PHYTOPATOMETRIC RESPONSE OF CHICKPEA (*Cicer acridinium* l.) GENOTYPES AGAINST ASCOCHYTA BLIGHT (*Ascochyta rabi*) DISEASE AT WEST BELESA DISTRICTS, NORTHWESTERN ETHIOPIA.

Misganaw Gelaye,[1] ,Assefa Sintayehu[2] (PhD), Yigrem Mengist[2] , Anteneh Adebabay[1]
Correspondence author: Misganaw Gelaye**;** misganaw.g@yahoo.com

Abstract

Ascochyta blight is a serious disease in chickpeas, can cause up to 100% yield loss. This study focuses on phytopatometric response of chickpea genotypes against Ascochyta blight, using 75 backcrossed disease resistance accessions and six varieties with local check.

Experiments were conducted in a 2 m x 0.6 m plots area, the spacing was 30 cm, 10 cm inter, and intra–row spacing respectively with each plot having two rows, between plots 0.3m, and between block 1m. Laboratory and greenhouse conditions on chickpea seedlings development, the study analyzed by using SAS software and Minitab's disease data from Ascochyta plants scored in a lattice design, revealing a wide range of responses from resistance to highly susceptible reactions.

The average severity index ranged from (16-25.5%), DZ-2012--CK-0253 (16.6), ICCU-92219 (20 %), ICCU-91212(21.11 %), Eshete (21.11 %), ICCU-13617 (22.22 %), Natoli (25.54 %), and DZ-2012-CK-0039 (25.5%), for resistance genotypes, with moderately resistance genotypes ranging from (31.5-52.54%) ICCMABCD-20 (31.583) MABC-2 (36.39) ICCU-13602 (38.05) ICCV-14106 (43.89) MABC-11(50.20) FLIP-2010-24C (51.74) ICCMABCD-23 (52.54). Moderately susceptible genotypes ranged from 56.8-100%. In general, 9% resistance 9%, moderately resistant, 2% moderately susceptible, 20% susceptible, and 45% highly susceptible were found, but none of the tested genotypes was highly resistant or immune.

The study suggests high yielder and new sources of resistance and moderate resistance against Ascochyta diseases those genotypes are used for next to breeding programs whereas Eshete directly used as varieties in areas having incidence of these diseases

Keywords: Ascochyta blight; Chickpea; Phytopathometric; Resistance; **Genotype:**

Background

Chickpea is a crucial grain legume, that is grown globally for human and animal consumption, contributing to soil fertility by converting atmospheric nitrogen [1]. 89.7% of the crop is grown in Asia, 5% in Africa, 2.6 in Oceania, 2.9 in the Americas, and 0.4 in Europe out of the more than 50 countries that grow it. [2]. Africa's chickpea production, primarily from Ethiopia, Malawi, Tanzania, Kenya, and Morocco, contributes 5% of the world's total, making Ethiopia the largest producer globally [3]. Chickpea is grown anywhere in the Amhara region, but it is most abundant in Central Gondar, North Shewa, South Gondar, East Gojam, West Gojam, and South Wollo. In general, Amhara Regional State has 55.5% of the crop and land coverage and 51.1% of its production in Ethiopia [4].

However, the yield potential of chickpeas is as high as 5 tons per hectare, in the study areas the productivity is 2.27 tons per hectare [5]. Numerous biotic and abiotic factors are to blame for the decline in chickpea productivity and production. Ascochyta blight (Ascochyta rabiei), Fusarium wilt (*Fusarium oxysporum* f.sp. ciceri), phytophthora root rot (*Phytophthora medicaginis*), and Botrytis grey mold (*Botrytis cinerea*) are a few examples of biotic agents (Li et al., 2021). Ascochyta blight is a prevalent and detrimental foliar disease that is responsible for substantial crop losses in Ethiopia's primary growing regions. It is considered the most significant fungal disease in terms of economic impact in the majority of chickpea-producing countries worldwide, including Ethiopia. [6].

It is one of the most important foliar fungal diseases of chickpeas and leads to yield losses of about 100%, in favorable environmental conditions, and susceptible varieties, In the earlier study's, indicated that from the study area (44.97%) relative grain yield loss was recorded from Teje chickpea variety [7]. On all leaf portions of the crop, the teleomorph and the anamorph (Ascochyta rabiei) may generate distinctive necrotic lesions that result in tissue collapse, stem breakage, and plant death. [8]. Frequent rainfall at flowering and pod formation stages can create a conducive environment for the infection and symptoms expression [9].

Due to seed exchanges and changes in rainfall patterns, foliar blight disease is becoming a more serious problem in Ethiopia [3]. At every physiological stage, from seedling to maturity, the weather has an impact on the development of the disease. The most significant contributors to the likelihood of disease and, thus, the development of disease epidemics are meteorological variables including temperature, relative humidity, continuous rainfall, the length of time leaves are wet and windy and overcast weather [10] and [11].

Cultural techniques like ideal plant populations, planting patterns, and fungicides have been used to reduce Ascochyta blight, but they are easily contaminated and spread over large areas. Seeds are primary inoculums for long-distance propagation, but they are costly due to repeated application requirements. Variability in pathogen genotypes is crucial for disease resistance. The reason why seed is the primary source of inoculums for long-distance propagation is because different fungicides are used for this disease in areas with low agricultural yield. Using these methods can be very costly due to their repeated application requirements, even though some have shown promising results as seed treatments. But Ascochyta blight is sporadic[12] and [8] due to this reason variability of the pathogen on the genotypes must be identified at the levels of disease resistance.

