

Abstract

Fusarium wilt (*Fusarium oxysporum* f. sp. *ciceris*) is an important biotic constraint to chickpea production worldwide. Host plant resistance is the most durable and economical way to manage these diseases. Fusarium wilt epidemics can devastate crops and cause up to 100% loss in highly infested fields under favorable conditions. The current study (funded by GRDC and ICARDA) aimed to identify new resistant genetic sources of chickpea against Fusarium wilt through multi-environment and multi-year screening. One hundred eighty chickpea genotypes were selected from the genetic resource section (GRS) of ICARDA based on the passport data using the focused identification of germplasm strategy (FIGS). The experiment was planted with an Alpha Lattice design in two locations (Terbol-Lebanon and Beja-Tunisia during the 2015, and 2016 seasons). The susceptible check (ILC482) was repeated every ten rows. The genotype (G) and genotype × environment interaction (GEI) have been conducted, and the GGE biplot analysis has indicated significant variations ($p \leq 0.001$) between genotypes and environments that are due to the genotype × environment interaction. Six genotypes (IG74725, IG9050, IG6049, IG9631, IG70283, and IG8914) were highly resistant to wilt (<10% mean disease incidence) across the two locations. Also, there are nine moderately resistant genotypes for wilt (<20% mean incidence). IG70283 had the highest stability in two locations and years. The resistant genotypes identified in this study were used in ICARDA breeding programs to develop new cultivars that are more resistant to FW and more stable in different environments.

Introduction

Chickpea (*Cicer arietinum* L.) is an important leguminous crop grown in a wide range of environments. It is mainly used for human consumption and is an essential constituent of the Mediterranean diet, with a total production of 15.9 million tons (FAO, 2021). Global legume production is severely challenged by a variety of fungal diseases, of which wilt is caused by *Fusarium oxysporum* one of the major biotic stresses limiting chickpea production is its susceptibility to fungal diseases. Fusarium wilt has become a major threat to chickpea production, and the yield losses range from 10 to 90%, depending upon the severity of the disease and climatic conditions (Figure 1). Reducing the losses due to this stress is important to enhance crop tolerance and production. The selection of many varieties, including chickpea suitable for the production environment is often challenged by the existence of (GEI) in the variety development process. The objective of this study in chickpea is to underscore the significance of multi-environment trials (MET) in the context of genotype × environment (GE) interactions. Furthermore, our study aims to emphasize the importance of biplot analysis as an important statistical tool in the pursuit of identifying chickpea genotypes resistant to Fusarium wilt (FW).



Figure 1. The symptoms of Fusarium wilt in chickpea plants under different severity of the disease and climatic conditions.

Materials and Methods

One hundred eighty chickpea genotypes were selected from the genetic resource section (GRS) of ICARDA and were screened for their level of resistance/susceptibility against fusarium wilt under two field conditions (Terbol-Lebanon and Beja-Tunisia during the 2015, and 2016 seasons). The experimental layout was an Alpha Lattice design with two replications. The susceptible check (ILC482) was repeated every ten rows at each location and year (Figure 2).



Figure 2. The susceptible chickpea repeated check (ILC482).

The scale for disease incidence (DI) was grouped as: 0-10%: Highly resistant; 11-20%: Resistant; 21-30%: Moderately resistant; 31-50%: Susceptible; 51-100%: Highly susceptible (Figure 3). $DI (\%) = (\text{Number of plants wilted} / \text{Total number of plants}) \times 100$



Figure 3. Evaluation of the level of resistance and susceptibility of plants.

Result and Conclusion

The analysis of variance (ANOVA) revealed highly significant differences ($P < 0.001$) among genotypes (G) and genotype X environment interactions (GEI), with significant differences ($P < 0.05$) observed for environments (Table 1). Genotypes accounted for 51.3% of the variation, GEI for 32.1% and the environment for only 11%. Notably, the high broad-sense heritability ($h^2 = 0.76$) indicated substantial genetic variation among the genotypes.

Table 1. Analysis of variance of fusarium wilt disease for 180 chickpea genotypes grown at two locations.

Source of variation	Df.	Sum of Squares	Mean of squares	%SS	Significance
Environment	3	277563.4	92521.1	13.3	*
Genotype	179	864766.4	4831.1	41.3	***
Genotype x Environment	513	561244.1	1094	28.8	***
Error	692	359186.4	519.1		
Total	1391	2094438.7			

* Indicates statistical significance at 0.05 level ($Pr(<F) < 0.05$).

*** Indicates highly significant results at 0.001 level ($Pr(<F) < 0.001$).

The average of disease incidences varied from 0 to 75% in Terbol and from 0 to 54% in Baja. For example, genotype IG5892 showed high resistance to Fusarium wilt in Baja with only 5% disease incidence but was highly susceptible with 60% disease incidence in Terbol. This demonstrates the importance of multi-environment testing to identify resistance genotypes that can perform well across different locations and pathogen populations. Six genotypes (IG74725, IG9050, IG6049, IG9631, IG70283, and IG8914) were highly resistant to wilt (<10% mean disease incidence) across the two locations. Also, there are nine moderately resistant genotypes for wilt with <20% mean incidence (Figure 4).

