Virulence gene regulation by L-arabinose in *Salmonella enterica*

Javier López-Garrido, Elena Puerta-Fernández, Ignacio Cota,
and Josep Casadesús

SUPPORTING INFORMATION

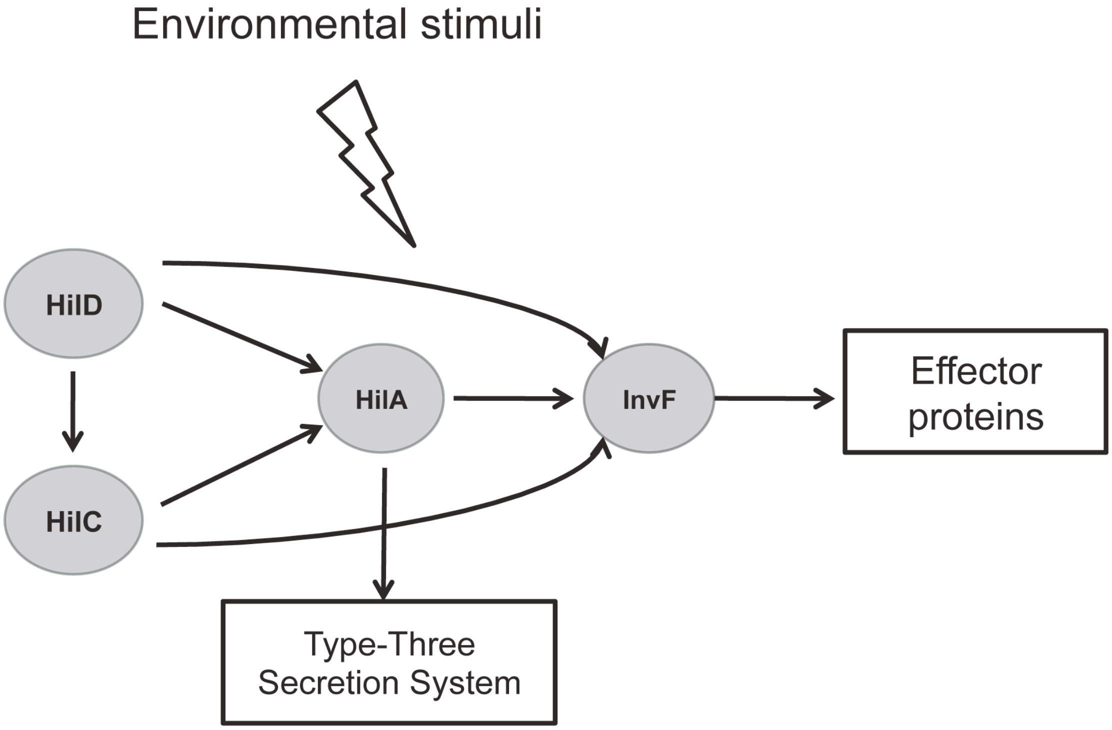

Figure S1 Diagram representing the regulatory network of SPI-1-encoded transcriptional activators.

