

FIG S3. *Rickettsia* biosynthesis of glycerophospholipids contains a pathway hole for the conversion of *sn*-glycerol 3-P to lysophosphatidic acid.

(A) The pathway from dihydroxyacetone phosphate to CDP-diacylglycerol (CDP-DG) contains two characterized enzymes that generate lysophosphatidic acid (LPA) from *sn*-glycerol 3-phosphate (G3P): the G3P acyltransferases PlsB and PlsY, both of which can utilize either acyl-CoA or acyl-ACP as the fatty acyl donor. The phosphate acyltransferase PlsX converts acyl-ACP to acyl-PO₄, which is also a donor for PlsY (1, 2), and both enzymes occur exclusively in bacteria (3). The bar graph indicates that the LPA-generating acyltransferases are variably-encoded across 3830 bacterial genomes, while the remaining enzymes of the pathway are highly conserved. The star depicts the pathway hole (no PlsB, PlsX or PlsY) in the *Rickettsia* glycerophospholipid biosynthesis pathway.

(B) The predominant bacterial glycerophospholipid biosynthesis pathway utilizes the PlsX/Y acyltransferases to generate LPA, with other pathways far less common. The “*Rickettsia*-like” pathway for generating LPA (i.e., sans any of the characterized G3P acyltransferases) occurs in 433 bacterial genomes (excluding *Rickettsia* genomes). The pathway hole (no PlsB, PlsX or PlsY) is noted with red Xs.

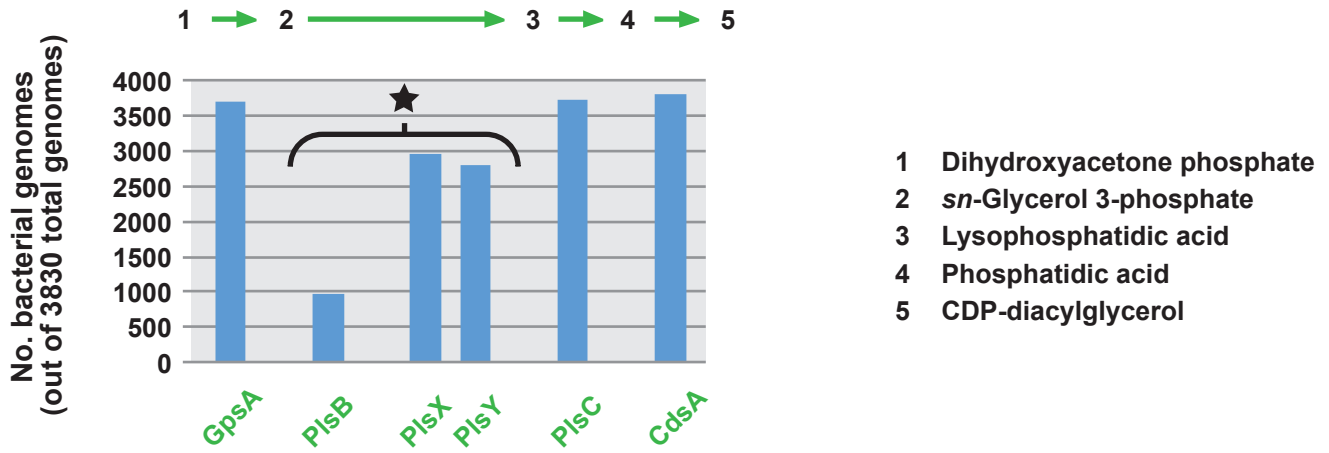
(C) Taxonomic breakdown of bacterial species containing the “*Rickettsia*-like” glycerophospholipid biosynthesis pathway (433 total genomes). Genomes from intracellular species represent 3% of the total number of “*Rickettsia*-like” pathways.

REFERENCES

1. Lu Y-J, Zhang Y-M, Grimes KD, Qi J, Lee RE, Rock CO. 2006. Acyl-phosphates initiate membrane phospholipid synthesis in Gram-positive pathogens. *Mol Cell* **23**:765–72.
2. Lu Y-J, Zhang F, Grimes KD, Lee RE, Rock CO. 2007. Topology and active site of PlsY: the bacterial acylphosphate:glycerol-3-phosphate acyltransferase. *J Biol Chem* **282**:11339–46.

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A



B

Pathway	Composition (enzymes)	No. genomes
<i>E. coli</i> -like	GpsA, PlsB, PlsX and PlsY, PlsC, CdsA	650
Predominant	GpsA, PlsB , PlsX and PlsY, PlsC, CdsA	1938
PlsB + PlsX	GpsA, PlsB, PlsX and PlsY , PlsC, CdsA	650
PlsB + PlsY	GpsA, PlsB, PlsX and PlsY, PlsC, CdsA	27
PlsB only	GpsA, PlsB, PlsX and PlsY , PlsC, CdsA	240
PlsX only	GpsA, PlsB , PlsX and PlsY , PlsC, CdsA	190
PlsY only	GpsA, PlsB , PlsX and PlsY, PlsC, CdsA	31
<i>Rickettsia</i> -like	GpsA, PlsB , PlsX and PlsY , PlsC, CdsA	433

C

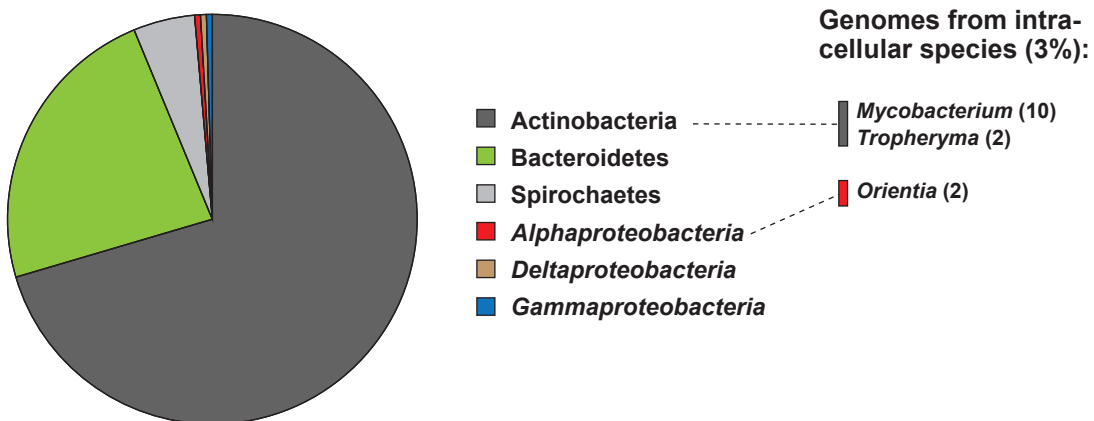


FIG. S3