The primary (PC1) and secondary (PC2) components explained 74.97% and 16.28% of genotype main effects and $G \times E$ interaction respectively (Figure 5). IG70283 had the highest stability in two locations and years. The resistant genotypes identified in this study were used in ICARDA breeding programs to develop new cultivars with improved FW resistance and improved stability across different environments.

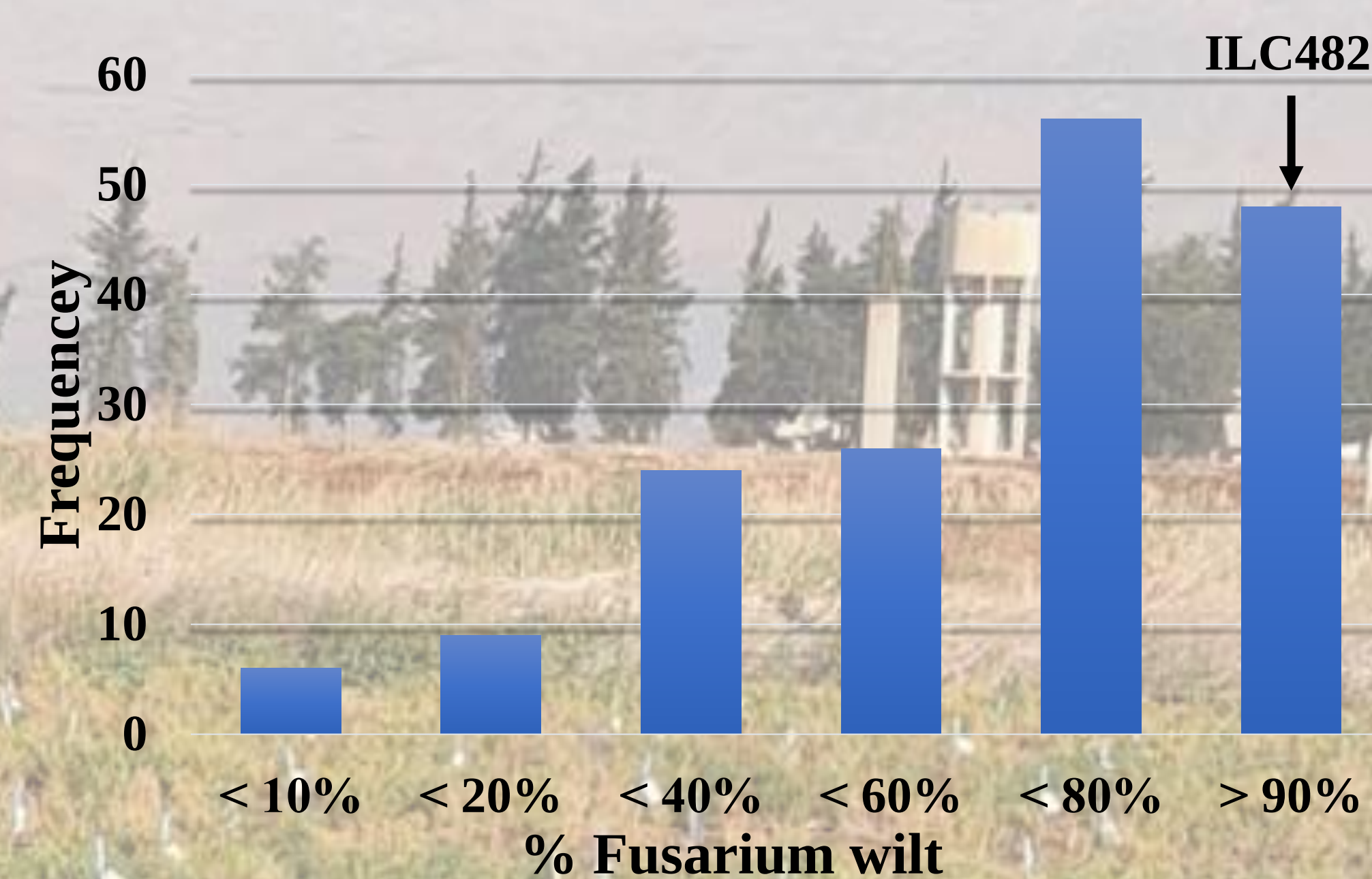


Figure 4. Frequency distribution of % fusarium wilt infection. The mean performance of the susceptible check (ILC482) is indicated above the bars.

Figure 5. Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for the means performance and stability of genotypes. Green and blue numbers stand for genotypes and environments, respectively.

