

Title of file for HTML: Supplementary Information

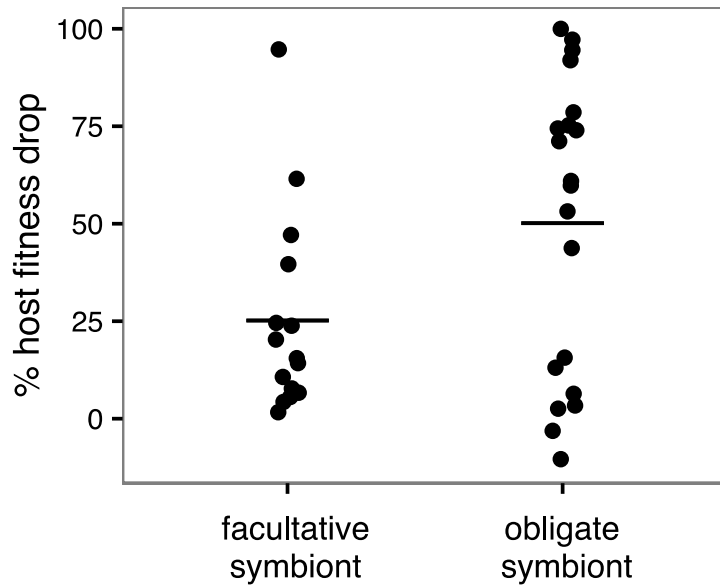
Description: Supplementary Figures, Supplementary Tables and Supplementary References

Title of file for HTML: Supplementary Data 1

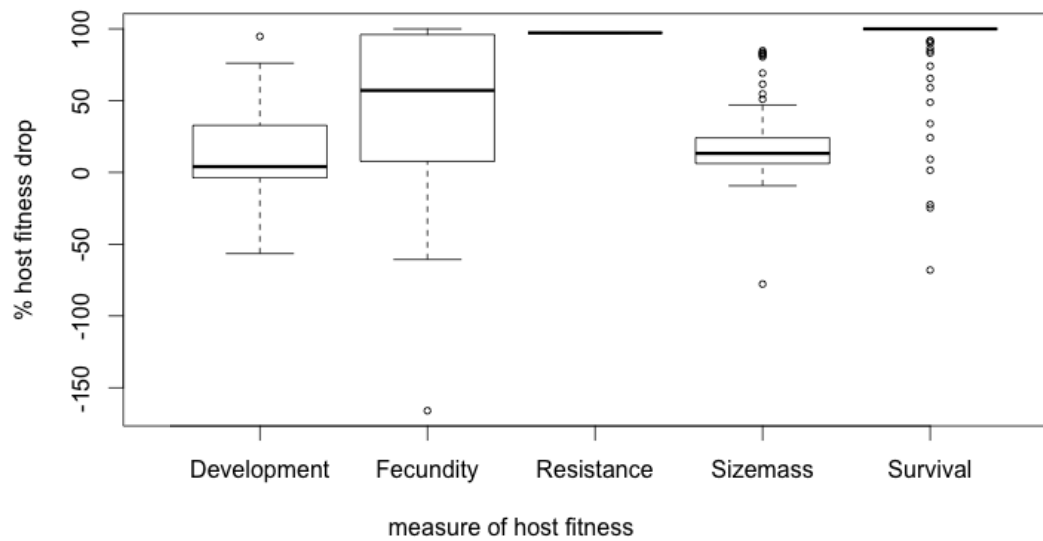
Description: Supplementary R code

Title of file for HTML: Peer Review File

Description:



Supplementary Figure 1. Obligate symbionts lead to a higher reduction in host fitness when removed. Each data point represents one host-symbiont combination and the mean % host fitness reduction for symbionts that are facultative and obligate are shown as horizontal bars (facultative symbiont = 25.19 and obligate symbiont = 47.49). Mean host fitness reduction was higher for hosts with obligate symbionts (symbiont phylogeny: BPMM, posterior mode = -23.95, CI = -48.36, 10.64, pMCMC = 0.02). $N_{\text{symbioses}} = 35$ and $N_{\text{datapoints}} = 284$.



