

Table S1. Sequence of the primer pairs, and their use in the study. Primer names are based on the human *Pgm-1* exon number, but do not always correspond to the exon/intron nomenclature in *A. pompejana*, due to the comparative fusion of some exons (case of AP-exon3 with corresponds to exon2, exon3 and exon4 in human). Lower-case sequences correspond to intronic regions and upper-case sequences correspond coding regions.

Primers	5' Sequence 3'	Localization/Method
Anchor-OligodT	5-CTCCTCTCCTCTCCTC-T(17)-3	Primer for reverse-transcription of polyA+ mRNA
AP_PGMcDNAF1	5-GTNGTYGGNGGNGAYGGNBG-3	Pgm-1 cDNA fragment amplification
AP_PGMcDNAF2	5-YCAYAAAYCCNGGNGGNCC-3	
AP_PGMcDNAR	5-NGTRATNACNGTNGGWKC-3	
Ap_PGMex1F	5-AAG AGG CAT CAG AGA AGA TA-3	Gene structure determination
Ap_PGMex2R	5-GAC CAC CTG GGT TAT GAG AT-3	(amplification of exon1-intron1)
Ap_PGMex2F	5-TAG GTA AAG ATG GCA TAC TT-3	Gene structure determination
Ap_PGMex4R	5-CCG CTG AGA GCA TTG ACA AG-3	(amplification of exon2-exon3)
Ap_PGMex5F	5-AA GAC TTT GGA GGA GGA CAT C-3	Chromosome walking along the gene
Ap_PGMex7R	5-ATC CAT AAG GTT ACC AAA GAA CTT CCA-3	(exon3-exon5)
Ap_PGMex7F	5-AGT TCT TTG GTA ACC TTA TGG ATG CT-3	Gene structure determination
Ap_PGMex9R	5-ATT TTA TCA AGG TTG GCC ATC ATC TG-3	(amplification of exon5-intron6)
Ap_PGMex9F	5-AC CTT GAT AAA ATG GCA GCT GAC-3	Gene structure determination
Ap_PGMex10R	5-GA ATC TGA CTC ATA GCT ATC AAT GTA-3	(amplification of exon7-exon8)
Ap_PGMex10F	5-ATG TAC ATT GAT AGC TAT GAG TCA GAT-3	Gene structure determination
Ap_PGMex11R	5-AAA TTT AAG TAA TAA CAG TAG GCT GCT-3*	(amplification of exon8-exon9) *anchored with the stop codon
Ap_PGMint1R1	5-tgtgtatataagacgttctttactgtgg-3	Chromosome walking to obtain the
Ap_PGMint1R2	5-tcatgtaaaattctgtatatacttacacc-3	5'UTR and the first exon with w1, w2, w3 and wc (Mishra et al., 2002)
Ap_PGMex1Rn	5-GTA GCC TTT CTC AGA CCA CTA GT-3	Genotyping EQ mutations in exon3
Ap_PGMint4F	5-tgttaggtageatgecteca-3	
AP_PGMex5R	5-TCC TCC AAA GTC TTC CAG TG-3	Genotyping intron1-exon2
Ap_PGMex1F	5-AAG AGG CAT CAG AGA AGA TA-3	
Ap_PGMex2R	5-GAC CAC CTG GGT TAT GAG AT-3	
Ap_PGMex6F	5-ttt tag GAC AGA AAC ATG ATA CTT GGT-3	Genotyping intron4-exon5
Ap_PGMint7R	5-taatattac CT GAT GTG ATC TGA TCC-3	
Ap_PGMex9F	5-AC CTT GAT AAA ATG GCA GCT GAC-3	Genotyping exons 6 and 8
Ap_PGMex10R	5-GA ATC TGA CTC ATA GCT ATC AAT GTA-3	
AP_PGMmut78F	5-AAG TGA TAG ACT CTG TGC AGG ATT ATA TGG AC-3	Directed mutagenesis to produce allele 78 from allele 100
AP_PGMmut78R	5-TAG TCC ATA TAA TCC TGC ACA GAG TCT ATC AC-3	
AP_PGMmut90F	5-TTG ACA CAA AAG ATC ACA CAA TAC CAC ACT GTG C-3	Directed mutagenesis to produce allele 90 from allele 100
AP_PGMmut90R	5-AGG CAC AGT GTG GTA TTG TGT GAT CTT TTG TGT C-3	
Pet20_PGMXhol	5-CTC GAG AGT AAT AAC AGT AGG CTG CTG TC-3	Cloning in Pet20 overexpression vector
Pet20_PGMAsel	5-ATT AAT GAG TCT GAA GTC GGT GAC AGT GGC T-3	
PetDuet_PGMBamHI	5-GGA TCC GAG TCT GAA GTC GGT GAC AGT GGC T-3	Cloning in PetDuet overexpression vector
PetDuet_PGMNotI	5-GCG GCC GCT TAA GTA ATA ACA GTA GGC TGC TGT C-3	

