*Plant Archives* Vol. 25, No. 2, 2025 pp. 1805-1812 e-ISSN:2581-6063 (online), ISSN:0972-5210

# Plant Archives

**Journal homepage: http://www.plantarchives.org**
**DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.2.261**

# ASSESSMENT OF COMBINING ABILITY AND HETEROSIS FOR ANTHRACNOSE UTILIZING HYBRIDS DERIVED FROM EXOTIC AND INDIGENOUS COLLECTIONS IN CHILLI (*CAPSICUM ANNUUM* L.)

**Bidwan Rath[1, 2]*, A. Mohan Rao[1], Premakumar[2], V. Prashantha[1], K. M. Shirisha[1], Channabasava[1], Jenia Roy[2], Firos T. M. Basha[2] and Rohit Sarkar[2]**

[1] Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Bangalore, Karnataka, India-560065

[2]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi, India-110012

(Date of Receiving : 03-08-2025; Date of Acceptance : 07-10-2025)

**ABSTRACT**

Anthracnose, primarily caused by *Colletotrichum capsica*, is a major constraint in chilli production, necessitating the identification of resistant parental lines and hybrids for sustainable disease management. In this study, 48 experimental hybrids developed from four cytoplasmic male sterile (CMS) lines and 12 fertility restorer testers using a line × tester mating design were evaluated under controlled laboratory conditions and disease response was assessed through overall lesion size (OLS) and true lesion size (TLS). Analysis of variance revealed significant variability among crosses, with line × tester interaction being predominant, indicating the role of non-additive gene action in governing response to anthracnose. Among parents, CMS7A and AV31 were identified as desirable general combiners with significant negative GCA effects, while CMSUAA × AV16 and CMS7A × AV48 recorded significant negative SCA effects for TLS. A significant positive correlation was observed between SCA effects and hybrid per se performance. Standard heterosis analysis revealed CMS7A × AV31 followed CMS7A×AV59 by showing the highest level of significant heterosis in desirable direction. These results highlight the potential of CMS7A × AV31 as a promising hybrid and reinforce the role of non-additive genetic effects in breeding anthracnose-resistant hybrid chilli cultivars.

***Keywords*** **:** Chilli anthracnose, combining ability, heterosis, GCA, SCA.

## Introduction

Chilli (*Capsicum annuum* L.) is among the world's most widely cultivated vegetables and spice crops, valued both for its culinary and industrial uses. The genus *Capsicum* is native to South and Central America, with evidence of early domestication dating back to 6000 years ago (Xue-xiao, 2022). Over centuries, chilli spread globally via human migration and trade; in India, it is believed to have been introduced by the Portuguese in the 15th century, integrating rapidly into local cuisines and agriculture (Shah, 2023). *Capsicum* belongs to the Solanaceae family and is diploid with 2n = 2x = 24 chromosomes (Haque *et al*., 2016). Of the ~30 recognized *Capsicum* species, five (namely *C. annuum, C. frutescens, C. pubescens, C. chinense,* and *C. baccatum*) are commonly grown worldwide (Bosland and Votava, 2012). In *C. annuum*, natural out-crossing rates under field conditions may range from 7 % to 36 %, making it an often-cross-pollinated species (Sarfaraz *et al*., 2022). India occupies the highest area (0.85 mha) under chilli cultivations and is the leading producer (2.78 mt) and exporter (0.48mt) of dry chilli and pepper in the world (FAOSTAT, 2023).

Biotic stresses including diseases caused by virus, fungi and bacteria are major production constraint in Chilli. Anthracnose is one of the devastating diseases of chilli caused by the fungus *Colletotrichum* spp. Five different species of *Colletotrichum* have been reported viz., *C. acutatum* (Simmonds), *C. capsici* (Syd.) Butler and Bisby, *C. gloeosporioides* (Penz.) Penz. and Sacc., *C. cocodes* (Wallr.) S.Hughes and *C. dematium* (Pers.) Grove. Among these, *C. capsici* and *C. gloeosporioides* are most predominant in India

(Prathibha, 2011). Chilli anthracnose a seed, soil, and air-borne disease (Meon *et al*., 1988; Saxena *et al*., 2016) and temperature of 27°C and 80% RH are congenial for the growth and sporulation of the pathogen (Roberts, 2011). It primarily attacks pepper fruits at both green and red fruit stages. Anthracnose on pepper leaves and stem are characterized by dark lesions while on fruits very dark, sunken lesions, containing spores with concentric rings of acervuli are produced. Potentially, the pathogen is known to cause up to 50% losses (Oo and Oh, 2016) as even a single anthracnose speck on the fruit reduces its marketability considerably (Than *et al*., 2008).