MATERIAL AND METHODS

Description of Study Area

The field experiments were carried out in West Belesa, located at longitude 120 20' 59'' N, latitude 370 47' 39'' E, and altitude minimum and maximum were respectively, 1777m to 1806 m a.s.l and annual rainfall 800-1200 ml, and annual temperature of 15.5 and 30^0_c According to the meteorological data of the center. The study was conducted during the 2023 main cropping season at West Belesa district in North Western Ethiopia, the Area is one of the moisture stress areas, whereas, agriculture and allied activities are the predominant income sources, chickpea, Teff, and Sorghum are the major crops cultivated in the area [5].

Treatments and Experimental Design

This study was conducted under field, laboratory, and greenhouse conditions to evaluate the phytopathogenic responses of different chickpea genotypes, particularly their resistance to Ascochyta blight. A total of 75 accessions, which were molecularly crossed materials aimed at disease control, were assessed alongside five released varieties and one local variety. The accessions were obtained from the Debre Zeit Agriculture Research Center, while the other six released varieties, including the local variety, were sourced from the Gondar Agricultural Research Center. The released varieties included Grarie, Natoli, Dimitu, Eshetete, Dalota, and the local check variety (Table 1).

The experiment utilized a simple lattice design and was conducted in a total area of 19 m x 5.4 m, with individual plots measuring 2 m in length and 0.6 m in width. The planting was arranged with inter-row spacing of 30 cm and intra-row spacing of 10 cm. Each plot consisted of two rows, with a distance of 0.3 m between plots and 1 m between blocks.

Pathogen Isolation and Identification

The morphological characterization and identification of the chickpea Ascochyta blight pathogen were conducted at the University of Gondar, specifically in the College of Agriculture and Environmental Sciences (CAES) plant protection laboratory. Samples of Ascochyta blight-

infected chickpea plants were collected from a hotspot area in West Belesa, where the disease was prevalent and spreading rapidly.

To prepare the samples, the stems, pods, and seeds were thoroughly cleaned with tap water. Diseased tissue was cut into small pieces and surface sterilized for 30 seconds using either 70% ethyl alcohol or 0.5% sodium hypochlorite. This sterilization was followed by rinsing the pieces three times with sterile distilled water for two minutes each time. The sterilized tissue was then aseptically placed on separate Petri plates containing sterilized potato dextrose agar (PDA) media.

After five days of incubation at 25°C, colonies of the Ascochyta blight fungal pathogen were transferred to fresh PDA. The fungi were sub cultured and purified by transferring the hyphal tip into PDA slants, which were maintained as stock cultures for further studies. The identification of the fungi was based on cultural (morphological) characteristics, focusing primarily on growth patterns and pigmentation. Additional microscopic examinations of mycelial and conidial structures were performed using an identification manual of illustrated genera of imperfect fungi. For morphological characterization, a small amount of mycelium was taken from ten day old pure culture plates using a sterile needle and transferred to a cleaned glass slide. Mycelium samples were collected from five different positions on the culture plate four from adjacent sides and one from the center. The mycelium was stained with 0.1% lactophenol cotton blue and observed under a compound microscope.

Pathogenicity Test

The pathogenicity test was conducted at the Gondar Agricultural Research Center greenhouse. The experiment involved planting susceptible Dimtu variety seeds in pots filled with sterilized soil, arranged in a simple plot with three replicates. The pots were regularly watered to maintain high relative humidity, and the seedlings were inoculated with a spore suspension of 1×10^6 spores per milliliter using a micropipette, as described by[13].

Data Collected and Calculated

Ascochyta blight Assessments

Disease incidence is the proportion of pathogen-caused disease in crop populations, influenced by the disease being assessed and its epidemiology [13]. The study used a 1-9 rating scale to assess the severity of Ascochyta blight disease on 5 randomly selected plants during the main cropping season.

The scoring scale of[13] infection percentage is 1-10 and the scoring scale (1-<2) =No infection or small lesions highly resistant and 11-30, 2-< 4 = some stem lesions - minor stem breakage in upper foliage 1-2 branches broken. Several girdling stem lesions low down on some branches resistant 31-50, 4-< 6 = large basal stem lesions or several branches broken near to main stem, half foliage dead moderately resistant. 51-60, 6-<7 =half foliage dead or dying, but young shoots still actively growing from base moderately susceptible 61-80, 7-<9 = most foliage dead - some healthy stem tissue with lateral buds ,Most foliage dead, no healthy lateral buds in leaf axils susceptible. 81-100, 9-<10 = most foliage dead, decreasing areas of living stem tissue, Plants completely dead highly susceptible.

Disease incidence

Calculated as No. of infected plants / Total number of plant assessed [15].

Severity: the area or volume of plant tissue that is (visibly) diseased, usually relative to the total plant tissue [16], the severity grades were converted into a percentage severity index (PSI) for analysis.

Area under Disease Progress Curve (AUDPC)

The area under disease progress curve (AUDPC) from PSI were obtained the followed the formula as described by [17].