Supplementary Figure 2. No differences in host fitness drop between different methods of measuring host fitness. Mean % host fitness drop for each of the 5 categories of how host fitness was measured. In our sensitivity analyses, we removed the category ‘resistance’ due to the fact we only had one observation of host fitness measured in this way. We found no overall differences in % host fitness drop between different methods of measuring host fitness, when controlling for both symbiont and host phylogeny (Supplementary Tables 8 and 9). Bold horizontal bars show the median value for each treatment, boxes show the first and third quartiles and whiskers show the minimum and maximum values.

Supplementary Table 1. Summary of full dataset. Raw means are presented for % host fitness drop and symbiont genome size for each level of each fixed effect.

		Mean host fitness drop	Mean symbiont genome size (Mb)
Transmission mode	Horizontal	21.18	7.09
	Vertical	51.78	1.52
Symbiont function	Nutritional	42.71	2.12
	Defensive	28.25	2.49
Intra/extracellular	Intracellular	38.56	2.13
	Extracellular	56.06	3.45

Supplementary Table 2. Analysis of the effect of transmission mode, intra/extracellular and symbiont function on fitness drop of host on symbiont removal and symbiont genome size, taking into account symbiont phylogenetic relationships using MCMCglmm. $N_{\text{symbioses}} = 106$, $N_{\text{symbiont species}} = 58$, $N_{\text{studies}} = 84$, $N_{\text{datapoints}} = 378$.

Response: Fitness drop				
Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	125	14.33 (-32.64, 57.09)	
	Vertical	253	46.65 (13.66, 84.20)	
	Difference		-36.58 (-67.54, -8.45)	0.01
Intra/extracellular	Intracellular	269	-15.05 (-56.12, 32.29)	
	Extracellular	109	12.55 (-40.43, 50.96)	
	Difference		19.10 (-3.88, 49.16)	0.07
Function	Defensive	27	7.28 (-41.41, 50.63)	
	Nutritional	207	41.98 (11.60, 67.08)	
	Unknown	144	24.98 (-12.63, 68.87)	
	Difference (Defensive & Nutritional)		-28.75 (-66.80, 2.79)	0.03
Response: Genome size				
Fixed Effect		N	Posterior mode	pMCMC
Transmission mode	Horizontal	125	8.46 (5.87, 9.96)	
	Vertical	253	2.77 (0.83, 4.41)	
	Difference		-5.56 (-6.74, -4.10)	<0.001
Intra/extracellular	Intracellular	269	6.27 (4.68, 8.85)	
	Extracellular	109	8.44 (6.04, 9.93)	
	Difference		1.34 (0.06, 2.85)	0.03
Function	Defensive	27	8.07 (5.84, 9.93)	
	Nutritional	207	7.74 (6.44, 9.85)	
	Unknown	144	8.79 (7.29, 11.38)	
	Difference (Defensive & Nutritional)		-0.08 (-1.47, 1.65)	0.52
Correlations				
Fitness drop : Genome size	Phylogenetic correlation		0.02 (-16.23, 3.75)	0.38
	Phenotypic correlation		0.03 (-0.20, 0.20)	0.51

Supplementary Table 3. Analysis of the effect of transmission mode, intra/extracellular and symbiont function on fitness drop of host on symbiont removal and symbiont genome size, taking into account host phylogenetic relationships using MCMCglmm. $N_{\text{symbioses}} = 106$, $N_{\text{host species}} = 89$, $N_{\text{studies}} = 84$, $N_{\text{datapoints}} = 378$.

Response: Fitness drop				
Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	125	6.98 (-40.04, 40.73)	
	Vertical	253	44.13 (6.58, 77.69)	
	Difference		-39.33 (-67.96, -9.13)	0.003
Intra/extracellular	Intracellular	269	-20.30 (-54.07, 21.18)	
	Extracellular	109	0.48 (-32.24, 46.09)	
	Difference		20.16 (-6.31, 44.57)	0.06
Function	Defensive	27	5.18 (-37.09, 42.21)	
	Nutritional	207	38.28 (9.70, 62.06)	
	Unknown	144	23.57 (-10.76, 62.47)	
	Difference (Defensive & Nutritional)		-24.93 (-63.44, -4.84)	0.01
Response: Genome size				
Fixed Effect		N	Posterior mode	pMCMC
Transmission mode	Horizontal	125	7.97 (5.72, 9.27)	
	Vertical	253	3.41 (1.94, 4.97)	
	Difference		4.21 (3.09, 5.56)	<0.001
Intra/extracellular	Intracellular	269	6.30 (4.46, 7.96)	
	Extracellular	109	7.78 (6.07, 9.61)	
	Difference		-0.0001 (0.27, 2.74)	0.005
Function	Defensive	27	8.14 (6.02, 9.58)	
	Nutritional	207	7.17 (5.59, 9.08)	
	Unknown	144	8.07 (6.50, 10.33)	
	Difference (Defensive & Nutritional)		0.52 (-0.64, 1.60)	0.19
Correlations				
Fitness drop : Genome size	Phylogenetic correlation		-0.62 (-0.84, 0.89)	0.49
	Phenotypic correlation		-0.01 (-0.21, 0.19)	0.53