Table S2. Frequencies of EE, EQ and QE *Pgm-1* alleles, heterozygosities and Fis (*: significant with 1000 permutations) in northern and southern populations of *Alvinella pompejana*. Note: Allele QQ was not found in any of the populations.

Site	N	EE	EQ	QE	Hobs	He(n.b.)	Fis
South EPR overall	126	0.051	0.139	0.810	0.293	0.324	+0.094
Krasnov (21°33'S, hot)	23	0.044	0.217	0.739	0.434	0.413	-0.053
Bordreaux (21°25'S, hot)	30	0.033	0.100	0.867	0.267	0.242	-0.105
Fromveur (18°25'S, hot)	32	0.000	0.047	0.953	0.094	0.091	-0.033
Rehu Marka (17°25'S, cold)	41	0.110	0.195	0.695	0.390	0.472	+0.176
North EPR overall	94	0.718	0.277	0.005	0.404	0.410	+0.014
Jumeaux (13°N, hot)	19	0.605	0.395	0.000	0.684	0.491	-0.410*
Julie (13°N, cold)	28	0.696	0.286	0.018	0.429	0.441	+0.028
Genesis (13°N, cold)	27	0.741	0.259	0.000	0.296	0.391	+0.246
Elsa (13°N, cold)	20	0.825	0.175	0.000	0.250	0.296	+0.159

Table S3. Summary statistics of structured coalescent simulations (n=1000) obtained with the msms software and the pylibseq librairies in order to test a model of asymmetric migration across a barrier with and without selection and two levels of recombination in order to examine the genetic expectations of overdominance and the two-niches (2 demes/2 habitats) models. *: selection coefficient was set to 100 (low=ls) and 10 000 (high=hs) for the selection models. For comparison purpose, the within deme values correspond to parameters estimated for the exporting deme in the migration asymmetry. Values between brackets represent the confidence interval of the parameter's simulations at 95%. D: Tajima's D, AM: Asymmetric migration across a barrier with no selection, AM_OD: Asymmetric migration across a barrier with overdominance, AM_2N: Asymmetric migration across a barrier with a two-niches model.

