

New Sources of Resistance and Heritability to Wilt/Root Rot Complex Diseases in Kabuli Chickpea

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Abstract

Chickpea wilt/root rot complexes are the most important yield-limiting factors in spring planted chickpea in the Mediterranean region, south Asia, and East Africa highlands. In West Asia and North Africa, *Fusarium* wilt caused by *Fusarium oxysporum* f.sp. *ciceri* (*Foc*) is a dominant pathogen in the disease complex. ICARDA Kabuli chickpea breeding program evaluates breeding lines in sick plots dominated with *Foc* pathogen for global elite lines supplies. In the 2021–2022 growing season, 240 genotypes were evaluated in sick plots at Terbol ICARDA research station in Lebanon and naturally infested experimental field at Merchouch ICARDA research station in Morocco. The experiment was laid out in an alpha lattice design with two replications. Percent plant mortality was scored on plot bases once the average mortality of the susceptible line (ILC482) reached over 95%. The analysis of variance (ANOVA) analysis has indicated that the genetic variation among genotypes was caused by genetic variation as broad sense heritability was high ($h^2 = 0.76$). However, only 51.3% of the changes were attributable to the genotypes, and only 11% to the environment (locations). Only four genotypes (S180005, S180022, S180071, and S180079) showed good levels of resistance (<20%) at both locations. These genotypes will be utilized for pyramiding additional resistance genes into other FW races and producing high-yield breeding varieties through the chickpea breeding program at ICARDA and will be shared with the national chickpea breeding programs in CWANA countries.

Introduction

Chickpea (*Cicer arietinum* L.) is the second grain legume cultivated in the world, with a total cultivated area of 15 million hectares and ranked third among the pulse crops; and accounts for 15.87 million tons annually (FAO, 2021). South Asia is by far the largest producer of chickpea (76%) in the world with a share of more than 80% area followed by the Middle East and North Africa. Global legume production is severely challenged by a variety of fungal diseases caused by *Fusarium* wilt is one of the most destructive. For instance, chickpea is affected by *F. oxysporum* f.sp. *ciceris* (*Foc*). *Fusarium* wilt has become a major threat to chickpea production, and the yield losses range from 10 to 100%, depending upon the severity of the disease and climatic conditions (Figure 1). Eight races 0, 1A, 1B/C, 2, 3, 4, 5, and 6 having been identified so far, are key elements in the development and management of the disease. Genotype × Environment interaction (GEI) is an important aspect of plant breeding programs. It may arise when certain genotypes are grown in a diverse set of environments. The lack of consistency in performance across environments encourages researchers to determine new sources of resistance genotypes to *Fusarium* wilt under different field conditions.



Figure 1. Comparative symptoms of *Fusarium* wilt in chickpea between two locations (Marchouch station in Morocco and Terbol station in Lebanon).

Materials and Methods

The International Center for Agricultural Research in the Dry Areas (ICARDA) selected 240 elite genotypes of Kabuli chickpea, with ILC482 as the susceptible check. The experiments were conducted during 2021/2022 in two locations, Terbol (Lebanon) and Merchouch (Morocco), using a two-replication Alpha Lattice design. Disease incidence (DI) was calculated as the ratio of wilt symptom-presenting plants to the total number of yellowing or wilting plants.

$$DI (\%) = (\text{Number of plants wilted} / \text{Total number of plants}) \times 100$$

Genotypes were grouped in classes regarding the scale for disease incidence: 0-10%: Highly resistant; 11-20%: Resistant; 21-30%: Moderately resistant; 31-50%: Susceptible; 51-100%: Highly susceptible.

Result and Conclusion

The analysis of variance 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 241 chickpea genotypes grown at two locations

Source of variation	df.	SS	MS	Var. %	Significance
Environment	1	84351.49	84351.49	40.31	*
Genotype	240	394370.65	1643.21	20.71	***
Genotype x Environment	240	246745.51	1028.11	12.96	***
Error	480	38088.85	79.35	4.23	
Coefficient of variation	8.8%				

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

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

The evaluation identified 10% of the genotypes as moderately resistant, with a wilt incidence rate of <20%. Among them, four genotypes (S180005, S180022, S180071, and S180079) exhibited excellent resistance at both locations (Figure 2). These promising, highly resistant genotypes will serve as valuable sources for creating desired recombinants and high-yield breeding varieties through ICARDA's chickpea breeding program. Additionally, they will be distributed to national chickpea programs in CWANA countries.

