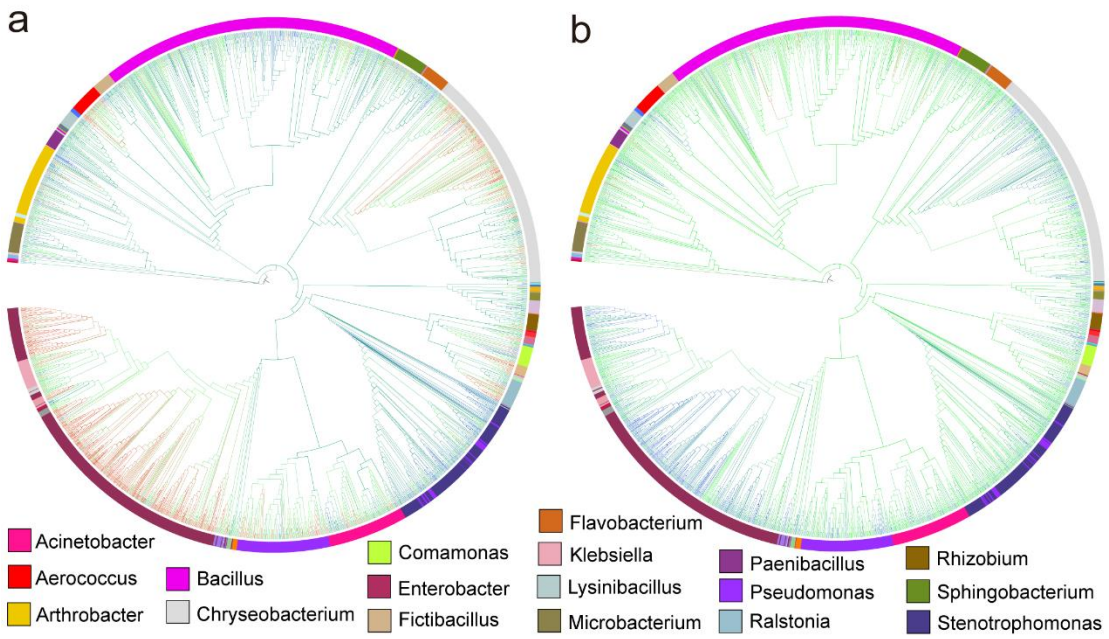
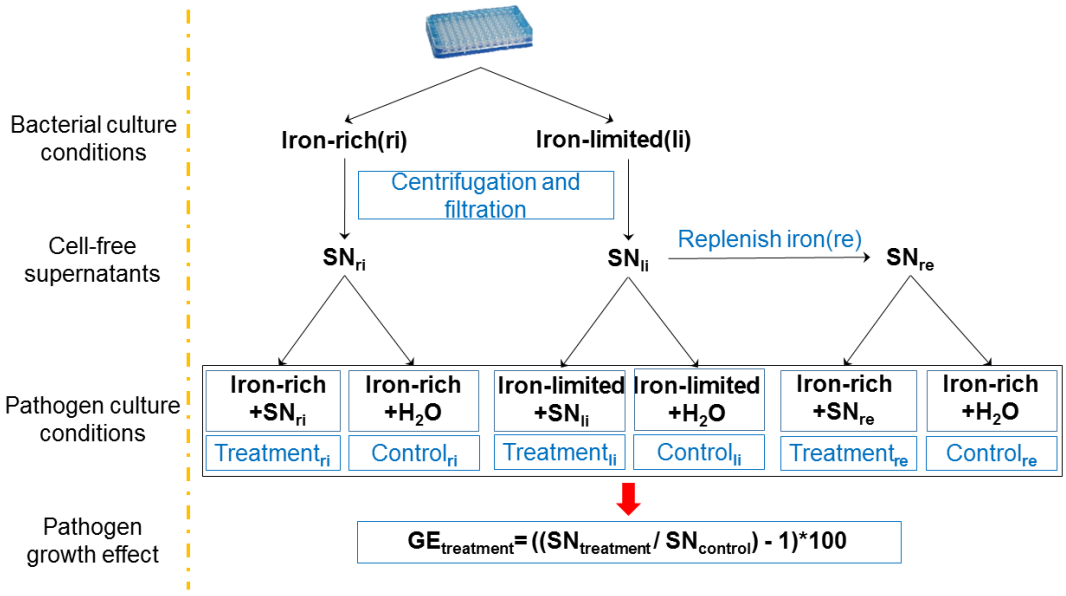
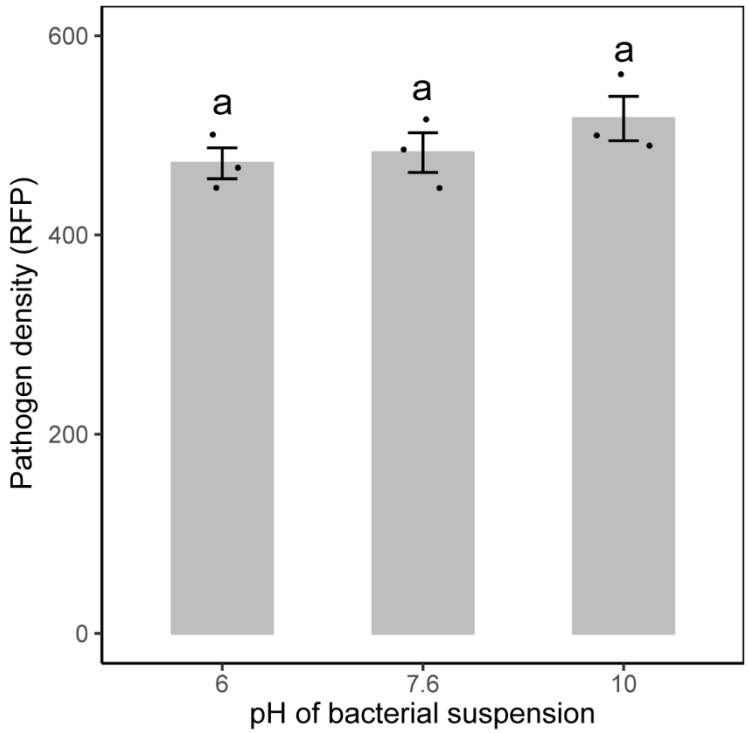


