Supplementary data

Genome Insights into the Novel Species *Jejubacter calystegiae,* a Plant Growth-promoting Bacterium in Saline Conditions

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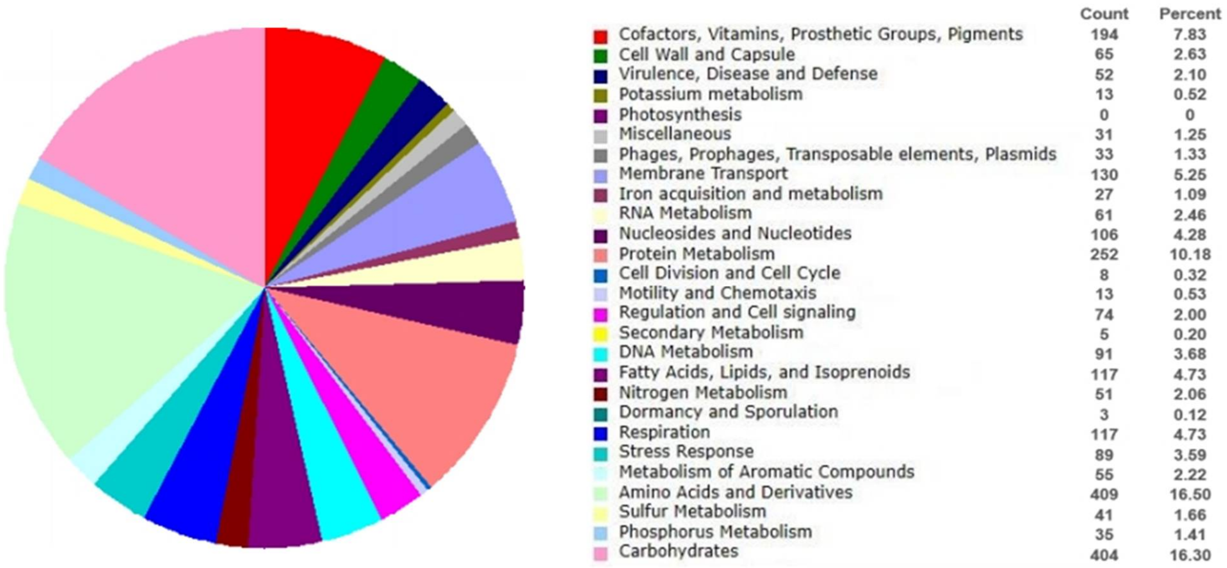

	Count	Percent
■ Cofactors, Vitamins, Prosthetic Groups, Pigments	194	7.83
■ Cell Wall and Capsule	65	2.63
■ Virulence, Disease and Defense	52	2.10
■ Potassium metabolism	13	0.52
■ Photosynthesis	0	0
■ Miscellaneous	31	1.25
■ Phages, Prophages, Transposable elements, Plasmids	33	1.33
■ Membrane Transport	130	5.25
■ Iron acquisition and metabolism	27	1.09
■ RNA Metabolism	61	2.46
■ Nucleosides and Nucleotides	106	4.28
■ Protein Metabolism	252	10.18
■ Cell Division and Cell Cycle	8	0.32
■ Motility and Chemotaxis	13	0.53
■ Regulation and Cell signaling	74	2.00
■ Secondary Metabolism	5	0.20
■ DNA Metabolism	91	3.68
■ Fatty Acids, Lipids, and Isoprenoids	117	4.73
■ Nitrogen Metabolism	51	2.06
■ Dormancy and Sporulation	3	0.12
■ Respiration	117	4.73
■ Stress Response	89	3.59
■ Metabolism of Aromatic Compounds	55	2.22
■ Amino Acids and Derivatives	409	16.50
■ Sulfur Metabolism	41	1.66
■ Phosphorus Metabolism	35	1.41
■ Carbohydrates	404	16.30

Figure S1. Distribution and count of the subsystem categories of *Jejubacter calystegiae* KSNA2^{T} based on RAST annotation.

