

Mitogenomics of southern hemisphere blue mussels (*Bivalvia: Pteriomorphia*): Insights into the evolutionary characteristics of the *Mytilus edulis* complex

Juan Diego Gaitán-Espitia^{1,2*}, Julian F. Quintero-Galvis^{1,3}, Andres Mesas^{1,3} & Guillermo D'Elía¹

¹ Instituto de Ciencias Ambientales y Evolutivas, Universidad Austral de Chile, Casilla 567 Valdivia, Chile.

² CSIRO Oceans and Atmosphere, GPO Box 1538, Hobart 7001, TAS, Australia

³ Programa de Doctorado en Ciencias mención Ecología y Evolución, Facultad de Ciencias, Universidad Austral de Chile, Valdivia, Chile.

* **Corresponding author:** Juan Diego Gaitán-Espitia. Instituto de Ciencias Ambientales y Evolutivas, Facultad de Ciencias, Universidad Austral de Chile, Casilla 567 Valdivia, Chile.

Tel: +56 63 221704; fax: +56 63 221673. Email address: juadiegaitan@gmail.com

Supplementary Figure Legends

Supplementary Figure S 1. Alignment of the Atp8 gene among species of the Family Mytilidae.

Supplementary Figure S 2. Mitochondrial genome syntenies of pteriomorph bivalves.

M. chilensis
Frame 1
Complement

M. platensis
Frame 1
Complement

M. edulis
Frame 1
Complement

M. galloprovincialis
Frame 1
Complement

M. californianus
Frame 1
Complement

M. coruscus
Frame 1
Complement

M. trossulus
Frame 1
Complement

P. viridis
Frame 1
Complement

M. senhousia
Frame 1
Complement

B. exustus
Frame 1
Complement

M. chilensis
Frame 1
Complement

M. platensis
Frame 1
Complement

M. edulis
Frame 1
Complement

M. galloprovincialis
Frame 1
Complement

M. californianus
Frame 1
Complement

M. coruscus
Frame 1
Complement

M. trossulus
Frame 1
Complement

P. viridis
Frame 1
Complement

M. senhousia
Frame 1
Complement

B. exustus
Frame 1
Complement

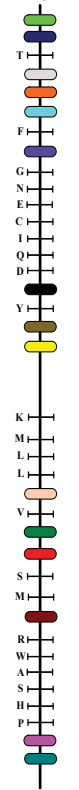
1 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150

1 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150

160 170 180 190 200 210 220 230 240 250 258

160 170 180 190 200 210 220 230 240 250 258

Mytilus edulis
complex



Mytilus trossulus



Perna viridis



Musculista senhousia



Brachidontes exustus



Anadara sativa



Scapharca broughtonii



Argopecten irradians



Chlamys farreri



Placopecten magellanicus



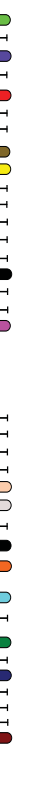
Crassostrea gigas



Ostrea denselamellosa



Saccostrea mordax



Pinctada margaritifera



Atrina pectinata



Supplementary Table 1. Mitogenome size and general features in Bivalvia. Columns represent protein coding genes with their lengths (bp). Start and stop codons for the protein coding genes are enclosed in parentheses.