Traditional control measures (chemical sprays and cultural practices) often lose efficacy under high disease pressure, and persistent or indiscriminate fungicide use leads to residue accumulation, regulatory restrictions, environmental harm, and loss of pathogen sensitivity (Bhandari *et al*., 2019; Chen *et al*., 2022; Shi *et al*., 2023). In this context, breeding for genetic resistance provides a more sustainable and ecofriendly strategy (Putra *et al*., 2024; Ridzuan *et al*., 2018). The development of resistant or tolerant cultivars, ideally in hybrid form, can offer durable disease suppression while maintaining yield potential. Hybrid breeding in chilli hinges on understanding the combining ability of parental lines and the manifestation of heterosis (Karim *et al*., 2021). Because chilli allows commercial hybrid seed production (via controlled pollination and cytoplasmic genetic male sterility systems (Channabasava *et al*., 2023), heterosis breeding is a practical route for trait improvement. However, success depends on identifying parents with desirable general combining ability (GCA) and cross combinations with favourable specific combining ability (SCA) for target traits, including disease resistance (Karim *et al*., 2021; Saengarun *et al*., 2025). In this study, we aim to evaluate general combining ability of exotic and indigenous parental genotypes and specific combining ability of hybrids derived from them for response to anthracnose in chilli. The extent of better parent heterosis (BPH) and standard heterosis (SH) was also analysed in hybrids.

## Material and Methods

### Experimental Materials

The experimental material consisted of 48 experimental hybrids derived involving four cytoplasmic male sterile (CMS) lines and 12 fertility restorer testers hybridized following line×tester mating design (Kempthorne, 1957) and two released hybrid (RH) checks. The parents include diverse set of germplasms with 13 exotic collections (10 advanced breeding lines (ABL) and three CMS lines) and three indigenous collections (two working collections (WC) and one CMS line) (Table1).

### Experimental Design

Seeds of hybrids, parents and checks were sown in nursery during late kharif 2021. Subsequently, 40 days old seedlings were transplanted to the experimental plot of 'K' block, Department of Genetics and Plant Breeding (GPB), University of Agricultural Sciences (UAS), GKVK, Bengaluru, which is situated at an altitude of 930 meters above mean sea level (MSL), 12º58' North latitude and 77º35' East longitude. Planting of hybrids and parents was carried out using simple lattice design with two replications following as spacing of 0.75m between rows and 0.45 m between plants with in a row.

### Artificial Inoculation

Pathogen responsible for anthracnose was isolated from infected chilli fruits (collected from the experimental plots, Department of GPB, K-Block) and subsequently purified through pure culture on potato dextrose agar medium under laboratory conditions until sporulation. Sporulation was verified by staining lactophenol cotton blue and observing under a light microscope at 10X magnification (Figure 1). Presence of sickle shaped conidia confirmed the identity of the pathogen as *Colletotrichum.* To ensure continuous supply of inoculum during the experiment, the culture was periodically sub-cultured. For stock solution of inoculum preparation, spores from sporulating culture were suspended in sterile distilled water under aseptic conditions in a laminar airflow cabinet. An aliquot of this suspension was mixed with lactophenol cotton blue (1:1) and examined with an improved Neubauer ruled haemocytometer under 10X magnification to determine spore concentration (Figure 1). The mean spore count from five grids was calculated and corrected for dilution to estimate the stock concentration ($S_c$). A working suspension containing approximately $5\times10^5$ spore $mL^{-1}$ (Chanchaichaovivat *et al*., 2007) was prepared from the stock using the required dilution formula to achieve the desired volume ($V_w$).

$$\text{Volume of aliquot to be taken from stock solution (VS)} = \frac{5\times10^5 \times V_W}{S_C}$$

Working suspension was obtained by diluting $S_c$ with ($V_w$ - $V_s$) mL of sterile distilled water.

**Laboratory challenged screening**

During early summer 2022, hybrids, parents and checks were evaluated for their response to anthracnose infection following protocol by Sun *et al*. (2015). From each genotype, ten fruits at the colour break stage were randomly collected and transported to the Hot Pepper Improvement Unit, Department of Genetics and Plant Breeding, UAS, Bangalore, for artificial inoculation under aseptic conditions. In the laboratory, fruits were surface sterilized using non-absorbent cotton dipped in 70% ethanol to prevent secondary infections. They were then placed in plastic boxes (approximately 26 × 15 × 7 $cm^3$) with sterile blotting paper at bottom moistened with distilled water to maintain a relative humidity of ~95%. Artificial inoculation was performed by puncturing the fruits using Hamilton's microliter syringe attached to with a repeating dispenser adjusted to release 1 µL of spore suspension. Depending on fruit length, two to three punctures were made in the mesocarp at ~10 mm intervals on both sides of the fruit. At each puncture, 1 µL of spore suspension (from the calibrated working solution) was introduced. Eight days after inoculation, fruits were examined for characteristic anthracnose lesions. Lesion diameter was measured using a specialized scale marked with circles of known diameters in milli meters. The overall lesion size (OLS) (Voorrips *et al*., 2004) was subsequently calculated based on these measurements.

