

VARIABILITY AND HERITABILITY OF THE COMMON WHEAT GROWTH CHARACTERS TO THE INTERACTION WITH THE PATHOGENIC AGENTS OF THE ROOT ROT

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The article presents data on the action of culture filtrates (CF) of the *Fusarium oxysporum*, *F. solani*, *Drechslera sorokiniana* fungi on the root and strain of 8 common winter wheat genotypes. There were identified: 1) the genotypes with different reaction when treating grains with CF; 2) the share of the genotypic factor in the growth organs reaction to the fungal pathogens; 3) the level of the coefficients of genotypic and phenotypic variation, the coefficient of heritability in the broad sense, the genetic progress for the growth organs in treating the grains with CF of the phytopathogenic fungi. It was concluded that at 5% selection pressure the efficiency of selecting wheat resistant genotypes will be more successful for *F. solani* and *D. sorokiniana*.

Keywords: wheat, root rot, fungi, variability, heritability.

INTRODUCTION

Root rot is among the most widespread and harmful diseases worldwide in various cereal crops, including wheat (*Triticum aestivum* L.), causing tissue damage to the underground part of the plant, root system, first internode, ability to maintain the plant upright, significant fruit losses (Kaur, 2016; Kiecana *et al.*, 2016; Moya-Elizondo *et al.*, 2011). Unfavorable climatic conditions, especially the drought of the last decade, cause the disease to increase in incidence and severity in various cereal cultivating countries (Fernandez, Conner, 2011). Root rot is considered a complex disease, caused by different pathogens in different geographical areas or different pathogens in the succession of the ontogenetic stages of plants. As the above mentioned diseases present serious problems for many cereal cultivating countries, in order to obtain high quality and wheat and barley crops, extensive research has been initiated on the pathogens involved, the environmental factors

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associated with these diseases and the loss of the harvest. Root rot caused by *Fusarium* spp., was found in 57% cases, and by *Bipolaris sorokiniana* (syn. *Drechslera sorokiniana*) – in 93% cases, under the conditions of Canada. The geographical distribution of the disease produced by these pathogens depends on the latitude of the region, soil type and temperature. Both types of rot can cause fruit loss within 3 ... 35%. In the pathogenesis of root rot caused by *Fusarium* spp., the species *F. culmorum*, *F. pseudograminearum*, *F. graminearum*, *F. acuminatum*, *F. equiseti*, *F. nivale* were mainly involved, among which *F. culmorum* dominated. The fact that out of 91 fields investigated, in 45 there was no root rot produced by *Fusarium* spp., led to the conclusion that these pathogens are not endemic, but depend a lot on the environmental conditions and the agroecological areas. The species *F. culmorum* has been more widespread in cold areas, and *F. pseudograminearum* – in warm areas. A possible antagonism between *B. sorokiniana* and *Fusarium* spp. is allowed (Moya-Elizondo *et al.*, 2011).

Under the conditions of the Republic of Moldova, the base stem rot in the common winter wheat is caused mainly by the *F. oxysporum*, *F. solani*, *D. sorokiniana* species which at different ontogenetic stages have different prevalence (Lupăscu, Gavzer, 2018).

Many of the *Fusarium* spp. that cause root rot have been associated with fungi that cause spike fusariosis, such as *F. avenaceum* (teleomorph *Gibberella avenacea* Cook). Colonization of the roots and basal part of the stem by *Fusarium* pathogens, as well as their survival, and their subsequent multiplication in these tissues, after harvesting plays an important role in the further development of spike fusarium, thus contributing to the easier spread of spores. The presence of *Cochliobolus sativus* and *Fusarium* spp. in the subterranean tissue of the plant is influenced by crop rotation, soil processing method and chemical preparations utilization. Differences in data, respectively, and conclusions regarding the presence or prevalence of *Fusarium* spp. in tissues from the underground part of wheat plants can be attributed to the limited identification of isolates, fluctuating environmental conditions, the prevalence of one or another agricultural practice and / or differences of the varieties genetic resistance to different species of the fungal complex (Fernandez, Conner, 2011). Infection of the stem base of the wheat plant with fungal pathogens depends largely on the agrotechnical cultivation system – organic, integral, conventional, monoculture, and vegetation stage. Among the pathogenic species, *Fusarium* spp. dominates in all systems, but their number is smaller in the organic cultivation system and higher in the integrated system (Lukanowski, 2009).