Selected model	R	Overall π	Overall θ_w	Overall D	Fst	Within deme π	Within deme θ_w	Within deme D
Obs. data*	1	8.2	8.4	-0.12	0.27	8.0	7.6	+0.20
AM	0	34.2 [32.6, 35.9]	17.1 [16.5, 17.7]	+2.73 [+2.6, +2.8]	0.85 [0.83, 0.86]	3.1 [3.0, 3.2]	3.1 [3.0, 3.1]	-0.05 [-0.1, +0.0]
AM	1	34.4 [32.6, 36.3]	17.1 [16.4, 17.8]	+2.65 [+2.6, +2.7]	0.84 [0.83, 0.85]	3.1 [3.0, 3.3]	3.1 [3.0, 3.2]	-0.04 [-0.1, +0.0]
AM	100	34.8 [33.1, 36.5]	17.3 [16.7, 18.0]	+2.75 [+2.6, +2.8]	0.85 [0.84, 0.86]	3.1 [3.0, 3.2]	3.1 [3.0, 3.1]	-0.04 [-0.1, +0.0]
AM_OD-ls*	1	37.0 [35.4, 38.6]	19.5 [18.8, 20.1]	+2.59 [+2.5, +2.7]	0.73 [0.72, 0.75]	6.4 [6.2, 6.5]	4.6 [4.5, 4.7]	+1.20 [+1.1, +1.3]
AM_OD-hs*	1	37.0 [35.5, 38.6]	19.4 [18.7, 20.0]	+2.61 [+2.5, +2.7]	0.74 [0.73, 0.75]	6.3 [6.1, 6.4]	4.5 [4.4, 4.6]	+1.21 [+1.1, +1.3]
AM_OD-hs*	100	35.1 [34.3, 35.8]	17.6 [17.3, 17.9]	+3.20 [+3.1, +3.3]	0.90 [0.89, 0.90]	3.2 [3.1, 3.3]	3.1 [3.0, 3.2]	+0.05 [-0.0, +0.1]
AM_2N	1	21.8 [21.1, 22.6]	16.9 [16.5, 17.3]	+0.83 [+0.7, +0.9]	0.45 [0.44, 0.47]	14.6 [13.8, 15.3]	12.6 [12.2, 13.1]	+0.44 [+0.3, +0.5]
AM_2N	100	22.7 [22.4, 23.0]	17.4 [17.3, 17.6]	+0.98 [+0.9, +1.0]	0.50 [0.49, 0.51]	15.0 [14.7, 15.2]	12.8 [12.6-13.0]	+0.58 [+0.5, +0.6]

Figure S1. Entire sequence of the *Pgm-1* gene of *A. pompejana* and its translated exons

(1) Structure of the *Pgm-1* gene. Grey zones represent positions where forward and reverse primers have been designed. Exons are indicated by the use of uppercase and introns are in lowercase. Highlighted codons in yellow* represent polymorphic non-synonymous changes between alleles found at a frequency of more than 10%, and in green below 5% but which are likely to change the net charge of the protein. # symbol represents methylated codons found at the end of exon 5.

ATGAGTCTGAAGTCGGTGACAGTGGCTACGAAGCCCTCGATGGGCAGAAGGCCGGGCACTAGTG
GTCTGAGAAAGGCTACGAAGATATTATGCAAGAACATTACACA **GAA**ACTTC**GTG**CAATGTAC
GTTGTCTGCCATGGCGACAAATTAAAGGGATGTACACTAGTAGTTGGAGGTGATGGAAGGTAT