Subclass	Species	Total Size	ATP6	ATP8	COX1	COX2	COX3	CYTB	ND1	ND2	ND3	ND4	ND4L	ND5	ND6	%A	%C	%G	%T	%A-T	%G-C
Pteriormorpha	<i>Mytilus platensis</i>	16765	717 (ATG/AAA)	255 (ATG/AAG)	1665 (ATA/CAA)	729 (ATG/T)	937 (ATG/T)	1308 (ATG/ATA)	916 (GTG/GTG)	948 (ATG/ATT)	351 (ATG/GGT)	1308 (ATG/CCT)	282 (ATG/TCC)	1707 (ATA/ATA)	466 (ATG/AAA)	30.2	11.4	28.8	29.8	60	40
	<i>Mytilus chilensis</i>	16765	717 (ATG/T)	255 (ATG/AAG)	1665 (ATA/CAA)	729 (ATG/T)	937 (ATG/T)	1308 (ATG/ATA)	916 (GTG/GTG)	948 (ATG/ATT)	351 (ATG/GGT)	1308 (ATG/CCT)	282 (ATG/TCC)	1707 (ATA/ATA)	466 (ATG/AAA)	30.2	11.4	28.6	29.8	60	40
	<i>Mytilus galloprovincialis</i>	16744	717 (ATG/T)	255 (ATG/AAG)	1665 (ATA/CAA)	729 (ATG/T)	936 (ATG/T)	1308 (ATG/ATA)	916 (GTG/GTG)	948 (ATG/ATT)	351 (ATG/GGT)	1308 (ATG/CCT)	282 (ATG/TCC)	1705 (ATA/TTT)	465 (ATG/AAA)	29.4	12.2	29.4	29.0	58.4	41.6
	<i>Mytilus trossulus</i>	18652	717 (ATG/T)	255 (ATG/AAG)	1656 (ATA/CAA)	729 (ATG/T)	933 (ATG/T)	1308 (ATG/ATA)	918 (GTG/GTG)	948 (ATG/ATT)	351 (ATG/GGT)	1308 (ATG/CCT)	282 (ATG/TCC)	1707 (ATA/ATA)	465 (ATG/AAA)	31.8	12.2	25.9	30.2	62	38
	<i>Mytilus californianus</i>	16730	717 (ATG/T)	255 (ATG/AAG)	1656 (ATA/CAA)	729 (ATG/T)	936 (ATG/T)	1308 (ATG/ATA)	916 (GTG/GTG)	948 (ATG/ATT)	351 (ATG/GGT)	1308 (ATG/CCT)	282 (ATG/TCC)	1710 (ATA/ATA)	465 (ATG/AAA)	31.0	10.6	28.6	29.8	60.8	39.2
	<i>Mytilus coruscus</i>	16642	717 (ATG/T)	255 (ATG/AAG)	1656 (ATA/CAA)	729 (ATG/T)	936 (ATG/T)	1308 (ATG/ATA)	918 (GTG/GTG)	948 (ATG/ATT)	351 (ATG/GGT)	1308 (ATG/CCT)	282 (ATG/TCC)	1710 (ATA/ATA)	465 (ATG/AAA)	31.0	11.4	27.5	30.2	61.2	38.8
	<i>Mytilus edulis</i>	16740	717 (ATG/T)	255 (ATG/AAG)	1656 (ATA/CAA)	729 (ATG/T)	933 (ATG/T)	1308 (ATG/ATA)	918 (GTG/GTG)	948 (ATG/ATT)	351 (ATG/GGT)	1308 (ATG/CCT)	282 (ATG/TCC)	1707 (ATA/ATA)	467 (ATG/AAA)	29.8	11.4	29.4	29.4	59.2	40.8
	<i>Musculista senhousia</i>	20612	714 (ATG/T)	189 (ATG/GTT)	1584 (ATG/GTA)	813 (ATG/GTA)	855 (ATG/GTA)	1197 (ATA/T)	966 (ATG/GTA)	945 (ATA/AGT)	375 (ATG/TCT)	1329 (ATA/TGT)	216 (ATA/TTT)	1765 (ATA/TTT)	438 (ATA/AGC)	45.7	8.7	19.6	26.1	71.7	28.3
