FIG S2. *Rickettsia* diaminopimelate biosynthesis contains a pathway hole for the conversion of *N*-Succinyl-L-2-amino-6-oxopimelate to *N*-Succinyl-LL-2,6-diaminopimelate.

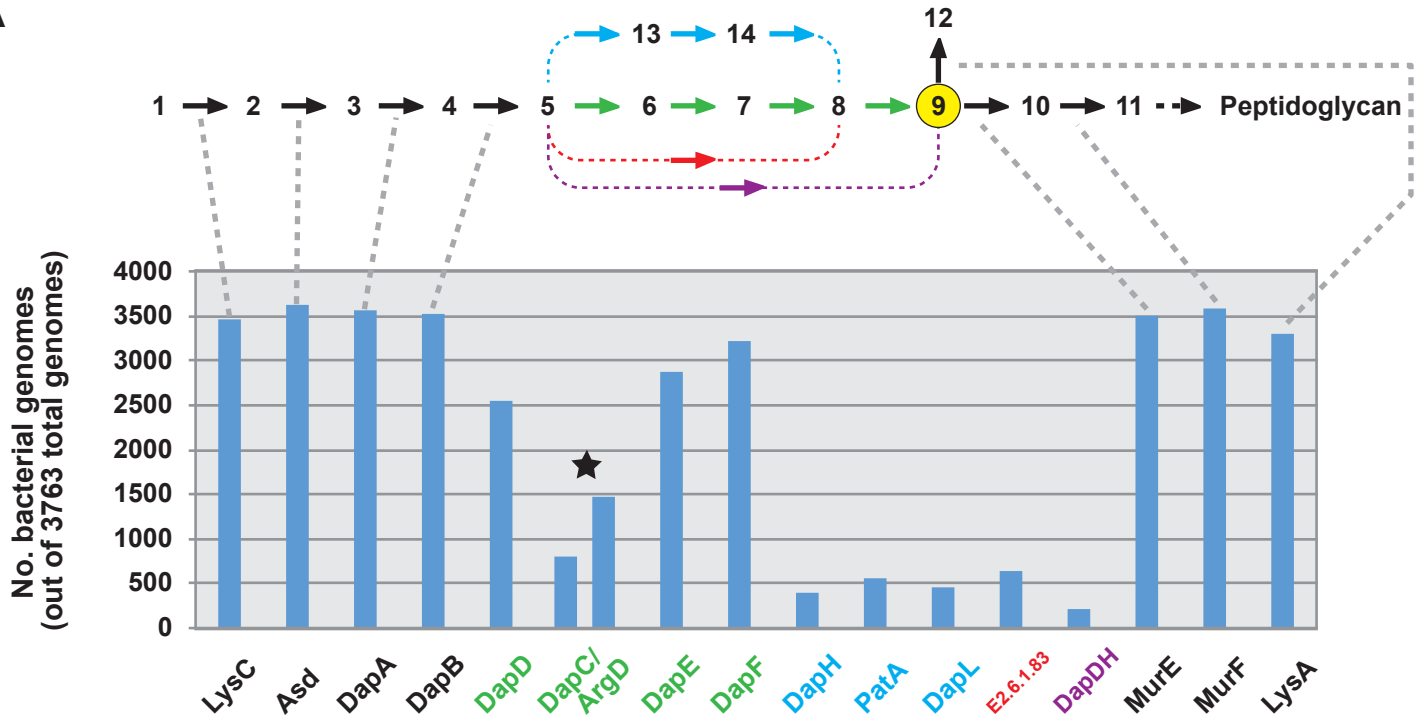
(A) The pathway from L-Aspartate to *meso*-2,6-Diaminopimelate (DAP) has several characterized routes for conversion of 2,3,4,5-Tetrahydrodipicolinate to DAP (model at top, with different colors depicting alternative pathways). Bar graph illustrates the distribution of all DAP pathway enzymes across 3763 analyzed genomes (all prokaryotic genomes with an available DAP biosynthesis pathway at KEGG). Dashed gray lines connect conserved proximal and distal enzymes to the model above, with less conserved enzymes of the alternative pathways colored accordingly. The star depicts the pathway hole (no DapC or ArgD) in the *Rickettsia* DAP pathway.