Supplementary Table 4. Analysis of the effect of transmission mode, intra/extracellular and symbiont function on fitness drop of host on symbiont removal and symbiont genome size, taking into account symbiont phylogenetic relationships using MCMCglmm. $N_{\text{symbioses}} = 106$, $N_{\text{symbiont species}} = 58$, $N_{\text{studies}} = 84$, $N_{\text{datapoints}} = 378$, with transmission specific correlations between genome size and host fitness drop.

Response: Fitness drop

Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	125	0.14 (-36.70, 51.90)	
	Vertical	253	55.52 (10.88, 92.76)	
	Difference		-41.16 (-75.87, -8.72)	0.007
Intra/extracellular	Intracellular	269	-5.29 (-55.99, 26.93)	
	Extracellular	109	7.47 (-33.77, 51.33)	
	Difference		17.60 (-7.24, 46.55)	0.08
Function	Defensive	27	6.62 (-39.82, 48.97)	
	Nutritional	207	42.38 (11.57, 68.79)	
	Unknown	144	19.42 (-13.28, 70.13)	
	Difference		-36.54 (-68.65, 4.93)	0.05

Response: Genome size

Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	125	8.15 (5.23, 12.19)	
	Vertical	253	3.35 (1.56, 4.65)	
	Difference		4.63 (1.86, 8.68)	0.008
Intra/extracellular	Intracellular	269	6.43 (3.10, 10.20)	
	Extracellular	109	8.52 (5.08, 12.43)	
	Difference		1.92 (0.71, 3.12)	0.003
Function	Defensive	27	8.48 (5.01, 12.17)	
	Nutritional	207	7.12 (4.35, 11.16)	
	Unknown	144	8.80 (5.56, 12.45)	
	Difference (Defensive & Nutritional)		0.46 (-0.73, 1.76)	0.19

Transmission specific correlations

Fitness drop : Genome size	Horizontal	1.03 (-31.51, 61.49)	
	Vertical	-0.14 (-30.54, 6.65)	
	Difference	1.17 (-0.98, 54.85)	0.25

Supplementary Table 5. Analysis of the effect of transmission mode, intra/extracellular and symbiont function on fitness drop of host on symbiont removal and symbiont genome size, taking into account host phylogenetic relationships using MCMCglmm. $N_{\text{symbioses}} = 106$, $N_{\text{symbiont species}} = 89$, $N_{\text{studies}} = 84$, $N_{\text{datapoints}} = 378$, with transmission specific correlations between genome size and host fitness drop.

Response: Fitness drop				
Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	125	0.06 (-32.27, 40.46)	
	Vertical	258	37.39 (9.12, 78.69)	
	Difference		-32.75 (-77.23, -7.87)	0.03
Intra/extracellular	Intracellular	274	-10.12 (-52.38, 22.97)	
	Extracellular	109	4.91 (-33.16, 50.38)	
	Difference		16.65 (-4.96, 46.05)	0.08
Function	Defensive	27	-0.93 (-40.38, 39.37)	
	Nutritional	212	33.30 (10.67, 64.44)	
	Unknown	144	30.79 (-16.18, 58.46)	
	Difference (Defensive & Nutritional)		-38.28 (-62.70, -7.37)	0.01
Response: Genome size				
Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	125	7.95 (3.52, 13.01)	
	Vertical	258	3.95 (2.44, 4.88)	
	Difference		4.07 (-0.51, 8.78)	0.04
Intra/extracellular	Intracellular	274	5.65 (2.24, 10.20)	
	Extracellular	109	7.84 (4.07, 11.84)	
	Difference		1.31 (0.07, 2.58)	<0.001
Function	Defensive	27	8.24 (4.19, 12.20)	
	Nutritional	212	7.29 (2.97, 10.96)	
	Unknown	144	8.74 (4.85, 12.75)	
	Difference (Defensive & Nutritional)		0.98 (0.44, 1.53)	<0.001
Transmission specific correlations				
Fitness drop : Genome size	Horizontal		0.15 (-38.88, 49.94)	
	Vertical		-0.11 (-23.30, 8.47)	
	Difference		0.72 (-42.59, 58.77)	0.37