Disease Progress Rate: Logistic, ln [(Y/1-Y)], [18] and Gompertz, -ln[-ln(Y)], (Berger, 1981) models were compared for estimation of disease progression parameters from each treatment. The transformed data were regressed over time (DAP) to determine the rate. The goodness of fit the models was selected based on the magnitude of the coefficient of determination (R^2), sum square of error (SSE), Mean Square of error (MSE) and Root Mean Square of error

(RMSE) obtained using each model[20]. Then the appropriate model was used to determine the disease progress rate (r).

RESULTS

Evaluation of chickpea Ascochyta blight disease intensity

Disease Incidence

High disease pressure most genotypes exhibit a high disease incidence (ins), ranging from 28% to 100%. The mean disease incidence is 88.6%, which indicates that the majority of the tested genotypes are significantly affected by the disease.

Disease incidence was evaluated based on the number of diseased plants or plant deaths caused by Ascochyta blight. A highly significant difference was found ($P \leq 0.0001$). The analysis of variance revealed a range of disease incidences across the genotypes, from lower to higher values. The resistant genotypes exhibited incidences ranging from 28% in ICCU-92219 to 67.5% in Natoli. For example, *ICCU-92219* had a low incidence of 28%, followed by *Eshete* at 32%, *DZ-2012--CK-0253* at 35%, *ICCU-91212* at 42%, *DZ-2012 CK-0039* at 55%, and *Natoli* at 67.5%. Moderate resistance genotypes showed incidences ranging from 42.4% in *FLIP-2010-24C* to 100% in *ICCU-13602*, with other varieties like *ICCMABCD-23* (43.7%), *MABC-2* (80%), *ICCV-14106* (85%), *ICCMABCD-20* (85%), and *MABC-11* (100%) showing varying degrees of susceptibility. On the other hand, genotypes that were moderately susceptible to highly susceptible exhibited incidences ranging from 80% to 100%.

During the cropping season, pathogen infection affected 81 genotypes, with Ascochyta blight symptoms first appearing at the seedling stage and worsening during the flowering and podding stages. These findings align with those of [21], where the highest disease incidence (90.1%) was recorded in the *Dimtu* variety, while the lowest (18.6%) occurred in the *Arerti* variety.

This observation also supports [22],who reported that plants are more susceptible to Ascochyta blight during the podding stage. The pathogen's incidence is believed to be initiated by zoospores, sporangia, or oospores washed in rainfall or precipitation from chickpea foliage and deposited in the seeds, or possibly by the pathogen diffusing through the xylem and phloem into the seeds. Therefore, the present study indicates that the damage to foliage or pathogen diffusion into the plant tissues directly contributes to disease incidence. The observed differences in disease incidence across various genotypes may be attributed to variations in genetic resistance to the pathogen (Figure.1).

Disease Average Percent Severity Index

The severity index of Ascochyta blight progress was found to be very highly significant ($p \leq 0.0001$). The overall mean performance of severity for the tested genotypes was 74.4 with minimum and maximum values of 16.6% from the resistance genotype and 100% highly susceptible genotypes. Among the resistance genotypes the lowest severity were recorded range from (16.6-25.5%), 16.6-25.5%, DZ-2012--CK-0253 (16.6%), ICCU-92219 (20%) ICCU-91212 (21.1%) Eshete (21.1%), ICCU-13617 (22.2%) Natoli (25.5%), DZ-2012-CK-0039 (25.5%) and moderately resistance (31.5%-52.54%), ICCMABCD-20 (31.58%) MABC-2 (36.39%) ICCU-13602 (38.05%) ICCV-14106 (43.89%) MABC-11 (50.20%) FLIP-2010-24C (51.74%) ICCMABCD-23 (52.54%) were obtained respectively. Whereas, from moderately susceptible up to highly susceptible genotypes average severity were ranged from 56.8% -100 (Table 2). This study in line with findings of Edeo (2021), the highest disease severity were (90.6%, and 89.6%) recorded from the Shasho and Dimtu variety respectively were recorded. In addition to this result similar with the finding of[13] resistance genotypes had les severity than susceptible genotypes.

According to this average percent severity index were used to recognized the disease reaction for susceptible, moderately susceptible, highly susceptible, moderately resistance, resistance. This results coincides with the investigation of [23] chickpea genotypes showing moderate resistance or tolerance against Ascochyta blight disease are good for use as commercial cultivars after testing their other agronomic characteristics, or may be used in breeding programs to develop Ascochyta blight resistant varieties.

Disease Progress Curve

The disease progress curve on Ascochyta Blight resistance genotype average percent severity index corresponding with average percent severity value of highly susceptible genotype found during the first date of severity assessment 42 days after planting 21.1% was found on resistance genotypes while maximum was 87% on highly susceptible genotypes. At 52 days after planting average percent severity value were minimum 24.6 % on resistance genotypes and maximum 87.7 % on highly susceptible genotypes. At 62 days after planting average percent severity value were minimum 20 % on resistance genotypes and maximum 88.5 % on highly susceptible genotypes. At 72 days after planting average percent severity value were minimum 20.7 % on resistance genotypes and maximum 88.9 % on highly susceptible genotypes (Figure 2). Hence, the result showed that the disease progress curve lower on resistant genotypes and constantly moved when the environment was unfavorable to this disease, the crops become rehabilitated. This finding agrees with [24], Slower disease progress curve Where hade been obtained from resistances genotypes.

