

Research Article

Screening of Chickpea Genotypes for *Fusarium* Wilt (*Fusarium oxysporum*) Resistance Under Field Condition in West Hararghe, Oromia

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Abstract

Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *ciceris*, is a major constraint to chickpea production worldwide, resulting in substantial yield reduction and deterioration of crop quality. The effectiveness of host resistance is often challenged by the emergence of new pathogen races, necessitating the continuous identification of resistant germplasm for breeding programs. This study was conducted to identify chickpea genotypes with resistance to *Fusarium* wilt and to select promising materials for further breeding. A total of 47 chickpea genotypes, along with two standard checks (Geletu and Dimtu), were evaluated under field conditions during the 2022 and 2023 main cropping seasons using an augmented experimental design. Disease incidence was recorded at both seedling and flowering stages, and genotypes were classified according to the ICRISAT disease rating scale. Considerable variation in disease response was observed among the tested genotypes. Two genotypes exhibited resistant reactions, while seventeen were categorized as moderately resistant. Overall, nineteen genotypes demonstrated desirable levels of resistance and were identified as valuable sources of resistance for future chickpea improvement programs. These genotypes can be advanced to subsequent breeding stages for the development of *Fusarium* wilt-resistant chickpea varieties.

Keywords

Chick Pea Genotypes, Chickpea *Fusarium* Wilt, Resistant

1. Introduction

Chickpea (*Cicer arietinum* L.) is one of the most widely cultivated grain legumes in the world and contributes substantially to food and nutritional security, particularly in developing countries [9, 13, 19]. Globally, the crop is grown on more than 13 million hectares with an annual production exceeding 13 million tons; however, its average productivity remains below its attainable yield potential [9, 30]. Chickpea is valued for its high nutritional content, serving as an affordable source

of protein and carbohydrates that constitute a major proportion of its dry matter [22, 33]. The crop is consumed in various forms and is an important component of traditional diets in Asia, Africa, and other regions of the world [6, 10].

Despite its economic and nutritional importance, chickpea production is constrained by several biotic and abiotic factors that limit productivity and yield stability [18]. Among the biotic stresses, *Fusarium* wilt caused by *Fusarium oxysporum* f.

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sp. ciceris is considered one of the most destructive diseases affecting chickpea production worldwide [1, 8, 12, 17, 24, 28, 32]. The disease is widely distributed in chickpea-growing areas, particularly under warm and relatively dry environmental conditions favorable for pathogen development [4].

The pathogen infects plants through the root system and subsequently colonizes the vascular tissues, impairing the movement of water and nutrients within the plant. Infected plants commonly exhibit symptoms such as yellowing, drooping, vascular discoloration, wilting, and eventual death [12]. Disease infection may occur throughout the crop growth cycle, although severe damage is frequently observed during flowering and pod development stages [20]. Depending on environmental conditions, cultivar susceptibility, and pathogen virulence, yield losses may range from 10% to 90%, and in severe cases complete crop failure can occur [11, 14, 23, 27]. In addition to reducing yield, the disease adversely affects seed quality and market value [16, 29].

The deployment of resistant cultivars remains the most practical, economical, and environmentally sound approach for managing Fusarium wilt [15]. Consequently, the identification and utilization of resistant germplasm have become important objectives in chickpea breeding programs [5, 7, 31]. However, resistance is often challenged by the emergence of new pathogen races and pathotypes capable of overcoming previously effective resistance genes [2, 3]. As a result, varieties that initially exhibit resistance may become susceptible over time, highlighting the need for continuous screening of chickpea germplasm to identify new and durable sources of resistance.

In Ethiopia, particularly in West Hararghe, information regarding the resistance status of available chickpea genotypes against Fusarium wilt is limited. Therefore, the present study was conducted to evaluate chickpea genotypes for resistance to Fusarium wilt under field conditions and to identify promising sources of resistance for advancement in subsequent chickpea breeding programs.

2. Materials and Methods

2.1. Description of the Experimental Sites

Field experiments were conducted during the 2022 and 2023 main cropping seasons at Bareda Farmers Training Center, Oda Bultum University Research Site, and the Badessa Field Gene Bank of the Ethiopian Biodiversity Institute, located in West Hararghe Zone, eastern Ethiopia. Oda Bultum District is situated approximately 362 km east of Addis Ababa at 8° 54' 31" N latitude and 40° 21' E longitude, with an altitude of about 1,703 m above sea level. The area receives an average annual rainfall of approximately 1,053 mm and has a mean annual temperature of 20°C, with average maximum and minimum temperatures of 28°C and 13°C, respectively.

