

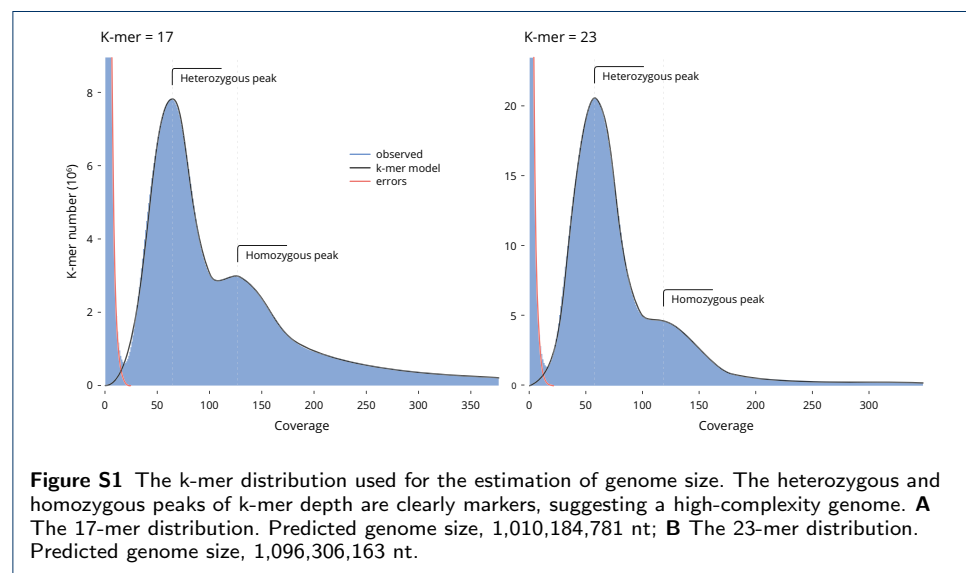
RESEARCH

Evidence of multiple genome duplication events in *Mytilus* evolution

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Supplementary Figure



Supplementary Tables

Table S1 Sequencing data, summary statistics. * Estimation based on *M. galloprovincialis* and *M. coruscus* genomes size.

Category	Number/length
Total number of long reads	15,945,130
Total number of bases	111,654,433,463
Mean length	7,002 nt
Maximum read length	672,255 nt
Coverage*	64x
Total number of PE short reads	652,465,784
Total number of bases	195,739,735,200
Read length	150 nt
Coverage*	113x
Total number of RNA-seq PE short reads	50,593,080
Total number of bases	15,177,924,000
Read length	150 nt
Coverage*	9x

Table S2 RepeatMasker statistics. * repeats fragmented by insertions or deletions have been counted as one element. † LTR.Finder results: 255,413 LTR pairs over 4,932 regions and 151,703,353 bp.

Element	Number of elements*	Length occupied	Percentage of sequence
SINEs	10,261	2,030,467 bp	0.11%
ALUs	0	0 bp	0.00%
MIRs	0	0 bp	0.00%
LINEs	343,643	130,980,160 bp	7.17%
LINE1	11,902	5,537,561 bp	0.30%
LINE2	7,970	3,762,443 bp	0.21%
L3/CR1	6,535	4,167,698 bp	0.23%
LTR elements†	4,932	151,703,353 bp	8.30%
DNA elements	99,267	25,504,172 bp	1.40%
hAT-Charlie	2,603	433,449 bp	0.02%
TcMar-Tigger	0	0 bp	0.00%
Unclassified	2,976,814	707,039,397 bp	38.70%
Small RNA	133	25,717 bp	0.00%
Satellites	2,252	400,532 bp	0.02%
Simple repeats	224,100	10,280,290 bp	0.56%
Low complexity	50,703	2,473,133 bp	0.14%
Total repeats		1,029,206,554 bp	56.33%

Table S3 Summary of annotation results for *M. edulis* gene models using a range of databases. * InterPro covers 12 databases (CDD-3.17, Coils-2.2.1, Gene3D-4.2.0, Hamap-2020_01, MobiDBLite-2.0, PANTHER-14.1, PRINTS-42.0, ProSitePatterns-2019_11, ProSiteProfiles-2019_11, SFLD-4, SMART-7.1, SUPERFAMILY-1.75, TIGRFAM-15.0).

