

Tables for main text

Are ecological communities the seat of endosymbiont horizontal transfer and diversification? A case study with soil arthropod community.

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Table 1: Allele profiles of MLST genes for 36 unique host-*Wolbachia* combinations. (Bold numbers represent new alleles and STs).

Sample ID	Class	Order	Family	Genus	<i>gatB</i>	<i>coxA</i>	<i>hcpA</i>	<i>ftsZ</i>	<i>fbpA</i>	ST	Supergroup
Morph0023	Insecta	Hymenoptera	-	-	near 301	303	317	near 32	353	ST- N1	A
Morph0076	Arachnida	Araneae	Phrurolithidae	<i>Orthobula</i>	310	7	320	32	471	ST-544	A
Morph0080	Insecta	Diptera	Phoridae	<i>Dohrniphora</i>	46	288	321	266	472	ST-547	A
Morph0082	Insecta	Hymenoptera	Platygastridae	-	311	304	322	267	473	ST-548	A
Morph0095	Insecta	Hymenoptera	Formicidae	<i>Cardiocondyla</i>	3	305	356	258	474	ST-550	A
Morph0152	Insecta	Hymenoptera	Platygastridae	<i>Dicroscelio</i> sp.	313	241	323	3	17	ST-553	A
Morph0171	Insecta	Hymenoptera	Diapriidae	<i>Trichopria</i> sp.	87	111	103	70	120	ST-554	A
Morph0182	Insecta	Hymenoptera	Platygastridae	<i>Idris</i> sp.	314	307	324	3	120	ST-555	A
Morph0189	Insecta	Hymenoptera	Bethylidae	<i>Laelius</i>	22	308	24	3	23	ST-556	A
Morph0269	Insecta	Hymenoptera	Platygastridae	<i>Scelio</i> sp.	315	311	328	271	477	ST-562	A
Morph0293	Insecta	Hymenoptera	Platygastridae	<i>Telenomus</i>	316	313	330	272	351	ST-564	A
Morph0294	Insecta	Hymenoptera	Platygastridae	-	317	7	344	273	479	ST-565	A
Morph0324	Insecta	Hymenoptera	Platygastridae	-	322	313	330	272	351	ST-575	A
Morph0330	Arachnida	Araneae	Uloboridae	<i>Uloborus</i>	319	315	1	3	217	ST-567	A
Morph0352	Insecta	Coleoptera	Corylophidae	-	320	15	348	6	17	ST-569	A
Morph0375	Insecta	Coleoptera	Chrysomelidae	<i>Monolepta</i>	321	316	349	154	122	ST-570	A
Morph0376	Insecta	Hymenoptera	Formicidae	<i>Pheidole</i>	3	305	350	258	474	ST-571	A
Morph0001	Insecta	Orthoptera	Gryllidae	<i>Neonemobius</i>	9	224	30	20	25	ST-541	B
Morph0098	Insecta	Hemiptera	Aphididae	<i>Phorodon</i>	9	224	30	20	25	ST-541	B
Morph0213	Insecta	Hemiptera	Psyllidae	<i>Heteropsylla</i>	250	66	88	15	417	ST-559	B
Morph0220	Insecta	Hemiptera	Delphacidae	-	250	66	88	15	417	ST-559	B
Morph0009	Insecta	Hemiptera	Pyrrhocoridae	<i>Dysdercus</i>	309	287	316	265	7	ST-542	B
Morph0026	Insecta	Orthoptera	Gryllidae	<i>Loxoblemmus</i>	9	224	318	20	25	ST-543	B
Morph0111	Insecta	Hemiptera	Delphacidae	<i>Nilaparvata</i>	107	87	29	35	27	ST-163	B
Morph0210	Insecta	Coleoptera	Chrysomelidae	<i>Bruchus</i>	39	310	326	270	27	ST-558	B
Morph0214	Insecta	Hemiptera	Delphacidae	<i>Muellerianella</i>	9	2	327	36	9	ST-560	B
Morph0285	Insecta	Diptera	Phoridae	-	39	14	40	36	4	ST-41	B
Morph0288	Insecta	Hemiptera	-	-	9	312	329	7	478	ST-563	B
Morph0329	Insecta	Hemiptera	Cicadellidae	<i>Balclutha</i>	318	314	345	274	480	ST-566	B
Morph0343	Insecta	Hymenoptera	Encyrtidae	-	near 217	7	346	275	359	ST- N2	B
Morph0348	Insecta	Coleoptera	Chrysomelidae	-	16	14	347	23	4	ST-568	B
Morph0381	Insecta	Hemiptera	Cicadellidae	<i>Agalliopsis</i>	109	87	351	35	27	ST-572	B
Morph0386	Insecta	Hemiptera	Cicadellidae	-	126	66	352	15	136	ST-573	B
Morph0396	Insecta	Hemiptera	Lygaeidae	<i>Nysius</i>	16	14	353	73	4	ST-574	B
Morph0148	Arachnida	Araneae	Gnaphosidae	<i>Zelotes</i>	312	306	319	268	475	ST-552	F
Morph0206	Insecta	Hymenoptera	Formicidae	<i>Paratrechina</i>	73	309	325	269	476	ST-557	F

Table 2: Recombination events detected in the *Wolbachia* MLST sequences. Putative breakpoints indicate concatenated sequences of MLST genes in the order (*gatB-coxA-hcpA-ftsZ-fbpA*). p-value was kept at < 0.01.

Recombination event		STs potentially involved	Gene: Putative breakpoints	Detection methods positive for recombination
Between supergroup	A and B supergroup	ST-N2/565	<i>coxA</i> : 370-771	<i>RDP, GENECONV, BootScan, MaxChi, Chimaera, SiScan</i>
	A and B supergroup	ST-560/550	<i>coxA</i> : 370-771	<i>RDP, GENECONV, BootScan, MaxChi, Chimaera</i>
	A and F supergroup	ST-544/552	<i>gatB</i> : 179-369	<i>RDP, GENECONV, BootScan, 3Seq</i>
Within supergroup	A supergroup	ST-565/555	<i>gatB</i> : 255-369 <i>fbpA</i> : 1650-1800	<i>MaxChi, SiScan, 3Seq</i>
	A supergroup	ST-547/564	<i>gatB</i> : 118-369 <i>hcpA</i> : 771-885	<i>MaxChi, Chimaera, SiScan, 3Seq</i>
	A supergroup	ST-570/550	<i>hcpA</i> : 998-1215 <i>fbpA</i> : 1650-1988	<i>MaxChi, Chimaera, SiScan</i>
	A supergroup	ST-544/570	<i>fbpA</i> : 1650-1988	<i>MaxChi, SiScan, 3Seq</i>
	A supergroup	ST-N1/567	<i>gatB</i> : 80-369	<i>Chimaera, SiScan, 3Seq</i>