	<i>Perna viridis</i>	16014	714 (ATG/AAA)	150 (ATT/TGA)	1536 (ATG/T)	690 (GTG/T)	825 (ATG/GTA)	1152 (ATG/TCA)	1188 (ATG/TTC)	945 (ATG/AAT)	956 (ATA/AGT)	354 (ATA/TGT)	1317 (ATA/TTT)	1683 (ATA/TTT)	540 (ATA/AGC)	29.2	9.3	21.0	40.5	69.7	30.3
	<i>Brachidontes exustus</i>	16600	747 (ATG/T)	114 (TTG/TTT)	1605 (ATG/T)	666 (ATG/GTA)	855 (ATG/TCA)	1278 (ATG/TTC)	933 (ATG/AAT)	963 (ATG/GTA)	351 (ATG/TGT)	1299 (GTG/TCT)	1731 (ATG/TTA)	465 (ATG/GTT)	468 (ATG/AAA)	17.6	14.8	28.6	30.0	56.6	43.4
<i>Anodara sativa</i>	48161	525 (ATA/T)	184 (ATG/AGA)	1584 (ATG/TTA)	813 (ATG/TTA)	855 (ATG/TCA)	1197 (ATA/T)	966 (ATG/GTA)	945 (ATA/AGT)	375 (ATG/TCT)	1329 (ATA/TGT)	216 (ATA/TTT)	1765 (ATA/TTT)	438 (ATA/AGC)	27.5	17.4	20.3	34.8	62.3	37.7	
<i>Scapharca broughtonii</i>	46985	525 (ATA/AGG)	184 (ATG/AGA)	1584 (ATG/TTA)	813 (ATG/TTA)	855 (ATG/TCA)	1197 (ATA/T)	966 (ATG/GTA)	945 (ATA/AGT)	375 (ATG/TCT)	1329 (ATA/TGT)	216 (ATA/TTT)	1765 (ATA/TTT)	438 (ATA/AGC)	25.3	8.8	22.5	43.4	68.8	31.2	
<i>Argopecten irradians</i>	16211	750 (GTG/T)	160 (ATA/AGG)	699 (GTG/TCT)	825 (GTG/TCT)	1158 (TTG/TCT)	1158 (GTG/GTT)	945 (TTG/CCT)	956 (ATA/GAT)	348 (ATG/CCT)	1317 (ATA/GGT)	275 (ATG/TCT)	1683 (ATG/GAT)	540 (ATG/GAT)	18.9	14.1	29.6	37.4	56.3	43.7	
<i>Argopecten purpuratus</i>	16266	636 (ATA/T)	160 (ATG/AGG)	671 (ATG/TCT)	828 (ATA/TTT)	1158 (TTG/TCT)	1158 (GTG/GTT)	945 (ATA/TTT)	957 (ATA/GAT)	348 (ATG/CCT)	1317 (ATA/GGT)	275 (ATG/TCT)	1683 (ATG/GAT)	540 (ATG/GAT)	17.6	14.8	28.6	30.0	56.6	43.4	
<i>Chlamys farreri</i>	21695	789 (ATG/AGG)	164 (ATG/AGG)	671 (ATG/GTT)	852 (ATG/AGG)	1155 (ATG/AGG)	1155 (ATG/AGG)	948 (ATG/CCT)	957 (ATA/TTT)	353 (ATA/TGC)	1284 (ATG/TTA)	318 (ATA/T)	1779 (ATG/GTT)	495 (ATA/AGA)	20.4	12.5	27.5	39.6	60	40	
<i>Minchamys senatori</i>	17383	882 (ATG/AGG)	153 (ATG/AGG)	671 (ATA/GTT)	864 (ATG/GAG)	1264 (ATG/TTA)	1264 (TTG/TTA)	966 (ATG/GAT)	966 (ATG/GAT)	333 (ATG/ATG)	1245 (ATG/GTA)	324 (ATG/TGT)	1746 (ATG/AGG)	495 (ATG/AGG)	18.2	14.7	27.7	39.4	57.6	42.4	