Database	Number annotated
PfamA	61,453
InterPro*	48,772
SwissProt	11,211
KEGG	51,091
GO	31,620
All	9,089
Total	69,246

Table S4 Mytilinae (subfamily) mitochondrial genomes.

Accession	Genome size	Species name	Common name
NC_018362.1	16,014 bp	<i>Perna viridis</i>	Asian green mussel
NC_044131.1	16,253 bp	<i>Septifer bilocularis</i>	-
NC_044128.1	17,582 bp	<i>Crenomytilus grayanus</i>	-
NC_030633.1	16,765 bp	<i>Mytilus chilensis</i>	Chilean mussel
NC_028706.1	18,145 bp	<i>Limnoperna fortunei</i>	Golden mussel
NC_026288.1	18,415 bp	<i>Perna perna</i>	Brown mussel
NC_024733.1	16,642 bp	<i>Mytilus coruscus</i>	Hard-shell mussel
NC_006886.2	16,744 bp	<i>Mytilus galloprovincialis</i>	Mediterranean mussel
NC_006161.1	16,740 bp	<i>Mytilus edulis</i>	Blue mussel
NC_007687.1	18,652 bp	<i>Mytilus trossulus</i>	Bay mussel
NC_015993.1	16,730 bp	<i>Mytilus californianus</i>	California mussel

Table S5 Bivalvia (class) genome where Ka & Ks estimations were possible: All exhibit evidences of α -WGD and β -WGD. * this study.

Species	Peak/Mean (α -WGD)	Std. dev. (α -WGD)	Peak/Mean (β -WGD)	Std. dev. (β -WGD)
<i>M. edulis</i> *	0.6132	0.1939	1.8196	0.7103
<i>M. galloprovincialis</i>	0.6010	0.1934	1.8109	0.7011
<i>M. coruscus</i>	0.5635	0.1996	1.7977	0.7082
<i>C. gigas</i>	0.6299	0.3699	1.6350	0.4601
<i>C. virginica</i>	0.4787	0.4921	1.7627	0.3479
<i>M. yessoensis</i>	0.6612	0.2278	1.7064	0.4722
<i>P. maximus</i>	0.6392	0.2759	1.8794	0.4541

Table S6 Bivalvia (class) genome and availability of gene models and annotations. * this study.

