Endophytic bacteria isolated from garden pea (*Pisum sativum* L.)Vasileva E.N.¹, Afonin A.M.¹, Akhtemova G.A.¹, Zhukov V.A.¹, Tikhonovich I.A.^{1,2}¹All-Russia Research Institute for Agricultural Microbiology, Saint Petersburg, Russia; ²Saint Petersburg State University, Saint Petersburg, RussiaE-mail: evasilieva@arriam.ru

Key message. Endophytic bacteria were isolated from surface-sterilized aerial parts of pea. Taxonomic status of isolated strains was determined by sequencing of 16S rRNA gene. Moreover, genomes of growth-promoting endophytes were sequenced.

Keywords: endophytic bacteria, *Pisum sativum*, pea, symbiosis

Background. Endophytic bacteria – microorganisms living inside plants – may have a positive impact on host-plant growth and development, which can be used in the environment-friendly crop production. Due to the possibility of using this kind of microorganisms in agriculture, the interest in studying associations of endophytes and plants is constantly increasing.

Our main aim was to study the diversity of endophytic bacteria from garden pea (*Pisum sativum* L.).

Materials and methods. To conduct an experiment, three genotypes were selected: K-8274 which is highly responsive to inoculation with beneficial soil microorganisms (‘effective macrosymbiont’), K-3358 – low-responsive genotype (‘non-effective’), and commercial cultivar “Triumph”, the ‘effective’ descendant of K-8274. Endophytic bacteria were isolated from surface-sterilized leaves and stems of plants at the flowering stage using the set of different growth media. Taxonomic status of isolated strains was determined using sequencing of 16S rRNA gene.

Results. Eight strains identified as *Bacillus* sp., *Rahnella* sp., *Enterobacter* sp., *Serratia* sp., and *Acinetobacter* sp. have shown significant growth promoting effect on lettuce roots. Furthermore, the genomes of growth-promoting endophytic strains were sequenced. Surprisingly, the analysis revealed that the isolated endophytic cultures were not pure and contained hidden minor components. This data made us talk about the endophytic consortia, and not about single strains. Interestingly, every consortium contained *Rahnella* sp., which thus could play a role of «core», or consortium-forming, bacteria. New results require detailed study: it is planned to visualize the penetration of consortia into host-plant using fluorescent in situ hybridization (FISH) technique.

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