# Supplementary Materials

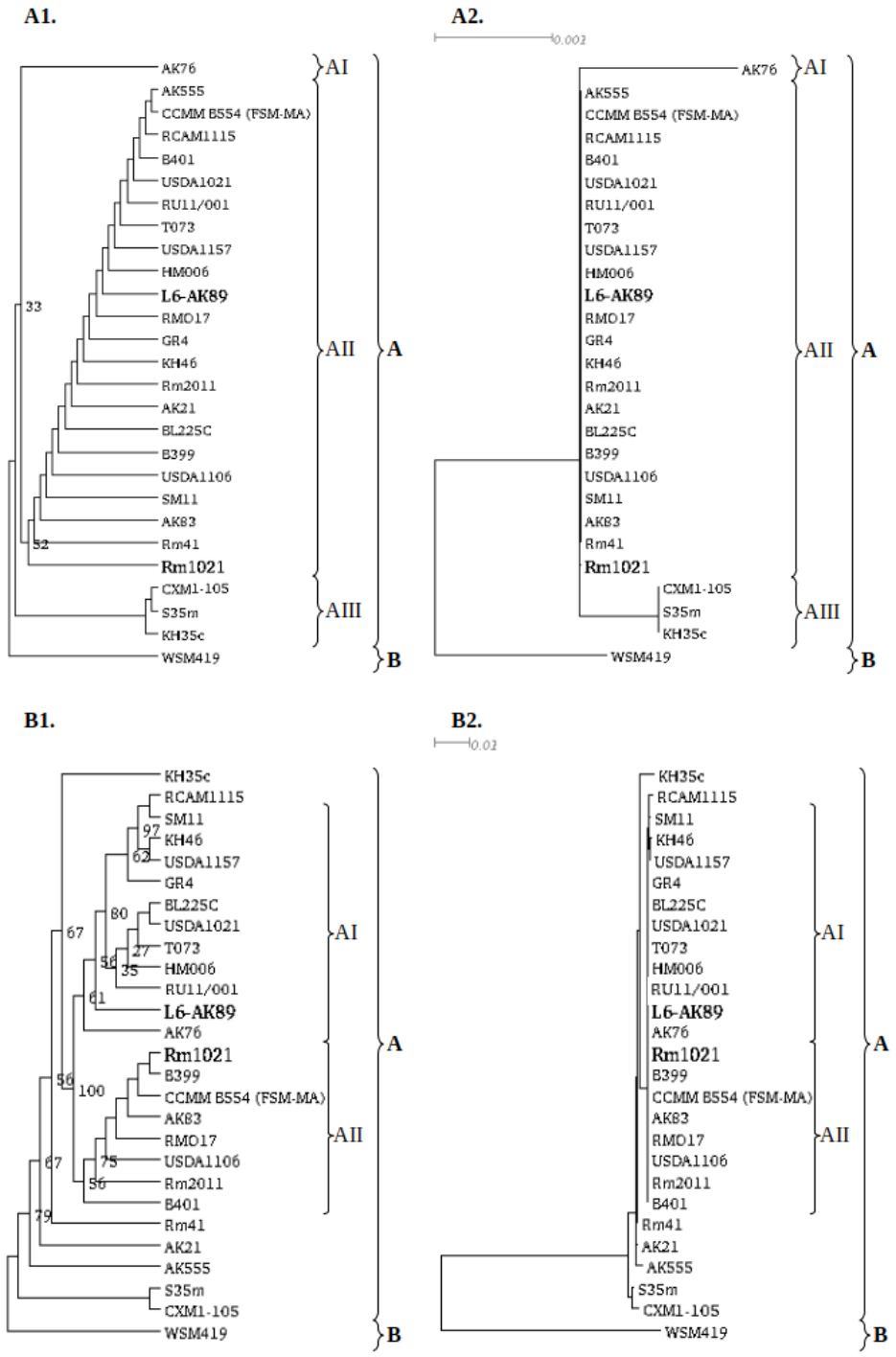


**Figure S1.** Phylogenetic analysis of (A) consensus 16S rRNA gene nucleotide sequences and (B) concatenated *recA–atpD–glnII–gyrB–dnaJ* gene nucleotide sequences in *Ensifer* spp. Trees A1 and B1 are drawn as rectangular cladograms and A2 and B2 as rectangular phylograms. Nucleotide substitution models selected for analysis were HKY + F for consensus 16S rRNA gene sequences and TIM2 + F + I for concatenated *recA–atpD–glnII–gyrB–dnaJ* sequences. Scale bars = 0.001 for gene consensus sequences and 0.01 for concatenated nucleotide sequence substitutions per site. Rooted trees were created by using maximum likelihood algorithm. Statistical support for internal nodes was determined by 1000 bootstrap replicates.