2.2. Experimental Materials, Design, and Crop Management

A total of 47 chickpea genotypes were evaluated along with two released varieties, Geletu and Dimtu, which served as standard checks. The experimental materials were obtained from Bishoftu Agricultural Research Center.

The trial was established using an augmented design in which the test genotypes were unreplicated while the check varieties were repeated across blocks. The experimental field was divided into blocks separated by 1 m, whereas adjacent plots were spaced 0.5 m apart. Each plot measured 3.0 m × 0.6 m and consisted of two rows. Row-to-row spacing was maintained at 0.30 m throughout the experiment.

Seeds of each genotype were planted in two rows following the recommended agronomic practices for chickpea production in the area. All field management operations, including land preparation and weed control, were carried out uniformly across treatments. Weeding was performed manually whenever necessary. No insecticides were applied during the study period.

2.3. Disease Assessment

Fusarium wilt incidence was assessed twice during the growing season, at the seedling and flowering stages. Disease reaction of each genotype was classified according to the ICRISAT wilt rating scale based on plant mortality percentage. Genotypes were categorized as Resistant (R) when mortality ranged from 0-10%, Moderately Resistant (MR) when mortality ranged from 10.1-20%, Moderately Susceptible (MS) when mortality ranged from 20.1-30%, Susceptible (S) when mortality ranged from 30.1-50%, and Highly Susceptible (HS) when mortality exceeded 50%.

Disease incidence was determined as the proportion of wilted plants relative to the total number of plants assessed in each plot and expressed as a percentage using the following equation [25]:

$$\text{Disease incidence\%} = \frac{\text{Number of plants exhibiting wilt symptoms}}{\text{Total Number of plants evaluated}} \times 100$$

Data analysis

Data on disease incidence were subjected to descriptive statistics.

3. Results and Discussion

Considerable variation in Fusarium wilt response was observed among the evaluated chickpea genotypes during both cropping seasons, indicating the existence of genetic variability for disease resistance. In 2022, disease assessment at the seedling stage revealed that seven genotypes were classified

as resistant, nineteen as moderately resistant, ten as moderately susceptible, nine as susceptible, and two as highly susceptible (Figure 1). However, disease severity increased at the flowering stage, where only two genotypes remained resistant, while twenty-two, seven, fourteen, and two genotypes were categorized as moderately resistant, moderately susceptible, susceptible, and highly susceptible, respectively. The reduction in the number of resistant genotypes from seedling to flowering stage suggests that resistance expression varied across growth stages.

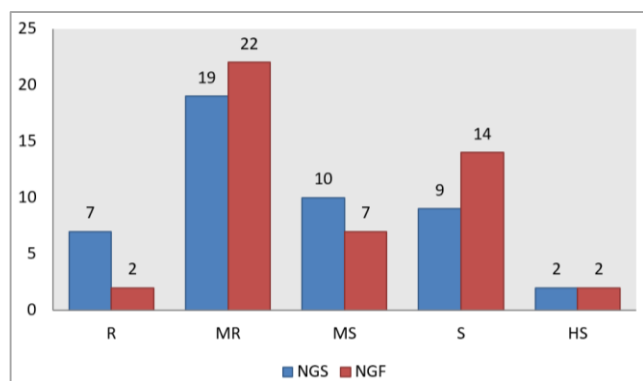


Figure 1. Response of genotypes to chick pea *Fusarium* wilt at seedling and flowering stage in 2022.

Note: NGS=number of genotypes at seedling stage, NGF=number of genotypes at flowering stage

Similarly, the 2023 evaluation showed differences among genotypes in their reaction to *Fusarium* wilt. At the seedling stage, twelve genotypes were resistant, fourteen moderately resistant, eleven moderately susceptible, nine susceptible, and one highly susceptible. In contrast, assessments made at the

flowering stage indicated that only two genotypes maintained a resistant reaction, whereas seventeen, seven, twenty, and eleven genotypes were classified as moderately resistant, moderately susceptible, susceptible, and highly susceptible, respectively (Figure 2). These results indicate that disease pressure increased as plants advanced to reproductive growth stages.