<i>Placopecten magellanicus</i>	32115	730 (ATA/AAG)	1513 (ATG/GTG)	685 (ATG/TGG)	828 (ATA/GGT)	1188 (TTG/TAC)	1188 (ATG/TGG)	942 (GTG/CCT)	966 (ATG/GAT)	372 (ATG/ATG)	1284 (GTG/GGG)	297 (ATG/CCA)	1860 (ATA/AGT)	567 (ATG/CCA)	14.8	13.4	34.9	48.3	51.7	48.3	
<i>Crassostrea angulata</i>	18408	684 (ATA/T)	1617 (ATG/TGT)	702 (ATG/GGA)	876 (ATG/TCT)	1239 (CTA/T)	936 (ATG/ATT)	999 (ATG/TAC)	999 (ATG/GAT)	351 (ATG/ATG)	1350 (ATG/GCT)	283 (ATG/GCT)	1671 (ATG/GTT)	474 (ATT/TTT)	27.6	14.7	22.1	35.6	63.2	36.8	
<i>Crassostrea ariakensis</i>	18414	675 (ATG/T)	1617 (ATA/TGT)	702 (ATG/GGA)	864 (ATG/TCT)	1233 (TTA/TTT)	936 (ATG/TTC)	999 (ATG/TAC)	999 (ATG/AGG)	351 (ATG/GCA)	1350 (ATG/GCA)	283 (ATG/GTT)	1671 (ATG/TAC)	480 (ATG/TAC)	26.8	15.2	22.5	35.5	62.3	37.7	
<i>Crassostrea gigas</i>	18225	684 (ATG/T)	1617 (ATG/TGT)	702 (ATG/GGA)	876 (ATG/TCT)	1239 (CTA/AAT)	936 (ATG/ATT)	999 (ATG/TAC)	999 (ATG/GAT)	351 (ATG/ATG)	1353 (ATG/ATG)	283 (ATG/GCT)	1671 (ATG/GTT)	477 (ATG/TTC)	24.6	15.1	22.0	38.2	62.9	37.1	
<i>Ostrea denselamellosa</i>	16277	675 (GTG/GCC)	669 (ATG/ATC)	1596 (ATG/GGA)	880 (ATG/TCC)	1161 (ATA/GAG)	1161 (ATG/ATG)	933 (ATG/TAC)	999 (ATG/AGC)	354 (ATG/TTT)	1350 (GTG/GAA)	283 (ATA/ATG)	1671 (ATG/AAA)	468 (ATG/AAA)	22.9	16.2	23.8	37.1	60	40	
<i>Ostrea edulis</i>	16320	669 (ATA/GTA)	693 (ATG/ATC)	1566 (ATG/ATC)	888 (ATA/TCT)	1161 (ATC/GAG)	1161 (ATG/ATA)	916 (ATG/TAC)	1008 (ATG/AGC)	354 (ATG/TTT)	1350 (ATG/GAG)	282 (ATG/ATT)	1548 (ATA/TCA)	468 (ATG/TTT)	26.5	13.0	20.9	39.5	66	34	
<i>Ostrea lurida</i>	16344	570 (ATG/T)	102 (ATA/TTA)	1611 (ATA/T)	693 (ATG/AAT)	880 (ATG/TCT)	1053 (ATA/GAG)	858 (ATG/ATA)	1005 (ATG/AGC)	353 (ATG/ATT)	1350 (ATA/GAG)	264 (ATG/GTT)	1671 (ATG/TCA)	474 (ATG/TCA)	26.5	13.0	20.9	39.5	66	34	
<i>Saxostrea mordax</i>	16532	678 (ATG/AAA)	682 (ATG/AAA)	1656 (ATG/T)	896 (ATG/T)	1173 (ATG/TCT)	1173 (ATG/TCT)	948 (ATG/TTT)	975 (ATA/TAT)	354 (ATG/AAT)	1350 (ATG/CCT)	282 (ATG/GAA)	1671 (GTG/CCC)	468 (GTG/CCC)	20.9	13.9	25.2	40.0	60.9	39.1	
