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Bacteria species diversity on winter grain crops of the field experimental station of RSAU-MTAA named after K.A. Timiryazev

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Motivation and Aim: According to the data of the Federal Customs Service, Russia annually supplies about 17 million tons of grain to countries where grain bacteria pathogens are subject to regulation. The use of species-specific PCR tests is the fastest and most reliable method to diagnose plant pathogens. Diagnostic PCR tests for many grain bacterioses have not been developed or validated. To create a correct algorithm for bioinformatic prediction of a species-specific PCR target, information on the bacterial microbiota species composition of grain crops is required. Both the target bacterial isolates and the accompanying microbiota are needed to validate the designed primers. The purpose of the study is detection and identification of bacteria in cereal crops.
Methods and Algorithms: The objects of the study were bacterial isolates from plants of winter wheat, triticale, and rye. The plants were collected in May 2020 on the field experimental station of the Russian State Agrarian University named after K.A. Timiryazev. Bacterial cultures were isolated on CRL medium [4]. Isolates were identified by NCBI alignment of sequences obtained by PCR with primers PSF/PSR [2], PsyF/PsyR, SyD1/SyD2 [1], 16SPSEfluF/16SPSER [3], and 8UA/519B [5]. PCR testing was carried out in accordance with the scheme (Fig. 1).

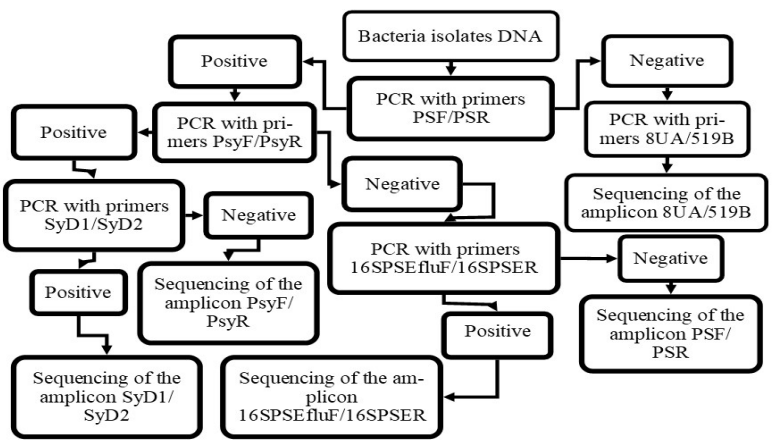

Fig. 1. The scheme for identification of bacterial isolates

Results: Bacteria were isolated from 55 different winter grain crop varieties, 47 of which are wheat, 2 ryes, and 6 triticale. The total number of identified isolates is 168. Among them: *Pseudomonas extremorientalis, P. trivialis, P. poae, P. graminis, P. synxantha, P. cichorii, P. chlororaphis, P. viridiflava, P. fluorescens, P. extremorientalis, P. frederiksbergensis, P. cannabina* pv. *alisalensis*, *P. savastanoi* pv. *savastanoi*, *P. amygdali* pv. *morsprunorum, P. syringae* pv. *lapsa, P. syr.* pv. *coronafaciens, P. syr*. pv. *aptata, P. syr*. pv. *atrofaciens, P. syr*. pv. *maculicola, P. syr*. pv. *cerasicola, Erwinia papaya, E. billingae, Frigoribacterium faeni, Clavibacter michiganensis, Kineococcus* sp., *Pantoea agglomerans, Curtobacterium flaccumfaciens, Arthrobacter chlorophenolicus, Streptomyces* sp., *Serratia plymuthica, Staphylococcus warneri, Sanguibacter inulinus, S. keddieii, Phycicocous* sp., *Cellulomonas* sp., *Oerskovia paurametabola, Microbacterium phyllosphaerae, M. foliorum, Frondihabitans* sp., *Sphingomonas* sp., *Micrococcus luteus*, *M. yunnanensis, Rothia kristinae, Bacillus pumilis, Rathayibacter festucae, Plantibacter* sp., *Actinobacterium* sp., *Rhodococcus cerastii, R. yunnanensis, R. fascians, Agreria* sp., *Lysinimonas* sp., *Subtercola pratensis* and *Pseudoclavibacter helvolus*.

Conclusion: The result of detection and identification of bacteria showed that the microbiota diversity of grain crops on the surveyed area is represented by at least 49 species belonging to 29 genera. The vast majority of isolates belong to *Pseudomonas* spp.

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