Pathogenic micromycetes feed crop rhizoplane

A A Postovalov
Federal State Budgetary Educational Institution of Higher Education "Kurgan State Agricultural Academy named after T.S. Maltsev", Kurgan region, Ketovsky district, the village of Lesnikovo, 641300, Kurgan, Russia

E-mail: p_alex79@mail.ru

Abstract. Studies have shown that during the vegetation period, the active colonization of root systems of forage crops (spring barley, peas, spring rape) was carried out due to the phytopathogenic micro-mycetes of the genus Fusarium Link; their abundance was from 6.1 to 49.7%. The most common species causing root rot were *F. culmorum*, *F. heterosporum*, *F. oxysporum*, *F. solani*, *F. sporotrichiella*. In addition, Bipolaris sorokiniana parasitized on the roots of spring barley with abundance of 6.5%, and on the roots of spring rape - *fungi p. Alternaria* is 26.9%. The development of root rot on spring barley and peas increased 2-3 times with the aging of plants and by the time of harvest was 23.2% and 53.4%, respectively. Rapeseed was affected by fusarium aetiology - root rot and tracheomycosis (*Fusariasis*). Fusarium lesion was observed throughout the whole vegetation period and did not exceed 12.7%; the root rot development index was 17.5%.

1. Introduction
The study of factors influencing the process of colonization of the root surface by various microorganisms is an important contribution to solving the problem of phytopathogenesis. Studies in this field are necessary for solving the problems of control and management of microorganisms populations possessing both useful and unfavorable properties for plants [6,7].

Particular attention should be paid to root rot and fusariasis as the most common diseases of crops in all areas of cultivation. In order to determine the causes of root system diseases and their development, it is necessary to determine the composition and representation of different micromycte taxonomic groups on plant roots [2,8,9,13]. Knowledge of the composition of pathogens of the root system, their biological and environmental characteristics of development is a prerequisite for the development of methods of biocontrol of phytopathogenic microorganisms and the justification of measures to combat them [8, 9, 12].

In order to obtain high and stable yields of fodder crops (spring barley, peas and spring rape) it is necessary to assess the phytosanitary situation in agrocenoses of fodder crops and develop methods of its optimization.

In this regard, the aim of the studies is to assess the structure of mycocenosis of fodder crops rhizoplane, to determine the place in it of populations of phytopathogenic fungi and their impact on the development of the disease.
2. Research conditions, materials and methods

The objects of research are the root system of spring barley (Prairie variety), peas (Aksai mustache 55 variety) and spring rape (Ratnik variety). Soil of the pilot plot is leached low-powered, medium-humus loamy soil. The hydrothermal conditions during the period of experiments, although characterized by certain features, were generally favorable for the cultivation of agricultural crops.

Rhizoplane micromycetes were studied using the method of root segments arrangement on the sterile medium of Chapek (with streptomycin). The roots were washed off the soil in sterile tap water, cut into fragments with a sterile scalpel and placed in Petri dishes on a sterile nutrient medium [4,5]. Identification of micromycetes was carried out on the basis of cultural and morphological features after 7 days of incubation according to the corresponding determinants [1,3].

Root rot of forage crops was accounted for according to the existing methods [4,10,11]. The prevalence and development of the disease was determined.

3. Results and discussion

When comparing the complexes of micromychetes of root system of fodder crops we noted significant differences in the composition of both saprotrophic and pathogenic microflora. Among soil micromycetes, pathogenic species of the genus *Fusarium* Link are widespread, which inhabited the root system of plants of agrocenosis during the entire vegetation period. Analysis of micromychete complexes on barley roots showed that the share of phytopathogenic fungi from *Fusarium* Link genera was 25.9% (*F. culmorum*, *F. oxysporum*, etc.), and the specialized pathogen *Bipolaris sorokiniana* in the structure of mycocenosis occupied 6.5% (Figure 1).

In the early stages of plant development, the colonization of underground organs with phytopathogens was carried out by various species of the genus *Fusarium* and *Bipolaris sorokiniana* on the primary roots, epicotyl and stem base. By the end of the vegetation period, the situation was changing, with the species of the genus *Fusarium* dominating the primary and secondary roots, leaving epicotyle and stem base for *Bipolaris sorokiniana*. A characteristic feature of the root system of barley was the presence of representatives of genera *Acremonium* with an abundance of 20.4%, *Penicillium* and *Aspergillus* accounted for an average of 5.5-6.5%.