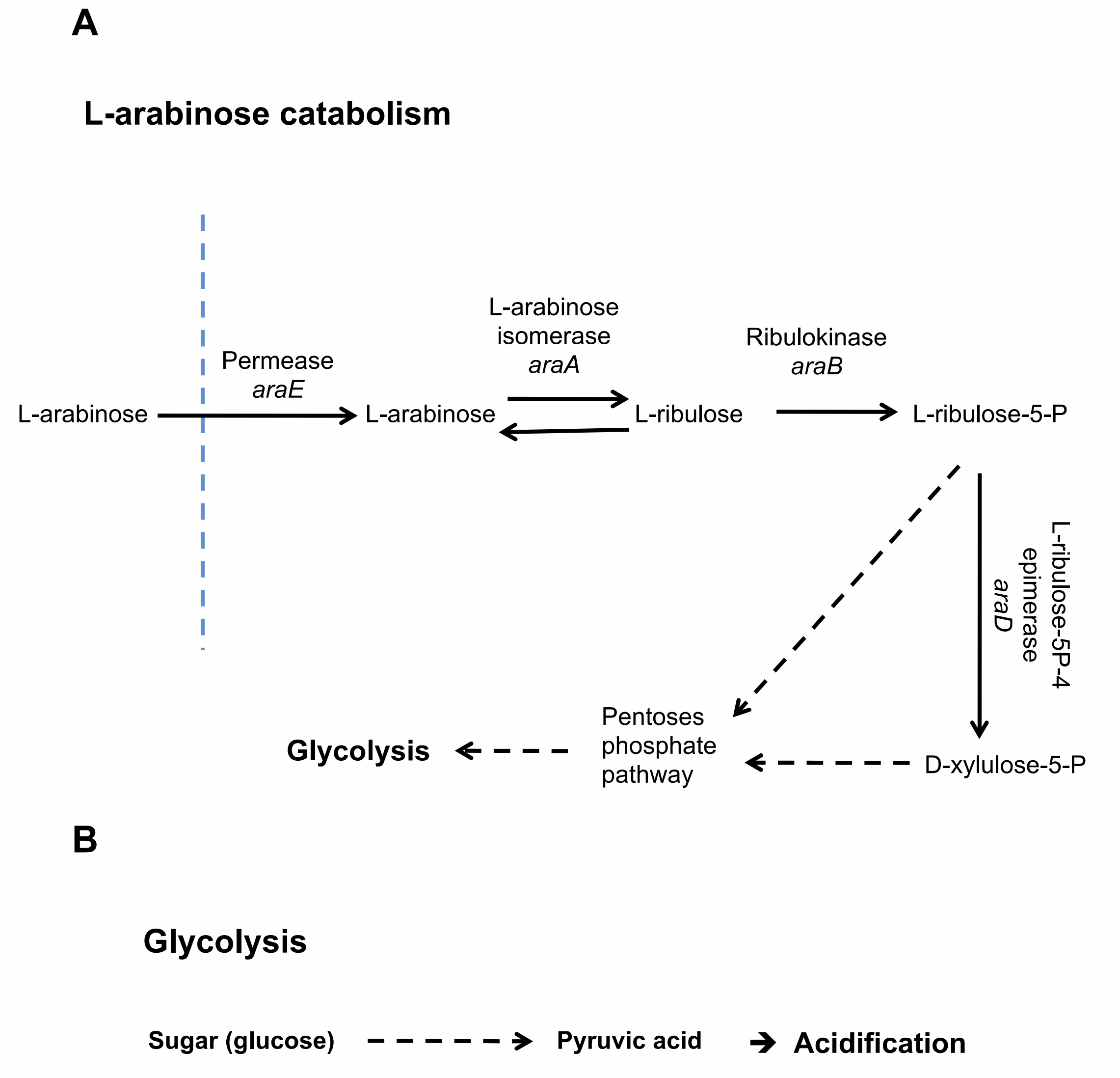

Figure S2 **A.** L-arabinose catabolism in *Salmonella*. Main steps in L-arabinose catabolism, enzymes involved and genes encoding the enzymes (in italics). **B**. Cause of culture medium acidification upon addition of a metabolizable sugar to LB.