Assembly	Reference	Species name	Common name	Gene Models
GCA_014843695.1	ASM1484369v1	<i>Archivesica marissinica</i>	Deep-sea clam	-
GCA_004382765.1	QAU_Acon.1.1	<i>Argopecten irradians concentricus</i>	Bay scallop	-
GCA_004382745.1	QAU_Airr.1.1	<i>Argopecten irradians irradians</i>	Bay scallop	-
GCA_002080005.1	Bpl.v1.0	<i>Bathymodiolus platifrons</i>	Cold seep mussel	-
GCA_001632725.1	ASM163272v1	<i>Corbicula fluminea</i>	Asian clam	-
GCF_902806645.1	cgigas.uk.roslin.v1	<i>Crassostrea gigas</i>	Pacific oyster	yes
GCA_005518195.2	NWPU_Cgig.v2	<i>Crassostrea gigas</i>	Pacific oyster	-
GCF_000297895.1	oyster.v9	<i>Crassostrea gigas</i>	Pacific oyster	-
GCA_000297895.2	ASM29789v2	<i>Crassostrea gigas</i>	Pacific oyster	-
GCA_011032805.1	ASM1103280v1	<i>Crassostrea gigas</i>	Pacific oyster	-
GCA_015776775.1	ASM1577677v1	<i>Crassostrea hongkongensis</i>	Hong Kong oyster	-
GCA_002022765.1	C.virginica.1.0	<i>Crassostrea virginica</i>	Eastern oyster	-
GCA_002022765.3	C.virginica-2.0	<i>Crassostrea virginica</i>	Eastern oyster	-
GCF_002022765.2	C.virginica-3.0	<i>Crassostrea virginica</i>	Eastern oyster	yes
GCA_012932295.1	ASM1293229v1	<i>Cyclina sinensis</i>	Venus clam	-
GCA_000806325.1	ASM80632v1	<i>Dreissena polymorpha</i>	Zebra mussel	-
GCA_007657795.1	UV_Dro.v1.1	<i>Dreissena rostriformis</i>	Quagga mussel	-
GCA_003130415.1	ASM313041v1	<i>Limnoperna fortunei</i>	Golden mussel	-
GCA_008271625.1	LuRhyn.1.0	<i>Lutraria rhynchaena</i>	Snout Otter Clam	-
GCA_016163765.1	CUHK_oyster.2.0	<i>Magallana hongkongensis</i>	Hong Kong oyster	-
GCA_015947965.1	ASM1594796v1	<i>Margaritifera margaritifera</i>	Freshwater pearlshell mussel	-
GCA_016617855.1	ASM1661785v1	<i>Megaloniaias nervosa</i>	Washboard	-
GCA_014805675.1	ASM1480567v1	<i>Mercenaria mercenaria</i>	Northern quahog	-
GCF_002113885.1	ASM211388v2	<i>Mizuhopecten yessoensis</i>	Yesso scallop	yes
GCA_002113885.1	ASM211388v1	<i>Mizuhopecten yessoensis</i>	Yesso scallop	-
GCA_002080025.1	Mph.v1.0	<i>Modiolus philippinarum</i>	Philippine horse mussel	-
GCA_017311375.1	Mcoruscus.HiC	<i>Mytilus coruscus</i>	Hard-shell mussel	-
GCA_011752425.2	MCOR1.1	<i>Mytilus coruscus</i>	Hard-shell mussel	yes
GCA_011752425.1	MCOR1	<i>Mytilus coruscus</i>	Hard-shell mussel	-
GCA_905397895.1*	MEDL1	<i>Mytilus edulis</i>	Blue mussel	yes
GCA_019925275.1	PEIMSO	<i>Mytilus edulis</i>	Blue mussel	-
GCA_900618805.1	MGAL_10	<i>Mytilus galloprovincialis</i>	Mediterranean mussel	yes
GCA_000715055.1	mussel1.0	<i>Mytilus galloprovincialis</i>	Mediterranean mussel	-
GCA_001676915.1	ASM167691v1	<i>Mytilus galloprovincialis</i>	Mediterranean mussel	yes
GCA_903981925.1	v081	<i>Ostrea lurida</i>	Olympia oyster	-
GCA_902825435.1	PGEN-v1.0	<i>Panopea generosa</i>	Pacific geoduck	-
GCF_902652985.1	xPecMax1.1	<i>Pecten maximus</i>	King scallop	yes
GCA_002216045.1	PinMar1.0	<i>Pinctada imbricata</i>	Akoya pearl oyster	-
GCA_016161895.1	ASM1616189v1	<i>Pinna nobilis</i>	Noble penshell	-
GCA_016746295.1	UT_Pstr.1.0	<i>Potamilus streckersoni</i>	Brazos heelsplitter	-
GCA_009026015.1	ASM902601v1	<i>Ruditapes philippinarum</i>	Manila clam	-
GCA_003671525.1	Sgl1.0	<i>Saccostrea glomerata</i>	Sydney rock oyster	-
GCA_007844125.1	ASM784412v1	<i>Sinonovacula constricta</i>	Chinese razor clam	-
GCA_009762815.1	ASM976281v1	<i>Sinonovacula constricta</i>	Chinese razor clam	-
GCA_013375625.1	ASM1337562v1	<i>Tegillarca granosa</i>	Blood clam	-
GCA_003401595.1	ASM340159v1	<i>Venustaconcha ellipsiformis</i>	Ellipse	-

Table S7 Genes involved in immunity, stress response and shell formation under positive selection in *M. galloprovincialis*, *M. edulis* and *M. coruscus*.