The genetic method of fighting the disease by creating resistant genotypes is considered a safe and ecologically harmless way of diminishing the consequences of root rot. It should be mentioned, however, that this problem is quite difficult to solve because of the specificity of the plant x pathogen species / isolate interaction, which most directly reflects on the variability and heritability of growth traits.

The character heritability pattern is important for the plant breeding because it provides information to the extent that a particular character can be transmitted from parent to descendants (Syukur *et al.*, 2012; Bello *et al.*, 2014), and heritability estimation provides information about the level of genetic control of character (Taneva *et al.*, 2019).

Heritability in the broad sense indicates the contribution of the genotypic component in the manifestation of the character, and being associated with the genetic progress, the contribution of the additive genetic variance in the expression of the character is highlighted, thus the selection based on these traits plays a vital role in improving the quantitative traits (Laghari *et al.*, 2010).

The genotypic coefficient of variation is considered to be the best index for assessing genetic variance (Wolde *et al.*, 2016), and for quantifying variability and character comparison, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advantage is assessed according to Snedecor, Cochran (1994).

In relation to the complexity of the systems of factors on which the manifestations of root rot in wheat depend on the growth organs, the purpose of the research was to establish their variability and heritability when interacting with some important pathogens in the initiation and development of the disease – *F. oxysporum*, *F. solani*, *D. sorokiniana*.

MATERIAL AND METHODS

The research was carried out under laboratory conditions. As a material, 8 genotypes showing lines and varieties of common wheat of autumn were used – L 1/3/M 3, L Sel./Accent, L Bas./M 30, L M/M3, L Cub. 101/Bas., Moldova 16, Moldova 66, Moldova 11.

F. oxysporum, *F. solani*, *D. sorokiniana* fungi were isolated from common autumn wheat plants with signs of rot at the base of the stalk, on nutritional medium *Potato Dextrose Agar* (Tuite, 1969), and identified on the basis of morphological-cultural characteristics (Bilal, 1977; Barnett, Hunter, 1998) (Fig. 1).



Fig. 1. Isolation and identification of fungi from the base of wheat stems with signs of root rot.

The culture filtrates (CF) of the mentioned fungi were prepared based on the liquid medium Czappek (Tuite, 1969), numbered CF 1, CF 2, CF 3 for each species of fungus.

Wheat grains were treated with CF for 18 hours, then rinsed with distilled water and kept for 6 days in Petri dishes on moistened filter paper. As metric characters, they served the length of root and stem of plants that are associated with adaptation to biotic stress at early stages of plant ontogenesis.

To analyze the genetic variability of the growth traits of wheat seedlings, the methods proposed by Johnson *et al.* (1955), Hanson *et al.* (1956), Allard (1999) (cit. Adeniji, 2018; Balkan, 2018) have been used:

$\sigma^2_g = (MSS - MSE)/r$; $\sigma^2_{ph} = \sigma^2_e + \sigma^2_g$; $h^2 = \sigma^2_g / \sigma^2_{ph} \times 100\%$; $PCV = 100 \times \sqrt{\sigma^2_{ph}} / X$; $GCV = 100 \times \sqrt{\sigma^2_g} / X$; $GA = K \times (\sigma_{ph}) \times h^2$; $GAM, \% = 100 \times K \times h^2 \times \sigma_{ph} / X$, in which σ^2_g – genotypic variance; σ^2_{ph} – phenotypic variance; σ^2_e (error variance, or VE) = MSE; h^2 – coefficient of heritability in the broad sense; PCV, % – coefficient of phenotypic variation; GCV, % – coefficient of genotypic variation; GA, GAM (%) – genetic advantage; K – selection differential = 2.06 at 5% selection pressure; X – the general average of the character; σ_{ph} – the general standard deviation of the character.

The data were processed in the STATISTICA 8 software package.