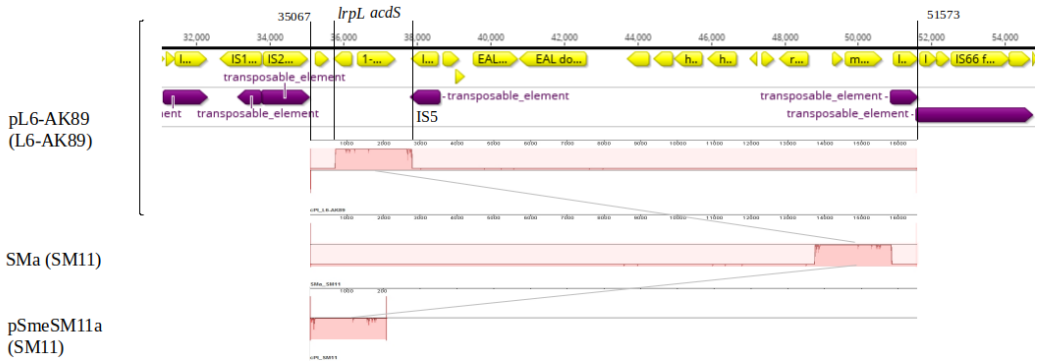


Figure **S2**. Localization of *acdS*–*lrpL* module on graphic linear part of cryptic plasmid of *E. meliloti* L6-AK89.

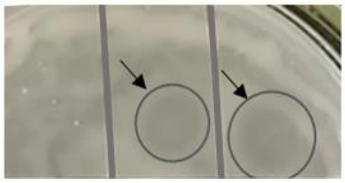

**Figure S3.** Lysis of L6-AK89 strain by bacteriophage no. 2. Arrows indicate lysis zones.

**Table S1.** IS elements and genes in head-to-tail orientation in genomes of strains L6-AK89 and Rm1021.[1]

| Strain | Replicon | IS element | Gene [4] | | Gene Product | Change in activity, microarray M-value | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | L6-AK89 | | Rm1021 | |
| | | | L6-AK89 | Rm1021 | | 1 h | 12 h | 1 h | 12 h |
| L6-AK89 | SMc | ISRm17[1] | LJD24_RS13335 | SMc02431 | MBL fold metallo-hydrolase | -0.32 | -0.03 | -0.13 | 0.09 |
| | | ISRel26 [3] | LJD24_RS08065 | SMc01195 | IS30 family transposase | -0.22 | 0.12 | -0.27 | -0.11 |
| | | ISRm2011-2 | LJD24_RS05500 | SMc02661 | peptidase domain-containing ABC transporter | 0.27 | 0.33 | 0.27 | -0.31 |
| | | ISRm2011-2 | LJD24_RS06570 | SMc01356 | hypothetical protein | 0.13 | 0.13 | -0.01 | 0.01 |
| | | ISRm2011-2 | LJD24_RS14505 | SMc03993 | MotA/TolQ/ExbB proton channel family protein | -0.09 | -0.22 | -0.01 | -0.00 |
| | pSymB | ISRm5 | NA [5] | SMb21403 | hypothetical protein | 0.15 | 0.02 | 0.61 | 0.55 |
| | | ISRm2011-2 | LJD24_RS31440 | SMb20691 | PepSYdomain-containingprotein | -0.14 | -0.37 | 0.37 | 0.47 |
| | pL6-AK89 | ISL3-NC1740 | LJD24_RS17720 | SMa0359 | helix-turn-helix domain-containing protein | -0.44 | -0.53 | 0.26 | 0.55 |
| Rm1021 | SMc | ISRm1 | LJD24_RS16750 [2] | **SMc03896**/SMc03899 | transcriptional regulator/hypothetical protein | 0.31 / 0.35 | **1.33 * / 0.38** | -0.79 / -0.64 | -0.59/ -0.64 |
| | | ISRm5 | LJD24_RS07810 | SMc01241 | hypothetical protein | -0.20 | 0.55 | -0.95 | 0.06 |
| | | ISRm5 | NA | SMc04866 | hypothetical protein | 0.62 | 0.61 | -0.56 | -0.43 |
| | | ISRm20 | LJD24_RS01350 | SMc00344 | GIY-YIG nuclease family protein; hypothetical protein | 0.03 | -0.31 | -0.16 | -0.09 |
| | | ISRm21 | LJD24_RS16735 | SMc03893 | amino-acid transport system permease ABC transporter protein | -0.49 | -0.52 | -0.55 | -0.01 |
| | | ISRm22 | LJD24_RS00705 | SMc04117 | pilus assembly protein; hypothetical protein | -0.24 | -0.06 | 0.01 | -0.24 |
| | | ISRm22 | NA [5] | SMc02718 | hypothetical protein | -0.14 | -0.22 | 0.51 | -0.28 |
| | | ISRm11 OR ISRm2011-2 | LJD24_RS16125 | SMc03748 | hypothetical protein | 0.37 | 0.34 | -0.00 | -0.01 |
| | pSymA | ISRm23 | NA [5] | SMa0775 | hypothetical protein | -0.21 | -0.27 | 0.41 | 0.83 |
| | | ISRm29 | LJD24_RS19845 | SMa2169 | IS3 family transposase; hp | 0.44 | 0.34 | -0.04 | 0.21 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | ISRm2011-2/ISRm11 | LJD24_RS24730 | SMa2377 | multidrug effflux MFS transporter; permease, MFS | -0.14 | -0.24 | 0.82 | **1.05 *** |
| | ISRm5 | LJD24_RS21420 | SMa5007 | possible transcriptional regulator | n.d. | n.d. | n.d. | n.d. |
| pSymB | ISRm1 | LJD24_RS28380 | SMb21232 | polysaccharide biosynthesis protein; nucleotide sugar epimerase dehydratase | 0.08 | 0.02 | 0.68 | 0.31 |
| | ISRm17 [3] | LJD24_RS31310 | SMb20664 | FadR family transcriptional regulator; GntR family transcriptional regulator | 0.35 | 0.27 | 0.01 | -0.32 |
| | ISRm19 | LJD24_RS32155 | SMb21706 | LacI family transcriptional regulator | 0.74 | 0.51 | 0.57 | 0.27 |

