

Figure S1. Phylogenetic tree inferred from the combined dataset of EF-1 α and β -tubulin based on the Neighbor-Joining method. *Fusarium foetens* isolate is the pathogen of potato wilt described in the study. The scale bar indicates genetic distance. Bootstrap values in 1000 replicates for major lineages at the nodes were shown as percentages.

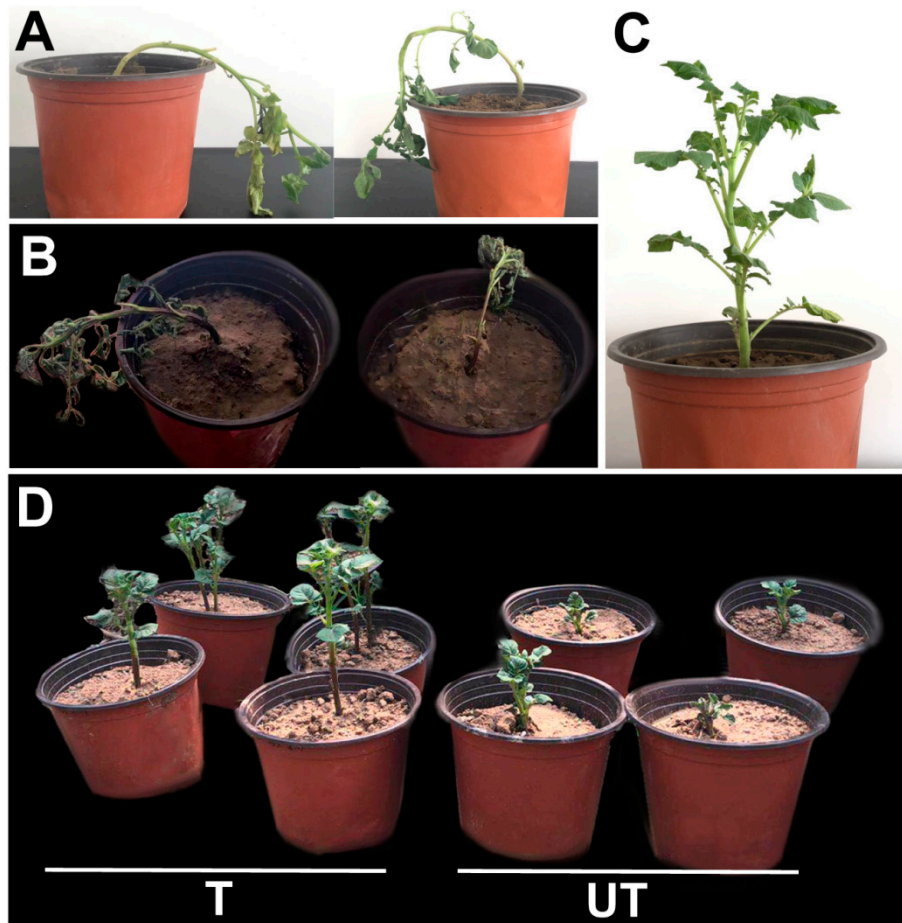


Figure S2. The effect of *B. subtilis* SF1 on the potato FW induced by *F. foetens*. **(A)** Seedlings inoculated with *F. foetens* cultured in pots put in the field for 9 days. **(B)** Seedlings inoculated with *F. foetens* cultured in pots put in the field for 2 weeks. **(C)** Healthy seedling. **(D)** Effect of *B. subtilis* SF1 on potato plants growth. The seedlings were transplanted into the pots with and without spores suspension of *B. subtilis* SF1 and then cultured in the greenhouse for 20 days. **(T)** the seedlings in the pots supplemented with 100 ml of spores suspension of *B. subtilis* SF1. **(UT)** the seedlings without any treatment.