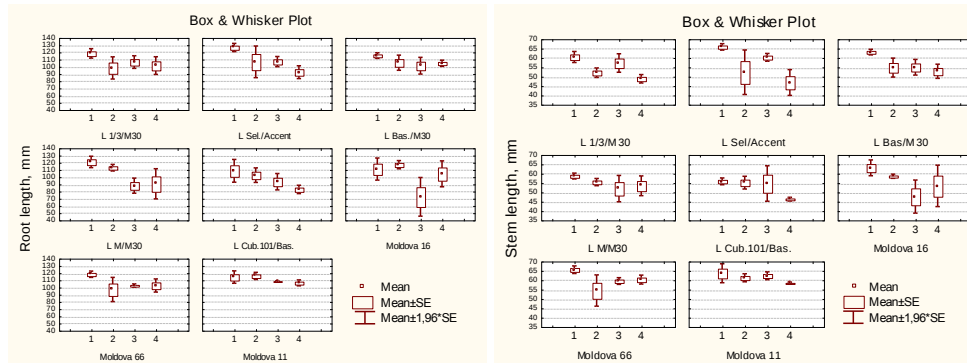
RESULTS AND DISCUSSIONS

***F. oxysporum* CF.** In most cases, it was found that under the influence of CF, inhibition of embryonic root growth occurred. Only in two cases – Moldova 16 and Moldova 11 in the CF1 action was there mild stimulation – 1.4... 5.4% compared to the control. In the other variants, the root length constituted 65.2... 94.9% of the variant with untreated seeds. The most pronounced inhibitions were observed in the

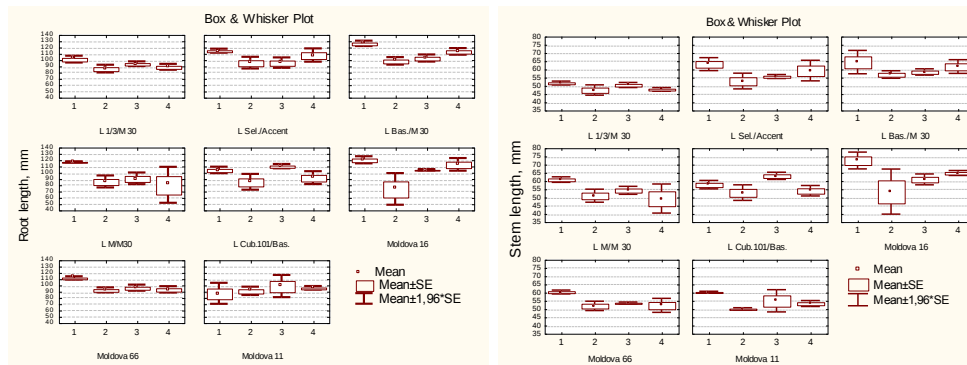
genotypes L Sel./Accent (-27.1% – CF 3), L M / M30 (-25.2, -27.3% – CF 2, CF 3, respectively), L Cub. 101 / Bas. (-23.8% – CF 3), Moldova 16 (-34.8% – CF 2). In the case of the stalk, the inhibition under the influence of CF was not as strong as in the case of the root. Thus, only in the case of L Sel./Accent (CF 3) and Moldova 16 (CF 2) genotypes, growth inhibition reached values of -28.9% and -24.4%, respectively. In the other variants the inhibition varied within the limits -2.0 ... -19.4%.

F. solani CF. It was found that only in the L Cub. 101 / Bas. (CF 2) and Moldova 11 (CF 1, CF 2, CF 3) variants was produced the stimulation of the growth of the embryonic root – +4.6... + 13.4% compared to the control. In the other cases there was inhibition which varied within the limits -6.1 ... -38.7%. The most sensitive genotype was L M/M30, where in the 3 variants with CF the root length was 26.9... 31.4% smaller than in the control variant. The genotypes L M/M30, Moldova 66 and Moldova 11 were the most resistant – in the first 2 genotypes in the variants with CF the root length constituted -7.2... -17.3% of the variant without treatment with CF. As for the stem, only at L Cub. 101/Bas. there was growth stimulation (+ 9.2%) under the influence of the fungus. In the other variants, inhibition was found that varied within the limits -2.3 ... -26.5%. The most sensitive proved to be Moldova 16: -10.5... -26.5%, and more resistant – L Cub. 101/Bas.: -8.4... + 9.2%, compared to the control.