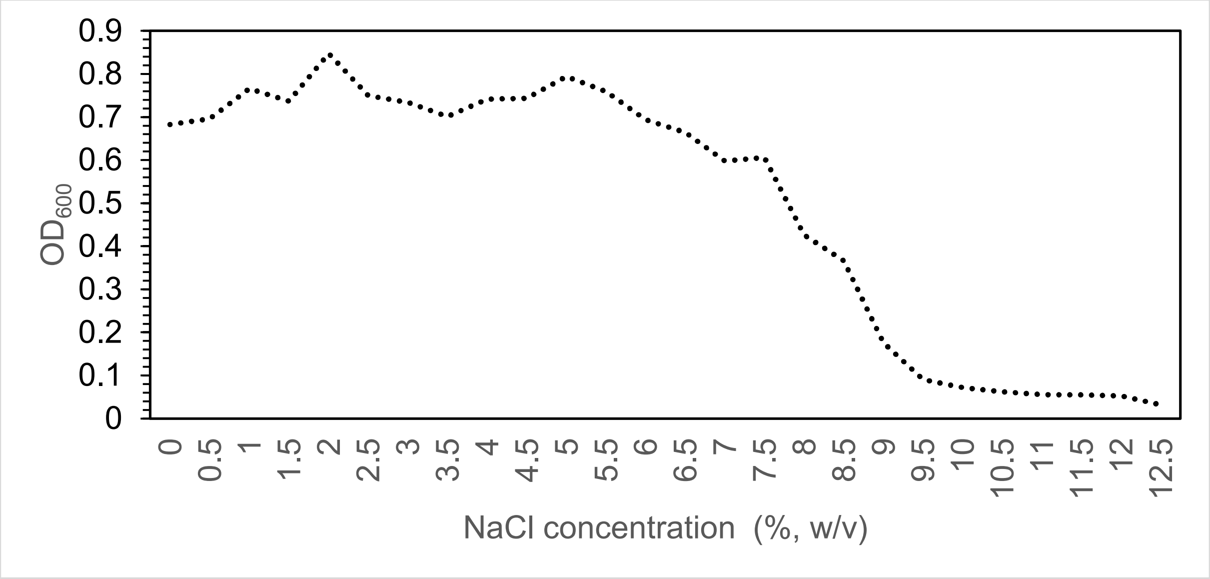

Figure S2. Growth of KSNA2^T in 0 to 12.5% (w/v) of NaCl.

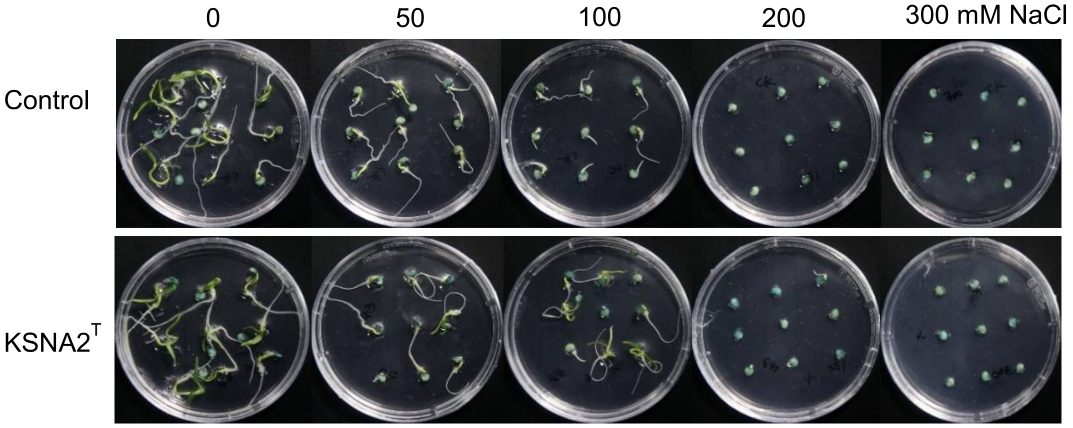

Figure S3. Effects of treatment with strain KSNA2^{T} on pepper seeds grown in different salt concentrations (0, 50, 100, and 300 mM NaCl).