$$\text{OLS (mm diameter)} = \frac{\text{Sum of lesion diameters across inoculation points}}{\text{Total number of inoculated points}}$$

However, all points of spore inoculation may not develop into infection. Since, OLS considers such inoculation points for estimation of the average, the lesion diameter would be under-estimated than actual value. Therefore, omitting such inoculation points that did not develop into lesion, true lesion size (TLS) (Voorrips *et al*., 2004) in mm diameter was calculated as,

$$\text{TLS (mm diameter)} = \frac{\text{Sum of lesion diameters across inoculation points}}{\text{Total number of inoculation points that developed lesions}}$$

Both estimates of OLS and TLS were considered for further statistical analysis.

**Statistical analysis**

Mean OLS and TLS estimates for responses to anthracnose of hybrids and parents were subjected to line×tester analysis (Kempthorne, 1957). Analysis of variance for line×tester mating design was carried out using 'INDOSTAT' software version 9.1 to estimate the GCA effects, SCA effects and standard heterosis. The corelation analysis between GCA effects and per se response to anthracnose in parental genotypes was carried out using 'R' software version 4.1.3.

## Results and Discussion

Presence adequate magnitude of significant variability among the crosses is prerequisite for conducting combining ability and heterosis analysis. The mean sum of squares (MSS) due to crosses has been found to be significant indicating suitability of conducting further analysis (Table 2). The significance of MSS due to line×tester effects was observed; however, line effects and tester effects were not significant (Table 2). This clearly indicates the importance of non-additive interaction and SCA effects resulted due to interaction alleles from line and tester parents for responses to anthracnose in chilli under current investigation. Studies by (Bal *et al*., 2024; Saengarun *et al*., 2025) has also reported significance of non-additive gene action controlling anthracnose response in chilli. Previous studies have reported significant variability for responses to anthracnose disease infection in chilli as well (Amorim *et al*., 2021; Pugalendhi *et al*., 2010).

General combining ability effect is a crucial estimate that indicates performance of a parent in a series of crosses involving it. Good general combiners are more likely to transmit their performance to their crosses. Among the female lines, CMS 7A (-1.63) and CMS UAA (2.74) registered significant GCA effects in negative and positive direction respectively. However, none of the female lines exhibited significant GCA effects for OLS (Table 3). Among the testers, AV 31 (-3.41) and AV47 (3.09) manifested significant negative and positive GCA effects for TLS. In case of OLS, AV59 (-1.86) and AV16 (2.29) has manifested significant GCA effects (Table 3). Since lower estimates of OLS and TLS are desirable since it indicates lower incidence of anthracnose; parents with significant negative GCA effects are the desirable for breeding hybrids against anthracnose in chilli. Hence, CMS7A and AV31 were found to be the desirable female and male general combiner against anthracnose in our study respectively. Study by Amorim *et al*. (2021) has identified chilli parental genotypes with varying extent of GCA effects including both desirable (negative GCA effect) and undesirable (positive GCA effect) general combiner for breeding against anthracnose. The correlation between per se responses

of parental lines and testers in terms of mean TLS estimates for anthracnose to their GCA effects were studied. Positive non-significant correlation coefficient was found for both lines (r = 0.81; p value = 0.18) and testers (r = 0.38; p value = 0.21) between their mean TLS estimates and GCA effect estimates. This indicates parental per se response to anthracnose in terms of TLS cannot be used as an inference to select good general combining parental lines and testers. Similar correlative study utilizing GCA effects has been conducted by Lata *et al*. (2023) for yield and related traits in chilli.

SCA effects is due to non-additive gene interaction between the genes contributed by parents involved in the cross. Among the 48 hybrids, five hybrids exhibited significant negative SCA effect for both OLS and TLS. In case of OLS and TLS, CMSUAA×AV16 (-8.59 and -9.04 respectively) followed by CMS7A×AV31 (-6.68) for OLS and CMS7A×AV48 (-7.28) for TLS registered for greater significant negative SCA estimates (Table 3). High levels of SCA effect clearly indicating the significant role of line×tester interaction due to non-additive gene effects contributing SCA effect under current investigation. Based on lesion area and area under disease progress curve, Amorim *et al*. (2021) has identified different chilli cross combination with significant negative and positive SCA effect for anthracnose in chilli. Significant positive correlation was obtained (r = 0.83; p value <0.001) between SCA effects and per se anthracnose response of hybrids. For yield and component traits, Lata *et al*. (2023) has also reported significant positive correlation between per se performance and SCA effects in chilli hybrids.

