

Supporting information

Table S1 List of the primers used for *Wolbachia* strain identification. A set of eleven MGE markers (the transposable element *Tr1* and ten WO prophages) were used for *Wolbachia* genotyping and five genes were used for *Wolbachia* neighbor-net analysis. For each gene are indicated: the locus code in the *wPip*(Pel) genome, the product, the name of the gene, PCR forward and reverse primers, sizes of the resulting PCR products, and the corresponding references. * Internal primers used to obtain full sequences.

Organim	Locus	Product	Gene	Primer (5'-3')	Size (bp)	References
<i>Wolbachia</i> (genotyping)	WPa_1362	Putative phage related protein	<i>GP1b</i>	F-AAGTGGCTGGAAAATGTATAAC R-TGAGTTTGCTATTTACTGCTAG	307	Duron <i>et al.</i> 2006b
	WPa_1304	Putative phage portal protein	<i>GP2a</i>	F-GCAAATATTTTAGGTGAGGCGC R-ACGGAGTTCTCCACAAAGTACT	363	Duron <i>et al.</i> 2006b
	WPa_0253	Putative phage portal protein	<i>GP2b</i>	F-CGTAGTGGCATTGAATTTAACC R-ACGGAGTTCTCCACAAAGTACT	642	Duron <i>et al.</i> 2006b
	WPa_0374	Minor capsid protein c (fragment)	<i>GP2e</i>	F-TTCTACAACAGATGATCAAACG R-CATCATCGGCCTACATAGCCA	306	Duron <i>et al.</i> 2006b
	WPa_1303- WPa_1301	Putative minor capsid protein c	<i>GP3a</i>	F-AAGTGGGTTTGTGAAAAATGT R-ACATCATCATGCGGAATGTGC	1339	Duron <i>et al.</i> 2006b
	WPa_0252	Putative minor capsid protein c	<i>GP3b</i>	F-CAGAGGCTTTCAATTGAAAAG R-GCGGTTATAAAATTTAAATGCA	428	Duron <i>et al.</i> 2006b
	-	Capsid protein	<i>GP3c</i>	F-CAGAGGCTTTCAATTGAAAAG R-AAGAACTTCAGTACGATACTTG	196	Duron <i>et al.</i> 2006b
	WPa_0426	Putative minor capsid protein c	<i>GP3d</i>	F-AAGTGGGTTTGTGAAAAATGT R-AAGAACTTCAGTACGATACTTG	360	Duron <i>et al.</i> 2006b
	WPa_1322a	Probable secretory protein	<i>GP15a</i>	F-TGTGACTACTAATGCTTCAGGA R-AAACTCGAATACTGTGAGGAAG	296	Duron <i>et al.</i> 2006b

	WPa_1322b	-	<i>GP15b</i>	F-GTAGAAGCAAAAGAGTTTGTG R-AAACTCGAATACTGTGAGGAAG	484	Duron <i>et al.</i> 2006b
	WPa_1312	Transposable element	<i>Tr1</i>	Tr1e-F1-ACTTTAGAGGGGTGCTTTCT Tr1e-R1-TTCATGGAGCTGAAGGTAT	583-1501	Duron <i>et al.</i> 2005
<i>Wolbachia</i> (sequencing)	WPa_0652	Ankyrin domain gene (wPip_ANK33)	<i>ank2</i>	F-CTTCTTCTGTGAGTGACGT R2-TCCATATCGATCTACTGCGT	313-511	Duron <i>et al.</i> 2007a
	WPa_0256	Ankyrin domain gene (wPip_ANK8)	<i>pk1</i>	F-CCACTACATTGCGCTATAGA	1260-1349	Duron <i>et al.</i> 2007a ; Sinkins <i>et al.</i> 2005
	WPa_0315	Ankyrin domain gene (wPip_ANK14)	<i>pk1</i>	R-ACAGTAGAACTACACTCCTCCA		
	WPa_1308	Ankyrin domain gene (wPip_ANK56)	<i>pk1</i>			
	WPa_0299	Ankyrin domain gene (wPip_ANK12)	<i>pk2</i>	F-ATTATGATAAAGCTTGGTAAGAA	453	Duron <i>et al.</i> 2007a ; Sinkins <i>et al.</i> 2005
	WPa_0413	Ankyrin domain gene (wPip_ANK25)	<i>pk2</i>	R-TTAGCCCTTCATAAATAGCTT		
	WPa_0258	DNA methylase-like protein	<i>GP12</i>	F-ATGAATTTAGCAATCCACTACT	1301-1324	This study
	WPa_0317	DNA methylase-like protein	<i>GP12</i>	R-TTACTAAATAACAGACATATTGCT		
	WPa_1310	DNA methylase-like protein	<i>GP12</i>			
	WPa_0429	DNA methylase-like protein	<i>GP12</i>			
	WPa_1322	Probable secretory protein	<i>GP15</i>	F1-ACCATTACAGAACTTGAGGA R1-TAGACGTTTCATAGGCAACCA F2-ACCTGACTCTGCAGTACTTGA* R2-ACTGCTTCTCATAAATTCA*	1511-1538	This study ; Duron <i>et al.</i> 2006b
<i>Culex pipiens</i> (genotyping)	<i>cytb</i>	mitochondrial cytochrome b gene		F-CTTTATTAGTAACTGTAAAAATTAC R-ACTAAAGGATTAGCAGGAATGA	853	This study
	<i>Ace1-exon3</i>	Acetylcholine esterase		F-CGCATGGATGGGCATTCCGTA R-GACTCCGACACGGTACTGCA	374	Weill <i>et al.</i> 2003