Species	Category	ClusterID	Gene Names / Function (Ortholog cluster)	Ka/Ks	Ortholog reference
<i>M. galloprovincialis</i>	Immunity	9813	NT1	2.5	[1]
<i>M. galloprovincialis</i>	Stress	6307	Potential tumour suppressor in tumour progression	1.4	[2]
<i>M. galloprovincialis</i>	Stress	1976	Arylesterase / Paraoxonase	1.4	[3]
<i>M. galloprovincialis</i>	Stress	8246	Confer resistance to organophosphate toxicity	1.4	[4]
<i>M. galloprovincialis</i>	Shell formation	18160	Serine/threonine kinase 17	1.2	[5]
<i>M. galloprovincialis</i>	Immunity	19933	Cellular processes, proliferation, apoptosis, and differentiation. Abiotic stress	1.1	[6]
<i>M. galloprovincialis</i>	Stress	1594	Peptidase inhibitor 16	1.1	[7]
<i>M. galloprovincialis</i>	Stress	973	Cardiac stress response	1.1	[8]
<i>M. galloprovincialis</i>	Stress	25447	EF-hand Ca ²⁺ -binding domain 6	1.1	[9]
<i>M. galloprovincialis</i>	Shell formation	12897	CaLP has two Ca ²⁺ -binding EF hand domains. Growth of nacre-prismatic layer	1	[10]
<i>M. galloprovincialis</i>	Stress	14603	Signal transducer-activator of transcription 5B	1	[11]
<i>M. galloprovincialis</i>	Immunity	14873	Mediate the signaling of cytokines and a number of growth factors	1	[12]
<i>M. galloprovincialis</i>	Immunity	3134	Pyruvate dehydrogenase E1 alpha subunit	1	[13]
<i>M. galloprovincialis</i>	Immunity	14056	Reduces OXPHOS and oxygen consumption	0.9	[14]
<i>M. galloprovincialis</i>	Stress	1893	DNA mismatch repair protein MSH6	0.9	[15]
<i>M. galloprovincialis</i>	Stress	7356	Responsive to oxidative stress and protection against ROS and DNA damage	0.9	[16]
<i>M. galloprovincialis</i>	Stress	3258	zinc finger MYM-type protein 2-like	0.9	[17]
<i>M. galloprovincialis</i>	Stress	5345	Significant correlations with salinity, temperature, As, Cd or lindane	0.9	[18]
<i>M. galloprovincialis</i>	Stress	5490	Ca ²⁺ -transporting ATPase, plasma membrane	0.9	[19]
<i>M. galloprovincialis</i>	Stress	5490	Catalyse the hydrolysis of ATP coupled with the transport of calcium	0.9	[20]
<i>M. edulis</i>	Immunity	1359	Inositol polyphosphate 1-phosphatase	2.4	[21]
<i>M. edulis</i>	Stress	5390	Mg ²⁺ dependent of inositol monophosphatase-like domain	2	[22]
<i>M. edulis</i>	Stress	13969	Galectin-4	1.7	[23]
<i>M. edulis</i>	Stress	9109	Regulators of immune cell homeostasis	1.7	[24]
<i>M. edulis</i>	Stress	10101	PRRT1	1.5	[25]
<i>M. edulis</i>	Stress	4324	Proline-rich transmembrane protein 1	1.3	[26]
<i>M. edulis</i>	Stress	4307	Metalloproteinase inhibitor 3	1.3	[27]
<i>M. edulis</i>	Stress	9741	Ligament-specific protein	1.2	[28]
<i>M. edulis</i>	Stress	7225	Solute carrier family 12	1.2	[29]
<i>M. edulis</i>	Stress	7276	Transport endogenous-exogenous substances. Potassium/chloride transporters	1.2	[30]
<i>M. edulis</i>	Stress	14877	Leucine-rich repeat domain superfamily	1.1	[31]
<i>M. edulis</i>	Stress	15346	Development, growth, and responses to abiotic and biotic stresses	1.1	[32]
<i>M. edulis</i>	Stress	2105	Heat shock protein 22 HSPB8	1	[33]
<i>M. edulis</i>	Stress	10990	Protecting cells, folding of nascent peptides, and responding to stress	1	[34]
<i>M. edulis</i>	Stress	20412	Mitogen-activated protein kinase 6 MAPK	0.9	[35]