Standard heterosis also known as economic heterosis is a measure of superior performance of hybrids over commercial checks. The practical utility of SH is more than better parent heterosis (BPH) since the better parent is not necessarily better than standard check and this has been reflected in our study as number of hybrids with significant negative BPH is higher than SH (Table 4). Since OLS estimates includes all inoculation points, therefore OLS is likely to under estimate the severity of infection due to inclusion of false positive inoculation points which is reflected from the number of crosses with significant negative heterosis for OLS is more than TLS. Among 48 hybrids three and five hybrids manifested significant negative standard heterosis over the checks i.e., Arka Meghana and Arka Khyati respectively for TLS (Table 4). Hybrid CMS7A×AV31 (-77.79%) followed by CMS7A×AV59 (-64.32%) and CMS7A×AV48 (-57.61%) manifested lower significant negative heterosis over the checks (Table 5, Figure 2). Previous studies have observed manifestation of significant negative heterosis over better parent against anthracnose in chilli as well (Amorim *et al*., 2021; Bal *et al*., 2024; Saengarun *et al*., 2025).

## Conclusion

The present study demonstrated significant genetic variability among chilli hybrids for anthracnose response, confirming the potential of heterosis and combining ability analysis in identifying promising sources of resistance. The predominance of line × tester interactions indicated that non-additive gene action plays a major role in governing resistance to *Colletotrichum capsici*. Among parental lines, CMS7A and AV31 were identified as desirable general combiners with significant negative GCA effects, while crosses such as CMSUAA × AV16 and CMS7A × AV48 expressed greater negative SCA effects for TLS. Significant correlation between SCA effects and hybrid per se performance further validated the utility of per se performance for identification of parents with desirable SCA effects in resistance breeding. Standard heterosis analysis revealed hybrids such as CMS7A × AV31 with substantial heterosis over commercial checks, highlighting their practical utility in hybrid breeding programs.

**Table 1:** Details of parental genotypes and checks used in the study

| Genotype | Kind of genetic material | Kind of collection | Source |
|---|---|---|---|
| CMS7A | CMS line | EC | WVC, Taiwan |
| CMS8A | CMS line | EC | WVC, Taiwan |
| CMS10A | CMS line | EC | WVC, Taiwan |
| CMSUAA | CMS line | IC | UAS, Bangalore, India[†] |
| AV16 | ABL | EC | WVC, Taiwan |
| AV31 | ABL | EC | WVC, Taiwan |
| AV43 | ABL | EC | WVC, Taiwan |
| AV44 | ABL | EC | WVC, Taiwan |
| AV47 | ABL | EC | WVC, Taiwan |

| | | | |
|---|---|---|---|
| AV48 | ABL | EC | WVC, Taiwan |
| AV49 | ABL | EC | WVC, Taiwan |
| AV53 | ABL | EC | WVC, Taiwan |
| AV59 | ABL | EC | WVC, Taiwan |
| AV99 | ABL | EC | WVC, Taiwan |
| PDL1 | WC | IC | UAS, Bangalore, India |
| S343 | WC | IC | Ludhiana, Punjab, India |
| Arka Khyathi | RH | IC | IIHR, Bangalore, India |
| Arka Meghana | RH | IC | IIHR, Bangalore, India |

*WVC – World Vegetable Centre; †UAS – University of Agricultural Sciences; #IIHR – Indian Institute of Horticultural Research

**Table 2:** Analysis of variance as per line×tester mating design for responses to anthracnose

| Source of variation | Degree of freedom | Mean sum of square | |
|---|---|---|---|
| | | OLS | TLS |
| Replication | 1 | 11.44 | 2.55 |
| Crosses | 47 | 29.76*** | 32.92*** |
| Line effect | 3 | 68.33 | 86.76 |
| Tester effect | 11 | 23.44 | 22.33 |
| Line * Tester effect | 33 | 28.36*** | 31.56*** |
| Error | 47 | 5.99 | 8.036 |

*Significance at P = 0.05 level; ** Significance at P = 0.01 level; *** Significance at P = 0.001 level

