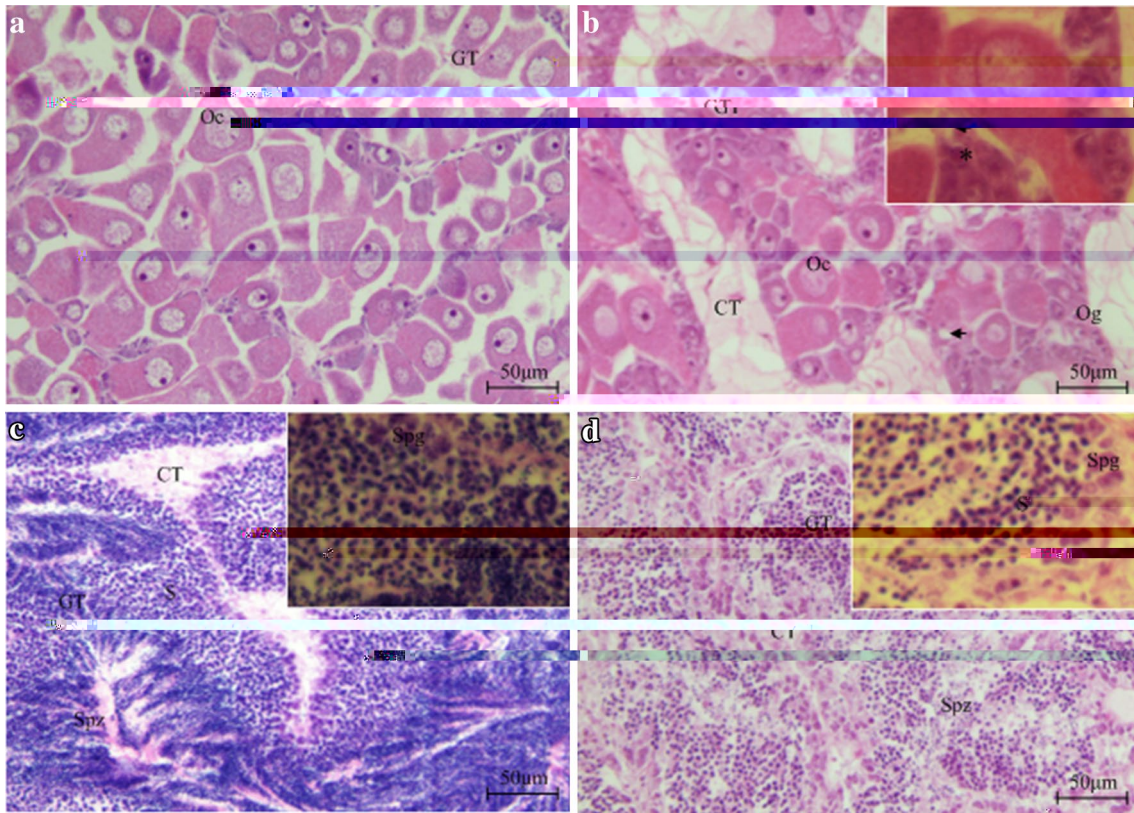
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G n mi DNA m m i
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 l (Li l. 2006). DNA n n in ni n
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 l mm n y m n . All i
 n i n l i n m
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 i l n i n i n in i
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 ll in 100 i in in in , 2000 100)
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 (// . n . /m im /in 1. ml).
 Bi l PCR (B -PCR) im in
 n i l -m i DNA m li y C G i l n
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 l, i in n P C l m DNA G l
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 A li Bi y m) n n ABI PRI M 3730 (A li
 Bi y m) m i n . A i l -
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 5-m yl y in m in n n . B n i
 i i, m yl i n l mir . C n -
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n ly n i n (Li n mi n 2001).
 l i mRNA l l n m li EF n i
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 l l m m , i l i . i i l i n n
 (l n l i . . g ; l y l m i . .) . D i l i

m l n n l l l l m m i -
 l i i i l () . C n l n i i ; O n i ;
 e O y ; m n i ; m i ; m

In l l n , n l y n i l y i n i n i -
 i n n i l i n i l i y : -
 i n l m n I I n e i n l -
 m n III . F i n n ,
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 n i n n l l l i m l (i n l -
 i n i) i n i n l 3 i
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 n i m i n i n , D N A m y l i n i n
 n n l y i n l l i n .