TATGGTAAAGAGGCATCAGAGAAGATAATTAAAATGTGCGCAGGTAAATGGT **gt**aagtatatcaa
gaattttacatgatgtgtaaacaattgttctactgacatcagaagccacagtaaagagaacg
tcttatatacacagataaatatgttaacacaacttcttcgttgcattaaatgcgggtatt
aattttgcttatttgaaactaccaagttatttaacgtatttattgttacaatttgaat
atgttatactgttacatgcctgaatttggttgaattgacgttttaatgtactaattacg
tttgggttttagactattgaatcattaccaggcatgctaatttgcatttgcatttgcatt
attgttgcatttgcatttgcatttgcatttgcatttgcatttgcatttgcatttgcatttgcatt
atttgtatgggtatttgcatttgcatttgcatttgcatttgcatttgcatttgcatttgcatt
agGTAGCAAAGGT
AATTATAGGTAAAGATGGCATACTTCTACACCAGCTGTGTCATGCTGATCAGAAAAATCAC
ACTGATGGAGGAATAATCCTCACTGCATCTCATAACCCAGGTGGTCAAATGCTGATTTGGCA
TAAAGTTAATATTGCCAACGGAG**gt**aatttgcatttgcatttgcatttgcatttgcatttgcatt
catacaaacaatccttatttgcatttgcatttgcatttgcatttgcatttgcatttgcatttgcatt
agctgaatgttaagtgttatgttatgttatgttatgttatgttatgttatgttatgttatgttat
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tggcactttagctgaccaaggacttgcatttgcatttgcatttgcatttgcatttgcatttgcatt
aggttgaaagctgaccaatgttatattttcatcac**ag**GACCAGCCCCAGCTGGAGTCACAG
ATCACATCTATGCCTGACACAAAAGATCACAC**GAA**TACCAACTGTGCTGACCTGAAGGCTGA
CATCTGTACAATAGGAAGCCAGACGTTACTGTTGATGATCATCCATTAAATATTGAAGTGATA
GACTCTGTG**GAG**GATTATATGGACTACATGAAGGAAATTGGACTTCAATTCCATCAGAGGCT
TATTGACTGGAGAAGGAGGACAAACAAAGCTAAAGGTCTGTCAATGCTCAGCGGAGTGGT
TGGCCCATATGTGAAGAGGATACTGTGCCAGGAGCTAGGCATGGATGAAGCCAGTGCTGTTAAT
TGTGTTCCACTGGAAGACTTGGAGGAGGACATCCAGATCCAACTTGACCTATGCAGCTGATT
TAGTGAATGAATTAAAGAAAGGTGTCATGATTTGGTGCATTGATGGC#GAC#GGC#**gt**a
agttaatttagttgtgatagatgtcttattttatgttgcatttgcatttgcatttgcatt
aaatacttcaaggatgtatgttatgttatgttatgttatgttatgttatgttatgttatgttat
cttatatatgttgcatttgcatttgcatttgcatttgcatttgcatttgcatttgcatttgcatt
ggtagcttt**ag**GACAGAAACATGATACTGGTAAGAATGGCTTCTTGTATGCCATGTGACT
CCCTGGCAGTCATAGCTGCACATTGGAGTGTATACCATAATTCAAGAAGTCTGGCATAAAAGG
TTATGCC**AGA**AGCATGCCAACTAGTGGGCCATTGAT**Ag****gt**aaatataaaaaatgtatcatctg
tggacctaattctgttatgtttcagttctttgtttaccttacttgcatttgcatttgcatttgcatt