**Table 3:** Estimates of significant GCA effects of parents and significant negative SCA effects of hybrids for OLS and TLS

| Parental genotypes | OLS | TLS | Crosses | OLS | TLS |
|---|---|---|---|---|---|
| CMS7A | -0.96 | -1.63 ** | CMS7A×AV31 | -6.68 *** | -6.30 ** |
| CMSUAA | 2.52 *** | 2.74 *** | CMS7A×AV48 | -5.01 ** | -7.28 *** |
| AV31 | -2.51 ** | -3.41 ** | CMS7A×AV59 | -5.26 ** | -6.36 ** |
| AV47 | 3.25 ** * | 3.09 ** | CMS10A×AV99 | -3.93 * | -4.29 * |
| AV59 | -1.86 * | -1.43 | CMSUAA×AV16 | -8.59 *** | -9.04 *** |
| AV16 | 2.29 * | 1.92 | - | - | - |

*Significance at P = 0.05 level; ** Significance at P = 0.01 level; *** Significance at P = 0.001 level

**Table 4:** Hybrids showing significant estimates of BPH (%) and SH (%) for OLS and TLS

| Crosses | BPH | | SH over Arka Khyati | | SH over Arka Meghana | |
|---|---|---|---|---|---|---|
| | OLS | TLS | OLS | TLS | OLS | TLS |
| CMS7A×AV31 | -86.46 ** | -85.78 ** | -80.12 ** | -79.88 ** | -74.66 ** | -77.79 ** |
| CMS7A×AV43 | -35.92 ** | -32.10 ** | 5.18 | 7.44 | 34.03 | 18.60 |
| CMS7A×AV44 | -42.75 ** | -39.90 ** | -6.03 | -4.90 | 19.75 | 4.98 |
| CMS7A×AV47 | -30.80 ** | -23.66 * | 13.58 | 20.79 | 44.75 * | 33.33 |
| CMS7A×AV48 | -70.94 ** | -70.94 ** | -60.17 ** | -61.60 ** | -49.24 * | -57.61 ** |
| CMS7A×AV49 | -46.77 ** | -45.34 ** | -12.63 | -13.51 | 11.34 | -4.53 |
| CMS7A×AV53 | -42.75 ** | -42.21 ** | -6.03 | -8.55 | 19.75 | 0.95 |
| CMS7A×AV59 | -76.87 ** | -76.87 ** | -66.47 ** | -67.67 ** | -57.27 ** | -64.32 ** |
| CMS7A×AV16 | -36.50 ** | -26.42 * | 4.22 | 16.43 | 32.82 | 28.53 |
| CMS7A×PDL 1 | -47.43 ** | -45.42 ** | -13.72 | -13.64 | 9.96 | -4.67 |
| CMS7A×S343 | -54.80 ** | -54.80 ** | -25.82 | -28.48 | -5.46 | -21.05 |
| CMS8A×AV31 | -36.43 ** | -35.51 ** | -6.69 | -8.74 | 18.91 | 0.74 |
| CMS8A×AV43 | -61.54 ** | -55.61 ** | -36.86 * | -29.75 | -19.54 | -22.46 |

| Crosses | BPH | | SH over Arka Khyati | | SH over Arka Meghana | |
|---|---|---|---|---|---|---|
| | OLS | TLS | OLS | TLS | OLS | TLS |
| CMS8A×AV44 | -56.70 ** | -52.44 ** | -28.92 | -24.73 | -9.41 | -16.91 |
| CMS8A×AV47 | -44.37 ** | -33.10 ** | -8.67 | 5.88 | 16.39 | 16.88 |
| CMS8A×AV48 | -32.91 ** | -19.94 | -8.04 | 5.79 | 17.18 | 16.77 |
| CMS8A×AV49 | -40.43 ** | -35.69 ** | -2.21 | 1.78 | 24.62 | 12.35 |
| CMS8A×AV53 | -36.71 ** | -30.05 * | 3.89 | 10.71 | 32.39 | 22.21 |
| CMS8A×AV59 | -52.87 ** | -43.74 ** | -31.68 | -21.39 | -12.94 | -13.23 |
| CMS8A×AV16 | -37.52 ** | -35.17 ** | 2.57 | 2.61 | 30.71 | 13.26 |
| CMS8A×PDL1 | -57.24 ** | -48.58 ** | -29.81 | -18.63 | -10.55 | -10.18 |
| CMS8A×S343 | -50.03 ** | -43.98 ** | -17.97 | -11.35 | 4.54 | -2.14 |
| CMS10A×AV31 | -46.26 ** | -42.61 ** | -28.03 | -25.91 | -8.28 | -18.21 |
| CMS10A×AV43 | -50.30 ** | -43.06 ** | -33.43 * | -26.48 | -15.17 | -18.84 |
| CMS10A×AV47 | -30.95 * | -30.31 * | -7.52 | -10.01 | 17.86 | -0.67 |
| CMS10A×AV53 | -46.55 ** | -39.36 ** | -28.42 | -21.71 | -8.78 | -13.58 |
| CMS10A×AV99 | -9.76 | -0.66 | -50.64 ** | -42.43 * | -37.10 | -36.46 |
| CMS10A×PDL1 | -59.77 ** | -54.11 ** | -46.13 ** | -40.75 * | -31.34 | -34.60 |
| CMS10A×S343 | -46.77 ** | -46.77 ** | -28.72 | -31.28 | -9.16 | -24.14 |
| CMSUAA×AV31 | -34.82 ** | -31.85 * | -4.32 | -3.56 | 21.93 | 6.46 |
| CMSUAA×AV43 | -54.64 ** | -45.31 ** | -10.95 | 3.53 | 13.49 | 14.28 |
| CMSUAA×AV44 | -48.08 ** | -48.08 ** | 7.42 | 3.56 | 36.89 | 14.32 |
| CMSUAA×AV47 | -34.50 ** | -34.50 ** | 35.51 * | 30.64 | 72.69 ** | 44.21 * |
| CMSUAA×AV49 | -57.98 ** | -56.45 ** | -13.06 | -13.13 | 10.80 | -4.11 |
| CMSUAA×AV53 | -41.04 ** | -38.37 ** | 21.99 | 22.92 | 55.46 ** | 35.68 |
| CMSUAA×AV16 | -63.63 ** | -60.76 ** | -38.15 * | -35.66 | -21.18 | -28.98 |
| CMSUAA×PDL1 | -39.92 ** | -38.59 ** | 16.12 | 14.43 | 47.98 * | 26.32 |

