

S_Figure 1.

Phylogenetic relationships of *Regiella insecticola* 5.15 with related best BlastP hit bacterial strains based on a 1,096 amino acid alignment from four concatenated *rfb* genes (*rfbA*, *rfbB*, *rfbC* and *rfbD*) using RAxML with 100 bootstraps.

S_Figure 2.

Enteric single copy ortholog amino acid phylogeny of *Regiella insecticola* 5.15 and related Enteric bacterial species using RAxML with 100 bootstraps. Based on a 1,639 amino acid alignment from four concatenated single copy ortholog genes (*accD*, *rpoS*, *gyrB*, and *murE*).

S_Figure 3.

PhoP phylogenetic tree displaying the relationship of *Regiella insecticola* 5.15 with best BlastP hit bacterial strains using RAxML on a 221 amino acid alignment with 100 bootstraps.

S_Figure 4.

PhoQ phylogenetic tree of *Regiella insecticola* 5.15 with best BlastP hit bacterial strains using RAxML with 100 bootstraps on a 435 amino acid alignment.