

## ABSTRACT

Local soybean rhizobial germplasm of twenty isolates collected from different governorates in Egypt was constructed. The symbiotic effectiveness of all isolates was evaluated under greenhouse conditions compared to the reference strains. The greenhouse results showed a positive symbiotic interaction between all tested rhizobial isolates/strains and soybean cultivar, *Giza 22*. Based on greenhouse results, four promising local rhizobial isolates (NGB-SR 3, 4, 7 and 14) were evaluated under field conditions as inoculants. During flowering stage, the field experiment results showed a prolific nodulation with all tested rhizobial isolates/strains. At harvest, rhizobial treatments showed significant increases in seed yield, seed N-yield and seed crude protein with a range of 10-38%, 12-50% and 4-9%, respectively compared to the un-inoculated control. The obtained results showed that, the symbiotic performance of the tested local isolates was higher than the reference strains as well as there was no significant differences in seed and seed N yields of soybean between tested rhizobial inoculants and full N-fertilizer treatments. Phenotypic characterization of local rhizobia germplasm under stress conditions (salinity, pH and high temperatures) was investigated *in vitro*. The tested isolates showed a high tolerance variation under different NaCl concentrations ranged from 0.1 to 6%. All tested isolates were able to grow in a pH range from 5 to 11, while seven local isolates were highly acid tolerant and survived at pH 4. Most of tested isolates were tolerant to 40 °C; however four local isolates were survived at 42°C. The genetic community of constructed germplasm was explored at higher levels using 16S rDNA comparative sequencing. 16S rDNA sequences of eight local representative isolates were identified, aligned and registered at National Center for Biotechnology Information (NCBI). On the basis of the phylogenies of 16S ribosomal gene, three soybean rhizobia genomic groups were identified: the *Bradyrhizobium* spp. complex (including *B. japonicum* and *B. yuanmingense* related genomic species) as well as *S. fredii* were the minor groups. While, *Rhizobium radiobacter* (syn. *Agrobacterium tumefaciens*) identified as a major group. Genotyping at the strain level using REP-PCR fingerprinting displayed a high level of genetic variation among local rhizobia related to *Rhizobium* and *Bradyrhizobium* genera in contrast with the genus *Sinorhizobium*.

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