gtcacagatgatatattgatcatcttattctgaactaggctacaaaataagagtggccagtct
 aataaaattaaattacactaactgctgttttatgatac**agA**GTGGCACAGAAGAAGGGC
 AAGGAGATGTTGAGGTGCCAACAGGCTGGAAGTTCTTGGTAACCTTACGGATGCTGGTAGAC
 TTCACTTGTGGAGAGGAGCTTGGGACAGGATCAGATCACATCAG**gta**atattacacaat
 gctacatgtgtcaaattcatttagaaataacttcatcttgtaagttgtatacacacttctgtaag
 ccgactagtagttccatttcagaattcatttaacatgttatcagtcatastatattctatatacg
 gatttgaattttaatgtgagctatccatagctgatattgacatattgctgctcagttgccta
 tatgagactaaggcagtcttatcttcattctggatgctgctatctataaaaccatttgaca
 taatacatcatcaaagtgtgtttgtattacatcattatgtgtgaaatgtgaaactgtttat
 tgtgttt**agA****GAA**AAGGATGGCTTATGGGCAGTTGGCCTGGCTCTATTAGCCTGCAA
 GAAGCAGTCAGTAGAAGAAATCTTAAAGGATCACTGGAAGACATATGGCAGGAACCTCTTCACT
Aggtaatatcatagatgtattacagtctcataaaatcatgtataaaattataatatttaatc
 acagtttgctgttaataatatgaaaacctacttgaaattgataagatgtgaaaaataactttgt
 ggctgttacttgcacccattttattttgtgtgactgacagttgcacccatttgc**ag**GTATG
 ATTATGAGAATGTTGAATCTGATCCAGCCAATCAGATGATGCCAACCTTGATAAAAATGGCAGC
TGACTCATCTATTGGCAAGGTGTTAGTCATGGTACAAATCATATAAAGTAGCCAAGATG
GACAACTTGAATACACTGACCCAATTGACAACAGTGTATCAAAAAACAG**gta**attctgtcat
 cttattaaattgtgcacacatacacaccccttgcacatttgcattttgtttaattatttgcctgtaaaa
 taaatactgcccaattcagaatgaaaaaaaaatgtcttcttacatcatgcaattgttattttg
 tgtcacccat**atag**GGCATCCGGATCATTGAGGATGGATCAAGGATTATATCCGTCTGAG
 TGGTACAGGAAGTGCTGGAGCAACAATCAGGATGTACATTGATAGCTATGAGTCAGATTCAAAC
 AACAGCTCCTAGATTCTCAG**gtt**ttcacagcttaatataacaagtgttatattctaaa
 ttgcagcattgtatgcataattgtgattaatatttagatataattttatattatgaaagac
 ctatcattaccactgcttatgaactgattgtttatgtattaaagttagttcttgagtggttat
 taggaaaggcatgtgcatttcatttctatgttagactatataaaatgctttaaaa
 atctatgcacaactcccactgaacaaatattattatattatcattccattctgc**ag**GTCA
 TGAAACCACGTATTGAGATAGCACTGAAATATCCCAGCTAGAGAGCTGACAGGAAGACAGCA
GCCTACTGTTATTACTTAAatttggatgcagccaacattttgtctcaattaccatgttagt
 ctatgtcatgtgatgagctatgcttagatgatctgtatgtaaaaaaaaaaaaaaaaaaaa
 aaaaaaaaaaaaa