References (Table S1)

1. Duron O, Fort P, Weill M (2006b) Hypervariable prophage WO sequences describe an unexpected high number of *Wolbachia* variants in the mosquito *Culex pipiens*. *Proceedings of the Royal Society B-Biological Sciences*, **273**, 495-502.
2. Duron O, Lagnel J, Raymond M *et al.* (2005) Transposable element polymorphism of *Wolbachia* in the mosquito *Culex pipiens*: evidence of genetic diversity, superinfection and recombination. *Molecular Ecology*, **14**, 1561-1573.
3. Duron O, Boureux A, Echaubard P *et al.* (2007a) Variability and expression of ankyrin domain genes in *Wolbachia* variants infecting the mosquito *Culex pipiens*. *Journal of Bacteriology*, **189**, 4442-4448.
4. Sinkins SP, Walker T, Lynd AR *et al.* (2005). *Wolbachia* variability and host effects on crossing type in *Culex* mosquitoes. *Nature*, **436**, 257-260.
5. Weill M, Lutfalla G *et al.* (2003) Insecticide resistance in mosquito vectors. *Nature*, **423**, 136-137.

Table S2 Genetic differentiation among *C. pipiens* populations from La Réunion. The upper half shows probabilities based on the null hypothesis of homogeneous distribution of *wPip* strains between populations. The lower half shows F_{st} values. The null hypothesis is rejected at $\alpha = 0.0005$, taking into account a Bonferonni's adjustment for 105 comparisons. Bold values indicate significant departure from homogeneous distribution of *wPip* strains.

Population	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1-Saint Denis		0.707	0.179	0.254	0.622	0.000	0.551	0.509	0.176	0.181	0.550	0.549	0.156	0.150	0.183
2-Sainte Suzanne	0.090		1.000	0.997	1.000	0.012	0.630	1.000	1.000	1.000	0.985	1.000	0.986	0.453	1.000
3-Saint André	0.126	0.000		0.940	1.000	0.000	0.078	0.828	1.000	1.000	0.677	1.000	0.237	0.033	1.000
4-Bras Panon	0.087	0.000	0.034		0.989	0.095	0.912	0.997	0.941	0.949	0.894	0.997	1.000	0.872	0.942
5-Saint Benoît	0.067	0.000	0.000	0.000		0.002	0.484	0.992	1.000	1.000	0.934	1.000	0.910	0.258	1.000
6-Sainte Rose	0.338	0.360	0.471	0.246	0.383		0.013	0.135	0.000	0.000	0.035	0.002	0.011	0.181	0.000
7-Saint Joseph	0.006	0.043	0.110	0.019	0.011	0.269		0.770	0.078	0.097	0.502	0.399	0.285	0.086	0.077
8-Saint Leu	0.078	0.000	0.050	0.000	0.011	0.224	0.021		0.825	0.825	0.999	0.998	0.994	0.834	0.826
9-La Possession	0.126	0.000	0.000	0.034	0.000	0.471	0.110	0.050		1.000	0.677	1.000	0.235	0.033	1.000
10-Plaine des Palmistes	0.118	0.000	0.000	0.030	0.000	0.458	0.102	0.044	0.000		0.680	1.000	0.487	0.033	1.000
11-Plaine des Cafres	0.050	0.001	0.044	0.000	0.018	0.249	0.033	0.000	0.044	0.038		0.944	0.831	0.709	0.679
12-Saint Pierre	0.103	0.000	0.000	0.000	0.000	0.380	0.051	0.000	0.000	0.000	0.002		0.910	0.251	1.000
13-Saint Louis	0.108	0.000	0.048	0.000	0.000	0.336	0.033	0.000	0.048	0.043	0.009	0.000		0.188	0.230
14-Etang Salé	0.090	0.084	0.155	0.015	0.092	0.148	0.061	0.011	0.155	0.146	0.015	0.092	0.059		0.033
15-Sainte Marie	0.126	0.000	0.000	0.034	0.000	0.471	0.110	0.050	0.000	0.000	0.044	0.000	0.048	0.155	

