

Supplementary Tables and Figures

Evolutionary genomics of APSE: a tailed phage that lysogenically converts the bacterium *Hamiltonella defensa* into a heritable protective symbiont of aphids

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Table S1. Regions of the bacterial genomes that share homology with APSE genomes.

Target species	Identification	Genomic region, contig, or chromosome
<i>Arsenophonus</i> sp. str. ENCA	NHNG01000131	scaffold 83; 5,323 bp
<i>Arsenophonus</i> sp. ex. <i>Aleurodicus floccissimus</i>	OUND01000001.1	loci WBAF_RS00520-WBAF_RS00780
<i>Arsenophonus</i> sp. ex. <i>Bemisia tabaci</i> Asia II 3	NZ_MASH01000127	scaffold 273; 20,407 bp
<i>Sodalis glossinidius</i> str. <i>morsitans</i>	DQ785801.1	pSOG3
<i>Sodalis glossinidius</i> str. <i>morsitans</i>	LN854557.1	SgGMMB4
<i>Morganella morganii</i>	TUM2748	loci DDA57-RS12540-DDA57-RS12300
<i>Morganella morganii</i>	NCTC12358	loci NCTC12358_01818-NCTC12358_01758
<i>Providencia alcalifaciens</i>	DSM30120	loci PROVALCAL_03397-PROVALCAL_03428
<i>Providencia alcalifaciens</i>	205/92	HMPREF1563_RS20015-HMPREF1563_RS20055
<i>Providencia sneebia</i>	DSM19967	loci O07_12289-O07_12234
<i>Proteus mirabilis</i>	CRK0056	loci B9475_005380-B9475_005540
<i>Providencia rettgeri</i>	DSM1131	loci PROVERT_06006-PROVERT_06027



Figure S1. Protein identity matrix for predicted genes in modules 1-4 for each sequenced APSE haplotype. Matrix identity tables were made for each predicted protein from amino acid alignments. Identities were color coded from low (green) to high identity (red). Note that predicted gene products in module 1 (G, H, HP20, L, HP21) and most predicted gene products in module 3 are present in only some haplotypes or a single haplotype (see Fig. 1 and main text) with grey backgrounds indicating that no identity comparison could be made.

