

## SUPPLEMENTARY INFORMATION

Supplementary materials include a table listing *Geopemphigus* samples used in this study, a table listing characteristics of genomes compared, and a figure of phylogenies for aphid-host genes.

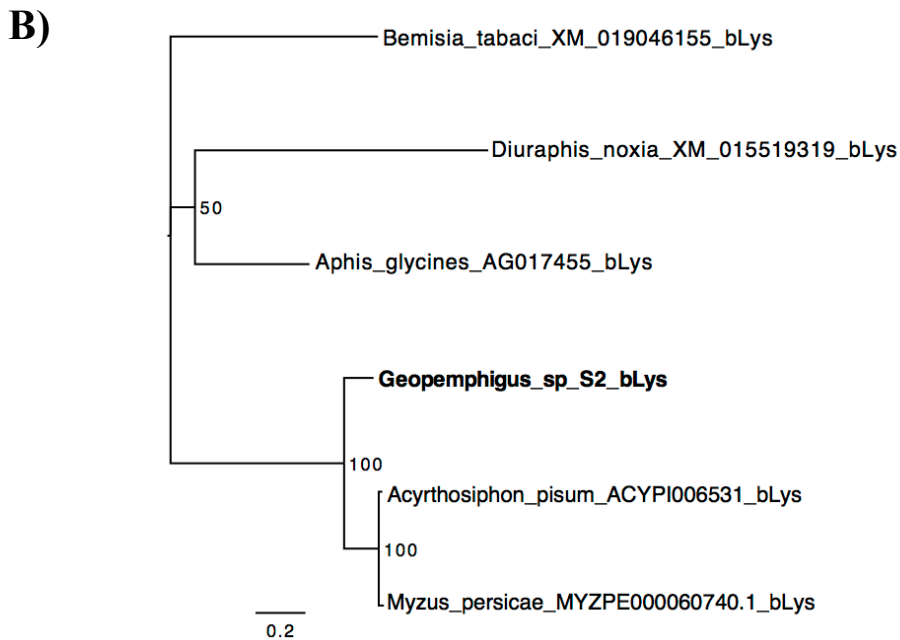
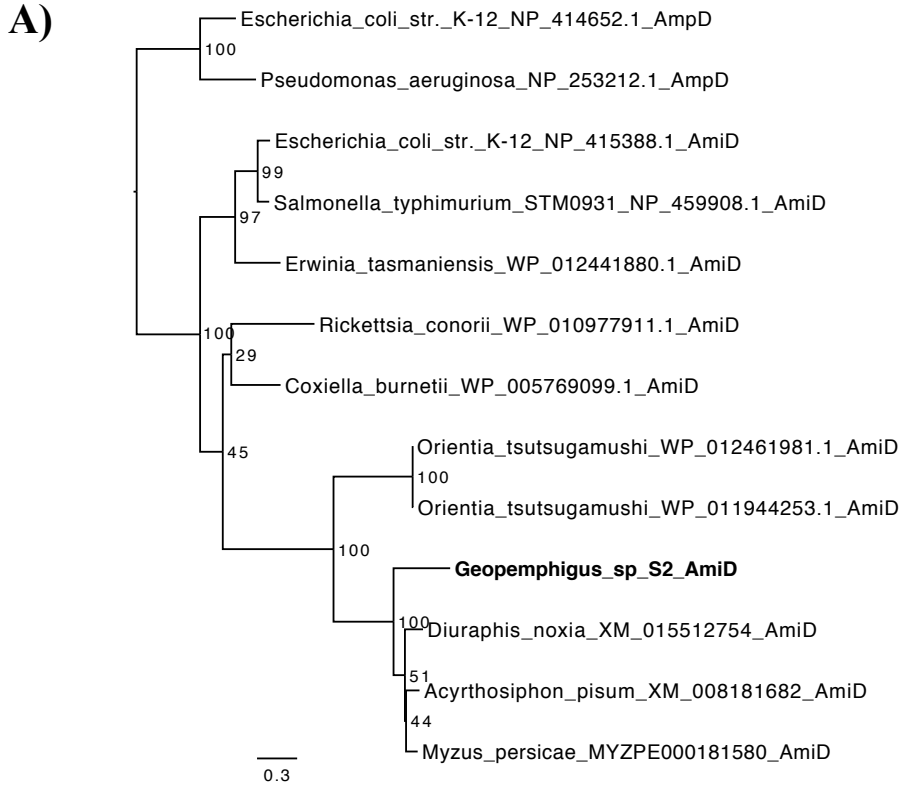
**Table S1.** List of *Geopemphigus* samples used for phylogenetic analysis and genome assembly and annotation.