Supplementary Table 6. Analysis of the effect of transmission mode and age of symbiosis on fitness drop of host on symbiont removal and symbiont genome size, taking into account symbiont phylogenetic relationships using MCMCglmm. This analysis uses a subset of the dataset where we have data on age of symbiosis: $N_{\text{symbioses}} = 54$, $N_{\text{symbiont species}} = 26$, $N_{\text{studies}} = 43$, $N_{\text{datapoints}} = 100$.

Response: Fitness drop

Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	35	33.51 (-11.41, 69.93)	
	Vertical	65	59.30 (25.54, 116.02)	
	Difference		-44.81 (-87.84, -5.41)	0.02
Age	Difference of slope from 0		0.14 (-0.27, 0.47)	0.3

Response: Genome size

Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	35	7.82 (1.39, 12.57)	
	Vertical	65	2.51 (0.58, 4.58)	
	Difference		4.16 (-0.58, 11.21)	0.04
Age	Difference of slope from 0		-0.01 (-0.02, 0.004)	0.1

Supplementary Table 7. Analysis of the effect of transmission mode and age of symbiosis on fitness drop of host on symbiont removal and symbiont genome size, taking into account host phylogenetic relationships using MCMCglmm. This analysis uses a subset of the dataset where we have data on age of symbiosis: $N_{\text{symbioses}} = 54$, $N_{\text{symbiont species}} = 53$, $N_{\text{studies}} = 43$, $N_{\text{datapoints}} = 100$.

Response: Fitness drop

Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	35	31.98 (-14.37, 80.06)	
	Vertical	65	77.84 (26.36, 124.39)	
	Difference		-40.25 (-94.28, 6.46)	0.04
Age	Difference of slope from 0		-0.0007 (-0.50, 0.36)	0.43

Response: Genome size

Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	35	6.10 (-2.66, 15.94)	
	Vertical	65	3.05 (0.78, 4.77)	
	Difference		4.51 (-5.42, 13.12)	0.13
Age	Difference of slope from 0		-0.003 (-0.01, 0.006)	0.28

Supplementary Table 8. Analysis of the effect of the way in which host fitness was measured on fitness drop of host, taking into account symbiont phylogenetic relationships using MCMCglmm. The category ‘resistance’ has been removed for this analysis due to lack of replication. $N_{\text{symbioses}} = 38$, $N_{\text{symbiontspecies}} = 27$, $N_{\text{studies}} = 37$, $N_{\text{datapoints}} = 300$.

Response: Fitness drop				
Fixed Effect		N	Posterior mode (CI)	pMCMC
Host fitness measure	Development	16	36.58 (14.57, 68.14)	
	Fecundity	97	47.19 (30.97, 80.69)	
	Size/Mass	107	45.02 (21.92, 74.47)	
	Survival	80	52.32 (23.12, 80.59)	
Differences	Diff between development time & fecundity		-18.86 (-29.64, -2.88)	0.01
	Diff between development time & size/mass		-8.91 (-22.84, 7.69)	0.18
	Diff between development time & survival		-10.17 (-30.01, 6.49)	0.09
	Diff between fecundity & size/mass		9.44 (-0.09, 18.90)	0.31
	Diff between fecundity & survival		3.02 (-14.33, 17.81)	0.36
	Diff between size/mass & survival		-8.77 (-24.22, 11.13)	0.25

Supplementary Table 9. Analysis of the effect of the way in which host fitness was measured on fitness drop of host, taking into account host phylogenetic relationships using MCMCglmm. The categories ‘resistance’ has been removed for this analysis due to lack of replication. $N_{\text{hostspecies}} = 31$, $N_{\text{studies}} = 40$, $N_{\text{datapoints}} = 304$.