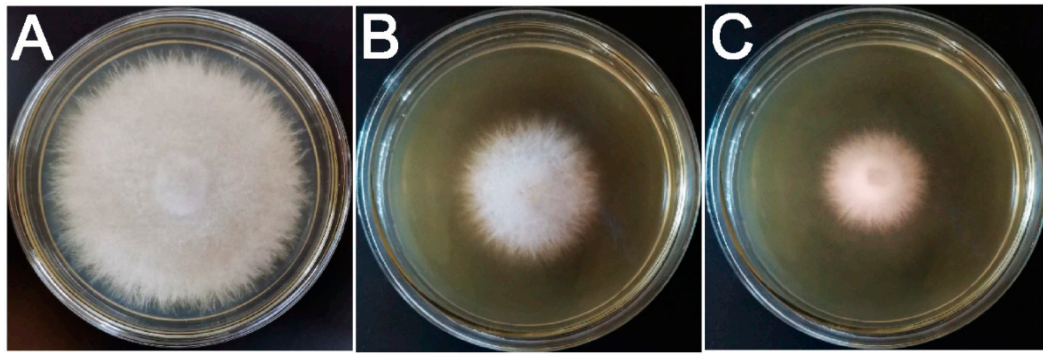


Figure S3. Effects of heat treatment on the antifungal activity of *B. subtilis* SF1 against *F. foetens*. The culture was incubated for 7 days at 25 °C. **(A)** Control: *F. foetens* on PDA. **(B)** *F. foetens* on PDA, replacing water by heated culture filtrate (105 °C for 10 min). **(C)** *F. foetens* on PDA supplemented with *B. subtilis* SF1 culture filtrate without heat treatment.

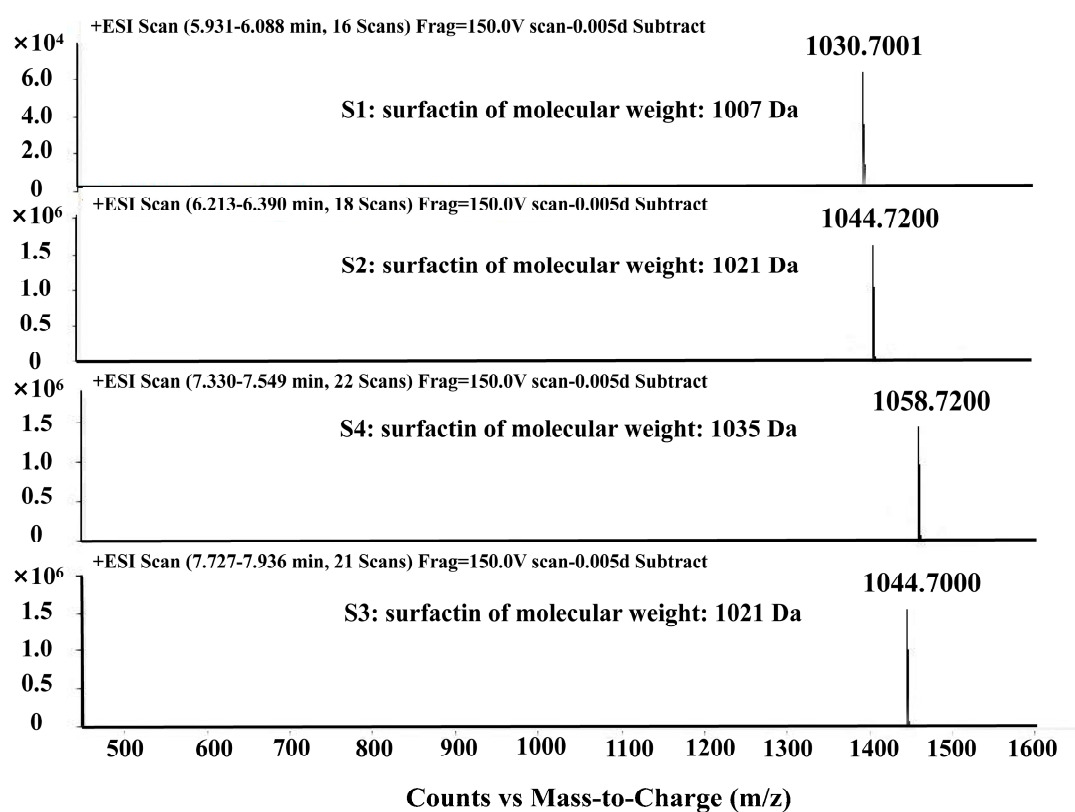


Figure S4. LC-MS spectrometry analysis of surfactin produced by *B. subtilis* SF1. The positive-ion MS spectrum of surfactin yielded the expected ion of $[M+Na]^+$ at m/z 1030 (S1), 1044 (S2), 1044(S3), and 1058 (S4), with molecular weights of 1007, 1021, 1021, and 1035 Da.

Table S1. The genes encoding beta-glucanase, endo-1,4-beta-glucanase, and extracellular protease in the genome of *B. subtilis* SF1.