<i>Arima pectinata</i>	16811	702 (GTG/CAG)	643 (ATG/CAG)	1560 (ATG/GCC)	887 (GTG/GTG)	1146 (ATC/CGT)	1146 (ATG/ATT)	931 (ATG/ATT)	999 (ATG/TCT)	345 (ATG/TTT)	1359 (ATG/GTT)	303 (ATG/GTT)	1755 (ATG/ATT)	471 (ATG/ATT)	20.6	8.7	28.2	42.5	63.1	36.9	
<i>Pinctada margaritifera</i>	15680	849 (ATG/AAA)	849 (ATG/AAA)	1557 (ATG/GAG)	781 (ATG/GAG)	1146 (ATG/GAG)	1146 (ATG/GAG)	936 (ATG/ATC)	970 (ATG/ATG)	345 (ATG/T)	1359 (ATG/GGG)	303 (ATG/ACC)	1755 (ATG/ACC)	471 (ATG/ACC)	21.1	10.2	29.2	39.6	60.7	39.3	
<i>Meretrix meretrix</i>	19826	849 (ATG/AAA)	849 (ATG/AAA)	1557 (ATG/GAG)	781 (ATG/GAG)	1146 (ATG/GAG)	1146 (ATG/GAG)	936 (ATG/ATC)	970 (ATG/ATG)	345 (ATG/T)	1359 (ATG/GGG)	303 (ATG/ACC)	1755 (ATG/ACC)	471 (ATG/ACC)	22.1	10.3	22.7	44.9	67	33	
<i>Loripes lacteus</i>	17321	645 (ATG/AGG)	118 (ATG/AGG)	1557 (ATA/AAA)	879 (ATA/AGG)	1140 (ATG/ATG)	1140 (ATG/ATG)	936 (ATG/AAA)	967 (ATG/GCT)	348 (ATG/TTA)	1350 (GTG/CAC)	327 (ATA/GTG)	1773 (ATA/TTG)	486 (ATA/TTG)	21.0	13.2	26.3	39.5	60.5	39.5	
<i>Lucinella divaricata</i>	18940	690 (ATA/GTA)	114 (ATP/TTT)	1554 (ATA/AGG)	930 (ATA/TCT)	1142 (ATG/GTT)	1142 (ATG/GTT)	939 (ATG/AAA)	1038 (ATA/ATC)	342 (ATG/GAA)	1350 (ATG/TTA)	282 (ATG/TTT)	1671 (ATG/TTT)	483 (GTG/TTT)	21.3	13.0	25.4	40.3	61.6	38.4	
<i>Mya arenaria</i>	17947	729 (ATG/T)	175 (ATA/TTA)	1434 (ATG/AAA)	861 (ATG/TTT)	1041 (ATA/TTA)	1041 (ATA/TTA)	912 (ATG/TTT)	1065 (ATG/ACT)	423 (ATG/AAA)	1365 (ATA/TTT)	384 (ATA/TTA)	1518 (ATA/AAAC)	546 (ATA/AAAC)	25.8	12.0	23.6	38.7	64.5	35.5	
<i>Palaeoheterodont</i>	<i>Anodonta anatina</i>	15637	702 (ATA/T)	165 (ATG/AAG)	1542 (TTG/AGG)	681 (ATG/T)	780 (ATG/TCT)	1155 (ATT/TTT)	855 (TTG/TTA)	966 (ATG/TTC)	357 (ATG/GTG)	1347 (ATT/CTA)	297 (GTG/TTT)	1737 (GTG/CTT)	489 (ATT/TTT)	36.7	18.4	18.4	35.7	72.4	27.6
<i>Protobranchia</i>	<i>Solemya velum</i>	15660	696 (ATG/CAT)	165 (ATG/AAA)	1536 (ATG/GCC)	887 (ATG/GCC)	1123 (ATG/AGG)	1123 (ATG/AGG)	924 (ATT/TGT)	1089 (ATG/ATT)	353 (ATG/TTA)	1344 (ATG/AAA)	297 (ATA/ATT)	727 (ATG/TGT)	501 (ATG/AGG)	47.5	20.8	8.6	23.2	70.7	29.3