Response: Fitness drop				
Fixed Effect		N	Posterior mode (CI)	pMCMC
Host fitness measure	Development	16	32.54 (5.14, 59.86)	
	Fecundity	99	48.76 (26.97, 79.06)	
	Size/Mass	107	37.12 (14.59, 66.13)	
	Survival	82	40.26 (10.34, 66.31)	
Differences	Diff between development time & fecundity		-22.23 (-32.77, -5.41)	0.004
	Diff between development time & size/mass		-6.51 (-25.28, 4.74)	0.12
	Diff between development time & survival		-9.96 (-25.59, 7.85)	0.18
	Diff between fecundity & size/mass		11.71 (0.54, 18.55)	0.02
	Diff between fecundity & survival		9.45 (-3.51, 24.04)	0.07
	Diff between size/mass & survival		0.76 (-14.67, 18.05)	

Supplementary Table 10. Analysis of the effect of transmission mode on fitness drop of host on symbiont removal and symbiont genome size, taking into account symbiont phylogenetic relationships using MCMCglmm. This analysis uses a subset of the dataset where host fitness was measured as fecundity: $N_{\text{symbioses}} = 26$, $N_{\text{symbiontspecies}} = 18$, $N_{\text{studies}} = 29$, $N_{\text{datapoints}} = 102$.

Response: Fitness drop				
Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	21	-15.96 (-82.24, 41.79)	
	Vertical	81	23.09 (-30.49, 84.30)	
	Difference		-50.89 (-85.68, -4.41)	0.02
Response: Genome size				
Fixed Effect		N	Posterior mode	pMCMC
Transmission mode	Horizontal	21	8.61 (6.68, 10.62)	
	Vertical	81	1.59 (0.36, 3.15)	
	Difference		7.02 (5.16, 8.47)	<0.001
Correlations				
Fitness drop : Genome size	Phylogenetic correlation		-0.73 (-0.95, 0.70)	0.34
	Phenotypic correlation		-0.07 (-0.31, 0.29)	0.48

Supplementary Table 11. Analysis of the effect of transmission mode on fitness drop of host on symbiont removal and symbiont genome size, taking into account host phylogenetic relationships using MCMCglmm. This analysis uses a subset of the dataset where host fitness was measured as fecundity: $N_{\text{hostspecies}} = 22$, $N_{\text{studies}} = 30$, $N_{\text{datapoints}} = 102$.

Response: Fitness drop				
Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	21	-34.20 (-84.73, 29.34)	
	Vertical	81	23.11 (-28.64, 72.20)	
	Difference		-43.32 (-86.98, -12.12)	0.006
Response: Genome size				
Fixed Effect		N	Posterior mode	pMCMC
Transmission mode	Horizontal	21	9.01 (6.37, 10.82)	
	Vertical	81	1.96 (0.03, 3.49)	
	Difference		7.37 (4.39, 9.68)	<0.001
Correlations				
Fitness drop : Genome size	Phylogenetic correlation		-0.52 (-0.89, 0.86)	0.50
	Phenotypic correlation		-0.02 (-0.30, 0.33)	0.49

Supplementary Table 12. Analysis of the effect of transmission mode, intra/extracellular and symbiont function on fitness drop of host on symbiont removal and symbiont genome size, taking into account symbiont phylogenetic relationships using MCMCglmm. Two symbiont species, *Verminephrobacter* and *Regiella insecticola* have been reassigned as horizontal transmission, to account for the possible influence of biparental transmission on host fitness drop. $N_{\text{symbioses}} = 106$, $N_{\text{symbiont species}} = 58$, $N_{\text{studies}} = 84$, $N_{\text{datapoints}} = 378$.

Response: Fitness drop

Fixed Effect		N	Posterior mode (CI)	pMCMC
Transmission mode	Horizontal	133	30.16 (-9.14, 62.49)	
	Vertical	245	58.56 (19.80, 97.33)	
	Difference		-26.64 (-53.44, -6.61)	0.002
Intra/extracellular	Intracellular	269	6.67 (-30.05, 37.90)	
	Extracellular	109	33.46 (-9.61, 62.70)	
	Difference		23.43 (-8.51, 43.74)	0.07
Function	Defensive	27	26.27 (-11.34, 59.76)	
	Nutritional	207	44.00 (17.67, 72.20)	
	Unknown	144	39.07 (-0.80, 70.95)	
	Difference (Defensive & Nutritional)		-27.27 (-49.91, 10.38)	0.12