Disease Progress Rate

To determine which model better fit the data about the rate at which the disease developed, tests were run on both Gompertz and logistic models. For every severity assessment date, the Logistic model had a higher coefficient of determination (R2) than the Gompertz model. Therefore, the Logistic model was used to calculate the rate at which chickpea Ascochyta blight disease progresses, and it was determined to be superior than the Gompertz model based on their coefficient of determination (R2) values. During cropping seasons, there was a substantial difference in the rate of Ascochyta blight progression ($P < 0.0001$) between the genotypes of chickpeas. Diseases progress rate for the 81 genotypes were ranged from 0.0015 (resistance) to 0.45 (highly susceptible. The mean performance of the tested genotypes were 0.095. The resistant genotypes significantly had lower disease progress rate. The result indicated that lower to higher values of among resistance genotypes were DZ-2012--CK-0253 (0.0015 units day-1), ICCU-91212 (0.0015 units day-1), ICCU-13617 (0.0015 units day-1), Eshete (0.0015 units day-1) ICCU-92219 (0.0016 units day-1) (DZ-2012-CK-0039 (0.002 units day-1), and Natoli (0.002 units day-1).

While from moderately resistance genotypes were FLIP-2010-24C (0.0025 units day-1), ICCMABCD-20 (0.0025 units day-1), MABC-11 (0.015 units day-1), MABC-2 (0.02 units day-1), ICCU-13602 (0.02 units day-1), ICCV-14106 (0.025 units day-1), ICCMABCD-23 (0.035 units day-1) (Table 2) those genotypes should be advance to next breeding program. They have been variation in Ascochyta blight disease progress rates among the genotypes because of genetic resistance levels and the significance of environmental factors that could either promote or inhibit the target pathogen's development during the growing period.

This study in line with findings of [21], The susceptible variety Shasho had the highest blight disease infection rate (0.176), which proceeded quickly, whereas the resistant variety Arerti had the lowest infection rate (0.021), which progressed slowly. and [25] shown that resistant genotypes could slow the field-wide spread of Ascochyta blight. It was determined that such genotypes and varieties had the lowest advancement rate. DZ-2012-CK-0253 (0.0015) that reduced disease progress rate by 99.6% as compared to genotypes ICCMABCD-18 (0.45) (susceptible).

Area under Disease Progress Curve

An extremely useful overview of plant disease epidemics is provided by the area under the disease progress curve (AUDPC), which takes into account the starting disease severity, the rate parameter, and the length of the epidemic to predict the end disease severity [26]. Hence, the effects of disease resistance on disease progress on crops can be evaluated using AUDPC.it was found that very highly statistical significant ($P \leq 0.0001$) difference was observed in the magnitude of the AUDPC among the genotypes. In this study, the genotypes were categorized in different susceptibility levels. For example, the AUDPC value calculated for resistant genotypes ranged between 522.3-763.6 %-days. Among the resistant genotype from lower to higher were recorded DZ-2012--CK-0253 (522.3%- days), ICCU-91212 (644.4) ICCU-13617 (666.6%- days) Eshete (644.4%- days) ICCU-92219 (600%- days) DZ-2012-CK-0039 (766.7%- days) Natoli (763.6%- days). and from moderately resistance genotypes were 956.61636.2 %- days

ICCMABCD-20 (956.6%- days), MABC-2 (1127.8 %- days), ICCU-13602 (1138.9%- days), ICCV-14106 (1477.8%- days), MABC-11 (1534.2), FLIP-2010-24C (1595.4%- days), ICCMABCD-23 (1636.2 %- days) While, the higher AUDPIC value recorded range from moderately susceptible to highly susceptible (1771.1 - 3000, %- days) (Table.1). Because of their genotypic resistance to blight reaction, the assessed genotypes' high degree of statistical significance difference in AUDPC values may generally be explained by this. A correlation between AUDPC and yield loss is known to exist, although the exact relationship between AUDPC and resistance levels varies throughout chickpea types.

Genotypes are more susceptible when the AUDPC is higher in an epidemic of disease. The result found in this study showed that while the AUDPC increases, the yield obtained decreases, this indicates the inverse relation between AUDPC and yield of chickpeas (Table 2). Similarly,[27], compared to the resistant variety, it was discovered that varieties with a higher area under the disease progress curve also had higher disease severity and were more vulnerable to the Ascochyta blight.

Reaction of Chickpea Genotypes against Chickpea Ascochyta Blight.

Significant variations have been noted in the genotype response to Ascochyta blight. Among the 81 genotypes that were tested, seven showed resistance to chickpea (11–30 percent), seven-showed moderate resistance (31–50 percent), two-showed moderate susceptibility (51–60 percent), twenty-showed susceptibility (61–80 percent), and the remaining forty-five showed high susceptibility (81–100 percent) (Figure 3).

Although the symptoms of Ascochyta blight are not absent in resistant genotypes, they may be limited due to genetic resistance. This result is consistent with that of[28], who found that resistance variants do not always present with no symptoms. In addition, these strains showed the presence of tiny black patches, which were unable to spread due to the genetic resistance.

