

Supplementary materials for the article:

Gao Y. et al. A Salt-tolerant *Streptomyces paradoxus* D2-8 from Rhizosphere Soil of *Phragmites communis* Augments Soybean Tolerance to Soda Saline-alkali Stress
Pol J Microbiol. 2022, Vol. 71, No 1, 43–53

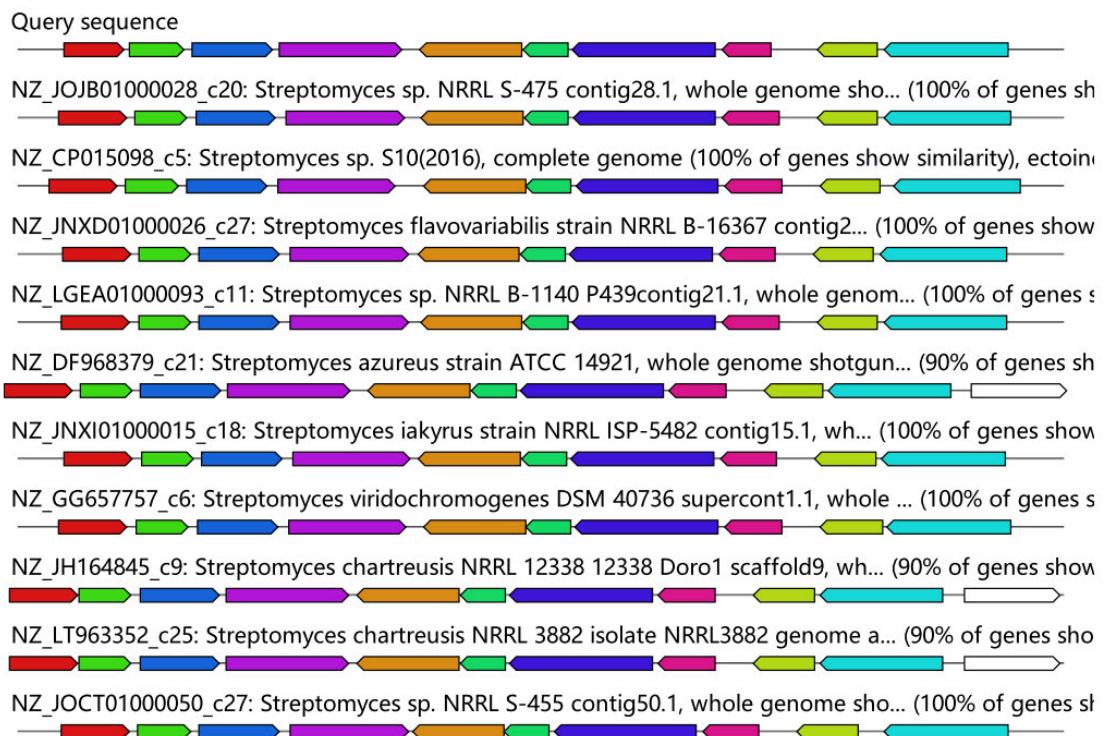


Fig. S1. BLAST analysis of the ectoine biosynthetic gene cluster in the D2-8 genome.

Table SI
The antagonistic activity of isolated actinomycetes against fungi.

| Actinomyces Inhibition radius (mm) | <i>Phytophthora sojae</i> | <i>Fusarium avenaceum</i> | <i>Fusarium solani</i> | <i>Gibberella zeae</i> |
|--|-------------------------------|-------------------------------|----------------------------|----------------------------|
| D2-8 | 28 ± 0.77 | 13.68 ± 2.7 | 11.9 ± 1.19 | 6.16 ± 3.49 |
| D2-1 | 9.53 ± 0.68 | N | N | N |
| D2-2 | 6.10 ± 2.35 | N | N | N |
| D2-3 | 8.55 ± 1.73 | N | N | N |
| D2-4 | - | N | N | N |
| D2-5 | 11.74 ± 1.43 | N | N | N |
| D2-6 | - | N | N | N |
| D2-7 | - | N | N | N |
| D2-9 | 16.33 ± 0.54 | N | N | N |
| D2-10 | - | N | N | N |
| D2-11 | 5.38 ± 1.45 | N | N | N |
| D2-12 | - | N | N | N |
| D2-13 | - | N | N | N |

N – not measured

- – no inhibition

Table SII
Growth features of strain D2-8 on different media.

| Medium | Growth | Substrate mycelium | Aerial mycelium |
|-----------------|----------|-------------------------|-----------------|
| ISP1 | moderate | pale yellow | grayish white |
| ISP2 | poor | brown | grayish white |
| ISP3 | good | red/violet | grayish white |
| ISP4 | moderate | red/violet | white |
| ISP5 | moderate | pale yellow | pale yellow |
| ISP6 | poor | grayish brown | grayish white |
| ISP7 | moderate | brilliant orange yellow | brown/violet |
| Bennett | moderate | brilliant orange yellow | |
| Glucose-nitrate | moderate | brilliant orange yellow | |
| Sucrose-nitrate | poor | brilliant orange yellow | |
| Czapek's agar | good | white | grayish white |

Table SIII
Characteristics of sequencing of the D2-8 genome.

| Property | Value |
|----------------------------------|--------------------|
| Reads num | 11,864,122 |
| Total bases (bp) | 2,883,887,826 |
| Q30 (%) | 80.42 |
| Total genome sequence length | 8,732,707 |
| Contig number | 72 |
| Scalfold number | 62 |
| N50 (bp) in contig | 280,139 |
| N50 (bp) in scalfold | 328,139 |
| ORF number | 8,019 |
| ORF density | 0.918 genes per kb |
| ORF / Genome (coding percentage) | 85.82 % |
| ORF average length | 934.55 |
| Protein annotation in NR | 7,703 |
| Protein annotation in Swiss-Prot | 4,818 |
| 5s rRNA | 5 |
| 16s rRNA | 2 |
| 23 s rRNA | 2 |
| tRNA | 67 |
| other ncRNA | 117 |