<i>M. edulis</i>	Stress	5702	involved in the regulation of Hsp expression in blue mussels	0.9	[36]
<i>M. edulis</i>	Stress	22962	LRP1B	0.9	[37]
<i>M. edulis</i>	Stress	11253	Low-density lipoprotein receptor-related protein	0.9	[38]
<i>M. edulis</i>	Stress	19695	E3 ubiquitin-protein ligase mind-bomb (MIB2)	0.9	[39]
<i>M. edulis</i>	Stress	11784	Antiviral immunity	0.9	[40]
<i>M. edulis</i>	Stress	12528	Mucolipin, Polycystin cation channel	0.9	[41]
<i>M. edulis</i>	Stress	8193	Calcium homeostasis	0.9	[42]
<i>M. edulis</i>	Stress	6739	RNF170, RING finger protein 170	0.8	[43]
<i>M. edulis</i>	Stress	8395	Ubiquitination and degradation of inositol 1,4,5-trisphosphate receptors	2	[44]
<i>M. edulis</i>	Stress	2491	Fibropellin-1	2	[45]
<i>M. edulis</i>	Stress	5530	Hypoxia responsive gene	1.6	[46]
<i>M. edulis</i>	Stress	9626	Carbohydrate-binding WSC	1.2	[47]
<i>M. edulis</i>	Stress	8044	Plasma membrane sensor for surface stress	1.1	[48]
<i>M. edulis</i>	Stress	17439	Lactamase-B	1.1	[49]
<i>M. edulis</i>	Stress	302	Drug resistance among gram-negative bacteria	1	[50]
<i>M. edulis</i>	Stress	6467	polycystin	1	[51]
<i>M. edulis</i>	Stress	2098	Calcium homeostasis	1	[52]
<i>M. edulis</i>	Stress	8921	Papain-like cysteine peptidase superfamily	1	[53]
<i>M. edulis</i>	Stress	13594	Prevent unwanted protein degradation	0.9	[54]
<i>M. edulis</i>	Stress	4996	Peptidase M12B	0.9	[55]
<i>M. edulis</i>	Stress	3709	Cell adhesion, signaling, cell-cell fusion, and cell-cell interactions	0.9	[56]
<i>M. edulis</i>	Stress	8284	ATP-dependent metalloprotease (YMEL1)	0.9	[57]
<i>M. edulis</i>	Stress	5847	Stress-sensitive mitochondrial protease	0.9	[58]
<i>M. edulis</i>	Stress	12429	P-loop - nucleoside triphosphate hydrolase	0.8	[59]
<i>M. edulis</i>	Stress	12587	This domain shows a high specificity for pathogens and parasites	0.8	[60]
<i>M. edulis</i>	Stress	12587	EF-hand Ca ²⁺ -binding domain	0.8	[61]
<i>M. edulis</i>	Stress	12587	CaLP has two Ca ²⁺ -binding EF hand domains (Growth of nacre-prismatic layer)	0.8	[62]
<i>M. edulis</i>	Stress	12587	C-type lectin superfamily 17 member A	0.8	[63]
<i>M. edulis</i>	Stress	12587	Mediate crucial cellular functions during immunity and homeostasis	0.8	[64]
<i>M. edulis</i>	Stress	12587	Fibrinogen-like protein A	0.8	[65]
<i>M. edulis</i>	Stress	12587	Immunopattern-recognition receptors.	0.8	[66]
<i>M. edulis</i>	Stress	12587	FYVE, RhoGEF and PH domain	0.8	[67]
<i>M. edulis</i>	Stress	12587	Signal transduction	0.8	[68]
<i>M. edulis</i>	Stress	12587	Perlucin-like protein	0.8	[69]
<i>M. edulis</i>	Stress	12587	Ca ²⁺ -dependent carbohydrate binding activity	0.8	[70]
<i>M. edulis</i>	Stress	12587	Clq-related factor	0.8	[71]
<i>M. edulis</i>	Stress	12587	Pattern recognition receptors. Activates innate immune response	0.8	[72]
<i>M. edulis</i>	Stress	12587	nicotinic acetylcholine receptor alpha-7	0.8	[73]
<i>M. edulis</i>	Stress	12587	Regulates immune response through the neuroendocrine-immune system	0.8	[74]
<i>M. edulis</i>	Stress	12587	TRIM56, tripartite motif-containing protein 56	0.8	[75]