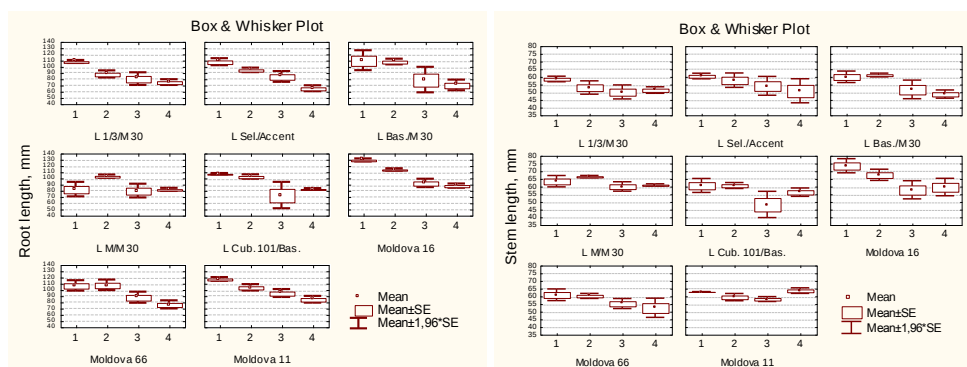
D. sorokiniana CF. Compared with *F. oxysporum* and *F. solani* CFs, a stronger inhibition of root growth was observed. For example, L M / M30, which showed relatively poor sensitivity in the first 2 fungi, had an inhibition of 18.6... 30.7% in the treatment with the 3 CFs compared to the control. A sharp decrease in root length was also observed in the genotypes L Sel./Accent, L Bas./M3, L Cub. 101 / Bas., Moldova 16 under the action of CF 2, CF 3 and Moldova 66 under the influence of CF 3 which varied within the limits -22.1... -39.8%. Less sensitive proved to be L M/M 30, whose reaction varied in the range -3.0 ... + 25.2% relative to the control. Regarding the strain, as in the case of the *F. oxysporum* and *F. solani* fungi, a weaker reaction was observed compared to the root, but the differentiation of the genotypes was nevertheless pronounced. Thus, the most resistant genotypes were L M/M 30 and Moldova 11, in which the deviations from the control constituted -3.9 ... + 4.7% and -7.6 ... + 1.2%, respectively. It should be mentioned that CF 1 acted the least on the increase of the strain in the first 7 genotypes, which shows the diminished pathogenicity of the isolate, for which reason a pronounced differentiation of the genotypes occurred based on the reaction on CF 2 and CF 3. Advanced sensitivity showed the genotypes of Moldova 16 (-18.9... -21.2%), L Bas./M 30 (-13.7... -18.8%), L 1/3/M 30 (-12.3 ... -14.4%) (Fig. 2).



F. oxysporum CF



F. solani CF



D. sorokiniana CF

Fig. 2. Influence of pathogenic fungi on some growth and developmental characteristics in wheat.

By correlational analysis, we found a pronounced dependence between the root length and the stem length in the variants with CF on the 8 studied genotypes. Thus, the correlation coefficient (r) was 0.80 *, 0.82 * and 0.78 * ($p \leq 0.05$) for *F. oxysporum*, *F. solani* and *D. sorokiniana*, respectively (Fig. 3).