It is confirmed that in this study, none of the tested genotypes have immunity and highly resistant against this pathogen (Ascochyta rabiei). This finding is in line with the finding of [29], There was no protection against this disease in any of the examined types. In Ethiopia, illness epidemics were a recurring event. [30] and Most of the types that are currently available are vulnerable to chickpea Ascochyta Blight [31]. So genotypes show that resistance and moderately resistance reaction test for next breeding program

Pathogen Isolation and identification of Ascochyta Blight

The pathogen Morphological characteristics of Ascochyta blight indicated that on PDA showed different, colony morphologies and colors, the color goes white to gray with septate and branched mycelium under microscope (Figure 4). The pycnidia were circular or ovular in shape, yellow to brown. Significant variations of isolates were observed in cultural and morphological characteristics. These results are similar to those of [32]. Ascochyta. rabiei the beginning are white then shortly turned to light gray because of the formation of pycnidia

Pathogenicity Test

During pathogenicity test, the inoculation and the appearance of the first symptoms of pathogen was appeared at 14 days. While. Re-isolation of isolated fungal pathogens. Furthermore, the inoculated fungi were re-isolated from plants that showed symptoms, while no symptoms were found on control plants (un sprayed). Re-Isolation of fungal Pathogens the causative agent in the diseased leaf parts was re-isolated on Potato Dextrose Agar (PDA). Then characteristics of the re-isolates were compared with those of the original parent cultures. For this step, similar to Koch's Postulates steps: first, identify the pathogen in all affected diseased and not in healthy ones; second, isolate and cultivate the pathogen in a pure culture; third, inoculate a healthy host with the cultured pathogen and see if the host develops the same disease; fourth, re-isolate the pathogen from the newly.

Grain Yield

At harvest, the yield performance of each genotype was evaluated based on the surviving 43 genotypes, with an average yield of 1261.89 kg/ha. The highest yield was recorded from the resistant genotype ICCU-91212 (3969.1 kg/ha), while the lowest yield came from the highly susceptible genotype ICCU-14106, with a yield of 163.4 kg/ha. Among the top-performing genotypes, five advanced disease-resistant lines showed high yields: ICCU-91212 (3969.1 kg/ha), Eshete (3695.9 kg/ha), ICCU-92219 (3383.3 kg/ha), DZ-2012-CK-0253 (3170.9 kg/ha), and ICCU-13617 (3071.6 kg/ha). Additionally, the moderately resistant genotypes, though slightly lower in yield, also performed well, with yields as follows: ICCU-13602 (2422 kg/ha), MABC-2 (2329.7 kg/ha), ICCMABCD-20 (2168.7 kg/ha), ICCMABCD-23 (1874.7 kg/ha), ICCV-14106 (1775.6 kg/ha), FLIP-2010-24C (1678 kg/ha), and MABC-11 (1573.1 kg/ha) (Table 2).

The results indicate that severe disease infection significantly affected the seed yields ($P \leq 0.0001$), emphasizing the crucial role of genetic variability in yield performance. The data demonstrate that resistant genotypes not only exhibit lower disease incidence and severity but also maintain higher yields compared to more susceptible varieties. Genetic variability is a key factor influencing seed yield, with resistant and moderately resistant genotypes showing notable resilience under disease pressure. This highlights the importance of selecting and breeding for genetic resistance in chickpeas to mitigate the impact of Ascochyta blight and improve overall yield stability.(Chongo, and Gossen, 2003). It has been confirmed that resistant genotypes in chickpea have a substantial impact on seed yield. This finding aligns with the results of Megersa (2016) and Muruiki *et al*. (2021) who reported that the highest seed yield obtained from resistance genotype were significantly increased grain yield.

Relative Yield Loss

Yield loss due to Ascochyta blight was quantified by comparing the yield of susceptible chickpea genotypes with that of the most resistant ones. Among the tested genotypes, ICCU-91212 achieved the highest yield of 3969 kg/ha, while the highly susceptible genotype ICC-8318 suffered a complete yield loss, with a yield of 0 kg/ha, resulting in a 100% yield reduction at West Belesa. This finding aligns with previous research by [33], which highlighted that Ascochyta blight, caused by *Ascochyta rabiei*, is one of the most devastating diseases, capable of causing up to 100% yield loss in susceptible chickpea varieties (Table 2).

Regression Analysis

In this study, linear regression was employed to model the relationship between the Area Under Disease Progress Curve (AUDPC) and yield, with AUDPC as the independent variable and yield as the dependent variable. The disease progress curve is highly sensitive to fluctuations in disease epidemic factors during its development, which makes it an unreliable predictor for the relationship between yield and disease impact[34]. Therefore, linear regression was used as a more effective analytical model to quantify the impact of disease severity on yield loss.

The regression model explained 81.4% of the variance in yield reduction due to Ascochyta blight. Specifically, for each unit increase in AUDPC, there was a corresponding 1.43 units of yield reduction in chickpeas, emphasizing the significant role of disease progression in determining yield loss (Figure 5).