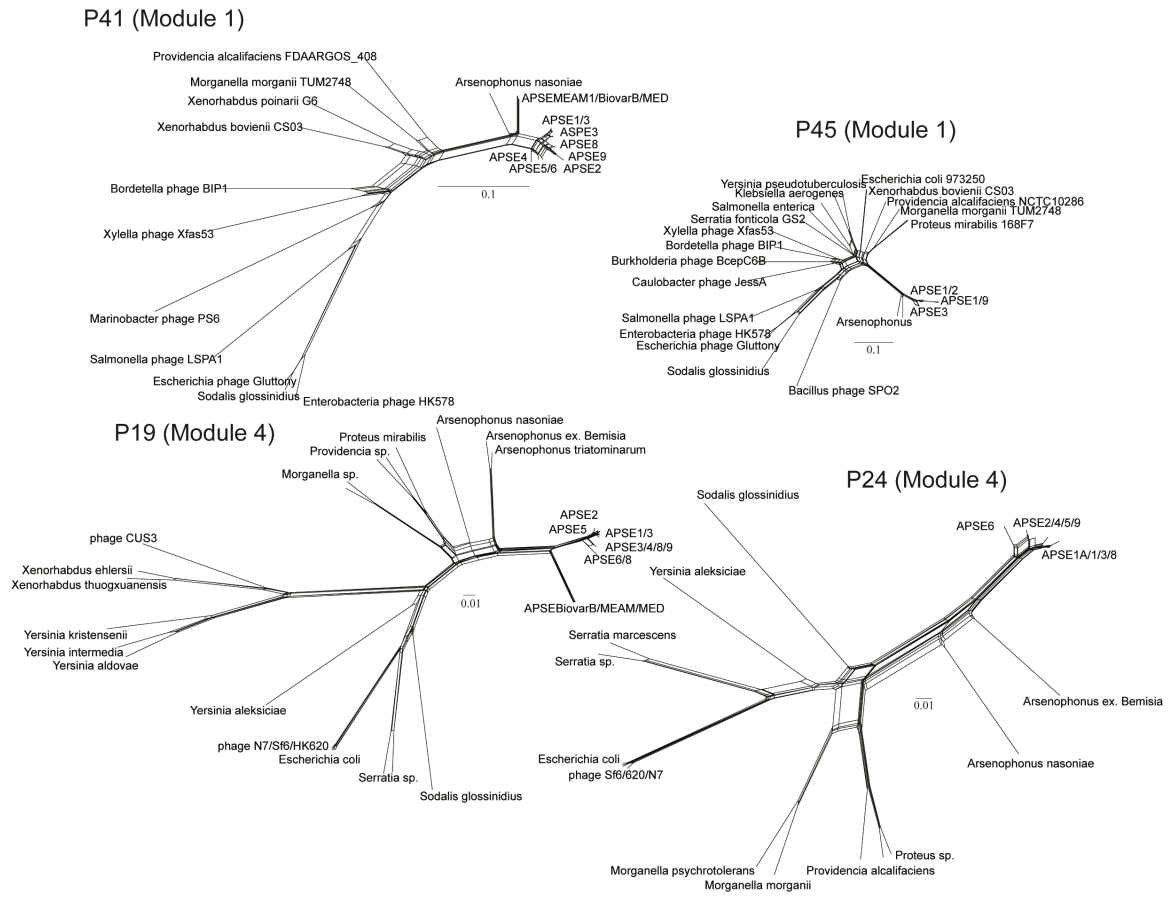


Figure S2. Phylogenetic networks depicting evolutionary relationships of the same genes analyzed in Fig. 5. Scale bars indicates nucleotide substitutions per site.

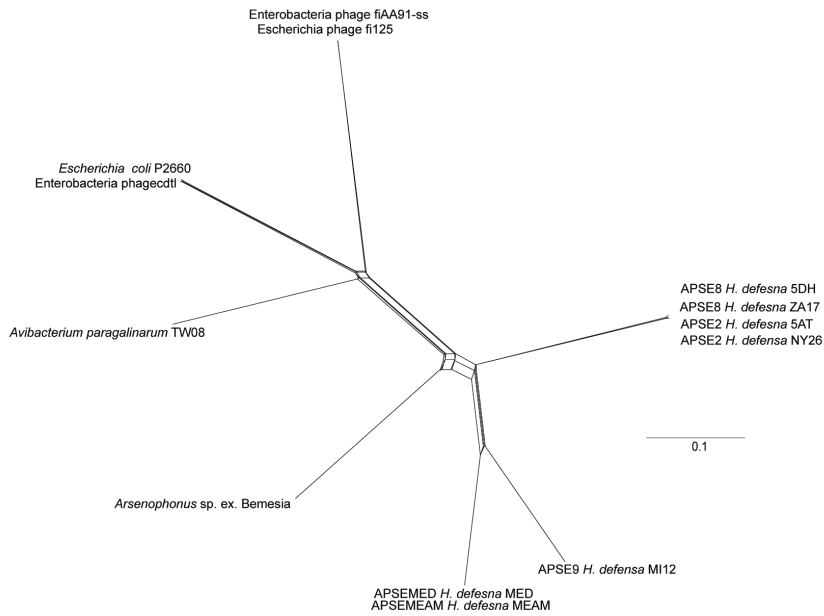
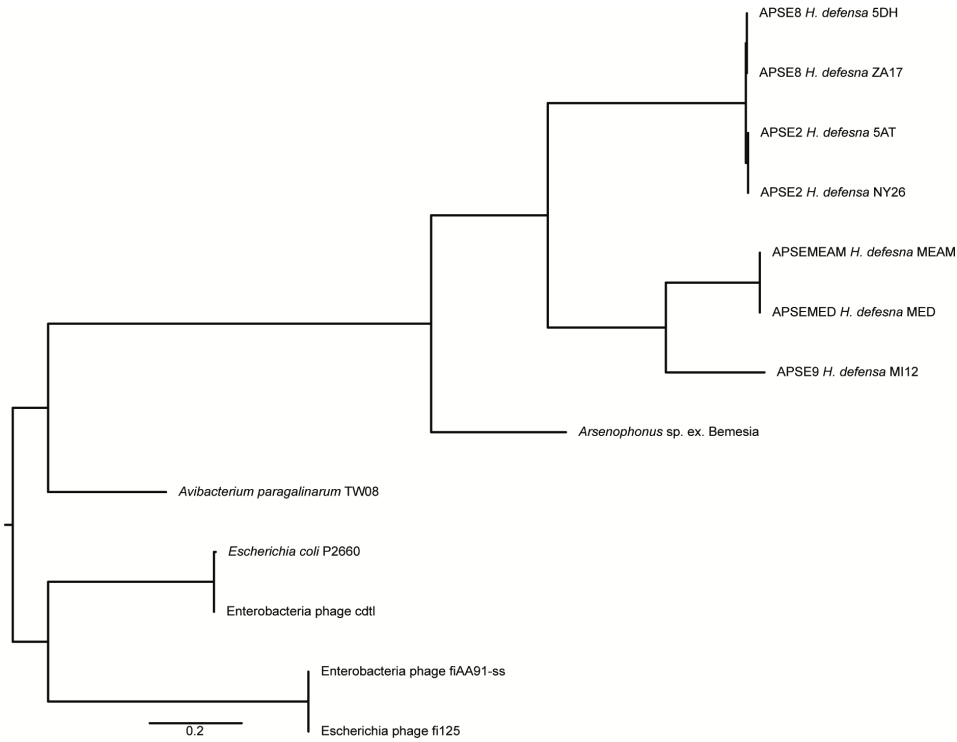


Fig. S3. Maximum-likelihood phylogram (A) and phylogenetic network (B) depicting evolutionary relationships for *ctdB* genes in different APSE haplotypes, other phages or phage elements in other bacteria in the order *Enterobacterales*.