(2) translated cDNA sequence of the AP-PGM enzyme (562 aa). Bold uppercase letters between parentheses are the three polymorphic sites for which the alternative allele has a frequency greater than 5%. Bold lowercase letters correspond to alternative mutations, which frequency is lower than 5% in genotyped regions. Other bold sites represent non-synonymous singlets in our set of sequenced individuals and, grey zones correspond to intronic regions linking the translated regions. *: stop codon.

MSLKSVTVATK**PFDQKPGTSLRKATKIFMQE**HYT (**E/q**) NF (**V/L**) QCTLSAM**GD**KLKGCT**L**
LVVGGDGRYYGKEASEKIIKMC**AGNGVAKVIIGKDILSTPAVSCLIR**KNHTDGGIILTAS
 HNPGGPNADFGI**KFNIANGGPAPAGVTDHIYALTQKIT** (**E/Q**) **YHTVPDLKADICTIGSQTF**
 TVDDHPFNIEV**IDSV** (**E/Q**) **DYMD**YMKEIFDFNSIRGLLTGEGGQTKLKV**LVNALS**GVVGPY
 VKRILCQELGMDEASAVNCVPLDFGGGHDPNL**TYAADLVNE**LKK**GVHDFGAAFDGDGDR** (**N/d**)
MILGKNGFFVSPCD~~S~~LA~~V~~IAAHLECIPFKKSGIKGYARSMPTSGAID (**R/i**) VAQKKG
 KEMFEVPT (**G/s,d**) WKFFGNL (**M/t**) DAGRLS**LCGEESFGTGS**DHIR (**E/k**) KDGLWAVLA
 WLSI**LACKQSVE**ILKDHWKTY**GRNFFTRYDYENVESDPANQMMANLDK**MAADSSIVGKVF
 SHGDKSYKVAKMDNFYTDPIDNSVSKQGIR (**I/l**) IFEDGSRI (**I/t**) (**F/l**) RLSGTGS
 AGATIRMYIDSYESDSNKQLLDSQVM**L**KPLIEIALEISQLRELTGRQQPTVIT*

Figure S2. Haplotypes network obtained by genotyping of the *Pgm-1* exon 3 on 187 individuals coming from the North and the South EPR. The red and the yellow correspond to the populations of the North and the South, respectively. The numeric values are the numbers of sequences forming each haplotype. Mutations non-synonymous and the concerning amino acids are presents on the branches.

