

## NEW APPROACHES FOR THE IDENTIFICATION AND DIAGNOSTICS OF THE PLANT-SYMBIOTIC AND PHYTOPATHOGENIC BACTERIA

Punina, N.V.<sup>1,2\*</sup>, Zotov V.S.<sup>2</sup>, Khapchaeva S.A.<sup>2</sup>

<sup>1</sup>Research Center for Medical Genetics RAMS, [hin-enkelte@yandex.ru](mailto:hin-enkelte@yandex.ru)

<sup>2</sup>A.N. Bach Institute of Biochemistry RAS, [adni83@yandex.ru](mailto:adni83@yandex.ru)

<sup>2</sup>A.N. Bach Institute of Biochemistry RAS, [hapchaeva.90@mail.ru](mailto:hapchaeva.90@mail.ru)

\* Correspondence author

**Abstract.** The investigation of the biodiversity and taxonomy structure of the pathogenic and symbiotic bacteria is very important task. In the first case, to prevent the crop damages and economic losses, in the second, to understand, maintain, and create beneficial host-symbiotic pairs to raise the effectiveness of symbiosis and crop capacity. In this work we investigated the large samples of pathogenic strains and isolates of *Xanthomonas* spp., *Ralstonia* spp., and symbiotic *Rhizobium* spp. and *Sinorhizobium* spp.. The classical phenotypic and genotypic (analysis of nucleotide sequences of the 16s rRNA, *gyrB*, *Xcc0006-0007*, saAFLP analysis) methods were used. All genotypic methods allowed determining of the genus and species belonging of the strains, but were failed at the inter-species level. Using saAFLP analysis we revealed the unique marker (*hin*-region), which was specific for every investigated genus, and also kept its uniqueness at the inter-species level. For every genus the DNA structure of *hin*-region was determined. The taxonomy revealed by *hin*-region was the same as existent for every genus though was more precise and accurate. This region had the promoters about 40 bp long in the down- and up-stream areas specific for both plant and bacteria. We supposed this region influence on the initiation, or effectiveness, plant-bacterial interaction getting involved with the specific signaling molecules of the host IR system. We designed PCR systems on the basis of *hin*-region conservative areas to provide the express-diagnostics of bacteria. All primers used in our work and also data are on the website [hin-project.com](http://hin-project.com).

**Key Words:** *hin*-regions, saAFLP, *Xanthomonas*, *Rhizobium*, *Sinorhizobium*, *Ralstonia*.