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Abstract:

Fusarium wilt (*Fusarium oxysporum* f. sp. *ciceris*) of chickpea is the major limitation to chickpea production worldwide. Host plant resistance is the major component in the management of fungal diseases in chickpea. This study was conducted with the aim to find new sources of resistance chickpea genotypes against fusarium wilt. The experiment was conducted in 2017-2018 at the sick plot at the International Center of Agricultural Research in the Dry Area (ICARDA), Terbol station, Bekaa valley, Lebanon. The experiment was laid out in an augmented block design (ABD), and the high susceptible check (ILC482) was repeated after each tenth row. The total number of the genotypes used in this study was 974, they included (34) accessions from the genebank, and (940) breeding lines from the chickpea breeding program at the ICARDA. Finally, 45 promising lines without symptoms were selected to be distributed through the chickpea fusarium wilt Nursery (CFWN) in 2021 for further testing in different locations. This is an important material in chickpea to enhance fusarium wilt chickpea resistance in the future.

Introduction:

Chickpea (*Cicer arietinum* L.) is cultivated in different parts of the world mainly in the Mediterranean, South Asia, North Africa, the Middle East, and North and Central America. Among biotic constraints affecting chickpea production, Fusarium wilt (FW) caused by *Fusarium oxysporum* f. sp. *ciceris* (FOC) is one of the widely distributed diseases of chickpea and cause yield loss up to 10–100% depending on varietal susceptibility and climatic conditions. The pathogen can stay alive in the soil in the absence of the host for at least 6 years. The wilt can be observed in the susceptible genotype within 25 days after sowing in the field. The pathogens attack the roots of plants and cause wilting as a result the whole plant shows drooping of leaves and paler color than healthy plants. The plant finally collapses and dies by showing gradual wilting symptoms. Such plants do not show external rotting and look healthy when cut vertically downward from the collar region, showing brown streaks of the internal tissues. Limited germplasm of chickpea resistant to Fusarium wilt is found in existing chickpea species so, this work aims to determine new sources of resistance for Fusarium wilt under field conditions.



Materials and methods:

During 2017/2018 cropping season, a total of 974 chickpea genotypes including 940 breeding lines and 34 germplasm accessions were screened for Fusarium wilt resistance in a sick plot at ICARDA. Out of a total, 713 promising lines having $\leq 10\%$ wilt incidence were selected primarily for further evaluation. The selected genotypes were further evaluated in 2020/2021 through augmented block design (ABD) in two replications. Each genotype was sown in a 3 m long row having a 45 cm row to row distance. A susceptible check (ILC482) was sown after every tenth row. Data for the number of wilted plants in each replication were recorded when the killing of ILC482 had occurred.

Percent disease incidence in each test genotype was calculated using the following formula:

$$\% \text{ Disease incidence} = (\text{No. of infected plants} / \text{Total no. of plants}) \times 100$$

Based on the mortality of plants to Fusarium wilt, the test genotypes were divided into four categories, highly resistant (0% plants infested), resistant (6-10% plants infested), moderately resistant (21-40% plants infested), susceptible (61-80% plants infested), and highly susceptible (100% plants infested).



Result and conclusion:

Analysis of variance (ANOVA) results showed significant variation ($P < 0.001$) among genotypes in response to disease. The first round of evaluation identified seven-hundred and thirteen lines (73%) were moderate resistant with wilt incidence $< 20\%$ infection rate. The second round of evaluation (2020/2021) confirmed the resistance of 129 genotypes with wilt incidence $< 10\%$ infection rate, and only 45 genotypes without any symptoms (Figure 1). The 129 resistance genotypes were used in the breeding program to improve the genetic variation for Fusarium wilt. A total of 45 highly resistant genotypes including susceptible check were selected to constitute Chickpea International Fusarium Elite Nursery (CIFEN) to be distributed to research stations in different locations in the world. Most of the genetic variability genotypes showing resistance to Fusarium wilt diseases could be utilized in a hybridization breeding program for transferring multiple resistance/ tolerance traits into high yielding elite cultivars. These promising genotypes with high resistance to wilt would be a good source for making desirable recombinants or may be used directly as a variety.