DISCUSSION

Disease Incidence: This study evaluated 81 chickpea genotypes for their susceptibility to Ascochyta blight, revealing significant variation in disease incidence. Resistant genotypes such as ICCU-92219 (28%), Eshete (32%), and DZ-2012-CK-0253 (35%) showed markedly lower disease

incidence compared to more susceptible ones. Moderately resistant genotypes had incidences ranging from 42.4% to 52.5%, while highly susceptible genotypes, such as Dimtu (90.1%), experienced near-total infection. These findings highlight that environmental factors like rainfall can significantly influence disease spread, especially during the podding stage.

Disease Severity: Disease severity ranged from 16.6% to 100%, with resistant genotypes like ICCU-92219 and Eshete showing low severity (16.6%-25.5%), while highly susceptible genotypes displayed severe symptoms (56.8%-100%). This confirms that resistant genotypes are less prone to disease progression and damage, making them suitable for breeding programs focused on enhancing Ascochyta blight resistance.

Disease Progress Curve: The disease progress curve confirmed that resistant genotypes had consistently lower disease severity across multiple time points (42, 52, 62, and 72 days after planting). For example, at 42 days, resistant genotypes showed a severity of 21.1%, while susceptible genotypes had 87%. These results align with previous studies, indicating that resistant genotypes slow disease progression, with environmental conditions also influencing the rate of disease spread.

Disease Progress Rate: The progression rate of Ascochyta blight was modeled using Gompertz and logistic models. The logistic model provided a better fit, with disease progression rates ranging from 0.0015 units/day in resistant genotypes to 0.45 units/day in highly susceptible ones. Resistant genotypes, such as DZ-2012-CK-0253, slowed disease spread, supporting the concept that resistant genotypes mitigate disease progression.

Area Under Disease Progress Curve (AUDPC): AUDPC values showed significant variation, with resistant genotypes having lower values (522.3%-days to 766.7%-days) compared to moderately resistant (956.6%-days to 1636.2%-days) and highly susceptible genotypes (1771.1%-days to 3000%-days). The study confirmed that higher AUDPC values correlated with increased disease severity and yield loss, emphasizing the importance of selecting genotypes with lower AUDPC values for improved resistance and yield stability.

Genotype Reactions: Out of 81 genotypes, 7 were resistant (11-30% severity), 7 were moderately resistant (31-50%), and the rest were varying degrees of susceptible. These results highlight the potential of resistant and moderately resistant genotypes for breeding programs aimed at developing more resilient chickpea varieties.

Pathogen Isolation and Identification: The pathogen responsible for Ascochyta blight, *Ascochyta rabiei*, was confirmed through morphological identification on Potato Dextrose Agar (PDA) and pathogenicity tests, which adhered to Koch's postulates, confirming the reliability of the findings.

Grain Yield: Grain yield data showed that resistant genotypes, like ICCU-91212 (3969.1 kg/ha) and Eshete (3695.9 kg/ha), significantly outperformed highly susceptible genotypes, such as ICCU-14106 (163.4 kg/ha). Disease severity inversely impacted yield, with higher severity correlating with lower yields. These findings support the notion that resistance to Ascochyta blight is essential for maintaining higher productivity under disease pressure.

Relative Yield Loss: Yield loss due to Ascochyta blight was assessed by comparing susceptible and resistant genotypes. At West Belesa, ICCU-91212 achieved a maximum yield of 3969 kg/ha, while susceptible genotypes like ICC-8318 had zero yield, resulting in a 100% yield loss. This supports earlier research by [35], which indicated that Ascochyta blight could cause up to 100% yield loss.

Regression Analysis: Linear regression was used to analyze the relationship between AUDPC and yield. The model explained 81.4% of the variance, with each unit increase in AUDPC resulting in a 1.43-unit reduction in yield. This confirms the strong correlation between disease severity and yield loss, demonstrating the utility of linear regression for predicting yield reductions based on disease progression.

Conclusion

Genetic resistance is a crucial factor in the effective management of Ascochyta blight in chickpeas. This study clearly demonstrated that resistant genotypes, such as ICCU-92219, Eshete, and DZ-2012-CK-0253, showed significantly lower disease incidence and severity compared to highly susceptible genotypes, which experienced substantial damage. The resistant genotypes not only exhibited slower disease progression but also maintained higher yields despite disease pressure. This underscores the importance of incorporating resistance into breeding programs to develop chickpea cultivars that can effectively withstand Ascochyta blight, ultimately leading to improved disease management and increased productivity.

Furthermore, the regression analysis reinforced the strong correlation between disease severity (as measured by AUDPC) and yield loss. This finding further highlights the necessity of prioritizing the development of chickpea varieties with enhanced resistance to Ascochyta blight. Resistant genotypes are integral to achieving sustainable chickpea production, as they mitigate the impact of the disease and improve crop yield stability.

Integration of Resistant Genotypes into Breeding Programs: The study emphasizes the need to focus breeding efforts on incorporating resistance to Ascochyta blight into chickpea varieties. Genotypes like ICCU-92219, Eshete, and DZ-2012-CK-0253, which demonstrated robust resistance, should be considered valuable sources of resistance for future breeding programs.