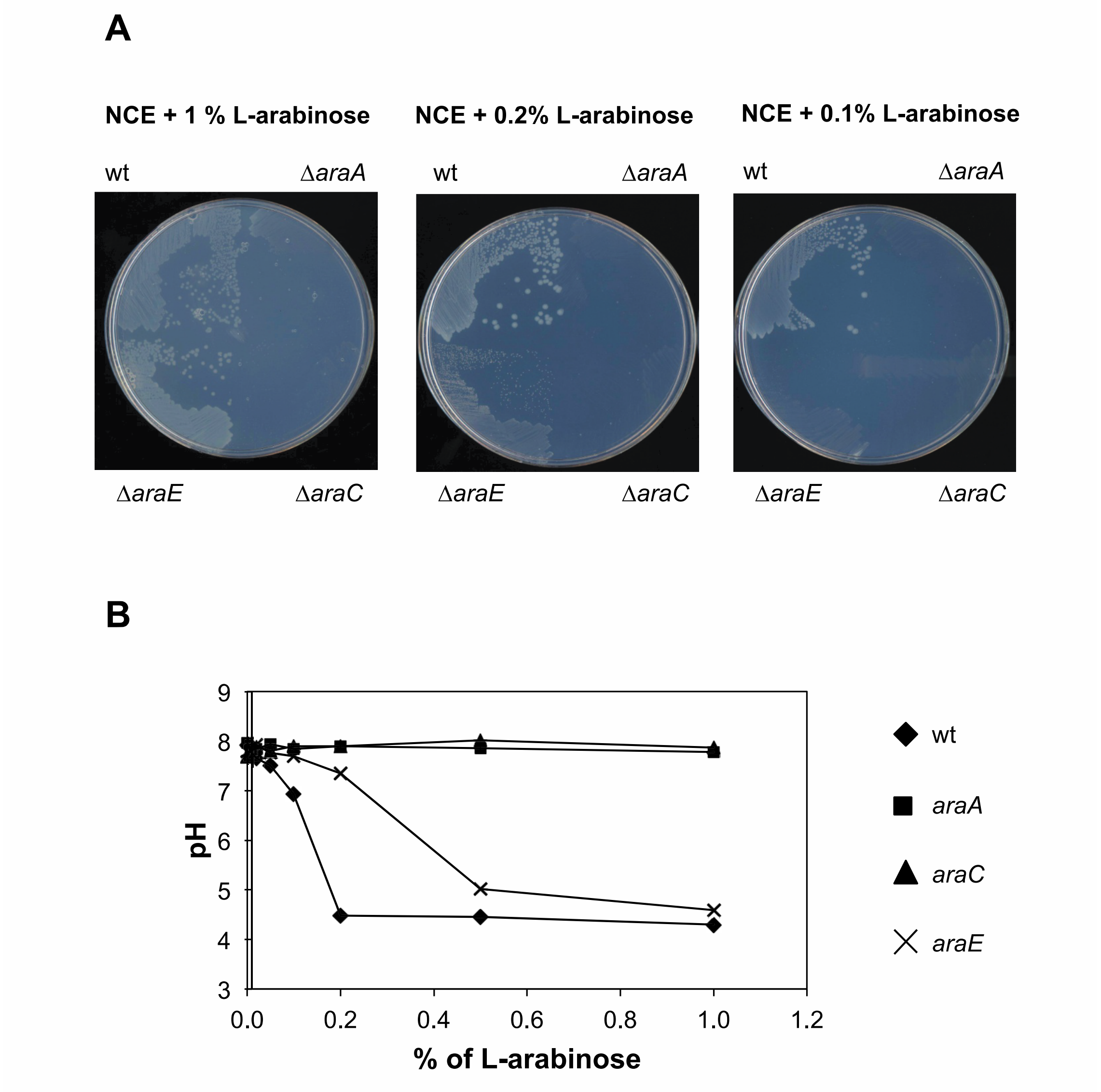

Figure S3 Phenotypes associated with *araA*, *araC*, and *araE* mutations. **A.** Growth of the wild type, AraA$^-$, AraC$^-$, and AraE$^-$ strains on minimal agar with 1%, 0.2% or 0.1% L-arabinose as sole carbon source. **B**. pH curves of the wild type, AraA$^-$, AraC$^-$ and AraE$^-$ strains.

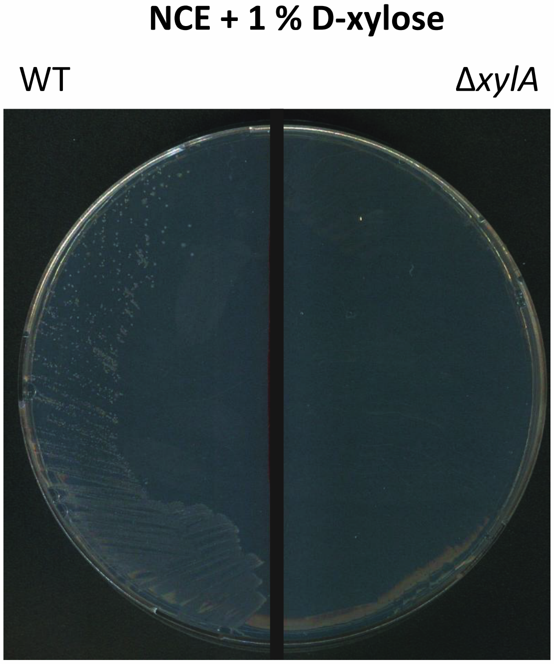

Figure S4 Growth of the wild type and an isogenic XylA^{-} strain on minimal agar with 1% D-xylose as sole carbon source.