Response: Genome size

Fixed Effect		N	Posterior mode	pMCMC
Transmission mode	Horizontal	133	5.62 (3.75, 7.81)	
	Vertical	245	1.19 (-0.51, 3.63)	
	Difference		4.23 (2.95, 5.72)	<0.001
Intra/extracellular	Intracellular	269	4.69 (2.52, 7.04)	
	Extracellular	109	5.91 (3.61, 8.01)	
	Difference		0.98 (-0.43, 2.64)	0.07
Function	Defensive	27	6.04 (3.63, 7.96)	
	Nutritional	207	6.37 (5.01, 8.89)	
	Unknown	144	7.61 (5.68, 9.78)	
	Difference (Defensive & Nutritional)		-0.94 (-3.02, 0.51)	0.12

Correlations

Fitness drop : Genome size	Phylogenetic correlation	-0.89 (-0.96, 0.84)	0.40
	Phenotypic correlation	-0.05 (-0.18, 0.20)	0.48

Supplementary Table 13. Summary of host fitness data. Studies from which we used data on mean % host fitness drop and the sample size (number of measures of host fitness) for each symbiont species. $N_{\text{datapoints}}$ is the number of host fitness measures found for removal of each symbiont species.

Symbiont	Mean % host fitness drop	Study Reference	Details	$N_{\text{datapoints}}$
Actinobacteria	87.03	17	Means and fitness change from Fig. 3 for aposymbiotic and control individuals	2
<i>Azospirillum</i>	12.28	18	Means taken from Tables 1, 2c, 3, 4, 5	
<i>Azospirillum</i>	5.57	3	Means taken from Tables 1 & 2	70
<i>Azospirillum</i>	4.28	4	Means taken from Table 3 (0 N fertilizer) & Table 4 (0 N fertilizer)	
<i>Blochmannia floridanus</i>	70.56	5	Means taken from text (page 4, Fig. 4)	2
<i>Blochmannia floridanus</i>	86.50	6	Means taken from text (page 3, Fig. 1)	
<i>Bradyrhizobium</i>	76.97	7	Means taken from Table 1 (local strains), only shoot dry weight	
<i>Bradyrhizobium</i>	36.86	8	Means taken from Table 5, seed yield, no phosphorus treatment	28
<i>Bradyrhizobium</i>	20.93	9	Means taken from Table 2, grain yield (0 N fertilizer)	
<i>Buchnera</i>	71.13	10	Means calculated from Fig. 1b, took end point	7
<i>Buchnera</i>	75.26	11	Means taken from Table 1 & 2	
<i>Burkholderia</i>	20.28	12	Means calculated from Fig. 3 C, D, E, F, both male and female	8
<i>Coriobacterium glomerans</i>	59.02	13	Means calculated from Fig. 1	1
<i>Coxiella</i>	59.75	14	Means taken from Table 1	7
<i>Erwinia</i>	23.81	15	Means taken from Table 1	
<i>Erwinia dacicola</i>	43.80	16	Means taken from text, page 4	10
<i>Frankia</i>	61.50	17	Means taken from Table 2, total plant dry weight only <i>Frankia</i>	1
<i>Glomeribacter gigasporarum</i>	53.17	18	Means calculated from Fig. 8 & Fig. 10, only end points taken	2
<i>Gordonibacter</i>	6.58	13	Means calculated from Fig. 1	1
<i>Hamiltonella</i>	13.10	19	Means taken from Table 2 &	13

