

RESISTANCE SOURCES OF WHEAT GENOTYPES FOR ROOT AND CROWN ROT DISEASE CAUSAL ORGANISM *Fusarium culmorum* (W.G. SMITH)

Gul Imriz^{1,*}, Fatih Ozdemir², Murat Nadi Tas², Birol Ercan², Ilker Topal² and Mehmet Sait Karaca²

¹Dicle University, Faculty of Agriculture, Department of Plant Protection, 21280 Diyarbakır, Turkey;

²Bahri Dadas International Agricultural Research Institute, 42020 Konya, Turkey.

*Corresponding author's e-mail: gul.imriz@dicle.edu.tr

Fusarium culmorum is a soil-borne fungus able to cause crown and root rot on different small-grain cereals, particularly in wheat and barley. For controlling such diseases, application of fungicides is inadequate in some cases besides their hazardous effects for environment and living organisms. As an alternative solution to chemicals, development and screening the resistant wheat genotypes has been emphasis in the recent plant defense studies. In the present study, totally 90 bread wheat genotypes developed for rainfed area were included in the experiment to be evaluated for resistance to *F. culmorum* in controlled conditions. The experiment was set up according to randomized complete block design with 4 replications for each entry. The wheat seeds were sown in the soil contaminated with *F. culmorum*, for control the seeds were sown in uncontaminated soil. The plants were kept in plant growth chamber at 23±2°C and 80% humidity for 8 weeks. The resistance levels of genotypes to *F. culmorum* were determined considering the 0-10 scale. The plant genotypes based on scale values were divided into 3 groups that were susceptible (≥3 scale value), moderately resistant (scale values between 1-3), and resistant (≤1 scale value). As a result, 2 genotypes were grouped as resistant, while 11 of genotypes were moderately resistant against *F. culmorum*. The rest of genotypes were taken to susceptible group with scale values above 3.

Keywords: Wheat, genotypes, soil-borne, *Fusarium culmorum*, resistance.

INTRODUCTION

Wheat is grown on 20% of the cultivated land area of the world and is a main food resource for 40% of the world's population (Braun *et al.*, 2010). In 2019, the forecast of wheat production is at nearly 771 million tonnes, up 5.6 percent from previous year's level (FAO, 2019). In 2050, the world's population is expected to reach 9 billion, thus it is estimated that cereal production needs to increase by 50% by 2030 (Alexandratos and Bruinsma, 2012). The wheat production is suffering substantial losses of biotic and abiotic stress factors. Among the biotic stress factors, *Fusarium* species causing foot and crown rots occur in winter cereals worldwide virtually wherever cereal-based farming system predominates (Burgess *et al.*, 2001).

Fusarium culmorum (W.G. Smith) is one of most important pathogens of wheat in Turkey and causing consequently grain yield and quality losses. *Fusarium* foot and root rot of cereals, caused by *Fusarium culmorum*, is a major constraint to cereal production in many parts of the world, especially in arid and semi-arid regions (Backhouse *et al.*, 2004; Chekali *et al.*, 2013; Rossi *et al.*, 1995; Mergoum *et al.*, 2004; Papendick and Cook, 1974; Van Wyk *et al.*, 1987).

It has a wide range of host plants, mainly cereals, such as wheat, barley, oats, rye, corn, sorghum and various grasses. In addition, it has been isolated from sugar beet, flax, carnation, bean, pea, asparagus, red clover, hop, leeks,

Norway spruce, strawberry and potato tuber. *F. culmorum* is known by its ability to grow at lower temperatures (Scherf *et al.*, 2013) and persists as hyphae in stubble residues and as chlamydozoospores in the soil matrix (Burgess, 2011). The disease symptoms on the wheat plant are defined as necrosis and dry rot of the crown bases in brown color and whitehead formation which is most severe, particularly, through the seasons with a wet start and dry climates (Matny, 2015). Damage to cereals is often unnoticed until white heads appear shortly before the crops mature or until shrivelled grains is noted during harvest (Burgess *et al.*, 2001). The water deficit in plants followed by limited water supply significantly increases disease severity in wheat caused by *F. culmorum* (Liu and Liu, 2016; Streit *et al.*, 2016). Moreover, the predicted climatic changes are expected to affect the pathogens' development and survival rates as well as the host sensitivity against the pathogens (Elad and Pertot, 2014; Kan *et al.*, 2017). It was projected that, with climate change, the *Fusarium* epidemics will be more severe by the 2050s (Madgwick *et al.*, 2011). *F. culmorum*, hence, might be a potential threatening agent with increasing importance for cereal production in arid and semi-arid regions as well as temperate climate countries.