[1] One exception to this table is case iii of IS location (see text). [2] Sequence disrupted by IS elements, corresponding to *expR* gene. [3] Fragment of IS element. [4] Genes annotated in L6-AK89 and Rm1021 strains. [5] No annotation; lines corresponding to genes with changed activity are colored. * Differences are significant ($P \leqslant 0.05$, $A \geqslant 7$, M-value $\geqslant 1$ or $\leqslant -1$; see Materials and Methods).

**Table S2.** Presence and localization of genes involved in response to stress in genomes of strains L6-AK89 and Rm1021.

| Replicon | Gene | Gene | | Presence of gene in genome | | Type of stress | Change in activity, microarray M-value | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | L6-AK89 | | Rm1021 | |
| | | L6-AK89 | Rm1021 | L6-AK89 | Rm1021 | | 1 h | 12 h | 1 h | 12 h |
| Chromosome | *aqpZ1* | LJD24_RS11135 | SMc01870 | + | + | ss | 0.05 | -0.02 | -0.91 | -0.82 |
| | *betA* | LJD24_RS04730 | SMc00093 | + | + | pss | 0.45 | 0.19 | 0.19 | -0.03 |
| | *betB* | LJD24_RS04735 | SMc00094 | + | + | pss | -0.37 | 0.06 | -0.18 | 0.12 |
| | *betC* | LJD24_RS04740 | SMc00127 | + | + | pss | -0.36 | -0.67 | -0.93 | -0.73 |
| | *betI* | LJD24_RS04745 | SMc00095 | + | + | pss | -0.08 | 0.08 | -0.47 | -0.61 |
| | *trkA* | LJD24_RS07355 | SMc01046 | + | + | ss | -0.22 | -0.05 | 0.63 | 0.25 |
| | *trkH* | LJD24_RS08255 | SMc00937 | + | + | ss | 1.87 | -0.31 | 0.16 | -0.03 |
| | *ropA1* | LJD24_RS05280 | SMc02396 | + | + | ph | -0.46 | -0.27 | -1.28* | -0.00 |
| | *ropA2* | LJD24_RS05290 | SMc02400 | + | + | ph | -0.92 | -0.66 | -1.94* | -0.70 |
| | *ropB1* | LJD24_RS05875 | SMc00604 | + | + | ph | -0.23 | -0.14 | 0.41 | 0.77 |
| | *ropB2* | LJD24_RS08615 | SMc00257 | + | + | ph | 0.10 | 0.02 | 0.17 | 0.07 |
| | *actR* | LJD24_RS00325 | SMc02584 | + | + | as | -0.11 | 0.03 | -0.47 | -0.30 |
| | *actS* | LJD24_RS00330 | SMc02585 | + | + | as | 0.36 | 0.18 | -0.44 | -0.64 |
| | *actJ* | LJD24_RS11990 | SMc02366 | + | + | as | 0.27 | -0.00 | -0.00 | -0.00 |
| | *actK* | LJD24_RS11995 | SMc02367 | + | + | as | 0.23 | 0.31 | -0.20 | 0.06 |
| | *chvI* | LJD24_RS00220 | SMc02560 | + | + | as | 0.60 | 0.45 | 0.15 | -0.40 |
| | *exoS* | LJD24_RS00215 | SMc04446 | + | + | as | 0.43 | 0.46 | -0.18 | -0.53 |
| pSymA | *aqpZ2* | - | SMa0627 | - | + | ss | n.d. | n.d. | -1.07 | -0.85 |
| | *betB2* | LJD24_RS19505 | SMa1731 | + | + | pss | 0.16 | 0.14 | 0.38 | 0.59 |