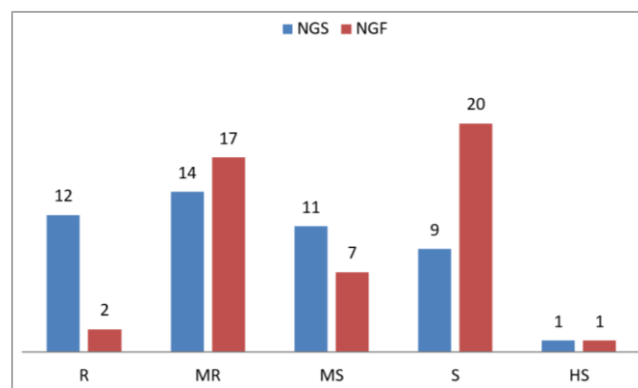


Figure 2. Response of genotypes to chick pea *Fusarium* wilt at seedling and flowering stage in 2023.

Note: NGS=number of genotypes at seedling stage, NGF=number of genotypes at flowering stage

The observed decline in resistance from seedling to flowering stage agrees with the findings of Muhammad [21], who reported that several chickpea genotypes expressing resistance during early growth stages became susceptible at later developmental stages. This may be attributed to differences in disease progression among genotypes, where resistant lines slow pathogen development while susceptible lines permit rapid colonization of plant tissues.

Table 1. Mean of disease incidence at seedling and flowering stage.

Genotype	2022		2023		Over all mean	
	DIS%	DIF%	DIS%	DIF%	DIS%	DIF%
DZ-2012-Ck- 0281	37.50	20.00	33.33	10.20	35.42	15.10
DZ-2012-Ck-0007	14.29	13.33	12.77	23.33	13.53	18.33
DZ-2012-ck-0212	50.00	45.45	58.33	44.74	54.17	45.10
DZ-2012-Ck-0245	16.67	16.00	11.11	16.67	13.89	16.33
DZ-2012-Ck-0220	42.86	41.67	37.50	42.31	40.18	41.99
DZ-2012-Ck-0224	36.67	31.58	31.71	33.33	34.19	32.46
DZ-2012-Ck-0070	34.62	35.29	36.36	30.00	35.49	32.65
DZ-2012-Ck-0288	20.00	20.83	14.29	20.00	17.14	20.42
DZ-2012-Ck-0282	9.09	13.33	7.32	10.42	8.20	11.88

Genotype	2022		2023		Over all mean	
	DIS%	DIF%	DIS%	DIF%	DIS%	DIF%
DZ-2012-ck-0265	7.41	4.00	9.09	15.38	8.25	9.69
DZ-2012-Ck-0246	33.33	35.71	22.22	37.50	27.78	36.61
DZ-2012-Ck-0266	11.76	20.00	11.11	38.46	11.44	29.23
DZ-2012-ck-0273	15.79	12.50	14.81	15.79	15.30	14.14
DZ-2012-ck-0255	23.81	31.25	25.00	33.33	24.40	32.29
DZ-2012-Ck-0202	28.57	30.00	25.00	35.71	26.79	32.86
DZ-2012-ck-0302	7.69	16.67	7.32	23.26	7.50	19.96
DZ-2012-ck-280	10.71	16.00	7.41	8.33	9.06	12.17
DZ-2012-Ck-0279	11.76	13.33	7.69	18.00	9.73	15.67
DZ-2012-Ck-0243	4.17	13.04	7.14	11.32	5.65	12.18
DZ-2012-Ck-0251	27.59	33.33	20.00	45.45	23.79	39.39
DZ-2012-Ck-0299	22.50	25.81	21.05	33.33	21.78	29.57
DZ-2012-Ck-0285	12.20	22.22	7.41	25.00	9.80	23.61
DZ-2012-Ck-0252	33.33	44.44	28.57	40.00	30.95	42.22
DZ-2012-Ck-0300	23.53	30.77	25.00	31.03	24.26	30.90
DZ-2012-Ck-0229	12.12	17.24	11.36	15.38	11.74	16.31
DZ-2012-Ck-0208	19.61	12.20	11.76	15.79	15.69	13.99
DZ-2012-Ck-0287	10.81	18.18	18.92	19.57	14.86	18.87
DZ-2012-Ck-0083	25.00	33.33	27.50	31.25	26.25	32.29
DZ-2012-Ck-0303	25.00	33.33	22.58	38.89	23.79	36.11
DZ-2012-Ck-0283	11.76	20.00	15.69	20.83	13.73	20.42
DZ-2012-Ck-0218	23.81	25.00	20.75	34.48	22.28	29.74
DZ-2012-Ck-0296	11.54	17.39	20.00	16.00	15.77	16.70
Flip -09-187c	10.53	17.65	3.64	21.95	7.08	19.80
Flip -07-128c	6.90	3.70	4.17	15.15	5.53	9.43
Flip -07-35c	14.29	11.11	10.00	10.81	12.14	10.96
Flip -09-159c	16.00	23.81	27.78	30.00	21.89	26.90
Flip -06-158c	3.85	12.00	5.71	8.70	4.78	10.35
DZ-2012-Ck-0268	5.71	12.12	5.13	12.50	5.42	12.31
DZ-2012-Ck-0199	11.76	16.67	10.53	11.76	11.15	14.22
Flip -93-146c	30.77	44.44	37.14	46.88	33.96	45.66
DZ-2012-Ck-0250	40.00	55.56	42.86	46.15	41.43	50.85
Flip -09-100c	23.08	30.00	25.64	33.33	24.36	31.67
Flip -09-154c	44.44	40.00	35.59	42.86	40.02	41.43
ICC- 3279	60.00	50.00	39.53	54.55	49.77	52.27
Flip -00-20c	10.53	17.65	18.64	12.96	14.59	15.31
Flip -13-298c	17.39	15.79	15.52	33.33	16.45	24.56