Even though, chemical protection with fungicides as seed application is highly efficient, they do not control for long besides their hazardous effects for environment and living organisms (Wegulo *et al.*, 2011). Breeding resistant varieties

as an effective alternative control method has come at first of necessity. As known, growing of resistant wheat cultivars is the more economic, environment-friendly and effective method to control the above-mentioned pathogen.

The aim of this research was to find out the sources of resistance in bread wheat genotypes developed for rainfed conditions in Bahri Dagdas International Research Institute against *F. culmorum*. We have determined some genotypes with high level of resistance that can be used for further breeding studies.

MATERIALS AND METHODS

Plant materials and pathogen isolate: In total, 90 bread wheat (*Triticum aestivum*) genotypes, developed for rainfed conditions in Bahri Dağdaş International Research Institute, were included in the study as plant materials. The identified pathogen isolate was obtained from of Prof. Dr. Berna Tunali's (19 Mayıs University, Samsun) culture collection.

Experimental design and management: The experiment was carried out in a growth room adjusted to 23±2°C and 80% relative humidity by using the pots, in 5 cm of diameter and 25 cm in depth, containing soil mix (3 field soil:1 sand). Trial was designed according to complete randomized block design with 4 replications each entry.

For inoculum preparation of pathogen, petri dishes containing PDA (Potato Dextrose Agar) were inoculated with a disc of *F. culmorum* isolate and incubated for 10 days till macroconidia sporulation. Ten days old pathogen culture was mashed with sterile distilled water by using a mortar and strained by a sieve. Conidia concentration of obtained suspension was checked under the light microscope by a haemocytometer. The soil mix was infested with the suspension adjusted 1×10^4 conidia per gram of soil (Lemmens *et al.*, 1993). The seeds were sown immediately, and the pots covered by a polyethylene for a week to provide favourite humid condition for max pathogen colonization. After sowing the seeds, the pots were kept in a growth room and the plants were observed for the typical symptoms of crown and root rot pathogen throughout 8 weeks. After this period, the symptom was evaluated according to 0-10 scale (Tinline *et al.*, 1975). The scale represented the first 10 cm from root-crown with area of lesion (0: No disease symptom, 1:1-4% with symptom, 2:5-9% with symptom, 3:10-19% with symptom, 4:20-29% with symptom, 5: 30-40% with symptom, 6: 50-69%, 7: 70-89% with symptom, 8: 90-99% with symptom, 10: dead plant). According to evaluation on scale values, the plant genotypes were divided into 3 groups that were susceptible-S (≥ 3 scale value), moderately resistant-MR-(scale values between 1-3), and resistant-R (≤ 1 scale value) (Erginbas *et al.*, 2008). The differences among the genotypes were statistically analyzed by One Way ANOVA using SPSS software. Means were separated by the Tukey HSD test ($p < 0.05$).

RESULTS AND DISCUSSION

Significant differences were observed between bread wheat genotypes with respect to disease symptom development. According to evaluation on scale values, the plant genotypes were divided into 3 groups that were susceptible (≥ 3 scale value), moderately resistant (scale values between 1-3), and resistant (≤ 1 scale value). Two genotypes were grouped as resistant genotypes (GN: 45, and 87), while 11 of genotypes (GN: 6, 14, 32, 40, 41, 47, 48, 50, 63, 72, 76) were moderately resistant against *F. culmorum* (Table 1). The rest of genotypes were taken to susceptible group with scale values above 3. The reactions of genotypes 45 (R) and 38 (S) can be seen in Figure 2. Statistically, there were significant differences among the genotypes for resistance level under controlled conditions ($F=41,158$, $df=89$, $P=0,001$) (Table 1). As shown in Figure 1, 2.24% of genotypes were resistant, 12.22% were moderately resistant and 85.56% were sensitive. Considering the number of genotypes used in this study, 14.44% (percentage of R+MR) is a percentage that can be considered good portion in terms of pathogen-resistance source.