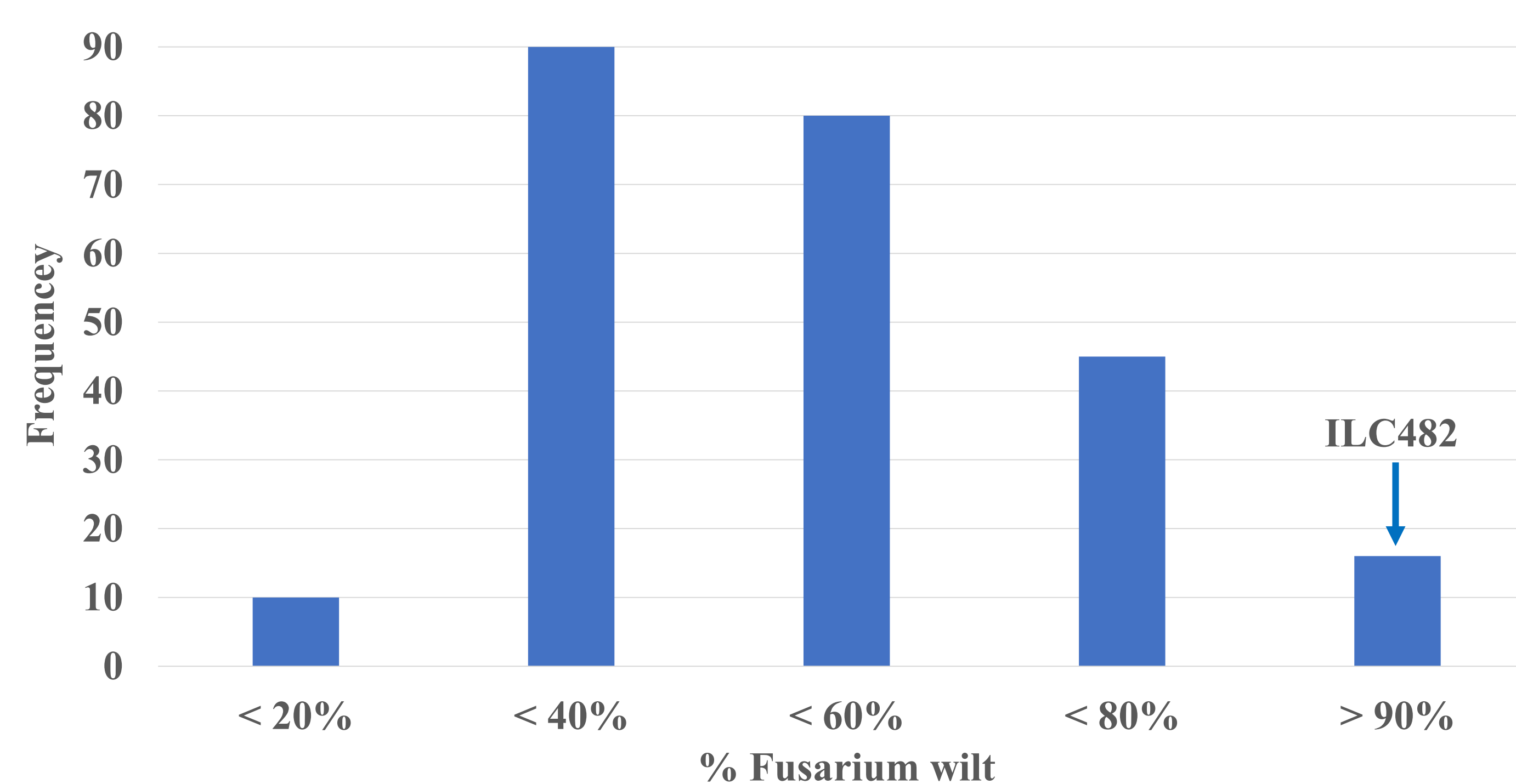


Figure 2. Frequency distribution of % *fusarium* wilt infection. The mean performance of the susceptible check (ILC482) is indicated above the bars.