

## Abstract

Ascochyta blight (AB) caused by *Ascochyta rabei* (Pass.) Labr. is a significant constraint that adversely affects the productivity and quality of chickpea (*Cicer arietinum* L.). Over the past two decades, numerous resistant genes/QTLs have been identified for this pathogen. To establish a comprehensive collection of chickpea genotypes with resistance to AB, the Global Ascochyta Blight Resistant Set Collection (GABRSC) was initiated through GRDC funding. The GABRSC comprises 200 Desi and Kabuli-released resistant varieties breeding lines, and landraces. Field Phenotyping of GABRSC was conducted in 2022 and 2023 cropping seasons at six AB hot spot sites in India (Punjab), Turkey, Tunisia, Lebanon, Morocco, and Ethiopia. The experimental design was Alpha Lattice with two replications. The primary objective of this study was to identify sources of resistance that exhibit stability across multiple environments that favor AB epidemics. Genotypes were rated using a 1–9 scale where 1= highly resistant and 9= highly susceptible. REML analysis revealed highly significant effects of environments, genotype, and genotype × environment interaction. Genotype and genotype × environment (GGE) biplot analyses of multi-environmental results showed four genotypes (S0110227, S160454, S0110088, and S0110028) consistently exhibited resistance (<3) across all the environments. The four genotypes were derived from the ICARDA breeding program, which involved the pyramiding of various resistant genotypes through crosses and demonstrated higher levels of resistance across diverse locations. The resistant genotypes identified in this study hold significant potential for integration into breeding programs as stable sources of resistance, facilitating the development of agronomically desirable Ascochyta blight-resistant varieties. These findings contribute to the advancement of sustainable and resilient chickpea cultivation, ultimately leading to increased chickpea yields.

## Introduction

Chickpea (*Cicer arietinum* L.) is the second most important grain legume in the human diet of Mediterranean and Asian countries that has been increasingly adopted as food globally. The seeds are used for both human and animal nutrition, as they contain a high level of proteins (20-23 %), carbohydrates (60.7 %), and dietary fibers (17.4 %). Ascochyta blight (AB), caused by *Ascochyta rabei* (Pass.) Labr. is an important disease of chickpea in many countries (India, Bangladesh, Algeria, Italy, Morocco, Nepal, Spain, Pakistan, Syria, Iran, Australia, and Canada) where cool and humid weather prevails during the flowering to podding stage. AB severely reduces the yield of chickpea and can cause complete yield losses of up to 100% under favorable conditions (Figure 1). Control of AB is essential to ensure stable chickpea production. The use of fungicides does not give complete protection and is usually uneconomical. Therefore, this research aimed to evaluate the performance and stability of Ascochyta blight-resistant chickpea breeding lines in different environments.



**Figure 1.** Ascochyta blight symptoms on chickpea stem, pods, and leaves under favorable conditions

## Materials and Methods

During the 2022 and 2023 cropping seasons the total of GABRSC comprises 200 Desi and Kabuli-released resistant varieties, breeding lines, and landraces established a comprehensive collection of chickpea genotypes with resistance to AB to screen at six AB hot spot sites in India, Turkey, Tunisia, Lebanon, Morocco, and Ethiopia. Alpha Lattice design trial was conducted with two replications at each location (Figure 2). Data were analyzed with GenStat software version 21 using REML- meta-analysis for multi-environments considering genotypes as random. Genotypes were rated using a 1–9 scale where 1= highly resistant and 9= highly susceptible.



**Figure 2.** The layout of the Ascochyta blight field with two replications.

## Result and Conclusion

The results of variance components (REML analysis) showed high significance ( $P < 0.001$ ) among genotypes (G), environment (E), and the interaction (G × E) for Ascochyta blight (Table 1). Genotype and genotype × environment (GGE) biplot analyses of multi-environmental results showed four genotypes (S0110227, S160454, S0110088, and S0110028) consistently exhibited resistance (<3) across all the environments. The four genotypes were derived from the ICARDA breeding program, which involved thorough crosses and demonstrated higher resistance across diverse locations.