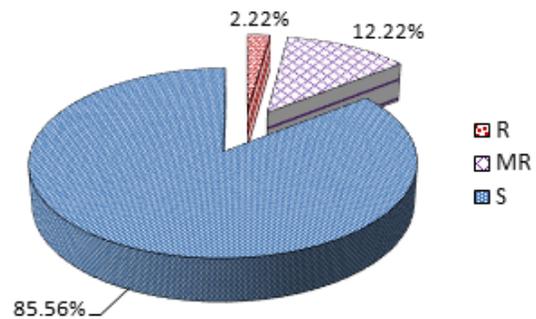


Figure 1. The percentage of genotypes in terms of resistance level; R: Resistant, MR: Moderately Resistant, S: Susceptible.



Figure 2. The reactions of wheat genotypes: No disease symptom on Genotype 45 on left (R); the lesion development matches with scale value of 6 on Genotype 38" (S).

Table 1. The numbers of genotypes (GN), means of lesion lengths (cm), resistance level group of genotypes (RLG).

GN	Means of lesion lengths in cm	RLG	GN	Means of lesion lengths in cm	RLG	GN	Means of lesion lengths in cm	RLG
1	3.000±0.4082 c-g	S	31	3.625±0.2500 e-i	S	61	5.000±0.8165 i-o	S
2	4.625±0.7500 h-m	S	32*	2.000±0.4082 a-d	MR	62	4.000±0.0000 f-k	S
3	3.750±0.5000 e-j	S	33	7.000±0.4082 rst	S	63*	2.500±0.4082 b-f	MR
4	3.375±0.4787 d-h	S	34	5.500±0.5774 k-r	S	64	5.000±0.4082 i-o	S
5	4.375±0.4787 g-l	S	35	7.250±0.2887 st	S	65	5.750±0.9574 l-s	S
6*	2.625±0.2500 c-f	MR	36	4.000±0.8165 f-k	S	66	5.000±0.0000 i-o	S
7	4.625±0.7500 h-m	S	37	3.750±0.5000 e-j	S	67	4.500±0.5774 g-m	S
8	5.250±0.5000 j-p	S	38	6.000±0.0000 m-s	S	68	4.500±0.5774 g-m	S
9	5.500±0.4082 k-r	S	39	3.500±0.5774 d-i	S	69	6.000±0.8165 m-s	S
10	5.500±0.4082 k-r	S	40*	2.000±0.4082 a-d	MR	70	6.000±0.0000 m-s	S
11	5.000±0.0000 i-o	S	41*	1.500±0.5774 abc	MR	71	4.250±0.2887 g-l	S
12	5.500±1.0000 k-r	S	42	5.000±0.4082 i-o	S	72*	2.250±0.2887 b-e	MR
13	3.250±0.2887 d-h	S	43	3.000±0.4082 c-g	S	73	4.250±0.2887 g-l	S
14*	2.500±0.5774 b-f	MR	44	3.250±0.5000 d-h	S	74	7.250±0.2887 st	S
15	7.000±0.7071 rst	S	45*	0.500±0.0000 a	R	75	4.250±0.2887 g-l	S
16	5.500±0.5774 k-r	S	46	5.250±0.2887 j-p	S	76*	2.500±0.5774 b-f	MR
17	7.000±0.8165 rst	S	47*	2.250±0.2887 b-e	MR	77	3.750±0.2887 e-j	S
18	5.000±0.0000 i-o	S	48*	2.000±0.0000 a-d	MR	78	4.000±0.0000 f-k	S
19	4.750±0.9574 h-n	S	49	3.000±0.0000 c-g	S	79	3.750±0.5000 e-j	S
20	5.500±0.4082 k-r	S	50*	1.500±0.4082 abc	MR	80	7.000±0.0000 rst	S
21	7.000±0.7071 rst	S	51	5.250±0.5000 j-p	S	81	6.750±0.5000 p-t	S
22	8.000±0.8165 t	S	52	5.500±0.4082 k-r	S	82	5.250±0.2887 j-p	S
23	6.500±0.7071 o-t	S	53	5.000±0.0000 i-o	S	83	4.750±0.5000 h-n	S
24	7.250±0.8660 st	S	54	5.250±0.2887 j-p	S	84	7.250±0.2887 st	S
25	7.000±0.7071 rst	S	55	7.250±0.2887 st	S	85	6.500±0.5774 o-t	S
26	5.250±0.5000 j-p	S	56	5.750±0.5000 l-s	S	86	3.500±0.5774 d-i	S
27	4.750±1.0408 h-n	S	57	5.250±0.6455 j-p	S	87*	1.000±0.0000 ab	R
28	6.250±0.5000 n-s	S	58	5.500±0.5774 k-r	S	88	4.500±0.5774 g-m	S
29	6.500±0.5774 o-t	S	59	3.500±0.5774 d-i	S	89	6.000±0.8165 m-s	S
30	5.250±0.5000 j-p	S	60	6.250±0.2887 n-s	S	90	6.250±0.2887 n-s	S