(B) Relative to the predominant "*E. coli*-like" pathway, the "*Rickettsia*-like" pathway for DAP biosynthesis is far less common, occurring in 315 bacterial genomes (excluding *Rickettsia* genomes). The pathway hole (no DapC or ArgD) is noted with a red X.

(C) Taxonomic breakdown of bacterial species containing the "*Rickettsia*-like" DAP biosynthesis pathway (315 total genomes). Genomes from intracellular species represent 11% of the total number of "*Rickettsia*-like" pathways.

(D) Top blastp hits against the NCBI *Rickettsia* database (taxid:780) using the alternative DAP pathway enzymes as queries. This analysis shows that, despite lacking DapC or ArgD homologs, *Rickettsia* genomes do not contain any alternative enzymes of the other characterized DAP biosynthesis pathways.

A

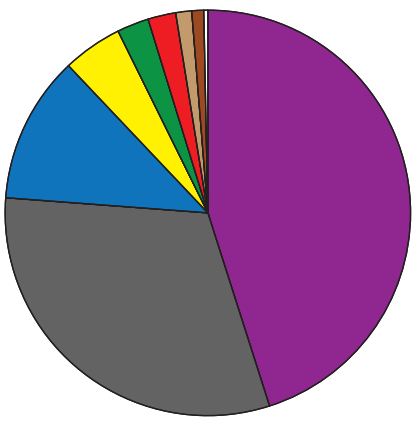


1	L-Aspartate	**9**	***meso*-2,6-Diaminopimelate (DAP)**
2	4-Phospho-L-aspartate	10	UDP-*N*-acetylmuramoyl-L-alanyl-gamma-D-glutamyl-*meso*-2,6-diaminopimelate
3	L-Aspartate 4-semialdehyde	11	UDP-*N*-acetylmuramoyl-L-alanyl-D-glutamyl-6-carboxy-L-lysyl-D-alanyl-D-alanine
4	(2S,4S)-4-Hydroxy-2,3,4,5-tetrahydrodipicolinate	12	L-Lysine
5	2,3,4,5-Tetrahydrodipicolinate	13	*N*-Acetyl-L-2-amino-6-oxopimelate
6	*N*-Succinyl-L-2-amino-6-oxopimelate	14	*N*6-Acetyl-LL-2,6-diaminoheptanedioate
7	*N*-Succinyl-LL-2,6-diaminopimelate		
8	LL-2,6-Diaminopimelate		

B

Pathway	Composition	No. genomes
E. coli-like	1 → 2 → 3 → 4 → 5 → 6 → 7 → 8 → 9	1589
Rickettsia-like	1 → 2 → 3 → 4 → 5 → 6 ✕ 7 → 8 → 9	315

C



- *Epsilonbacteria*
- Actinobacteria
- *Gammaproteobacteria*
- Firmicutes
- *Betaproteobacteria*
- *Alphaproteobacteria*
- *Deltaproteobacteria*
- Aquificae
- Other

Genomes from intra-cellular species (11%):

- *Frankia* (5)
- *Mycobacterium*
- *Carsonella* (3)
- *Coxiella* (6)
- *Coxiella*-like symbiont
- *Legionella* (2)
- *Ruthia*
- *Sodalis*
- *Tatlockia*
- *Vesicomyosocius*
- *Taylorella* (5)
- *Caedibacter*
- *Neorickettsia*
- *Acanthamoeba* symbiont
- *Wolbachia*
- *Bdellovibrio* (4)

D

	Top Hit
DapH	2e-22 (DapD)
PatA	2e-61 (AAT)
DapL	1e-04 (DapE)
E2.6.1.83	not significant
DapDH	not significant

FIG. S2