Table S1. Stress responses genes annotated by RAST SEED server.

Stress response	Subsystem	Count
Osmotic stress (21)	Osmoregulation	4
	Osmoprotectant ABC transporter YehZYXW of *Enterobacteriales*	4
	Synthesis of osmoregulated periplasmic glucans	4
	Choline uptake, betaine uptake, and betaine biosynthesis	9
Oxidative stress (30)	Oxidative stress	10
	Glutathione biosynthesis and gamma-glutamyl cycle	4
	Non-redox reactions	8
	Redox cycles	4
	Glutaredoxins	2
	Glutathionyl spermidine and trypanothione	2
Detoxification (16)	Nucleoside triphosphate pyrophosphohydrolase MaszG	1
	Nudix proteins	6
	Housecleaning nucleoside triphosphate pyrophosphatases	1
	Uptake of selenate and selenite	2
	Tellurite resistance and chromosomal determinants	3
	Glutathione-dependent pathway of formaldehyde detoxification	2
General stress response (24)	Universal stress protein family	5
	Phage shock protein (psp) operon	5
	Dimethylarginine metabolism	1
	Sugar-phosphate stress regulation	1
	Hfl operon	4
	Commensurate regulon activation	3
	Carbon starvation	5
Periplasmic stress response (7)	Periplasmic Stress Response	7

Table S2. Predicted secondary metabolite loci in *J. calystegiae* KSNA2^T.

Region	Type	From	To	Most similar known cluster	Similarity	MIBiG accession	Gene cluster from the organisms
Region 1	Bacteriocin	1163967	1174590				
Region 2	Acyl_amino_acids	2378582	2439403				
Region 3	Ectoine,ladderane, butyrolactone	2576144	2624004	Kosinostatin (NRP + Polyketide)	0.03	BGC0001073	*Micromonospora sp.* TP-A0468
Region 4	NRPS	2804510	2866079	Turnerbactin (NRP)	0.3	BGC0000451	*Teredinibacter turnerae* T7901
Region 5	Thiopeptide	3116323	3142588	O-antigen (Saccharide)	0.14	BGC0000781	*Pseudomonas aeruginosa*
Region 6	Arylpolyene	3296744	3340309	Aryl polyenes (Other)	0.77	BGC0002008	*Xenorhabdus doucetiae*
Region 7	Terpene	3730164	3751417				

Table S3. Predicted stress response proteins in *J. calystegiae* KSNA2^T.

