Abundant of CRISPR/Cas elements in genomes of nitrogen-fixing bacteria from the genus Sinorhizobium

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A putative CRISPR sequences and *cas* genes were searched in full genome sequenced reference strains among which were *S. meliloti* Rm1021, *S. medicae* WSM419, *S. fredii* NGR234 and *S. americanum* CCGM7. Genomes of all tested strains have a multireplicon organization and their sizes varied from 6.68 to 6.9 Mb. The 7 CRISPR sequences on the chromosome and the 6 CRISPR sequences on SMb were detected in *S. meliloti*, while in *S. medicae* the 2 and 1 corresponding sequences were identified, as well per the 4 *cas* genes were revealed in each strain by CRISPRCasFinder. In *S. fredii* and *S. americanum* the 2 and the 6 CRISPR sequences, as well 4 and 5 *cas* genes, were identified, respectively, all of which were located on corresponding chromosomes. Only one spacer was found in 84% tested CRISPR sequences of *Sinorhizobium* spp., while few others had 2 or 4 spacers. It was found that all identified *cas* genes encoded Cas proteins of the type I CRISPR/Cas system. The 4 non-homologous cas genes were detected in studied *Sinorhizobium* spp. strains. The homology between corresponding *cas* genes detected in strains related to different species was 80.5–90.3%. Since CRISPR sequences and *cas* genes were localized at a distance exceeded to 80 kb in all tested strains, therefore it was concluded that they are not clustered in *Sinorhizobium* spp. No prophages sequences next to regions of CRISPR sequences and cas genes were found (according to web server PHASTER). Thus, putative CRISPR sequences and cas genes detected in *Sinorhizobium* spp. are abundant on chromosome and on megaplasmids as well. All studied CRISPR sequences were short and not clustered with *cas* genes and presumably encoding proteins of the type I CRISPR/Cas system. The work was supported by the RSF 20-16-00105.

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