Further Evaluation of Moderately Resistant Genotypes: Although the study focused primarily on highly resistant genotypes, moderately resistant genotypes also exhibited promising results in terms of disease management and yield stability. These genotypes should be further explored and included in breeding programs to broaden the genetic base for resistance

Abbreviation

AB	Ascochyta Blight
ANOVA	Analysis of variance
AUDPC	Area under disease progress curve
CAEs	Collage of agriculture and environmental science
CSA	Central Statically Agency
CV	Coefficient variation
DAP	Days after planting
DPC	Disease progress curve
DPI	days post infection
Dr	Didemalia rabiei
DR	Disease Reaction
DZARC	Debre zeit Agriculture Research Center
GARC	Gondar Agriculture Research Center
Hr	Hypersensitive Response
PDA	Potato dextrose Agar
PSI	Percentage Severity Index
SAS	Statically analysis software

Acknowledgement

The author expresses gratitude to God, colleagues Asfaw Azanaw and Yonas Worku, from Gondar Agriculture Research Center, parents, siblings, friends, and my sensor lovely Ethiopia Yimenu for their unwavering support and guidance. They also thank Debre zeit Agriculture Research Center for suppling selective genotypes and Gondar Agricultural Research Center for admission and financial assistance. The author also thanks relatives and friends for their encouragement and moral support throughout the thesis writing process.

Ethics approval and consent to participate

The Ethics Committees of the Amhara Agriculture Research Institute (ARARI), Gondar Agriculture Research Center, and the University of Gondar, College of Agriculture and Environmental Sciences approved this study. Written informed consent was obtained from all participants before their involvement. The research was conducted in full compliance with the ethical guidelines outlined in the Memorandum of Understanding.

Consent for publication

All authors have reviewed and approved the final version of this manuscript for publication. There are no conflicts regarding authorship, and all contributors have consented to the submission and potential publication of this work

Data availability

The datasets generated and/or analyzed in this study are not publicly accessible due to privacy considerations. However, they can be made available upon reasonable request from the corresponding author. The Amhara Agriculture Research Institute (ARARI) and Gondar Agriculture Research Center (GARC) are dedicated to protecting the confidentiality of research participants. Any data distribution will be subject to compliance with relevant regulatory and ethical guidelines, including the establishment and approval of a formal data-sharing agreement.

Author contributions statement

Misganaw Gelaye: The person(s) who came up with the idea for the study and developed the overall research plan , conducted data analysis and wrote the first version of the manuscript Asefa Sintayehu: This person who verified the results or ensured the research methods were applied correctly, supervised the project, and provided oversight. Yigrem Mengist: this person who carried out the research or data collection. Antenehi Adebabaye: This person who organized and maintained the research data.

Author details

[1,4]Amhara Agriculture Research Institute (ARARI), Gondar Agriculture Research Center P.O. Box 1337, Gondar, Ethiopia, [2,3] University of Gondar, College of Agriculture and Environmental Sciences, Department of Plant Sciences P.O. Box 196, Gondar, Ethiopia

Declaration of No Funding

This research received no specific grant from any funding agency, commercial, or not-for-profit sectors. No funding was received for this stud. This work was conducted without external funding

References

1. Diapari, M., Sindhu, A., Bett, K. & Deokari, A. Genetic diversity and association mapping of iron and zinc concentration in chickpea (Cicer arietinum L). *Genome* **57**, 459-468. (2014).
2. FAOSTAT. *(Food and Agriculture Organization) Crop Production. Available*. (2014).
3. Abate, T. *et al.* A systems and partnership approach to agricultural research and development – lessons from Ethiopia. *Outlook on Agriculture* **40(3)**, 213–220 (2011).
4. CSA. *Agricultural Sample Survey: Report on Crop and Livestock Product Utilization, 7. Central Statistical Agency: Addis Ababa, Ethiopia, 2020/2021.* (2021).
5. CSA. *THE FEDERAL DEMOCRATIC REPUBLIC OF ETHIOPIA CENTRAL STATISTICAL AGENCY AGRICULTURAL SAMPLE SURVEY*. (2022).
6. Demissie Mitiku, Senait Regassa, Legesse Dadi, & Asnake Fikre. *Adoption of Improved Chickpea Varieties in the Central Highlands of Ethiopia*. (2005).
7. Yigrem Mengist, ytolgn Wassie & Tazebachew Asres. Response of chickpea varieties and sowing dates for the management of chickpea ascochyta blight (Ascochyta rabiei (Pass.) disease at West Belesa District, Ethiopia. *African Journal of Plant Science* **13(8):**, 231-238. (2019).
8. Pande, S. *et al.* Ascochyta blight of chickpea (Cicer arietinum L.): a review of biology, pathogenicity, and disease management. *Aust. J. Agric. Res.* **56**, 317 (2005).
9. Ali, Q. & Malik, A. Genetic response of growth phases for abiotic environmental stress tolerance in cereal crop plants. *Genetika* **53**, 419–456 (2021).
10. Ayoub, L. *et al.* Insect pests under changing climate and climate-smart pest management. (2022).
11. Jhorar, O. Crop-environment-disease interaction study on ascochyta blight of chickpea. (1996).
12. Gan, Y., Siddique, K., MacLeod, W. & Jayakumar, P. Management options for minimizing the damage by Ascochyta blight (Didymella rabiei) in chickpea (Cicer arietinum L.). *Field Crops Research*, **97:**, 121-134. (2003).
13. Banniza, S. *et al.* The long path to understanding the host–pathogen interactions of Colletotrichum lentis on lentil. *Canadian Journal of Plant Pathology* **40**, 199–209 (2018).
14. Agrios, G. Plant Pathology. 5th Edn Academic Press. *New York,–2005.–925 c* (2005).
15. Kadırı, A., Berrezoug, N., Hennia, A., Bennaceur, M. & Ighilhariz, Z. Essential Oil of Myrtus communis L. effects In Vitro and In Vivo Evaluation against Chickpea Blight (Ascochyta rabiei) Disease. (2021).
16. Wheeler, B. E. J. An introduction to plant diseases. *An introduction to plant diseases.* (1969).
17. Jones, D. G. An introduction to plant disease epidemiology. in *The Epidemiology of Plant Diseases* (ed. Jones, D. G.) 3–13 (Springer Netherlands, Dordrecht, 1998). doi:10.1007/978-94-017-3302-1_1.
18. Van der Plank, J. E. Plant diseases: Epidemics and control. *Academic Press, New York.* 334p (1963).
19. Berger, ., R. D. Comparison of the Gompertz and Logistic equation to describe plant disease progress. .*Phytopathology* **71**, 716-719. (1981).
20. Campbell, C. L. & Madden, L. V. *Introduction to Plant Disease Epidemiology.* (John Wiley & Sons., 1990).
21. EDEO, N. T. DISTRIBUTION OF ASCOCHYTA BLIGHT (Didymella rabiei) AND EVALUATION OF CHICKPEA (Cicer arietinum L.) VARIETIES TO THE DISEASE IN EAST SHEWA, CENTRAL ETHIOPIA. (2021).