Supplementary Fig. 1 | Ancestral character estimation. Cladograms relating the phylogenetic relationship among the 2150 isolates (based on the 16S rRNA gene sequences) to the estimated ancestral character state with regard to (**a**) siderophore production (from low [blue] over intermediate [green] to high [red]) and (**b**) siderophore-mediated growth effects (from inhibitory [blue] over neutral [green] to promotive [red]). Note that the ancestral character estimation suggests that high levels of both siderophore production and siderophore-mediated effects on pathogen growth evolved independently multiple times.



Supplementary Fig. 2 | Overview of the experimental design used to assess the effect of siderophores produced by rhizosphere bacteria on the growth of *Ralstonia solanacearum.* To explore how competition from iron affected interactions between the pathogen and rhizobacteria, we grew the pathogen in triplicates in presence of supernatant form each of our isolates. Do determine whether the supernatant-mediated effects on pathogen growth were due to iron competition or to other metabolites, we set up three different types of supernatant treatments: (i) supernatants collected from iron-rich conditions (rhizobacteria grown in iron-rich MKB medium, in which little siderophore is produced but other compounds are secreted, SN_{ri}); (ii) supernatants collected from iron-limited conditions (rhizobacteria grown in iron-limited MKB medium, which triggers siderophore production in addition to other secreted compounds, SN_{li}); and (iii) supernatants collected from iron-limited conditions that was subsequently replenished with 50 µM FeCl3 (SN_{re}). This supernatant still contains siderophores, but they are no longer relevant for iron uptake, as iron is available in excess. As a control, we used sterilized water instead of supernatant ($SN_{control}$). Subsequently, we calculated the rhizobacterial supernatant effect on pathogen growth relative to growth in the absence of supernatants, using the following formula: growth effect $GE_{treatment}$ = (($SN_{treatment}$ / $SN_{control}$)-1)*100, where SNtreatment = SN_{li}, SN_{ri}, or SN_{re}. For this calculation, we took the average supernatant effects across the three replicates. Values smaller and greater than zero indicate growth inhibition and facilitation, respectively, expressed as percentage fold-change in growth.