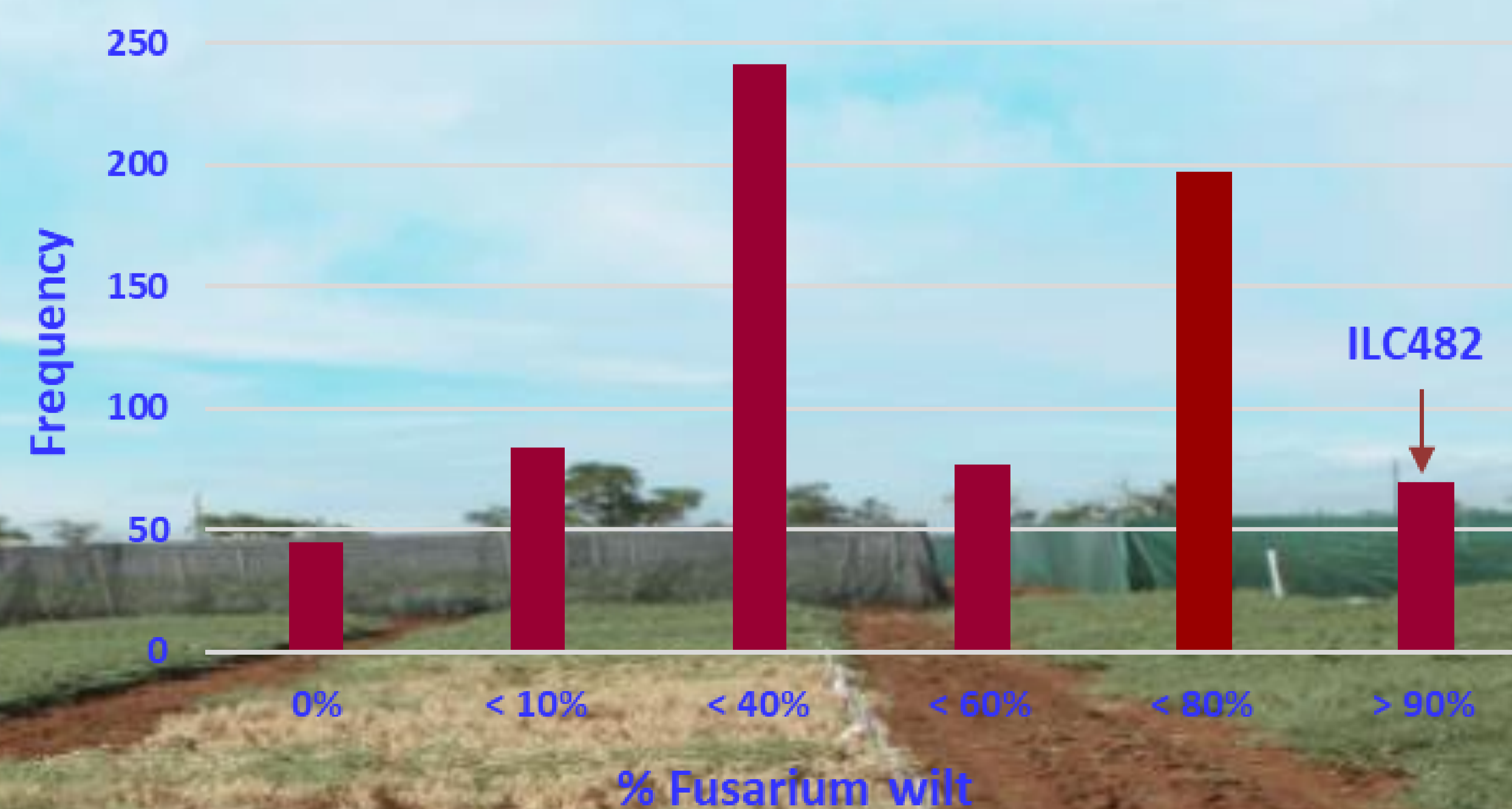


Figure. Frequency distribution of % fusarium wilt infection. The mean performance of the susceptible check (ILC482) is indicated above the bars