*Significance at P = 0.05 level; ** Significance at P = 0.01 level; *** Significance at P = 0.001 level

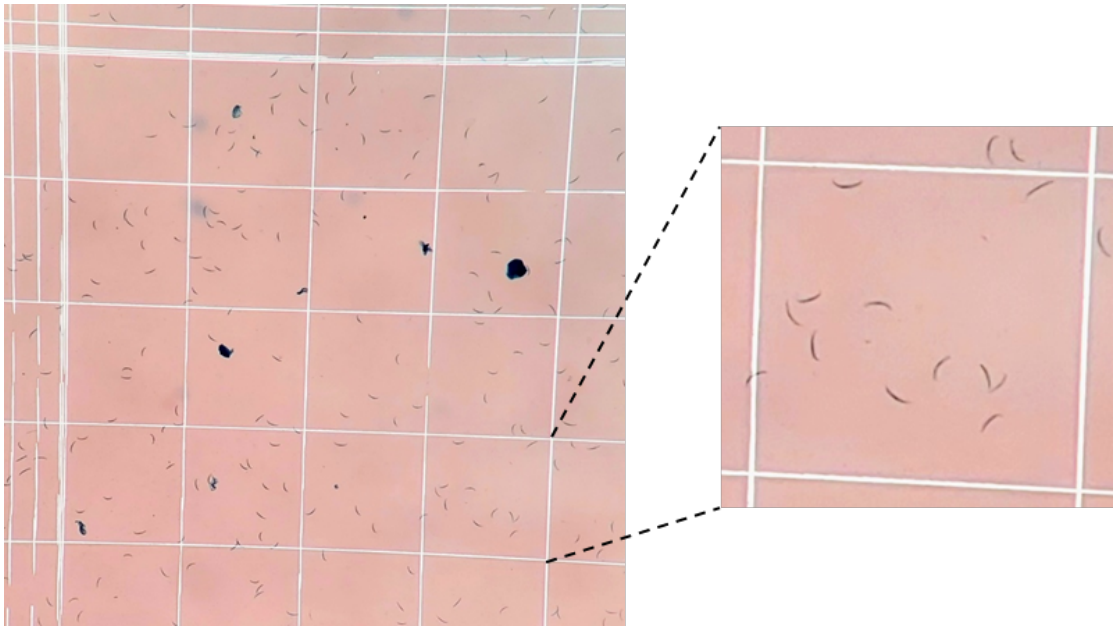

**Fig. 1:** Visualization of sickle shaped conidia of *Colletotrichum capsica* with hemocytometer under light microscope at 10X magnification

