

SUPPLEMENTARY INFORMATION

**Differential impact of lipopolysaccharide defects caused by loss of RfaH in
Yersinia pseudotuberculosis and *Yersinia pestis***

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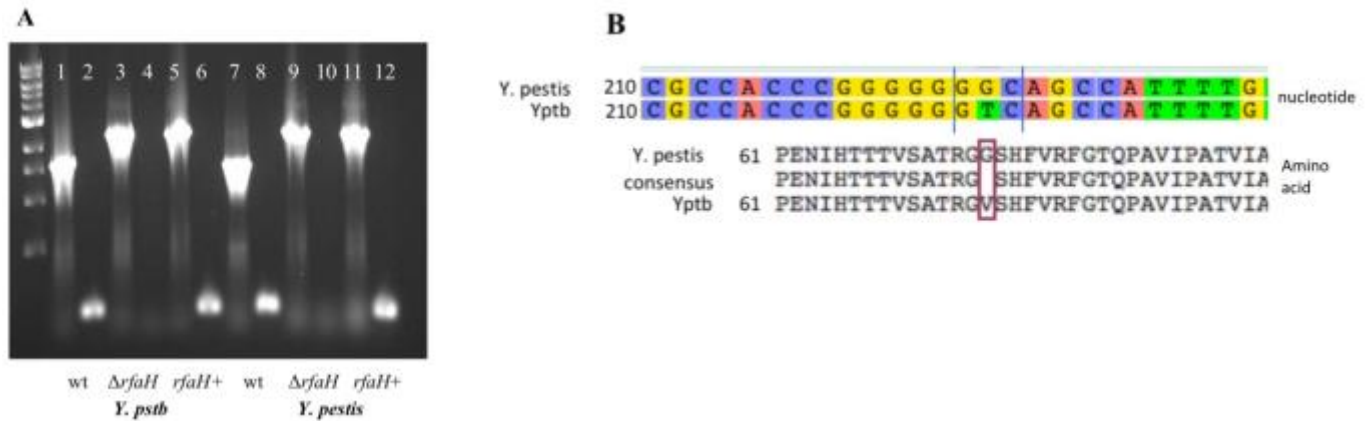
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Supplementary Table S1. Primers used in this study.

Primer name	Sequence (5' - 3')	Purpose
<i>rfaH</i> 500 F SacI	GCCGAGCTCGCCAATAATTTACCAACATCTCGC	<i>rfaH</i> gene deletion
<i>rfaH</i> 500 R KpnI	CCGGGTACCGCTAAGTATGCGTCTTGCTACTATG	<i>rfaH</i> gene deletion
<i>rfaH</i> F	GCCGCGTCGACTTCGGCGGCTATGGGATGCG	<i>rfaH</i> gene deletion and complementation
<i>rfaH</i> R	CCGCCTCTAGAGTGCAGGTGCGGATGGCGTA	<i>rfaH</i> gene deletion and complementation
<i>rfaH</i> internal F	GGCTCAAGCTTCCCTTAGGACACCTTCATGGAC	<i>rfaH</i> gene deletion
<i>rfaH</i> internal R	GCGTGTCTAGAGGCGTTTAGTTTTCGTTAACTTATCTGGGC	<i>rfaH</i> gene deletion
<i>lcrV</i> F	TCGCCGAATACACAATGGGA	Virulence plasmid verification
<i>lcrV</i> R	GAGCAGGTGGTGCCAAAGT	Virulence plasmid verification
<i>yopM</i> F	CGACAAGCCCATGAGCTAGA	Virulence plasmid verification
<i>yopM</i> R	GATTCCAGGCTCTGCGGTAA	Virulence plasmid verification
<i>attTn7</i> F	CGCTAACAACCCTGCGACTTCA	Tn7 insertion verification
<i>attTn7</i> R	GCGTGCTCGTGGTGGTTTGC	Tn7 insertion verification
<i>ddhD</i> F	TATTGGGGAATGCCAGCAGG	qPCR
<i>ddhD</i> R	TGGCTCCGGTCCAAGTACTA	qPCR
<i>ddhA</i> F	TCTACTTGGGAGCAGGAACC	qPCR
<i>ddhA</i> R	CACGCAACGTATCCATTGGC	qPCR
<i>ddhB</i> F	CGATGCTGAGGCTACTCCAGG	qPCR
<i>ddhB</i> R	ATGAGGGTGAGCATTGCCAT	qPCR
<i>wbyI</i> F	GCGGTACACTCGGAGTTGTA	qPCR
<i>wbyI</i> R	TCCAAAAATCATAATCACTGACAGGA	qPCR
<i>wbyK</i> F	TGCGCGTGGTGTTATAAGA	qPCR
<i>wbyK</i> R	ACTAGTGAATGCCCCCTCCAC	qPCR
<i>waaC</i> F	CGTGTGGTACAACAACGCAG	qPCR
<i>waaC</i> R	ACTTTTACAATCCGGCCCCGT	qPCR
<i>waaE</i> F	AACGGCACACGCTACTCAAT	qPCR
<i>waaE</i> R	CTCGATATCATGCGGCCCAT	qPCR
<i>waaQ</i> F	CAGCGTCATTGTCCCCGTAT	qPCR
<i>waaQ</i> R	AGAGCCATCGTTAACGGCAA	qPCR
<i>wabD</i> F	TGGCCACATTATGCCTGGT	qPCR
<i>wabD</i> R	TTGGGCCACGAGTGCTAATT	qPCR
<i>wabC</i> F	GAGCCACAATTGCAGGCAAA	qPCR
<i>wabC</i> R	ACTTATCCCAACTCCAGCGC	qPCR
<i>dnaE</i> F	TTTCGTCCCGGTCCGTTACAA	qPCR
<i>dnaE</i> R	ACAAGATTATGCCGTAGGTGCG	qPCR



Supplementary Figure S1. Deletion and complementation of *rfaH* in *Yptb* and *Y. pestis*. **A.** Agarose gel electrophoresis of PCR reactions. Reactions were performed using primers flanking the *rfaH* gene (500 F & R primers) to show an increased product size in $\Delta rfaH$ mutant (3, 9) and *rfaH*⁺ complemented strains (5, 11) in both *Y. pstb* and *Y. pestis*. The wild-type strains (1 and 7) gave a shorter product indicating the Km^R gene (which is larger than the *rfaH* gene) was inserted. Lanes 2, 6, 8, 12 were performed using the *rfaH* internal primers (150 bp product) which show *rfaH* gene present in wild-type and *rfaH*⁺ complemented strains, but not $\Delta rfaH$ (Lanes 4 and 10). **B.** Comparison between the *rfaH* gene in *Y. pestis* (top) and *Yptb* (bottom). They share a 99.8% identity with only one G-T nucleotide difference at position 224, resulting in a predicted Glycine-Valine difference at amino acid 75. Plasmids containing either the *Yptb* or *Y. pestis* versions of the *rfaH* gene were created for complementation analysis, and both gave identical results.