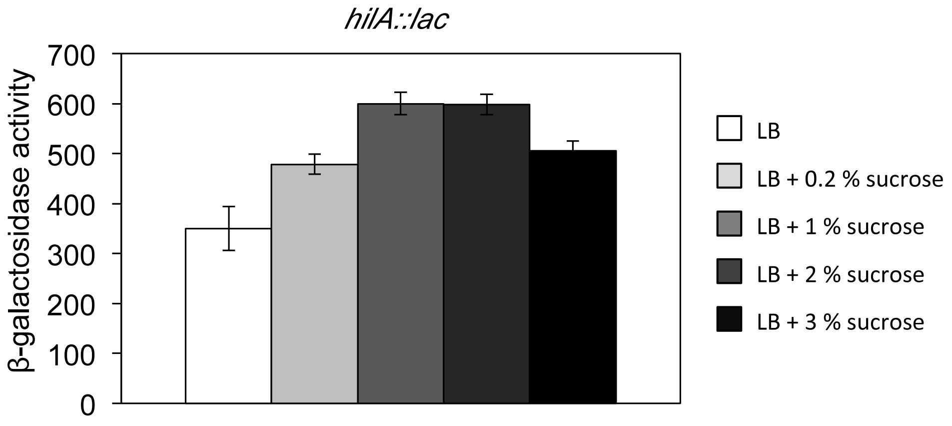

Figure S5 β-galactosidase activity of a *hilA::lac* fusion in LB and LB + 0.2%, 1%, 2%, and 3% sucrose.

