



Fig. S1. *Nicotiana benthamiana* infiltrated with *Pst* DC3000, *corR* and *hrpL* mutants, and water. **A**, Leaves infiltrated with *Pst* DC3000 and *hrpL* mutant at $OD_{600}=0.1, 0.01, 0.001$ and 0.0001 . **B**, Leaves infiltrated with *Pst* DC3000 and *corR* mutant at $OD_{600}=0.1, 0.01, 0.001$ and 0.0001 . **C**, Leaves infiltrated with *Pst* DC3000, *corR* and *hrpL* mutants, ($OD_{600}=0.001$), and water. Photographs were taken 48 h postinoculation. All experiments were repeated, and the results shown are typical of all experiments.

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PG4180 cfl      TATAACCAGAATC CGAAGCCATTTCGCTGGCACAAAAAAGCGGACGAGATTCTGGGTTCCGTTGCTCGCGCAGAAAAGCA 626
DC3000 corR    CTCCACTAAAACCTCCGTCCTCTCCACAAGCGTAAAAATGAGGACTGCAGGCCTGCTCCTGCACCGTGATTTTTTTGACA 384
DC3000 hrpL    TGGACCGTACTTGCGACGCAGCTGTTTGAGCTGCTGTGTCAGGACCACATGCTCGCCATCTCACCGTCGGCTTCGGCCT 614
CONSENSUS      CGA-GCC-CT-C-C-AGC--AAAAATGAGGAC-ACATGCT-GCTCCTGT--C-G

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Fig. S2. Alignment of the CorR-binding site upstream of the *cfl* gene in *Psg* PG4180 (DNaseI protected region; see Penaloza-Vazquez and Bender 1998) with potential CorR-binding sites in the promoter regions of *corR* and *hrpL* in *Pst* DC3000. Numbers on the right represent the nucleotide position relative to the translational start (ATG). Bases shown in red font with yellow highlighting indicate nucleotides with homology to the CorR-binding site in *Psg* PG4180. The alignment was constructed using the Pretty Multiple Sequence Alignment program of SeqWeb Version 2 (Genetics Computer Group, University of Wisconsin).