Sequence ID	KEGG Orthology	Encoded protein description
izh:FEM41_00615 izh:FEM41_02925 izh:FEM41_04465 izh:FEM41_05340 izh:FEM41_09770	K03307	Solute:Na$^+$ symporter, SSS family, sglT; sodium/glucose cotransporter
izh:FEM41_02330	K14445	Solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2/3/5
izh:FEM41_16595 izh:FEM41_22915	K14347	Solute carrier family 10 (sodium/bile acid cotransporter), member 7
izh:FEM41_07150	K03453	Bile acid:Na$^+$ symporter, BASS family
izh:FEM41_09220	K03313	Na$^+$:H$^+$ antiporter, NhaA family
izh:FEM41_07360	K24163	Na$^+$/H$^+$ antiporter
izh:FEM41_15120	K11928	Sodium/proline symporter
izh:FEM41_03110 izh:FEM41_11255	K14392	Sodium/pantothenate symporter
izh:FEM41_05805	K03312	Glutamate:Na$^+$ symporter, ESS family
izh:FEM41_07140	K03324	Phosphate:Na$^+$ symporter
izh:FEM41_17620	K03308	Neurotransmitter:Na$^+$ symporter, NSS family
izh:FEM41_05555	K02111	F-type H$^+$/Na$^+$-transporting ATPase subunit alpha
izh:FEM41_05565	K02112	F-type H+/Na+-transporting ATPase subunit beta
izh:FEM41_10350	K00346	Na$^+$-transporting NADH:ubiquinone oxidoreductase subunit A
izh:FEM41_10355	K00347	Na$^+$-transporting NADH:ubiquinone oxidoreductase subunit B
izh:FEM41_10360	K00348	Na$^+$-transporting NADH:ubiquinone oxidoreductase subunit C
izh:FEM41_10365	K00349	Na$^+$-transporting NADH:ubiquinone oxidoreductase subunit D
izh:FEM41_10370	K00350	Na$^+$-transporting NADH:ubiquinone oxidoreductase subunit E
izh:FEM41_10375	K00351	Na$^+$-transporting NADH:ubiquinone oxidoreductase subunit F
izh:FEM41_16580	K03617	Na$^+$-translocating ferredoxin:NAD$^+$ oxidoreductase subunit A
izh:FEM41_16575	K03616	Na$^+$-translocating ferredoxin:NAD$^+$ oxidoreductase subunit B
izh:FEM41_16570	K03615	Na$^+$-translocating ferredoxin:NAD$^+$ oxidoreductase subunit C
izh:FEM41_16565	K03614	Na$^+$-translocating ferredoxin:NAD$^+$ oxidoreductase subunit D
izh:FEM41_16555	K03613	Na$^+$-translocating ferredoxin:NAD$^+$ oxidoreductase subunit E
izh:FEM41_16560	K03612	Na$^+$-translocating ferredoxin:NAD$^+$ oxidoreductase subunit G
izh:FEM41_19430	K03315	Na$^+$:H$^+$ antiporter, NhaC family
izh:FEM41_19550	K03314	Na$^+$:H$^+$ antiporter, NhaB family
izh:FEM41_10380	K05952	nqrM; (Na$^+$)-NQR maturation NqrM
izh:FEM41_22260	K03319	Divalent anion:Na$^+$ symporter, DASS family
izh:FEM41_21195	K07114	Ca-activated chloride channel homolog

izh:FEM41_21190		
izh:FEM41_02835	K07301	Calcium/sodium antiporter
izh:FEM41_19275	K07300	$Ca2^{+}$:H^{+} antiporter
izh:FEM41_09935	K03281	Chloride channel protein, CIC family
izh:FEM41_05490	K03549	KUP system potassium uptake protein
izh:FEM41_11200	K05802	Potassium-dependent mechanosensitive channel
izh:FEM41_19525	K11105	Potassium/hydrogen antiporter
izh:FEM41_23555 izh:FEM41_06880	K03498	Trk system potassium uptake protein
izh:FEM41_03215	K03499	Trk system potassium uptake protein
izh:FEM41_13335	K01545	Potassium-transporting ATPase KdpF subunit
izh:FEM41_13330	K01546	Potassium-transporting ATPase potassium-binding subunit
izh:FEM41_13325	K01547	Potassium-transporting ATPase ATP-binding subunit
izh:FEM41_13320	K01548	Potassium-transporting ATPase KdpC subunit
izh:FEM41_09300	K11745	Glutathione-regulated potassium-efflux system ancillary protein KefC
izh:FEM41_09295	K11746	Glutathione-regulated potassium-efflux system ancillary protein KefF
izh:FEM41_03455	K11747	Glutathione-regulated potassium-efflux system protein KefB
izh:FEM41_03460	K11748	Glutathione-regulated potassium-efflux system ancillary protein KefG
izh:FEM41_21815 izh:FEM41_16950	K05847	Osmoprotectant transport system ATP-binding protein
izh:FEM41_21810 izh:FEM41_21820 izh:FEM41_16955 izh:FEM41_16965	K05846	Osmoprotectant transport system permease protein
izh:FEM41_21825 izh:FEM41_16960	K05845	Osmoprotectant transport system substrate-binding protein