

PP 3-36

GENETIC DIVERSITY OF *RHIZOBIUM* SP. IN RUSSIAN FEDERATION AND UKRAINE

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Genus *Rhizobium* forms a symbiotic association with leguminous plants and carry out biological nitrogen fixation (BNF). The BNF is most efficient way to supply the large amount of nitrogen used by plants to produce high-yielding crops. Only certain combinations of host plants and nitrogen-fixing rhizobia form the efficient BNF. The investigation of bacterial diversity is important to reveal the most efficient root-nodulating *Rhizobium* sp.

The genetic diversity within 73 rhizobial strains isolated from root nodules of 6 legume plants growing in different regions of Russia and Ukraine, together with 12 type strains of *Rhizobium* sp., was investigated by using different methods: (i) 16S rRNA gene and ITS full sequence analyses; (ii) PCR-restriction fragment length polymorphism (RFLP) of the rRNA intergenic spacer (IGS); (iii) single adaptor amplified restriction fragment polymorphism saAFLP analysis and (iv) specific PCR and sequence analyze of *hin*-regions (Zotov et al., 2010). The results showed high genetic diversity among these strains. 16SrRNA gene and ITS full sequence analyses revealed that most of investigated isolates and strains belonged *R. leguminosarum*, and 8 were from another *Rhizobium* species. The one isolate belonged to unnamed *Rhizobium* species.

IGS PCR-RFLP and saAFLP results were in a good agreement and divided strains into 20 RFLP genotypes and 27 saAFLP genotypes, respectively, most of the strains were grouped according to their host-plants. These clustering agreed with 16S rRNA gene and ITS full sequence analyses datas, but allowed to reveal high genetic diversity among *R. leguminosarum* strains.

Hin-region analyze confirmed the obtained dates. The 85 strains were clustered into 8 groups in accordance with length and DNA sequences of the region. 75 *R. leguminosarum* strains were reliably divided into 5 genotypes with 25.5%-89.9%/96.2%-99.9% levels of similarity beetween/within these groups.