(2)
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 13) . I n e , n l y C G i l n n i n n
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 n C G i n l i m i n . n i n
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 l l y n i l i i n y 99% .
 i n i n i n y i n i l i y
 i l m i i n n n y l -
 l i n l .

l 2 i m n m l i y C G
 i l n . i n E R - C G 2 i l n i l n -
 l l y m l i y n l n , i m l i i n i m -
 . i n i l m i i n n n i n , D N A
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 D N A m y l i n l y i n l i
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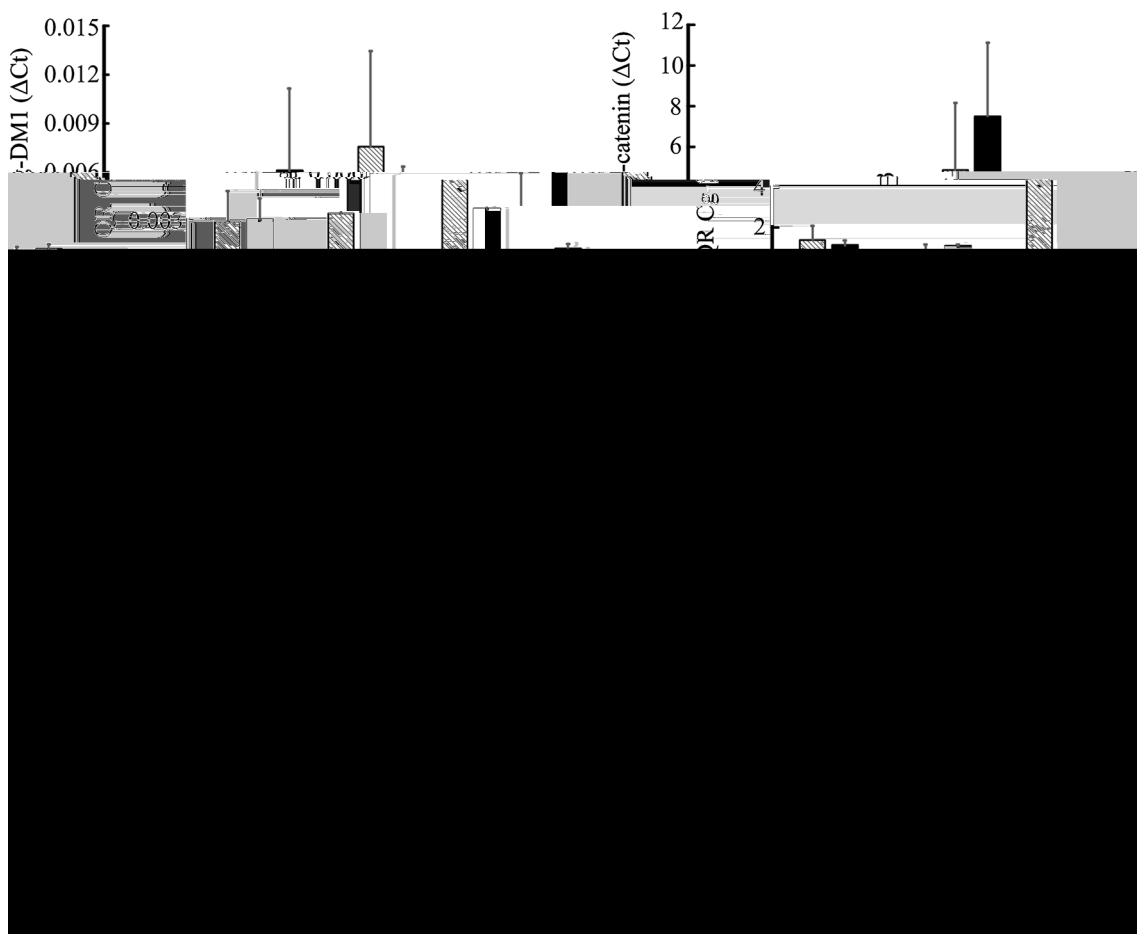


Fig. 4 Real-time PCR analysis of DMI and catenin expression in the liver of control (I), II, III, and IV groups. The results are expressed as mean ± SEM. Significant differences (p < 0.05) are indicated by different letters.

Sample ID	DMI (ΔCt)		catenin (ΔCt)	
	Mean	Di	Mean	Di
1	0.0850	11.3446	0.0069	0.0014
2	0.0380	6.3813	0.0034	0.0016
3	0.0531	3.9370	0.0036	0.0024
4	0.0236	3.6503	0.0085	0.0011
5	0.0130	7.0858	0.0050	0.0017
6	0.0642	6.7123	0.0071	0.0009
A	0.0461	0.0225	6.5186	2.3470
			0.0057	0.0017
			0.0015	0.0004

$$N = 100 * 2^{(C_{EF} - C_{CC} - n)}$$

6.10% of the total DNA, while in the liver of control (I) group, it was 95.47%. In the liver of control (I) group, the expression of DMI was 0.0069, while in the liver of control (I) group, it was 0.0014. In the liver of control (I) group, the expression of catenin was 6.5186, while in the liver of control (I) group, it was 2.3470. In the liver of control (I) group, the expression of DMI was 0.0057, while in the liver of control (I) group, it was 0.0017. In the liver of control (I) group, the expression of catenin was 0.0015, while in the liver of control (I) group, it was 0.0004.