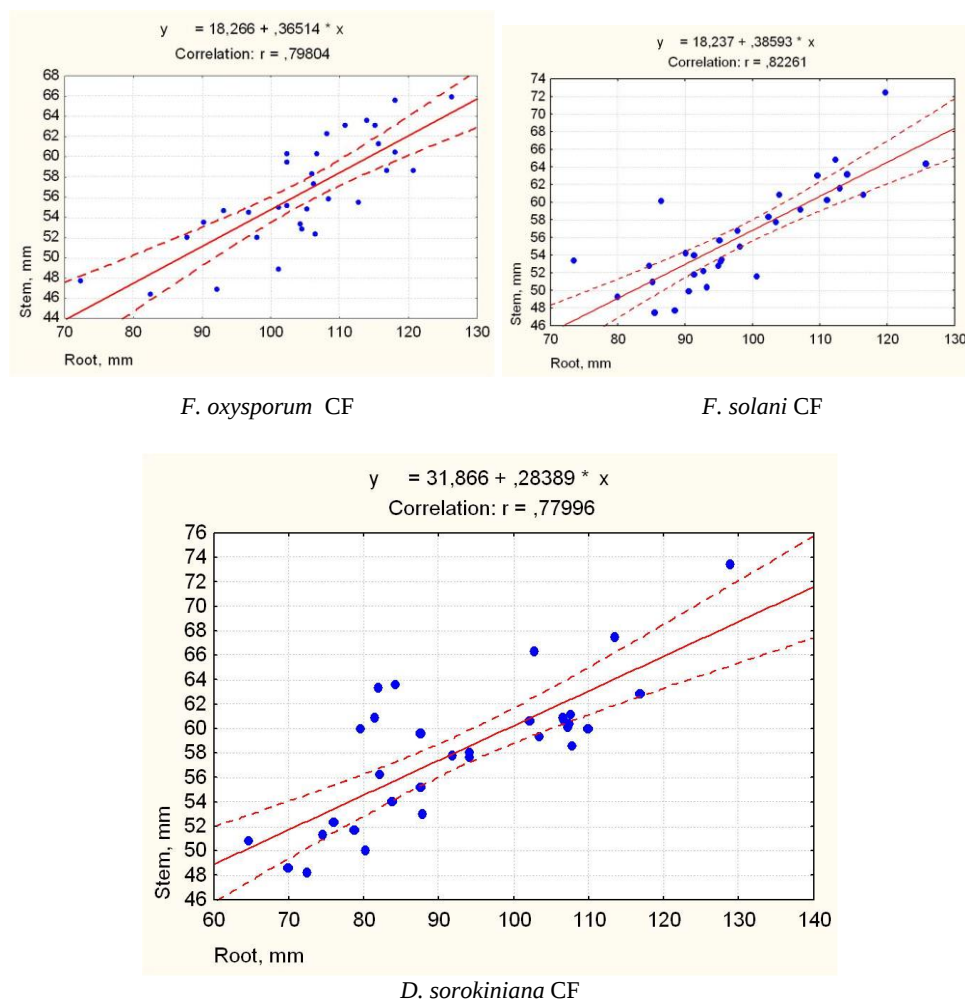


Fig. 3. Correlational dependence between wheat root and strain length on the interaction with culture filtrates of fungal pathogens.

Factor analysis of *plant x pathogen* relationships showed that the average sum of squares for genotype, isolated, *genotype x isolate* interaction, for the 3 fungi was much higher for root length than for stem length, which shows the higher variability of the first character. It was found that the share of genotype in the source of variation of the root length constituted 9.25, 17.24, and 8.99%, and of the

stem length – 17.67, 34.69 and 31.47%, respectively, for *F. oxysporum*, *F. solani*, *D. sorokiniana*, from which is why the role of the isolate was higher in the case of the root – 77.16, 70.7, 87.2%, than of the stem – 71.25, 58.56, 61.98%, respectively, *F. oxysporum*, *F. solani*, *D. sorokiniana* CFs, which shows that for the root, CFs were more toxic and significantly diminished the role of the genotype (Tab. 1).

Table 1

Factorial analysis of the influence of interactions *wheat* x *fungal pathogens* on growth organs

Source of variation	Degrees of freedom	Root length		Degrees of freedom	Stem length	
		The average sum of squares	Share of the source of variation, %		The average sum of squares	Share of the source of variation, %
F. oxysporum						
Genotype	7	234	9.25	7	94.2	17.67
F. oxysporum isolate	3	1953	77.16	3	379.9	71.25
Genotype x isolate	21	237	9.36	21	38.8	7.28
Error	64	107	4.23	64	20.3	3.81
F. solani						
Genotype	7	462.1	17.24	7	211.3	34.69
F. oxysporum isolate	3	1895.2	70.70	3	356.7	58.56
Genotype x isolate	21	243.4	9.08	21	25.8	4.24
Error	64	79.9	2.98	64	15.3	2.51
D. sorokiniana						
Genotype	7	533.1	8.99	7	191.3	31.47
F. oxysporum isolate	3	5172.3	87.19	3	376.7	61.98
Genotype x isolate	21	172.0	2.90	21	26.6	4.38
Error	64	54.9	0.93	64	13.2	2.17

*- $p < 0.05$.

From the presented data in Table 2, it can be seen that the genotypic (σ^2_G) and phenotypic (σ^2_P) variability were much higher in the case of root length than of the stem and, at the same time, higher in the case of the *D. sorokiniana* fungus, then *F. solani* and, finally, at a detached distance – of the fungus *F. oxysporum*. This shows that although there is a rather strong positive correlation between root and stem growth, the root response to CFs is much more differentiated than the stem. At the same time, root sensitivity was more specific for *D. sorokiniana* CF compared to other 2 fungi.

Table 2

Genetic parameters of wheat growth traits under the influence of culture filtrates of some phytopathogens

Parameter	<i>F. oxysporum</i> CF		<i>F. solani</i> CF		<i>D. sorokiniana</i> CF	
	Root length	Stem length	Root length	Stem length	Root length	Stem length
σ^2_G	42.33	24.63	127.4	65.33	159.4	59.37
σ^2_P	149.33	44.93	207.3	80.63	214.3	72.57
GCV, %	6.22	8.79	11.47	14.38	13.59	13.23
PCV, %	11.68	11.87	14.63	15.98	15.76	14.63
h^2 , %	28.35	54.82	61.46	81.02	74.38	81.81
Difference PCV–GCV, %	5.46	3.08	3.16	1.60	2.17	1.4
GA	8.23	7.27	18.14	10.91	25.53	10.75
GAM, %	7.87	12.88	18.43	19.41	27.48	18.46

This was reflected in an important parameter – the genotypic coefficient of variation (GCV,%) that followed the same trend as σ^2_G and had higher values in the treatment with *D. sorokiniana* CF (13.23... 13.59%) than in the treatment with *F. solani* CF (11.47... 14.38%) and *F. oxysporum* CF (6.22... 8.79%). Thus, GCV (%) was medium for *F. solani* and *D. sorokiniana*, and low for *F. oxysporum*.