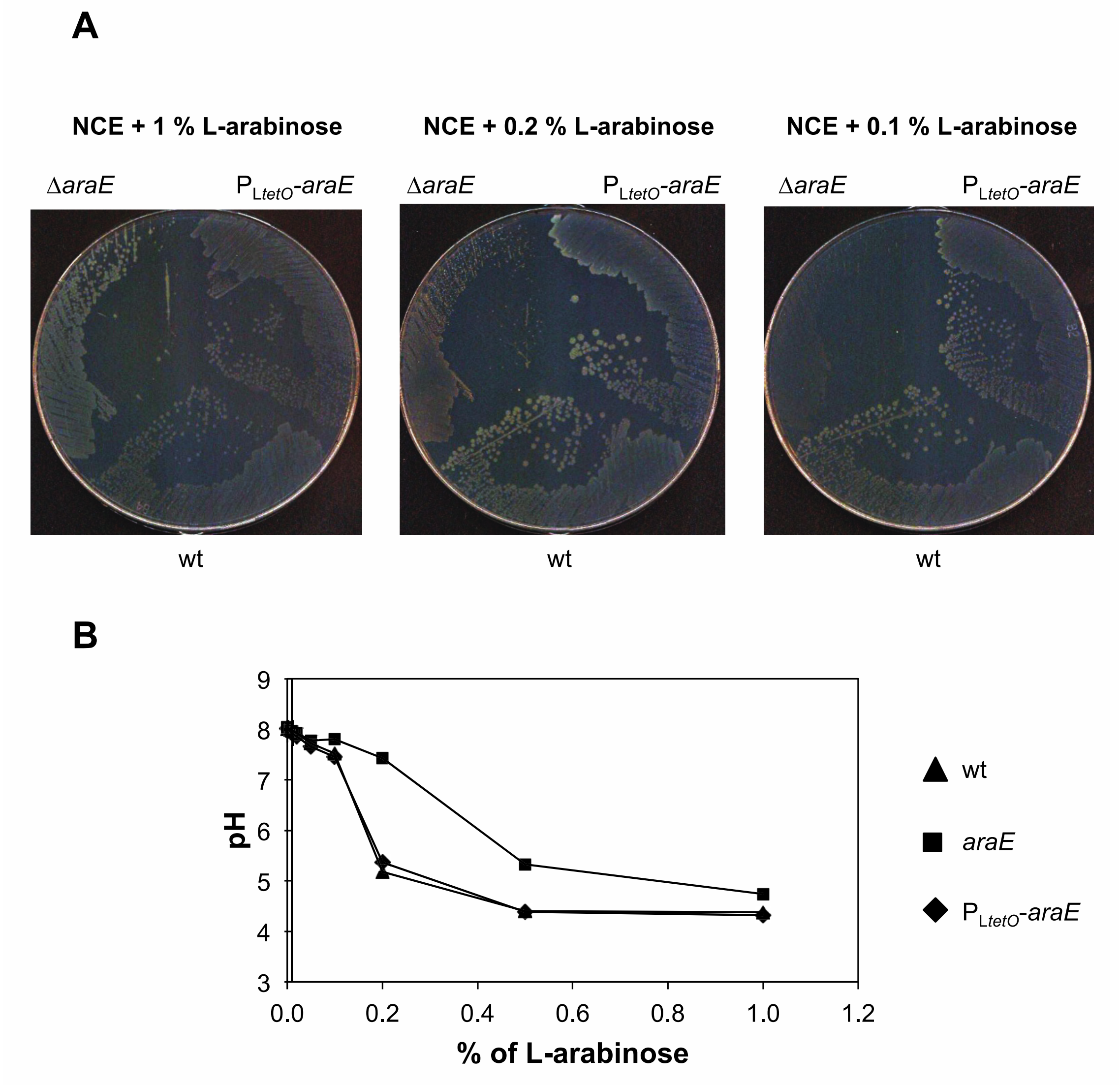

Figure S6 Phenotypes associated with *araE*. **A.** Growth of the wild type, AraE$^-$, and P$_{Ltet O}$-*araE* strains in minimal medium with 1%, 0.2% or 0.1% L-arabinose as sole carbon source. **B.** pH curves of wt, AraE$^-$, and P$_{Ltet O}$-*araE* strains.

Table S1 Oligonucleotides used in this study (5'→3')

Oligonucleotide	**Sequence**
araAUP	ctgactcattaaggacacgacaatgacgatttttgataatattccggggatccgtcgacc
araADO	gcaatccgtttcaccaattaacgtttgaacccgtaatacagtgtaggctggagctgcttc
araA-E1	tgcgacgtactgaatcgtcc
araA-E2	accaccaccatatcgtcagc
xylAUP	cgtttacttgccgtcttatctgattatggagctcactatgattccggggatccgtcgacc
xylADO	ggccgggctaacgcggagtcgcccggtagatagggttattgtgtaggctggagctgcttc
xylA-E1	aattcatcacagcaaacgg
xylA-E2	caggatagcttttacacccg
PLtetO-araE-UP	tgggtttaacttaatccatatattgttaaataatagctataggcttacccgtcttactgtc
PLtetO-araE-DO	ttaatagagaccatattttcctgccacaacagagtaagacgtgctcagtatctctatcactgatag
araEUP	tttcaggctatgtcttactctgttgtggcaggaaaatatgattccggggatccgtcgacc
araEDO	cggataacaggcgtcatccggcatgggaggggggattacagtgtaggctggagctgcttc
araE-E1	tataccatagcggtagatggc
araE-E2	agtcgattcccagctcatc
araCUP	tttgtttcttctctgaacatcggggggtagagaaatcatgattccggggatccgtcgacc
araCDO	gcttatgacatctttgtggacacatcattcactttttattgtgtaggctggagctgcttc
araC-E1	tcaatgtggacattccagc
araC-E2	gataaagtgttccagcagtgc
hilDUP1	agagcatttacaactcagatttttcagtaggataccagtcatatgaatatcctccttag
hilDUP930	aactacgccatcgacattcataaaaatggcgaaccattaacatatgaatatcctccttag
hilD-lacZUP	tgaacatctgaaaacggcgttctcctgtacgaaggatacacccgtcgttttacaacgtcg
hilD-lacZDO	gcaaatagttctcagagggaacggatgatgtataaatatgcgtgtaggctggagctgcttc
hilDDO2	gcaaatagttctcagagggaacggatgatgtataaatatggtgtaggctggagctgcttc
hilD-E1	agaccattgccaacacacgc

hilD-E2’	atcatcctcaggctggctcc
pXG10-hilD-UP	gtttttatgcataaggaacattaaaataacatcaac
pXG10-hilD-DO	gtttttgctagcggcaaatagttctcagaggg
pXG10-FOR	ttggaacctcttacgtgcc
pXG10-REV	gcatcaccttcaccctctc
hilDriboprobeUP	atggaaaatgtaacctttgtaag
hilDriboprobeDO	gtttttttaatacgactcactatagggaggtatatcgaaatccatgtggc
rnpBriboprobeUP	gaagaagtgaaactgaccgataagc
rnpBriboprobeDO	taatacgactcactataggccgaagctgaccagacagtcg