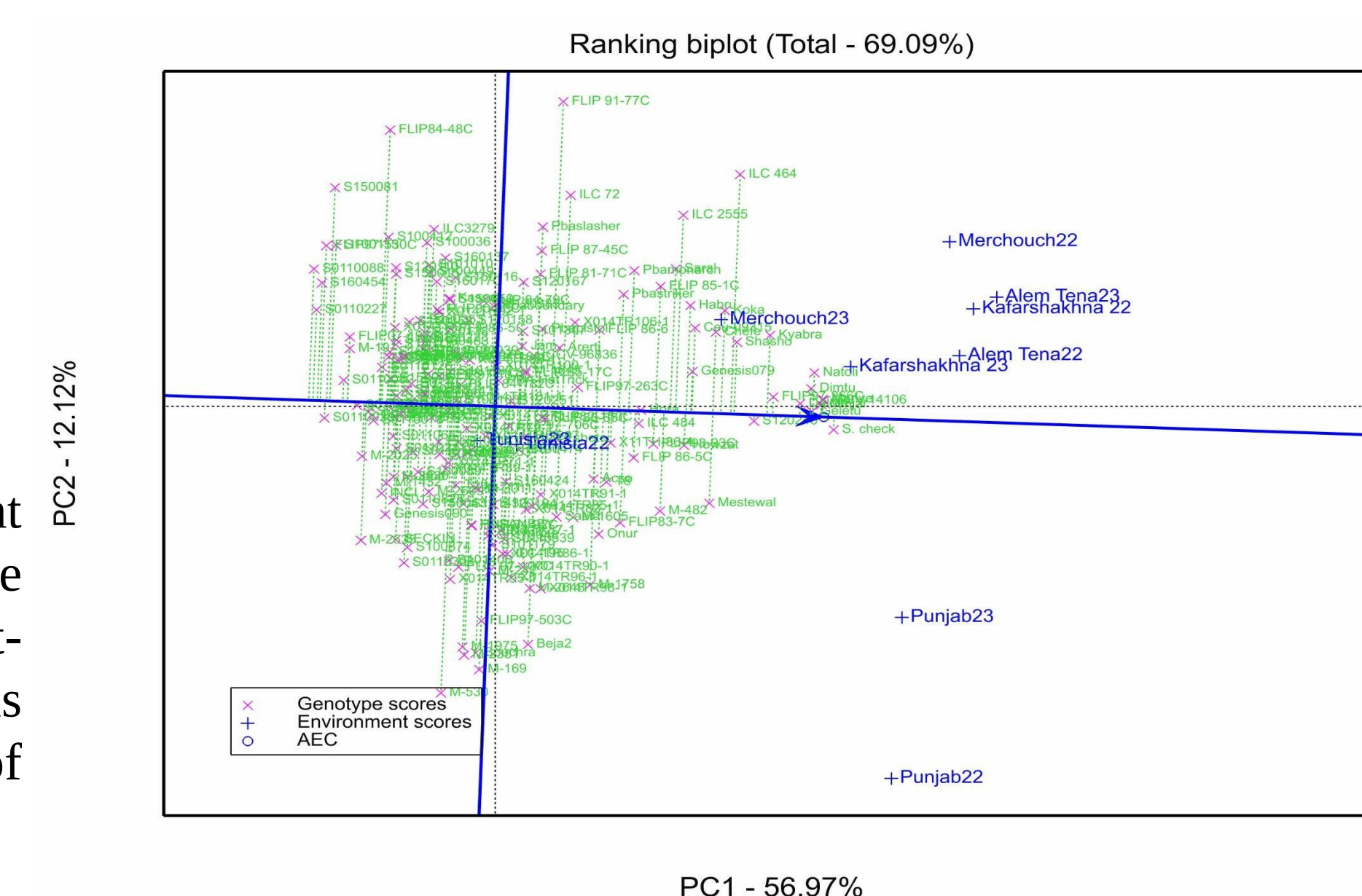
**Table 1.** Components of variance for Ascochyta blight score of 200 genotypes under multi-environment.

| Fixed term                    | Wald statistic | d.f  | Wald/d.f. | Chi-sq. probability |
|-------------------------------|----------------|------|-----------|---------------------|
| <b>Genotype</b>               | 7241.09        | 203  | 35.67     | <0.001              |
| <b>Environment</b>            | 301.64         | 7    | 43.09     | <0.001              |
| <b>Genotype x Environment</b> | 1764.42        | 1417 | 1.25      | <0.001              |

The GGE biplot for AB accounted for 69.09% of the variation due to G main effect and G × E interaction. The primary (PC1) and secondary (PC2) components explained 56.97% and 12.12% of genotype main effects and G × E interaction respectively (Figure 3).

The S100115 had the highest stability with an AB score (<4) in all locations and years.

**Figure 3.** Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for the means performance and stability of genotypes.



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