22. Ghanbarnia, K., Dilantha Fernando, W. G. & Crow, G. Comparison of disease severity and incidence at different growth stages of naturally infected canola plants under field conditions by pycnidiospores of *Phoma lingam* as a main source of inoculum. *Canadian Journal of Plant Pathology* **33**, 355–363 (2011).
23. Atta, B. M. & Shah, T. M. Stability analysis of elite chickpea genotypes tested under diverse environments. *Australian Journal of Crop Science* **3**, 249–256 (2009).
24. Silvar, C., Díaz, J., & F. Merino. Real-Time Polymerase Chain Reaction Quantification of *Phytophthora capsici* in Different Pepper Genotypes. *Phytopathology*® **95**, 1423–1429 (2005).
25. Malik, S. R., Iqbal, S. M. & Haqqani, A. M. Resistance screening to Ascochyta blight disease of chickpea in Pakistan. *International Chickpea and Pigeon pea Newsletter* **13**, 30-31. (2006).
26. Madden, L. V., Hughes, G. & van den Bosch, F. *The Study of Plant Disease Epidemics*. (The American Phytopathological Society, 2017). doi:10.1094/9780890545058.
27. Kiprop, C. J. Evaluation of chickpea (Cicer arietinum L.) genotypes for host plant resistance to Ascochyta blight (Ascochyta rabiei) in elgeyo-marakwet, uasin-gishu and baringo counties of Kenya. (2016).
28. Chongo, G. & Gossen. Diseases of Chickpea. In: Diseases of Field Crops in Canada, Bailey, K.L., Gossen, B.D., Gugel, R. and Morrall, R.A.A. (Eds.). Canadian Phytopathological Society, Saskatoon, 3: 185-190. *Canadian Phytopathological Society, Saskatoon,* **3**, 185-190. (2003).
29. Chen, w, Coyne, T., Peever, T. & Muehlbauer, ., F. chickpea differentials for pathogenicity assay of Ascochyta blight and identification of chickpea accessions resistant to Didymella rabiei.,. *Plant Pathol ogy* **53**, 759-769. (2004).
30. Asrat, Z. Epidemiology and Management of Ascochyta Blight (Didymella rabiei) on Chickpea in Central Rift Valley, Ethiopia. (Haramaya University, Haramaya, Ethiopia, 2015).
31. Megersa, T. Occurrence, distribution and management strategies for Ascochyta blight (Ascochyta rabei Pass.) of chickpea (Cicer arietinum L.) in Ethiopia. (Thesis, Kenyatta University of Agriculture and Technology, Kenya., 2016).
32. Mahiout, D., Bendahmane, B. S., Benkada, M. Y. & Rickauer, M. Physiological characterisation of Ascochyta rabiei (Pass.) Lab. isolated from diseased chickpea fields in six regions of northwestern Algeria. *Am. Eur. J. Agric. Environ. Sci* **15**, 1136–1146 (2015).
33. Muruiki, R., Kimurto, P., Towett, B. & Rao, G. Yield performance of chickpea (Cicer arietinum L.) genotypes under supplemental irrigation regimes in semi-arid tropics. *JPBCS* **13**, 177–189 (2021).
34. Fekede Girma. Management of late blight (Phytophthora infestans) of potato (Solanum tuberosum L.) through potato cultivars and fungicides in Hararghe highlands, Ethiopia. (Haramaya University, Haramaya, Ethiopia, 2011).
35. Kimurto, P. K. *et al.* Evaluation of chickpea genotypes for resistance to Ascochyta blight (Ascochyta rabiei) disease in the dry highlands of Kenya. *Phytopathologia Mediterranea* 212–221 (2013).