

Are cryptic plasmids of *Sinorhizobium meliloti* attractive within phage infection?

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The genome of root nodule bacteria *Sinorhizobium meliloti* is enriched by non-symbiotic cryptic plasmids. The attractiveness of such plasmids to phages was evaluated in this work for the first time. The 20 cryptic plasmids with sizes varied from 17.2 to 453.8 kb were identified in whole sequenced genomes of the 5 strains from the origin of plant diversity at the NW of the Big Caucasus Ridge (NCG) and of the 7 strains from the center of the introgressive hybridization of alfalfa at the Kazakhstan NW, subjected to salinity (PAG). Phage sequences (PS) were detected in the 7 out of the 8 analyzed plasmids of NCG strains, and in the 7 out of the 12 plasmids in PAG strains according to the PHASTER (<https://phaster.ca/>). The number of PS was varied from 1 to 11 per plasmid replicon, and their sizes ranged from 5.1 to 33 kb. PS related to *Siphoviridae* family were significantly prevailed (frequency 0.64; $P < 0.05$), then those which were homologous to *Podoviridae* were extremely rare in plasmids from NCG strains. Prophages related to both above families were found with the same frequency (0.37) in cryptic plasmids of PAG strains. PS related to *Myoviridae* were found with similarly equal frequencies (0.24 in average) on plasmids of NCG and PAG strains. Remarkable, but PS from all three families were detected on the same cryptic plasmid with a frequency of 0.40. Significant differences was revealed between the occurrence of intact, questionable and incomplete PS on plasmids of NCG and PAG strains ($P < 0.05$). Thus, incomplete prophages prevailed (0.67) on the plasmids of PAG strains and their active participation in intragenomic rearrangements in rhizobia adapted to extreme salinization environment is proposed. A significant portion of intact prophages detected on cryptic plasmids of *S. meliloti* strains from NCG is indicated at a high infection activity of phages from *Siphoviridae* family in this gene center of cultivated plants. The work was supported by the RSF 20-16-00105.

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