Analysis of the structure of the pathogenic complex of rhizoplane, which determines the phytosanitary situation in the agrocenosis of peas showed that it was annually affected by fusariosis. This is confirmed by the data obtained on the structure of the root system mycocenosis. The dominant micromycetes are *Fusarium* Link mushrooms, which accounted for 49.7% (Fig. 2). The most common species were *F. culmorum*, *F. heterosporum*, *F. oxysporum*, *F. solani*. Mould fungi. *Penicillium* and...
Aspergillus in the composition of mycocenosis occupied from 12.6 to 18.6%, i.e. their abundance was 2.0 and 3.5 times higher, respectively, than on the roots of spring barley. The group of sterile micelles on the roots of spring barley and peas occupied an average of 8 to 14%.

The mycological study found that the rhizosphere of spring rape was inhabited by micromycetes of different genera, which included pathogenic fungi, the agents of infectious diseases. The structure of spring rape mycocenosis was dominated by the genus Cryptococcus, which accounted for 31.0%. The pathogenic complex on the roots of rapeseed was represented by fungi, Alternaria and Fusarium Link with abundance not exceeding 26.9% and 6.1%, respectively (Figure 3). Among the fungi of the genus Fusarium Link, F. oxysporum, F. heterosporum, F. sporotrichiella, F. solani were most often found in the rape rhizosphere. Mould fungi were represented mainly in the mycocenosis. Penicillium, Aspergillus, Mucor with an abundance of 6.1-13.7%.

Thus, the share of phytopathogens found on the roots of spring barley accounted for 32.4% of all isolated micromycetes, on the roots of spring rape - 31.0%, and on the root system of peas - 49.7%, or
1.5 times more than on spring barley and rape. This, in turn, is also reflected in the assessment of the degree of rottenness of plants.

The following peculiarities were observed on the studied forage crops when taking into account the parameters of root rot. The prevalence of the disease on spring barley in the tillering phase was 24.7%, with a disease development index of 7.8% (Figure 4). During the wax ripeness phase, the prevalence of the disease increased 2.8 times, and the degree of root rot development increased to 23.2%, or 3 times compared to the previous phase of development.

We have established a close correlation between the development of the disease in agrocenosis and the yielding capacity of spring barley, which amounted to -0.79. The dependence of the yield of spring barley on its root rot is described by the regression equation, which looks as follows: \( y = 3.46 - 0.05x \).

![Figure 4. Parameters of root rot of spring barley, % (2002-2004).](image)

The abundance of fungi of the genus Fusarium Link on the roots of peas is 1.5 times higher than in other crops, so the parameters of root rot increased (Figure 5). The prevalence of root rot of peas in the sprouting phase was 63.0%, with the disease developing at 24.5%. By the time of harvest, 97.6% of plants in agrocenosis had been affected, and the disease development index had more than doubled to 53.4%. The dependence of pea yield on root rot can be described by the following regression equation: \( y = 6.26 - 0.08x \) (\( r^2 = 0.94 \)).

![Figure 5. Root rot parameters of peas, % (2005-2009).](image)
Annually, fusarium etiology diseases - root rot and tracheomycosis (fusariasis) - were detected on rapeseed. Fusarium was the most intensive in hot, dry years. Fusarium lesion was observed during the whole vegetation period and did not exceed 12.7%. Root rot was observed in the early stages of spring rape, with a prevalence of 75.8% and a 17.5% disease development index (Figure 6).

The dependence of spring rape yield on root rot can be described by the following regression equation: \( y = 26.62 - 9.32x \) (\( r^2 = 0.82 \)).

4. Conclusion
During the whole vegetation period, active colonization of root systems of forage crops was carried out due to phytopathogenic micromycetes of the genus *Fusarium Link*. Their abundance ranged from 6.1 to 49.7%. The most common pathogenic species were *F. culmorum*, *F. heterosporum*, *F. oxysporum*, *F. solani*, *F. sporotrichiella*. In addition, *Bipolaris sorokiniana* was parasitized on the roots of barley with an abundance of 6.5%, and on the roots of spring rape - fungi of the *p. Alternaria* is 26.9%.

Taking into account the degree of damage of spring barley and peas by root rot, it was found that the development of the disease increased by 2-3 times with the aging of plants and by the time of harvest was 23.2% and 53.4%, respectively. Rapeseed was affected by fusarium etiology - root rot and tracheomycosis (fusariasis). Fusarium contamination of spring rape plants with fusarium was observed during the whole vegetation period and did not exceed 12.7%. The prevalence of root rot was 75.8% with a 17.5% disease development index.

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