<i>defensa</i>			Fig. 1a	
<i>Hamiltonella</i>	6.40	20	Means calculated from raw data given in Appendix 1	
<i>defensa</i>			Means calculated from Fig. 1A for strains Co08, Co23, Co26 & Co37	
<i>Hamiltonella</i>	-10.45	21		
<i>defensa</i>				
<i>Nardonella</i>	15.68	22	Means calculated from Fig. 3, both male and female	5
symbiont of <i>Plautia stali</i>	99.08	23	Raw data provided by Takahiro Hosokawa	70
<i>Regiella insecticola</i>	-3.77	24	Means calculated from Fig. 1a	
<i>Regiella insecticola</i>	-2.47	19	Means taken from Table 2 & Fig. 1a	6
<i>Regiella insecticola</i>	34.15	25	Calculated means from raw data from Fig. 2 provided by Christoph Vorburger	
<i>Rhodococcus rhodnii</i>	7.73	26	Means taken from Table 1 sym <i>in vitro</i> and apo <i>in vitro</i> only for unfed individuals	1
<i>Rickettsia</i>	-26.17	27	Means taken from Table 1, excluding individuals infected with both symbionts.	
<i>Rickettsia</i>	-10.78	28	Means calculated from Fig. 1 and Table 1	
<i>Rickettsia</i>	-8.79	29	Means taken from Table 1	29
<i>Rickettsia</i>	0.93	30	Means taken from Table 1	
<i>Rickettsia</i>	33.60	31	Calculated means of Fig. 3 from raw data provided by Martha Hunter	
<i>Serratia symbiotica</i>	-23.67	27	Means taken from Table 1, excluding individuals	
<i>Serratia symbiotica</i>	81	28	Means calculated from Fig. 1 and Table 1	
<i>Serratia symbiotica</i>	15.07	32	Means calculated from Fig. 1	31
<i>Serratia symbiotica</i>	6.54	24	Means calculated from Fig. 1a	
<i>Serratia symbiotica</i>	23.21	19	Means taken from Table 2 & Fig. 1a	
<i>Serratia symbiotica</i>	-7.83	33	Means taken from Table 1	
<i>Sinorhizobium meliloti</i>	14.26	34	Means taken from Fig. 1 & 2	4
<i>Spirochaetes bacteria</i>	94.73	35	Means taken from Table 1, only when B and no S, F or P	1
<i>Spiroplasma</i>	-22.45	36	Means taken from Table 4	
<i>Spiroplasma</i>	37.72	37	Means calculated from Table 1 & Fig. 1	10
<i>Streptomyces</i>	91.96	38	Mean calculated from text page 3	1
<i>Verminephrobacter</i>	31.05	39	Means calculated from Fig. 4 (only hatched data)	2
<i>Wigglesworthia glossinidius</i>	74	40	Means calculated from Fig. 5, only took end point	10

<i>Wolbachia</i>	-1.98	41	Means taken from text page 5	
<i>Wolbachia</i>	-4.75	42	Means taken from Table 3	
<i>Wolbachia</i>	100	43	Means taken from Table 3 only from tetracycline	
<i>Wolbachia</i>	60.94	44	Means calculated from Fig 1., highest antibiotic concentration	
<i>Wolbachia</i>	17.83	45	Means taken from Table 1, only WxW and UxU	52
<i>Wolbachia</i>	94.24	46	Means taken from Table 2	
<i>Wolbachia</i>	-12.52	47	Means taken from Table 1	
<i>Wolbachia</i>	6.75	48	Means calculated from Fig. 2, 3 & 4	
<i>Wolbachia</i>	14.90	49	Means taken from Fig. 1 legend	
<i>Wolbachia</i>	74.41	50	Means calculated from Fig. 3	
chemoautotrophic symbiont of <i>Codakia</i>	47.06	51	Means taken from text on page 7	1

Supplementary Table 14. Summary of symbiont transmission modes, genome sizes and age of association with hosts.

