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Agrobacterium salinitolerans sp. nov., a saline-alkaline-tolerant bacterium isolated from root nodule of Sesbania cannabina

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Two Gram-staining-negative, aerobic bacteria (YIC 5082^T and YIC4104) isolated from root nodules of *Sesbania cannabina* grown in a high-salt and alkaline environment were identified as a group in the genus Agrobacterium (https://doi.org/10.1601/nm.1310) because they shared 100 and 99.7% sequence similarities of 16S rRNA and recA+atpD genes, respectively. These two strains showed 99.2/100% and 93.9/95.4% 16S rRNA and recA+atpD gene sequence similarities to Agrobacterium radiobacter (https://doi.org/10.1601/nm.1317) LMG140^T and Agrobacterium (https://doi.org/10.1601/nm.1310). pusense NRCPB10^T, respectively. The average nucleotide identities (ANI) of genome sequences were 89.95% or lower between YIC 5082^T and the species of the genus Agrobacterium (https://doi.org/10.1601/nm.1310) examined. Moreover, these two test strains formed a unique nifH lineage deeply separated from other rhizobia. Although the nodC gene was not detected in YIC 5082^T and YIC4104, they could form effective root nodules on S. cannabina plants. The main cellular fatty acids in YIC 5082^T were summed feature 8 ($C_{18:1}\omega 7c/C_{18:1}\omega 6c$), $C_{19:0}$ cyclo $\omega 8c$, summed feature 2 ($C_{12:0}$ aldehyde/unknown equivalent chain length 10.9525) and $C_{16:0}$. The DNA G+C content of YIC 5082^T was 59.3 mol%. The failure to utilize d-sorbitol as a carbon source distinguished YIC 5082^T from the type strains of related species. YIC 5082^T could grow in presence of 5.0% (w/v) NaCl and at a pH of up to 10.0. Based on results regarding the genetic and phenotypic properties of YIC 5082^T and YIC4104 the name Agrobacterium salinitolerans sp. nov. is proposed and YIC 5082^T (=HAMBI 3646^T =LMG 29287^T) is designed as the type strain.

The accession numbers of the 16S rRNA, atpD, recA, glnII and nifH genes for the type strain YIC 5082^T and YIC4104 (https://www.ncbi.nlm.nih.gov/nuccore?term=YIC4104) in GenBank are KP142169 (https://www.ncbi.nlm.nih.gov/nuccore?term=KR162868), KP142172 (https://www.ncbi.nlm.nih.gov/nuccore?term=KR154036), KP142170 (https://www.ncbi.nlm.nih.gov/nuccore?term=KP142170) and KR154036 (https://www.ncbi.nlm.nih.gov/nuccore?term=KP142170) and KR154036 (https://www.ncbi.nlm.nih.gov/nuccore?term=KP142170) and KR154006 (https://www.ncbi.nlm.nih.gov/nuccore?term=KR154006), KP202170 (https://www.ncbi.nlm.nih.gov/nuccore?term=KP202170) and KR154021 (https://www.ncbi.nlm.nih.gov/nuccore?term=KR154021) and KR154052 (https://www.ncbi.nlm.nih.gov/nuccore?term=KR154052) and KR154050 (https://www.ncbi.nlm.nih.gov/nuccore?term=KR154050), respectively. The genomes have been deposited in GenBank under the accession numbers of MRDH00000000 (https://www.ncbi.nlm.nih.gov/nuccore?term=MRDH00000000) for A. Salinitolerans YIC 5082^T, MRDG00000000 (https://www.ncbi.nlm.nih.gov/nuccore?term=MRDJ00000000) for A. pusense NRCPB10^T.

Two supplementary figures and one supplementary table are available with the online Supplementary Material.

Keyword(s): Agrobacterium salinitolerans sp. nov. (/search?value1=%27Agrobacterium+salinitolerans+sp.+nov.%27&option1=pub_keyword), Sesbania cannabina (/search?value1=%27Sesbania+cannabina%27&option1=pub_keyword), symbiosis (/search?value1=%27symbiosis%27&option1=pub_keyword), Polyphasic taxonomy (/search?value1=%27Polyphasic+taxonomy%27&option1=pub_keyword)

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