Genotype	2022		2023		Over all mean	
	DIS%	DIF%	DIS%	DIF%	DIS%	DIF%
Flip -10-260c	25.93	35.00	31.43	35.71	28.68	35.36
Mean	22.61	24.24	21.49	26.45	20.44	25.34

Note: DIS=disease incidence at seedling, DIF=disease incidence at flowering stage

Across the two years of evaluation, twenty-four genotypes exhibited resistant or moderately resistant reactions in 2022. However, five of these genotypes failed to maintain a consistent response in 2023, indicating the influence of environmental conditions and genotype-by-environment interactions on disease expression. Previous studies have also shown that variability in pathogen races and environmental conditions can affect the stability of resistance in chickpea germplasm [26].

Based on combined performance across years and growth stages, two genotypes, Flip-06-158C and DZ-2012-CK-280, consistently exhibited resistant reactions to Fusarium wilt. In addition, seventeen genotypes, namely DZ-2012-CK-0281, DZ-2012-CK-0282, Flip-07-35C, DZ-2012-CK-0243, DZ-2012-CK-0199, DZ-2012-CK-0268, Flip-00-20C, Flip-07-128C, DZ-2012-CK-0265, DZ-2012-CK-0229, DZ-2012-CK-0273, DZ-2012-CK-0208, DZ-2012-CK-0296, DZ-2012-CK-0245, DZ-2012-CK-0279, DZ-2012-CK-0287, and DZ-2012-CK-0288, were classified as moderately resistant. These genotypes represent valuable sources of resistance and could be utilized in chickpea improvement programs aimed at developing Fusarium wilt-resistant cultivars. The identified resistant and moderately resistant genotypes may also serve as parental materials for resistance breeding and adaptation studies in wilt-prone environments.

4. Conclusion and Recommendation

The present study demonstrated substantial variation in Fusarium wilt resistance among the evaluated chickpea genotypes under field conditions in West Hararghe, Ethiopia. Among the forty-seven genotypes screened, two genotypes exhibited stable resistance, while seventeen showed moderate resistance across the evaluation period. The identified resistant and moderately resistant genotypes constitute important genetic resources for the development of Fusarium wilt-resistant chickpea varieties.

Based on their consistent performance, nineteen genotypes are recommended for advancement to the next stage of breeding and evaluation. Further multi-location testing is recommended to verify the stability of resistance under diverse environmental conditions and pathogen populations. The resistant genotypes identified in this study can also be incorporated into chickpea breeding programs as potential sources of resistance genes for the development of improved cultivars.

Abbreviations

ICRISAT International Crops Research Institute for the Semi-Arid Tropics

Author Contributions

Daba Etafa: Conceptualization, Methodology, Investigation, Formal Analysis, Data curation, Visualization, Writing – original draft, Writing – review & editing

Conflicts of Interest

The author declares no conflict of interest.

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