| | *betI2* | LJD24_RS22905 | SMa1726 | + | + | pss | -0.11 | -0.20 | 0.49 | 0.29 |
| | *otsA* | LJD24_RS19545 | SMa0233 | + | + | pss | -0.19 | 0.26 | -0.01 | -0.01 |
| | *trkH2* | LJD24_RS22805 | SMa1691 | + | + | ss | -0.74 | -0.93 | 1.02 | -0.11 |
| | *kdpA* | LJD24_RS24625 | SMa2333 | + | + | ss | 0.15 | 0.58 | 1.05 | 1.12 |
| | *kdpB* | LJD24_RS24620 | SMa2331 | + | + | ss | -0.15 | 0.63 | 0.54 | 0.81 |
| | *kdpC* | LJD24_RS24615 | SMa2329 | + | + | ss | 0.12 | 0.01 | -0.00 | -0.00 |
| | *kdpD* | LJD24_RS24610 | SMa2327 | + | + | ss | -0.68 | -0.87 | -1.71* | -0.37 |
| | *kdpE* | LJD24_RS24605 | SMa2325 | + | + | ss | -0.09 | 0.40 | 0.32 | -0.02 |
| | *kdpF* | LJD24_RS24630 | SM_RS30995 | + | + | ss | n.d. | n.d. | n.d. | n.d. |
| pSymB | *treS* | LJD24_RS25300 | SMb20099 | + | + | pss | -0.03 | -0.06 | 0.38 | 0.22 |
| | *treZ* | LJD24_RS30855 | SMb21447 | + | + | pss | 0.35 | 0.17 | -0.09 | -0.39 |
| | *treY* | LJD24_RS31840 | SMb20574 | + | + | pss | 0.10 | 0.06 | 0.87 | 1.09 |
| pL6-AK89 | *acdS* | LJD24_RS17290 | - | + | - | as | n.d. | n.d. | n.d. | n.d. |

ss, salt shock; pss, prolonged exposure to salt stress; ph, lysis/resistance to lytic bacteriophages; ac, acid stress. "-" Gene is absent. * Differences are significant ($P \leqslant 0.05$, $A \geqslant 7$, M-value $\geqslant 1$ or $\leqslant -1$; see Materials and Methods).

**Table S3.** Phagotyping of *E. meliloti* strains.

| ***E. meliloti* strains** | **Bacteriophage (no.)** | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | **1** | **2** | **3** | **4** | **5** | **6** | **7** | **8** | **9** | **10** |
| L6-AK89 | - | + | + | + | + | - | - | - | - | - |
| Rm1021 | + | - | - | + | - | - | - | - | - | - |
| Md3/4 | + | - | + | - | + | + | + | - | - | + |

"+" Sterile spot on bacterial cover reflecting lysis of bacterial culture. "-" Absence of sterile spot. Bacteriophages 1-10 were isolated from soils of geographically different regions (Dagestan and NW Russia) and native isolate *E. meliloti* Md3/4 was from lab collection. L6-AK89 and Rm1021 were sensitive to 4 and 2 bacteriophages, respectively. Only bacteriophage 1 was specific to Rm1021, while 2, 3, and 5 were specific to L6-AK89, and the last two also lysed Md3/4 strain. Bacteriophage 2, isolated from soils of SW Dagestan and belonging to *Myoviridae* family, demonstrated specific lytic activity toward strain L6-AK89.