<b>ID</b>	<b>Sample</b>	<b>Location</b>	<b>Approximate Coordinates</b>	<b>Collection Date</b>	<b>Collector</b>
UNAM 2116	<i>Geopemphigus blackmani</i>	Mezquititlán Hidalgo, Mexico	20.53, -98.63	9 July 2015	A. L. Muñoz
UNAM 2053	<i>Geopemphigus sp. E</i>	Mezquititlán Hidalgo, Mexico	20.53, -98.63	9 July 2015	A. L. Muñoz
This study	<i>Geopemphigus sp. S2</i>	Langtry, Texas, USA	29.81, -101.56	24 July 2016	R.A. Chong N. A. Moran
This study	<i>Geopemphigus sp. C7</i>	Langtry, Texas, USA	29.81, -101.56	24 July 2016	R.A. Chong N. A. Moran

**Table S2.** Genome characteristics of free-living, facultative, and insect endosymbiont bacterial genomes.

GenBank	Species	Phylum	MB	GC %	CDS	rRNA	tRNA	Other RNA	Pseudo gene	Status
NC006347	<i>Bacteroides fragilis</i> _YCH46	Bacteroidetes	5.28	43.3	4578	18	74	0	0	Free living
CP012706.1	<i>Bacteroides fragilis</i> _S14	Bacteroidetes	4.90	43.2	3813	18	73	1	46	Free living
NC009614	<i>Bacteroides vulgatus</i> _ATCC 8482	Bacteroidetes	5.16	42.2	4077	22	83	2	146	Free living
NC000913	<i>Escherichia coli</i> _K12_MG1655	Proteobacteria	4.64	50.8	4140	22	89	67	184	Free living
NC003197	<i>Salmonella enterica</i> _st_LT2	Proteobacteria	4.86	52.2	4453	22	85	10	39	Free living
NC013454.1	<i>Blattabacterium</i> _sp_BGE	Bacteroidetes	0.64	27.1	557	3	34	2	19	Obligate
NC013418	<i>Blattabacterium</i> _sp_BPLAN	Bacteroidetes	0.64	28.0	580	3	33	2	12	Obligate
CP001981.1	<i>Sulcia muelleri</i> _CA RI	Bacteroidetes	0.28	21.2	246	3	29	2	2	Obligate
NC014004.1	<i>Sulcia muelleri</i> _DMI N	Bacteroidetes	0.24	22.5	226	3	31	1	0	Obligate
NC010118	<i>Sulcia muelleri</i> _GW SS	Bacteroidetes	0.25	22.4	227	3	31	2	0	Obligate
NC013062	Flavobacteriaceae_bacterium_3519-10	Bacteroidetes	2.77	42.7	2481	6	42	3	30	Free living
CP000685.1	<i>Flavobacterium johnsoniae</i> _UW101	Bacteroidetes	6.10	34.1	5113	18	60	3	53	Free living
CP016907.1	<i>Flavobacterium johnsoniae</i> _GSE09	Bacteroidetes	5.11	34.3	4239	15	66	3	56	Free living
CP003263.1	<i>Uzinura diaspidicola</i> _ASNER	Bacteroidetes	0.26	30.2	227	3	30	2	1	Obligate
NZCP006873.1	<i>Walczuchella monopylebidarum</i>	Bacteroidetes	0.31	32.6	271	3	33	2	16	Obligate
NC004545.1	<i>Buchnera aphidicola</i> _str_Bpistaciae	Proteobacteria	0.64	26.3	576	3	31	3	9	Obligate
NC011833.1	<i>Buchnera aphidicola</i> _str_Apisum_5A	Proteobacteria	0.62	25.3	517	3	31	3	3	Obligate
CP001277.1	<i>Hamiltonella defensa</i> _5AT	Proteobacteria	2.17	40.4	1915	9	42	4	210	Facultative
CP002295.1	<i>Serratia symbiotica</i> _str_Cinara_cedri	Proteobacteria	1.76	29.2	672	3	36	3	59	Facultative
NZACYF0000000.1	<i>Regiella insecticola</i> _LSR1	Proteobacteria	2.07	42.4	1658	12	41	4	469	Facultative
<i>This study</i>	Endosymbiont of <i>Geopemphigus</i> sp. S2 "Ca. Skilesia alterna"	Bacteroidetes	1.32	37.0	1611	3	35	0	-	Obligate

**Figure S1.** Maximum likelihood phylogenies based on amino acid alignments for aphid-host genes including laterally transferred genes, (A) *amiD*, (B) *bLys*, and (C) *rlpA*, and novel aphid-specific genes, (D) *SP*.



C)



D)