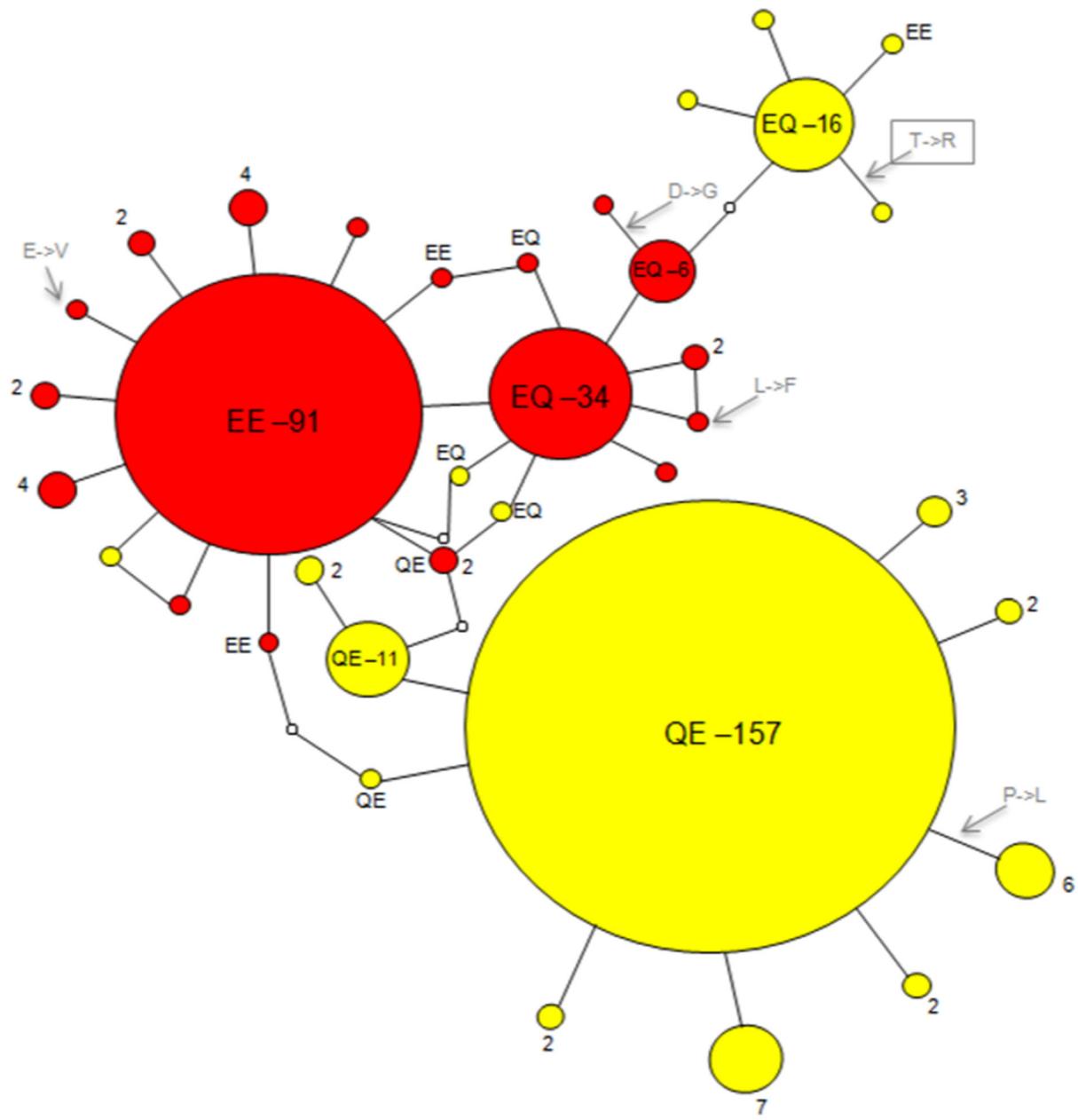
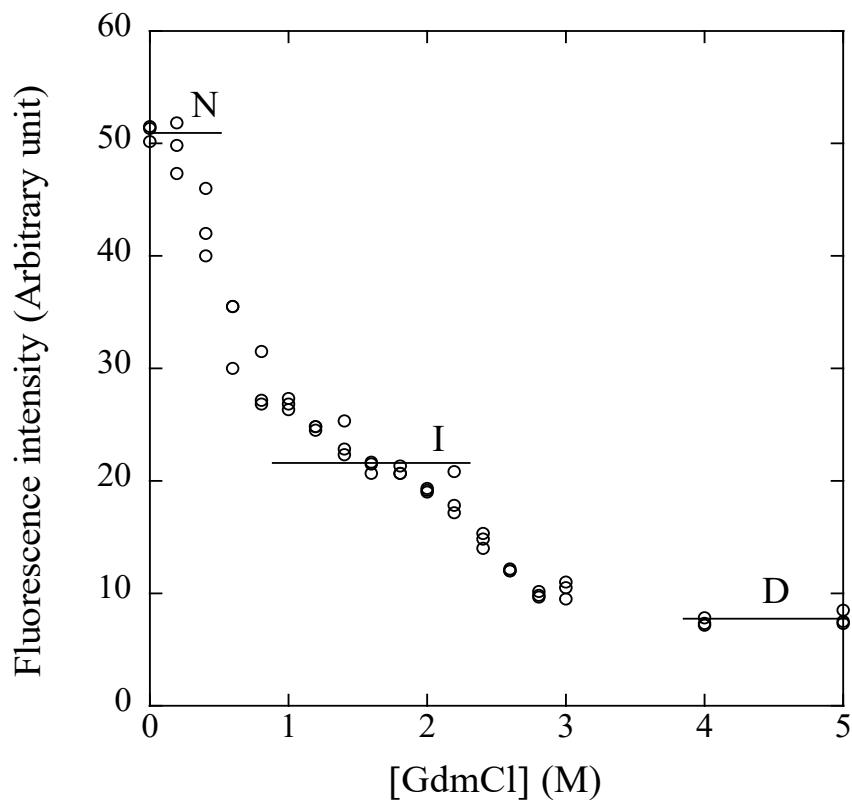