<i>M. edulis</i>	Stress	12587	virus-inducible E3 ubiquitin ligase that restricts pestivirus infection	0.8	[76]
<i>M. edulis</i>	Stress	12587	HMCN, hemicentin	0.8	[77]
<i>M. edulis</i>	Stress	12587	Immune recognition, signaling and regulation. insulin peptide receptor	0.8	[78]
<i>M. edulis</i>	Stress	12587	COL6A, collagen, type VI	0.8	[79]
<i>M. edulis</i>	Stress	12587	Adhesome molecules	0.8	[80]
<i>M. edulis</i>	Stress	12587	mucin-13-like	0.8	[81]
<i>M. edulis</i>	Stress	12587	Molluscan calcification	0.8	[82]
<i>M. edulis</i>	Stress	12587	serine-protein kinase ATM	0.8	[83]
<i>M. edulis</i>	Stress	12587	DNA damage sensor	0.8	[84]
<i>M. edulis</i>	Stress	12587	Hemicentin (HMCN)	0.8	[85]
<i>M. edulis</i>	Stress	12587	Extracellular ion-binding proteins in the biomineral matrix	0.8	[86]
<i>M. edulis</i>	Stress	12587	O-mannosyltransferase (TMTc)	0.8	[87]
<i>M. edulis</i>	Stress	12587	Ca ²⁺ -regulation and protein folding	0.8	[88]
<i>M. edulis</i>	Stress	12587	ADAR, adenosine deaminase	0.8	[89]
<i>M. edulis</i>	Stress	12587	DNA binding, antiviral effectors	0.8	[90]
<i>M. edulis</i>	Stress	12587	Caveolin-1, Caveolin-3	0.8	[91]
<i>M. edulis</i>	Stress	12587	Regulating neutrophil functional responses that underpin innate immunity	0.8	[92]
<i>M. edulis</i>	Stress	12587	Apoptosis regulator BAX	0.8	[93]
<i>M. edulis</i>	Stress	12587	Apoptosis regulator	0.8	[94]
<i>M. edulis</i>	Stress	12587	2-hydroxyglutaryl-CoA dehydratase (hgdC)	0.8	[95]
<i>M. edulis</i>	Stress	12587	Iron-sulfur cluster binding	0.8	[96]
<i>M. edulis</i>	Stress	12587	Mannose receptor, C type (MRC)	0.8	[97]
<i>M. edulis</i>	Stress	12587	Pathogen recognition receptor	0.8	[98]
<i>M. edulis</i>	Stress	12587	Inhibitor of growth protein 1 (ING1)	0.8	[99]
<i>M. edulis</i>	Stress	12587	Tumor suppressor gene	0.8	[100]
<i>M. edulis</i>	Stress	12587	BIRC2.3	0.8	[101]
<i>M. edulis</i>	Stress	12587	Physiological role in growth, immunity, and apoptosis	0.8	[102]
<i>M. edulis</i>	Stress	12587	Filamin	0.8	[103]
<i>M. edulis</i>	Stress	12587	Recognition of pathogens	0.8	[104]
<i>M. edulis</i>	Stress	12587	Proteasome regulatory (PSMD7)	0.8	[105]
<i>M. edulis</i>	Stress	12587	Recognition of polyubiquitin chains and cleavage of ubiquitin from degraded proteins	0.8	[106]
<i>M. edulis</i>	Stress	12587	NOTCH1	0.8	[107]
<i>M. edulis</i>	Stress	12587	Calcium signalling pathway and shell pigmentation	0.8	[108]
<i>M. edulis</i>	Stress	12587	Heat shock protein 90kDa beta (HSP90B)	0.8	[109]
<i>M. edulis</i>	Stress	12587	Heat shock protein	0.8	[110]
<i>M. edulis</i>	Stress	12587	Cell division control protein 42	0.8	[111]
<i>M. edulis</i>	Stress	12587	Roles in host defense	0.8	[112]
<i>M. edulis</i>	Stress	12587	Ammonium transporter (amt)	0.8	[113]
<i>M. edulis</i>	Stress	12587	Ammonium transporter	0.8	[114]
<i>M. edulis</i>	Stress	12587	RING finger protein 145	0.8	[115]
<i>M. edulis</i>	Stress	12587	Ubiquitination	0.8	[116]
<i>M. edulis</i>	Stress	12587	Lysine methyltransferase 4 (EEF1AKMT4)	0.8	[117]
<i>M. edulis</i>	Stress	12587	Enhances the function of heat shock factor 1 during the heat shock response	0.8	[118]

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