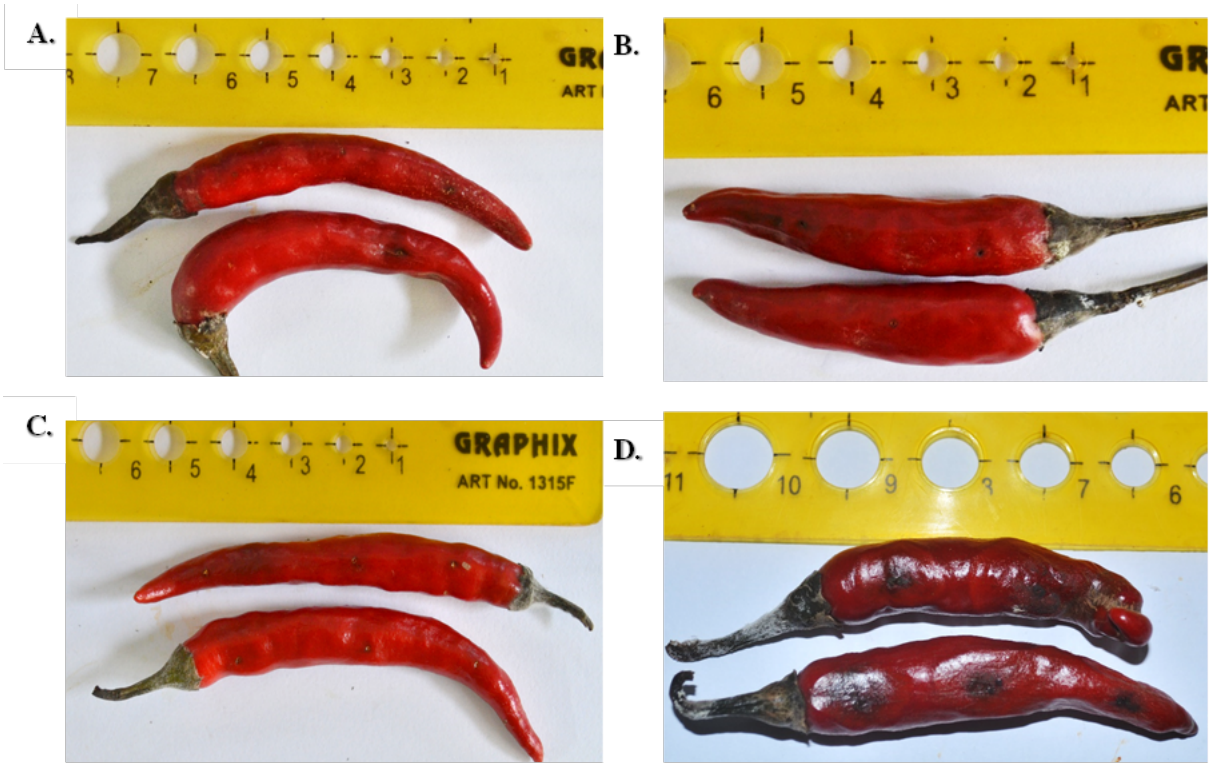


**Fig. 2 :** Response of CMS 7A×AV31 (A), CMS 7A×AV59 (B), CMS7A×AV48 (C) and Arka Khyati (D) to challenged anthracnose infection

## References


Amorim, A. F. S., Gilio, T. A. S., de Jesus, J. B., de Souza, L. H. A., dos Anjos, I. V., Araujo, K. L., Barelli, M. A. A., da Costa Preisigke, S., and Neves, L. G. (2021). Genetic improvement of Capsicum frutescens, hybrid vigor for anthracnosis resistance and production traits. *Euphytica* 217(4).

Bal, S., Karak, C., Mandal, A. K., and Chattopadhyay, A. (2024). Breeding chili pepper for simultaneous improvement in leaf curl virus and anthracnose disease tolerance and commercially important traits. *International Journal of Vegetable Science* **30**(1), 91–109.

Bhandari, G., Zomer, P., Atreya, K., Mol, H. G. J., Yang, X., and Geissen, V. (2019). Pesticide residues in Nepalese vegetables and potential health risks. *Environmental Research,* **172**, 511–521.

Bosland, P. W., and Votava, E. J. (2012) *Peppers, Vegetable and Spice Capsicums*. (Vol. 22). Wallingford, CABI Publishing.

Chanchaichaovivat, A., Ruenwongsa, P., and Panijpan, B. (2007). Screening and identification of yeast strains from fruits and vegetables, Potential for biological control of postharvest chilli anthracnose (*Colletotrichum capsici*). *Biological Control,* **42**(3), 326–335.

Channabasava, Ganesh, P., Siddu, C. B., Susmitha, B., Rao, A.M., and Ramesh, S. (2023). DNA marker-assisted identification of promising exotic advanced breeding lines as pollen fertility restorers and their validation based on field and laboratory assayable traits in chilli (*Capsicum annuum* L.). *Genetic Resources and Crop Evolution,* **70**(7), 1957–1969.

Chen, W., Wei, L., Hou, R., Zhao, Y., Zhao, Y., and Liu, F. (2022). Sterol demethylation inhibitor fungicide resistance in Colletotrichum siamense from chili is caused by mutations in CYP51A and CYP51B. *Phytopathology Research* **4**(1).