Figure S3. Guanidium chloride (GdmCl) denaturation curves for the three PGM1 overexpressed isoforms. The fluorescence intensity at 324 nm (excitation at 290 nm) is presented as a function of GdmCl concentration. (A) Evolution of the protein denaturation along the GdmCl gradient of isoform QE (78) showing the normal (N), intermediate (I) and denatured (D) states of the protein. (B) Denaturation curves f_u (*I*) and f_u (*II*) of the three isoforms showing that isoform differences stand during the first step of protein denaturation.



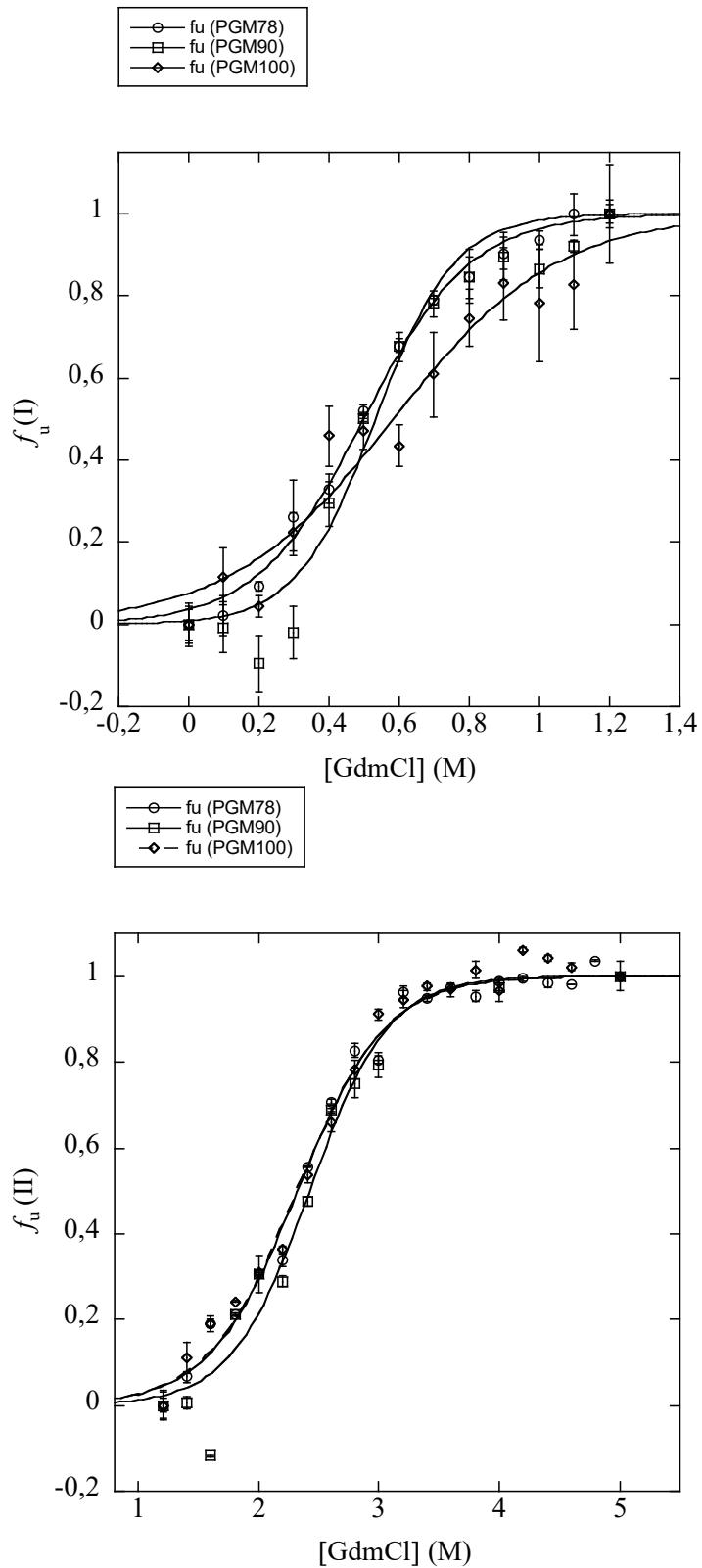


Figure S4. Modelled regression curves of the folded/unfolded protein states f_u (I) and f_u (II) of three PGM1 overexpressed isoforms for each transition according to the denaturation equilibrium $N \leftrightarrow I \leftrightarrow U$ (Native \leftrightarrow Intermediate \leftrightarrow Unfolded).

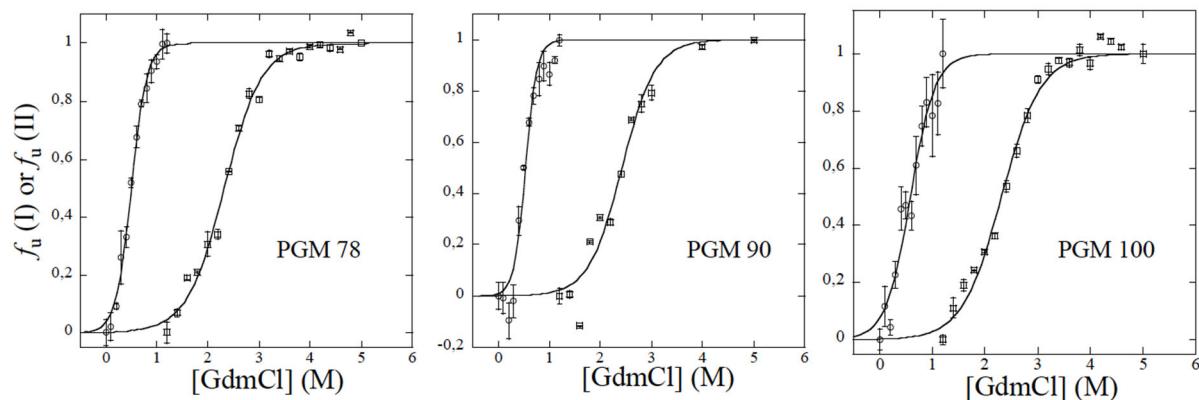


Figure S5. Scatterplots of female *A. pompejana* fecundities according to their PGM-1 allozyme genotypes. Corrected fecundities by female size were determined on board from mature females by counting coelomic oocytes from aliquots and the *Pgm-1* genotype was determined in the laboratory. The numbers above each category indicate the number of individuals.