Supplementary Table 2. Codons that may be under positive selection

Codon	Gene	SLAC		FEL		MEME	FUBAR	
		dN-dS	p-value	dN-dS	p-value	p-value	dN-dS	Post. Pr.
246	<i>Cytb</i>	0.43	0.30	0.26	0.12	0.03	-0.08	0.47
275	<i>Cytb</i>	0.36	0.54	0.18	0.29	0.00	-0.51	0.14
383	<i>Cytb</i>	0.50	0.43	0.84	0.27	0.02	-0.21	0.47
384	<i>Cytb</i>	-0.12	0.72	5.70	0.04	0.00	2.20	0.56
1016	<i>Nad4</i>	0.53	0.28	0.36	0.09	0.02	-0.24	0.39
1059	<i>Nad4</i>	0.28	0.47	0.83	0.45	0.02	-0.33	0.32
1267	<i>Nad4</i>	0.36	0.54	0.17	0.35	0.01	-0.55	0.11
1362	<i>Nad4</i>	0.58	0.20	0.28	0.09	0.02	-0.05	0.52
1941	<i>Nad2</i>	0.76	0.20	1.18	0.04	0.10	0.21	0.72
2092	<i>Atp8</i>	0.28	0.51	0.23	0.48	0.03	-0.59	0.09
3029	<i>Nad5</i>	0.71	0.17	0.36	0.04	0.05	0.06	0.69
3753	<i>Nad6</i>	0.54	0.33	0.67	0.57	0.00	-0.41	0.34
3764	<i>Nad6</i>	0.42	0.43	0.23	0.31	0.00	-0.59	0.13
3766	<i>Nad6</i>	0.17	0.53	0.07	0.87	0.00	-0.35	0.18

Supplementary Table 3. dN/dS comparisons

Gene	Number of codons	dN	dS	Normalized dN/dS
<i>Cytb</i>	446	0.33	1.15	0.144
<i>Cox2</i>	290	0.41	1.16	0.179
<i>Nad1</i>	333	0.40	1.20	0.168
<i>Nad4</i>	450	0.67	1.61	0.222
<i>Cox3</i>	312	0.49	1.56	0.159
<i>Nad2</i>	342	0.67	1.57	0.227
<i>Nad3</i>	125	0.40	1.20	0.176
<i>Atp8</i>	95	0.76	1.38	0.212
<i>Cox1</i>	556	0.48	2.15	0.096
<i>Atp6</i>	254	0.55	1.28	0.193
<i>Nad4L</i>	94	0.84	1.72	0.232
<i>Nad5</i>	603	0.56	1.29	0.214
<i>Nad6</i>	182	0.81	1.74	0.262

Supplementary Table 4. Best Partition Scheme (BPS) and best-fit models of molecular evolution for the subsets partitions of the mitochondrial protein-coding genes alignment.

Subset	Model	Partition for codon position
1	GTR+I+G	<i>Cox1_1, Cox2_1, Cox3_1, Cytb_1, Nad1_1, Nad3_1</i>
2	GTR+G	<i>Cox1_2</i>
3	HKY+I+G	<i>Cox2_2, Cox3_2, Cytb_2, Nad1_2, Nad3_2</i>
4	GTR+I	<i>Cox1_3, Cox2_3, Cox3_3, Cytb_3, Nad1_3, Nad3_3</i>
5	GTR+I+G	<i>Nad2_1, Nad4_1, Nad4L_1, Nad5_1, Nad6_1, Atp6_1</i>
6	HKY+I+G	<i>Nad2_2, Nad4_2, Nad4L_2, Nad5_2, Nad6_2, Atp6_2</i>
7	GTR+I	<i>Nad2_3, Nad4_3, Nad4L_3, Nad5_3, Nad6_3, Atp6_3</i>