Symbiont species	Transmission mode	General reference(s)	Symbiont genome size	Age of symbiosis in millions of years (mean)	Genome/age reference(s)
Actinobacteria	Vertical	^{1,52}	-	-	-
<i>Aliivibrio fischeri</i>	Horizontal	⁵³	4.27	60	Ned Ruby, pers.comm.
<i>Nostoc azollae</i> (<i>Anabaena azollae</i>)	Vertical	^{54,55}	5.49	140	⁵⁴
<i>Azobacteroides pseudotrichonymphae</i>	Vertical	⁵⁶	1.11	-	-
<i>Azospirillum</i>	Horizontal	-	7.39	-	-
<i>Baumannia cicadellincola</i>	Vertical	⁵⁷	0.68	70-100 (85)	⁵⁸
<i>Blattabacterium</i>	Vertical	⁵⁷	0.64	150	⁵⁹
<i>Blochmannia floridanus</i>	Vertical	⁵⁷	0.71	50	⁶⁰
<i>Bradyrhizobium</i>	Horizontal	-	9.21	62	⁶¹
<i>Buchnera</i>	Vertical	⁶²	0.64	180	⁵⁷
<i>Burkholderia</i>	Horizontal	¹²	6.96	-	-
<i>Burkholderia brachyanthoides</i>	Vertical	⁶³	3.55	12	⁶⁴
<i>Burkholderia calva</i>	Vertical	⁶³	4.21	12	⁶⁴
<i>Burkholderia crenata</i>	Vertical	⁶³	2.84	12	⁶⁴
<i>Burkholderia humilis</i>	Vertical	⁶³	5.15	12	⁶⁴
<i>Burkholderia kirkii</i>	Vertical	⁶³	4	12	⁶⁴
<i>Burkholderia pumila</i>	Vertical	⁶³	3.68	12	⁶⁴
<i>Burkholderia schumannianaie</i>	Vertical	⁶³	2.36	12	⁶⁴
<i>Burkholderia verschuerenii</i>	Vertical	⁶³	6.19	12	⁶⁴
<i>Carsonella ruddii</i>	Vertical	⁵⁷	0.16	120	^{57,65}
chemoautotrophic symbiont of <i>Codakia</i>	Horizontal	⁵¹	-	-	-
<i>Coriobacterium glomerans</i>	Vertical	¹³	2.12	-	-
<i>Coxiella</i>	Vertical	¹⁴	0.66	-	-
<i>Endoriftia persephone</i>	Horizontal	⁶⁶	3.2	-	⁶⁶
<i>Erwinia</i>	Horizontal	¹⁵	-	-	-
<i>Erwinia dacicola</i>	Vertical	¹⁶	-	-	-
<i>Frankia</i>	Horizontal	-	7.5	-	-
<i>Gilliamella apicola</i>	Vertical	⁶⁷	2.24	-	-
<i>Glomeribacter gigasporarum</i>	Vertical	¹⁸	1.73	-	-
<i>Gordonibacter</i>	Vertical	¹³	-	-	-
<i>Hamiltonella defensa</i>	Vertical	¹⁹	1.84	-	-
<i>Hodgkinia cicadinicola</i>	Vertical	⁶⁸	0.15	-	-
<i>Ishikawaella capsulata</i>	Vertical	⁵⁷	0.75	-	-

<i>Mesorhizobium loti</i>	Horizontal	-	7.33	62	61
<i>Moranella endobia</i>	Vertical	⁶⁸	0.54	-	-
<i>Nardonella</i>	Vertical	²²	-	-	-
symbiont of <i>Plautia stali</i>	Vertical	²³	-	-	-
<i>Regiella insecticola</i>	Vertical	¹⁹	2.04	-	-
<i>Rhodococcus rhodnii</i>	Vertical	⁶⁹	8.4	-	-
<i>Rickettsia</i>	Vertical	-	-	-	-
<i>Riesia pediculicola</i>	Vertical	⁵³	0.58	-	-
<i>Rosenkranzia clausaccus</i>	Vertical	⁷⁰	0.94	-	-
<i>Ruthia magnifica</i>	Vertical	⁶⁶	1.2	-	⁷¹
<i>Serratia symbiotica</i>	Vertical	¹⁹	3.19	-	-
<i>Sinorhizobium meliloti</i>	Horizontal	-	7	62	61
<i>Snodgrassella alvi</i>	Vertical	⁷²	2.33	-	-
<i>Spirochaetes</i> bacteria	Vertical	³⁵	-	-	-
<i>Streptomyces philanthii</i>	Vertical	⁷³	-	68	⁷³
<i>Sulcia muelleri</i>	Vertical	⁵⁷	0.21	260	⁵⁸
<i>Tremblaya princeps</i>	Vertical	⁶⁸	0.14	100-200 (150)	⁶⁵
<i>Uzinura diaspidicola</i>	Vertical	⁵⁷	0.26	100	⁷⁴
<i>Verminephrobacter</i>	Vertical	⁷⁵	5.6	62-136 (99)	⁷⁵
<i>Vesicomysocius okutanii</i>	Vertical	⁶⁶	1	-	⁷⁶
<i>Wigglesworthia glossinidius</i>	Vertical	⁵⁷	0.71	40	⁷⁷
<i>Wolbachia</i>	Vertical	-	-	-	-
<i>Zinderia insecticola</i>	Vertical	⁶⁸	0.21	-	-

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