Gene	Protein	Position	Description
<i>eglS</i>	endo-1,4-beta glucanase EglS	988,650-990,149	Hydrolytic activity against carboxymethylcellulose
<i>bglS</i>	beta-glucanase	835,782-836,510	Hydrolyze beta-glucans such as lichenan or barley beta-glucan
<i>nprE</i>	neutral metalloprotease NprE	586,981-588,546	Neutral metalloprotease
<i>epr</i>	protease Epr	762,622-764,559	Serine protease
<i>vpr</i>	serine protease Vpr	728,750-731,170	Fibrinolytic enzyme, a serine protease of the subtilisin family
<i>bpr</i>	bacillopeptidase F	646,231-650,532	Serine proteinase with esterolytic activity
<i>wprA</i>	cell wall-associated protease WprA	203,965-206,649	Subtilisin protease family

Table S2. Representative genes involved in plant growth promotion in the genome of *B. subtilis* SF1.

Gene	Position	Description
<i>spo0A</i>	1,433,063 to 1,433,866	Biofilm formation
<i>sigW</i>	424,349 to 424,912	Biofilm formation
<i>sinR</i>	1,467,687 to 1,468,028	Biofilm formation
<i>sinI</i>	1,467,659 to 1,467,486	Biofilm formation
<i>abrB</i>	45,441 to 45,725	Biofilm formation
<i>resE</i>	1,332,210 to 1,330,441	Biofilm formation
<i>lytS</i>	1,887,433 to 1,885,652	Biofilm formation
<i>ybdK</i>	397,849 to 396,863	Biofilm formation
<i>ycbA</i>	355,282 to 356,634	Biofilm formation
<i>EpsA to O</i>	332,476 to 348,216	Necessary for biofilm formation
<i>yqxM to</i>	1,468,121 to 1,470,287	Essential for biofilm formation
<i>tasA</i>	354,374 to 355,795	Root adhesion
<i>sacB</i>	1,453,155 to 1,453,712	Essential for swarming motility
<i>efp</i>	764,229 to 764,732	Essential for swarming motility
<i>swrB</i>	441,011 to 441,346	Essential for swarming motility
<i>swrA</i>	204,256 to 207,414	Self-resistance against surfactin
<i>swrC</i>	74,898 to 77,141	Regulator of surfactin production
<i>comP</i>	218,867 to 245,015	Necessary for surface motility and biofilm
<i>srfABCD</i>	213,097 to 213,744	formation
<i>yczE</i>	214,523 to 213,849	Necessary for surface motility and biofilm
<i>sfp</i>	127,632 to 130,324	formation
<i>escABC</i>	615,368 to 615,817	Necessary for surface motility and biofilm

<i>ylbF</i>	821,321 to 821,752	formation
<i>ymcA</i>	26,810 to 28,000	Protein secretion to extracellular matrix
<i>tuf</i>	452,303 to 453,799	Control of community development
<i>fliD</i>	454,379 to 455,293	Control of community development
<i>hag</i>	457,637 to 459,160	Elicitation of plant basal defence
<i>flgK</i>	468,046 to 478,310	Elicitation of plant basal defence
<i>tuaA to</i>		Elicitation of plant basal defence
<i>tagO</i>		Elicitation of plant basal defence
		Elicitation of plant basal defence

Table S3. The predicted secondary metabolites and the corresponding synthesis gene clusters in the genome of *B. subtilis* SF1.

Metabolite	Gene cluster	Size	Position	Bioactive spectrum
Surfactin	<i>srfABCD, ycxA,</i>	31.9 Kb	2,736,952	Mycoplasma, fungi,
	<i>sfp, yczE</i>		to 2,768,870	virus and tumor
Pilpastatin	<i>ppsABCDE</i>	37.7 Kb	1,429,921	Bacteria and fungi
			to 2,768,870	
Bacilysin	<i>bacABCDEFG</i>	6.7 Kb	3,657,315	Bacteria and
			to 3,664,002	<i>Candida albicans</i>
Bacillaene	<i>pksABCFGHIJKLM</i>	77.9 Kb	1,250,587	Bacteria
	<i>NRS,acpK</i>		to 1,328,470	
Bacillibactin	<i>dhbBCEF</i>	2.6 Kb	3,076,306	Microbial competitors
			to 3,078,940	
	<i>albABCDEFG</i>	6.7 Kb	3,625,712	Bacteria
Sublitolin			to 3,632,518	