DNA methylome in rice inbred lines

CG/ER-ID	mi (%)	Di (%)
-CG1	1.11	2.22
-CG2	0.91	0.91
-CG3	3.00	2.00
-CG4	2.86	3.57
-CG5	0.00	0.91
-CG6	1.81	2.73
ER-CG1	0.00	0.00
ER-CG2	3.08	3.85
ER-CG3	3.33	1.67
ER-CG4	96.67	96.67
ER-CG5	96.90	95.47

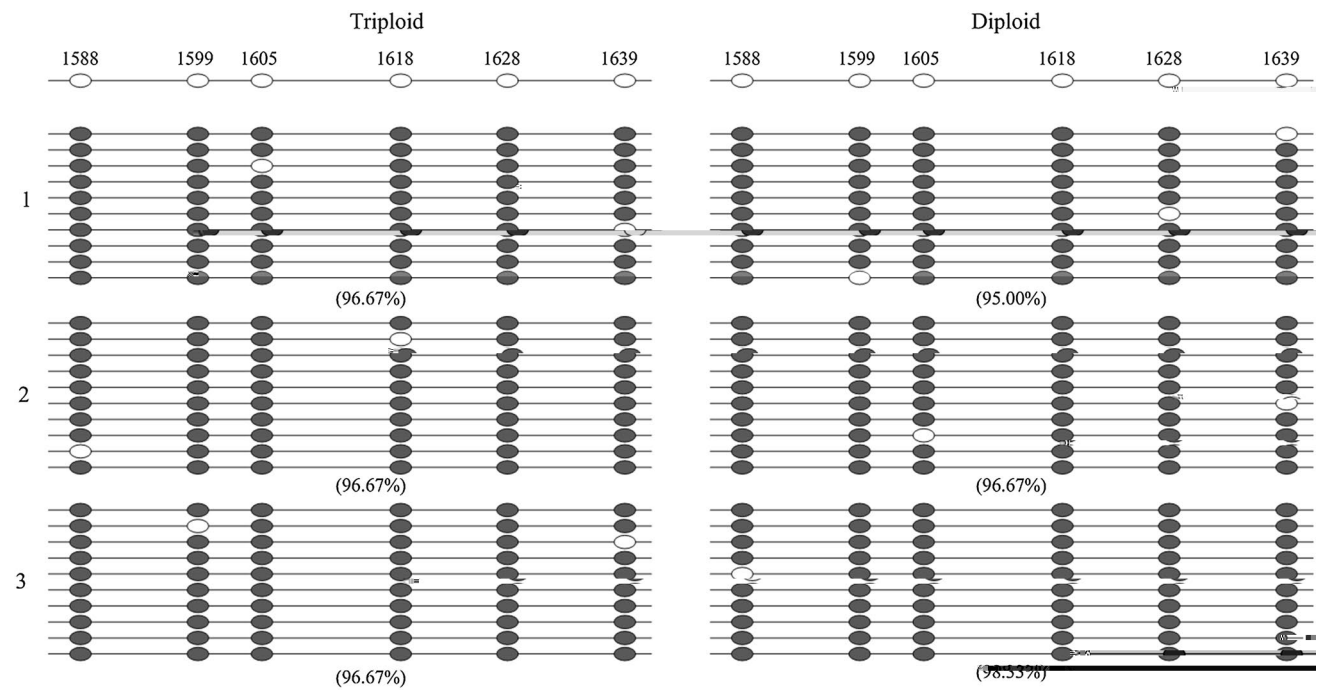
inbred lines in rice inbred lines

GRM

inbred lines in rice inbred lines

(2010): inbred lines in rice inbred lines

inbred lines in rice inbred lines



DNA methylome in rice inbred lines ER-CG4 (n=6) inbred lines

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 l m i n (n n C ll 2003, 2007). N -
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P i i in C. ... i i n
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 y l i n l l, m y l i n n i n i i l l
 n i n n i n i n i n . i i i n
 m i n i n i n n l y l m y l i n l l
 l i n i i l l i n i .

N i n l N l i n F n i n C i n (31372524), n n
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 N i n l N l i n F n i n C i n (31372524), n n
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I s

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 G n m - i i - l i n m in n n i n l n l y i
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