The influence of growth stage on the structure and formation of fungal microbiota in potato root

Akosah Y.A.¹, Pudova D.S.¹, Vologin S.G.², Mardanov A.M.¹

¹Institute of fundamental medicine and biology of KFU, Kazan, Russia; ²Tatar Research Institute of Agriculture, Kazan, Russia

E-mail: akosah2005@gmail.com

Key message. In the potato root, *Fusarium* populations greatly increase during the flowering stage of growth. At senescence, a decrease in their share and a significant surge in *Monographella* spp. is observed.

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The spread of fungal-related diseases in potato plants, including *Fusarium* wilt is an urgent problem for the Mid-Volga region of Russia. The aim of the study was to characterize the formation and change of the fungal microbiota of potato roots at different stages of vegetation. Potato plants of the Zhukovskij rannij cultivar were grown on alfisol and soil probes of the soil (SL), rhizosphere (RS) and rhizoplane (RP) were sampled during different vegetation periods: flowering (FP) and senescence (PS). Total DNA was isolated using the commercial FastDNA® SPIN Kit for Soil according to the manufacturer's protocol and amplicons of conserved ITS regions of 5.8S rRNA genes were sequenced via high-throughput sequencing (Illumina Hi-seq). The fungal community of SL, RS, and RP was represented by 3 primary phyla: *Ascomycota*, which comprised 89.99-97.35% in the SL, 89.47-93.85% in the RS and 94.67-99.09% in the RP; *Basidiomycota*, which covered 0.88-1.88%, 2.26-4.90% and 0.25-1.42% in the SL, RS and RP respectively; as well as *Zygomycota*, the shares of which were 0.72-2.89%, 1.19-8.16% and 0.66-3.85% in the SL, RS and RP, respectively. Besides *Sordariomycetes* being dominant (43.54-89.39%) in all three compartments during both stages of growth, the population of fungal classes differed considerably compartment-wise. For instance, *Eurotiomycetes* were registered significantly in almost all SL (22.06-30.99%) and RS (11.17-12.29%) probes but substantially low in the RP (1.29-1.32%). In contrast, *Agariomycetes* were only noted in the RP but at minimal proportions (1.18-2.24%). According to the analysis of similarity by the Bree – Curtis and UniFrac metrics, the structure of the microbiota clearly clusters into microbiomes of SL and RP, with the RS microbiome occupying an intermediate position between them. Assessment of alpha diversity by Shannon's, Simpson's and Chao1 indices indicates that the diversity of species is higher in RS in comparison to SL and RP. At both stages of growth, sequences of *Penicillium* spp. were appreciably registered in the SL (FP=18.12±4.17%, PS=27.74±2.59%), moderately noted in the RS (FP=8.97±1.64%, PS=10.81±2.94), but virtually lacking in the RP (FP=0.67±0.25%, PS=0.38±0.20). On the other hand, representatives of the *Fusarium* genus were present in all tested samples; no considerable variations were noted in the SL during FP (15.54±2.19%) and PS (14.82±2.81%). However, their populations contrasted significantly in the RP and RS, having a higher representation of OTUs during the FP (RS=16.30±4.87%; RP=43.50±9.75%), in comparison with the PS probes, which remained considerably low (RS=7.42±1.52%; RP=10.33±1.88%). During the PS, the RS and RP recorded a surge in presence of *Monographella* (RS = 50.30±5.17%; RP=47.05±7.42%) and *Verticillium* (RS=9.84±2.01%; RP=14.37±5.50), which were practically nonexistent in these compartments at FP. It was concluded that flowering conditions favor an increase in the proportion of *Fusarium* in the root zone of potatoes, which, in turn, may lead to the occurrence of *Fusarium* infections in potato plants. During the senescence period, a decrease in the proportion of *Fusarium* and a surge in the proportion of *Monographella* spp. demonstrates the significance of the later in the degradation and utilization of dead plant matter. In addition, the formation of *Fusarium* communities in RP in such large proportions could be likewise tied to their important role in the biospheric cycle of nutrients and interaction with terrestrial plants (i.e., their influence on the growth and development of the host plant). In this regard, the fight against *Fusarium*, related diseases must be focused on measures aimed at the conservation of beneficial species, such as bio-control methods, crop rotation approaches and a number of other environmentally safe methods.

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