Supplementary Fig. 3 | The stability of the mCherry tag fluorescence under a pH range. Pathogen density (in terms of fluorescence signal intensity; excitation: 587nm, emission: 610 nm) does not change along the pH of the culture media. Data represent the mean±s.d. of pathogen density in each pH suspension for three independent biological replicates (shown as black dots over the bars). The same lowercase letters above bars denote for nonsignificant differences based on analysis of variance (ANOVA) followed by Duncan's multiple range tests (all $P>0.5$).

Supplementary Table 2. ANOVA table summarizing the effect of relative siderophore production and phylogenetic distance on the siderophore-mediated effect on pathogen growth under iron-limited condition. n=2150 biologically independent rhizobacterial isolates and significant effects ($P < 0.05$) are highlighted in bold and the "up" and "down" arrows denote positive or negative effects, respectively.

	Siderophore-mediated effect on pathogen growth		
	Df	F	*P*
Phylogenetic distance	1	25.282 ↑	**5.4×10^{-7}**
siderophore production	1	712.83 ↓	**$<2.2\times10^{-16}$**
Residuals	2147		
Model summary	AIC: 1502.76, R^2 = 0.255, F=369		

Supplementary Table 3. ANOVA table summarizing the effect of soil pH and siderophore-mediated effects on pathogen growth (SIDE) on the co-occurrence/coexistence of rhizosphere bacteria with the pathogen across the 80 soil samples (correlation coefficient) in iron-limited condition. n=2130 biologically independent rhizobacterial isolates and significant effects ($P < 0.05$) are highlighted in bold and the "up" and "down" arrows denote positive or negative effects, respectively.

	Correlation coefficient value		
	Df	F	*P*
Soil pH	1	207.565 ↓	**$<2.2\times10^{-16}$**
SIDE	1	326.405 ↑	**$<2.2\times10^{-16}$**
Soil pH *SIDE	1	36.217 ↓	**2.07×10^{-9}**
Residuals	2126		
Model summary	AIC: 435.91, R^2 = 0.210, F=190		

Supplementary Table 5. ANOVA table summarizing the effect of the three bacterial genera and their siderophore-mediated effect on pathogen growth (SIDE), on the probability of the pathogen to infect tomato plants and the level of disease incidence and the pathogen density in greenhouse experiments. n=360 biologically independent rhizobacterial isolates for successful infection and pathogen density, n=77 biologically independent rhizobacterial isolates for disease severity. Significant effects (P < 0.05) are highlighted in bold and the "up" and "down" arrows denote positive or negative effects, respectively.

	Successful infection			Disease severity			Pathogen density		
	Df	F	*P*	Df	F	P	Df	F	*P*
Genus	2	0.64	0.53	2	0.26	0.77	2	0.43	0.64
SIDE	1	26.60 ↑	**4.17×10^{-7}**	1	14.05 ↑	**0.0004**	1	35.37 ↑	**6.52×10^{-9}**
Residuals	356			73			356		
Model summary	AIC:362.63 R^2=0.065, F=9.29			AIC:321.42 R^2=0.132, F=4.86			AIC:158.79 R^2=0.085, F=12.08		

Supplementary Table 6. Information of *Pseudomonads* strains used in siderophore pyoverdine purification study. SampleID refers to the rhizosphere samples from where the bacterial strains were isolated, as listed in the Extended Data Table 1. SIDE represent the siderophore-mediated effects on pathogen growth based on raw supernatant experiment.

Strain ID	Genus	Sample site	Sample ID	SIDE	Relative Fluorescence Units (RFU)
BS0048	*Pseudomonads*	Changsha	2	-0.33	5898.13
BS0408	*Pseudomonads*	Changsha	16	-0.46	7614.18
BS0599	*Pseudomonads*	Ningbo	3	-0.30	4857.84
BS1719	*Pseudomonads*	Nanning	6	-0.32	4431.08