*The genotypes which gave response at resistant and moderately resistant level

In the columns, values having the same letter are not statistically different at P<0.05 (Tukey HSD test).

Varietal resistance and tolerance to crown rot is limited and it is known that durum wheat varieties are more susceptible to *F. culmorum*, while other winter cereals exhibit varying levels of susceptibility (Sakr, 2019). In our study, 13 genotypes (2 resistant and 11 moderately resistant) gave hopes for resistance source to the crown rot. Next step would be field trials with the successful genotypes for further screening of resistant genotypes. Since the interaction between the agricultural practices have shown a synergistic effect, integrated multiple strategies including resistant variety development, in the areas characterized by a probable *F. culmorum* infection, would seem to be the effective management way of reducing the pathogen in wheat (Blandino *et al.*, 2013).

Wheat genotype resistant to crown rot is limited, therefore, developing and/or identifying a new genotype with acceptable level of resistance will greatly benefit wheat producers 'farmers'. Implementing the resistant germplasm with other

cultural practices such as crop rotation and other Integrated Pest Management (IPM) will ultimately reduce the damage and increase the grain yield (Erginbas Orakci *et al.*, 2010). The importance of soilborne pathogens, particularly caused by the *Fusarium* spp. on cereals are reported by many of researchers for wheat producing areas (Smiley *et al.*, 2005; Chakraborty *et al.*, 2010). Using resistant genotypes of high yielding potential is the most effective and economical way to control soil borne pathogens, especially the drought subjected areas. Researchers have been focused on Quantitative Trait Loci (QTLs) for crown rot around the world to find out resistance source (Erginbas Orakci, 2018). However, only few sources were identified with partial resistance (Wallwork *et al.*, 2004; Collard *et al.*, 2005; Ma *et al.*, 2009; Li *et al.*, 2010). The results of this study clearly show fine variation in the resistance level among the tested genotypes. All genotypes assessed for crown symptoms at seedling stage for seedling resistance in growth room showed

various reactions to the pathogen *F. culmorum*. As reported by Smiley and Yan (2009), a high degree of variation in response to crown rot disease over years and found it difficult to establish reliable tolerance standards in wheat genotypes. In this study, totally 13 wheat genotypes were found to be R (2) and MR (11) to the crown rot developed for rainfed conditions and those were recommended for crosses in the breeding programs.

Conclusion: The study indicated that the presence of resistance sources against *F. culmorum* among bread wheat breeding materials developed in Bahri Dagdas International Agricultural research Institute. Those thirteen genotypes were well adopted for rainfed areas where receive especially irregular rainfall. The promising genotypes were recommended for crosses in the breeding programs. Nevertheless, knowing the involved genes and the mode of inheritance will more facilitate the transfer of the resistance in the breeding studies.

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