The coefficient of heritability in the broad sense (h^2 ,%) is classified as weak (0–30%), moderate (31–60%) and high ($\geq 61\%$) (Gobu *et al.*, 2017), being also a good indicator of the influence of environmental conditions. Thus, in the case of *F. oxysporum*, h^2 was weak (28.35,%) for root length and medium (54.82,%) for stem length. In the variants with *F. solani* and *D. sorokiniana*, h^2 had high values for growth organs that varied within the limits 61.46 ... 81.81,%. This shows that root growth was more dependent on the influence of *F. oxysporum* CF than on *F. solani* CF and *D. sorokiniana* CF. At the same time, h^2 had higher values in the case of the strain, which denotes its less dependence on the culture filtrates compared to the root.

According to the authors Tuhina-Khatun *et al.* (2015), Gobu *et al.* (2017), the environmental effect is well demonstrated by the magnitude of the difference between PCV (%) and GCV (%). Thus, in our research it was found that this difference was more pronounced for *F. oxysporum* CF than for the other two fungi, and at the same time – greater for the root than for the stem. These data basically confirm the phenomenon established on the basis of h^2 values.

It was found that for growth organs, GAM (%) had relatively low values (7.87... 12.88,%) in the case of *F. oxysporum* fungus, and medium – high (18.43... 27.48,%) in the case of *F. solani* and *D. sorokiniana*. Considering the values of h^2 , we can conclude that at the selection pressure of 5% the efficiency of selecting resistant wheat genotypes will be more successful for *F. solani* and *D. sorokiniana*.

CONCLUSIONS

1. Treatment of the kernels of 8 common wheat genotypes with culture filtrates of the *F. oxysporum*, *F. solani*, *D. sorokiniana* fungi led in most of the cases to decrease of growth of the embryonic root and of the strain, the effect depending on the genotype and the tested organs.

2. In the case of the embryonic root, the most sensitive genotypes registered decreases of growth with 34.8% (Moldova 16), 31.4% (LM / M 30) and 30.7% (LM / M 30) under the action of *F. oxysporum* CF, *F. solani* CF and *D. sorokiniana* CF, respectively, and the length of the strain at the most sensitive genotype Moldova 16 in all 3 pathogens decreased by 21.2... 26.5%. The smallest deviations from the root length and stem length, that is, the most resistant genotypes were found to be Moldova 11, L 1/3 / M 30 and LM / M30, respectively, the *F. oxysporum*, *F. solani*, *D. sorokiniana* fungi.

3. Correlational analysis found a dependence (r) of $0.78 * \dots 0.82 *$ ($p \leq 0.05$) between root length and stem on the interaction of plants with CF of *F. oxysporum*, *F. solani*, *D. sorokiniana* fungi, which indicates that under conditions of fungal infection, the growth organs of wheat plants maintain a relative proportionality, which is a proof of the completeness of the response to pathogens.

4. The factorial analysis showed that in the wheat reaction to *F. oxysporum* CF, *F. solani* CF, *D. sorokiniana* CF, the growth of the embryonic root presented a much higher variability than the strain, which denotes a more specific interaction specificity in the first case.

5. The genotypic coefficient of variation (GCV, %) recorded higher values in the treatment of wheat grains with *D. sorokiniana* CF (13.23... 13.59%) than in the treatment with *F. solani* CF (11.47... 14.38%) and in particular – *D. sorokiniana* CF (6.22... 8.79%). Higher differences between PCV (%) and GCV (%) for “*F. oxysporum* CF” variant, compared to other 2 pathogens, denote the more pronounced action of *F. oxysporum* fungus.

6. For growth organs, the values h^2 (61.46... 81.81%) and GAM (18.43... 27.48%) were much higher in the variant “*F. solani* CF” and “*D. sorokiana* CF”, which offers chances of greater success when selecting resistant genotypes for these two pathogens.

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