Table S3 No effect of the host nuclear genome on CI expression. Sl(Pie-11), Sl(Su-132), Sl(Leu-118), Sl(Su-118) and Sl(Leu-58) lines correspond to Pie-11, Su-132, Leu-118, Su-118 and Leu-58, cytoplasm introgressed into the nuclear genome of the Slab strain. A: Crosses performed with original lines from La Réunion and B: Crosses performed with backcrossed lines. Compatible crosses (C, HR>90%); incompatible crosses (IC, 0% HR). Incompatible crosses are shaded and bidirectionally incompatible crosses are underlined. The number of egg rafts collected in each cross is indicated into brackets.

A

female strain	male strain								
	Pie-11	Su-132	Leu-118	Su-118	Leu-58	Istanbul	Slab	LaVar	MaClo
Pie-11	C	C (6)	C (8)	C (8)	C (7)	IC (13)	C (13)	IC (4)	C (5)
Su-132	C (7)	C	C (10)	C (6)	C (9)	IC (11)	C (7)	IC (9)	C (10)
Leu-118	C (8)	C (7)	C	C (5)	C (8)	IC (7)	C (5)	IC (9)	C (12)
Su-118	C (7)	C (7)	C (5)	C	C (6)	IC (9)	C (7)	C (3)	C (9)
Leu-58	C (9)	C (11)	C (9)	C (10)	C	IC (12)	C (10)	C (32)	C (30)
Istanbul	C (45)	IC (19)	IC (12)	IC (16)	IC (8)	C	IC (15)	IC (12)	C (10)
Slab	C (18)	IC (22)	C (17)	IC (28)	C (12)	C (18)	C	IC (18)	IC (12)
LaVar	C (11)	IC (12)	C (7)	IC (12)	C (9)	IC (7)	C (8)	C	C (12)
MaClo	C (15)	C (13)	C (10)	C (11)	C (14)	IC (14)	C (12)	C (6)	C

B

female strain	male strain								
	Sl(Pie-11)	Sl(Su-132)	Sl(Leu-118)	Sl(Su-118)	Sl(Leu-58)	Istanbul	Slab	LaVar	MaClo
Sl(Pie-11)	C	C (22)	C (26)	C (22)	C (25)	IC (22)	C (26)	IC (21)	IC (20)
Sl(Su-132)	C (25)	C	C (25)	C (22)	C (23)	IC (22)	C (20)	IC (24)	IC (24)
Sl(Leu-118)	C (23)	C (20)	C	C (24)	C (24)	IC (28)	C (22)	IC (30)	IC (32)
Sl(Su-118)	C (24)	C (27)	C (21)	C	C (23)	IC (24)	C (20)	C (25)	C (24)
Sl(Leu-58)	C (22)	C (25)	C (24)	C (29)	C	IC (31)	C (26)	C (15)	C (22)
Istanbul	C (19)	IC (23)	IC (28)	IC (28)	IC (22)	C	IC (15)	IC (12)	C
Slab	C (27)	IC (23)	C (24)	IC (23)	C (24)	C (18)	C	IC (18)	IC (12)
LaVar	C (24)	IC (24)	C (26)	IC (22)	C (17)	IC (7)	C (8)	C	C (12)
MaClo	C (31)	C (15)	C (31)	C (32)	C (22)	IC (14)	C (12)	C (6)	C

Figure S1 Schematic representation of the MGE genetic differences among La Réunion *w*Pip strains. Strains in clear boxes differ from *w*11 by a single MGE marker (symbolized by one bar) and between them by two MGE markers. Strains in shaded boxes differ from *w*11 by two MGE markers and finally *w*135 (dark shaded) differs from *w*11 by three markers. Strains shown in bold were isolated as isofemale lines. The frequency of *w*Pip strains identified from field samples are indicated into brackets. No frequency is indicated for the strain *w*133 found during the establishment of isofemale lines.