*FAOSTAT, 2023. https,//www.fao.org/faostat/en/#data/QCL* (n.d.).

Haque, S. M., Paul, S., and Ghosh, B. (2016). Karyological studies of two hot chilli pepper cultivars from two different geographical regions of India, Bhut jolokia, Capsicum chinense Jacq. and Bullet Lanka, *Capsicum annuum* L. *Nucleus (India)* **59**(3), 227–233.

Karim, K. M. R., Rafii, M. Y., Misran, A. B., Ismail, M. F. Bin, Harun, A. R., Khan, M. M. H., and Chowdhury, Mst. F. N. (2021) Current and Prospective Strategies in the Varietal Improvement of Chilli (*Capsicum annuum* L.)

Specially Heterosis Breeding. *Agronomy* **11**(11), 2217.

Kempthorne, O. (1957) *An introduction to genetic statistics.* Wiley.

Lata, H., Sharma, A., Thakur, H., Thakur, A., Rana, R. S., and Kaur, M. (2023) Heterosis and combining ability vis-à-vis association for green fruit yield and component traits involving male sterile lines in chilli (<scp> *Capsicum annuum* </scp>) under wet temperate zone of North Western Himalayas. *Plant Breeding,* **142**(4), 547–562.

Meon, S., Zainun, W., and Nik, W. (1988). *Seed-borne Infection and Development of Colletotrichum capsici in Naturally Infected Chili Seed*. *Pertanika* (Vol. 11).

Oo, M.M. and Oh, S.-K. (2016). Chilli anthracnose (Colletotrichum spp.) disease and its management approach. *Korean Journal of Agricultural Science,* **43**(2), 153–162.

Prathibha, V.H. (2011, November 18) *Pathological and variability studies on colletotrichum spp. causing anthracnose (Fruit rot) disease of chilli (Capsicum annuum L.)*. University of Agricultural Sciences, Bengaluru.

Pugalendhi, L., Veeraragavathatham, D., Sathiyamurthy, V. A., and Natarajan, S. (2010). *High yielding and moderately resistant to fruit rot disease chilli hybrid-CCH 1 (TNAU Chilli Hybrid CO 1)*. *Electronic Journal of Plant Breeding* (Vol. 1).

Putra, F., Carsono, N., Widiantini, F., Bakti, C., Mitalo, O. W., and Kang, S. W. (2024). Breeding Methods for Antrachnose Resistant Chili Pepper in the Last Decade, A Review. *AGROSAINSTEK, Jurnal Ilmu dan Teknologi Pertanian,* **8**(2), 76–90.

Ridzuan, R., Rafii, M., Ismail, S., Mohammad Yusoff, M., Miah, G., and Usman, M. (2018). Breeding for Anthracnose Disease Resistance in Chili, Progress and Prospects. *International Journal of Molecular Sciences* 19(10), 3122.

Roberts, P. D. , P. K. L. and K. T. A. (2011) Anthracnose caused by *Colletotrichum* spp. on pepper responsible for anthracnose diseases of various fruits. *Plant Disease* **82**(6), 596–605.

Saengarun, P., Suwor, P., Inprasert, H., Kumsee, N., Tsai, W. S., Techawongstien, S., Tainta, T., Kumar, S., Jeeatid, N., Chatchawankanphanich, O., and Kramchote, S. (2025). Combining ability analysis in anthracnose-resistant introgression inbreds and developing improved resistant lines of pepper (*Capsicum annuum* L.). *Scientia Horticulturae,* **339**, 113899.

Sarfaraz, V., Yadav, S. and Srivastav, P. (2022). *Organic Horticulture*. (Vol. 147). Bright Sky Publications.

Saxena, A., Raghuwanshi, R., Gupta, V. K., and Singh, H. B. (2016). Chilli Anthracnose, The Epidemiology and Management. *Frontiers in Microbiology* 7.

Shah, N. C. (2023). Origin, introduction, and cultural history of capsicum in India. *Indian Journal of History of Science,* **58**(4), 312–319.

Shi, N., Zhao, D., Qiu, D., Wang, H., Wu, L., Chen, F., Chen, Q., and Du, Y. (2023). Resistance risk and resistance-related point mutations in cytochrome b of florylpicoxamid in Colletotrichum scovillei. *Pesticide Biochemistry and Physiology* 196, 105617.

Sun, C., Mao, S. L., Zhang, Z. H., Palloix, A., Wang, L. H., and Zhang, B. X. (2015) Resistances to anthracnose (*Colletotrichum acutatum*) of Capsicum mature green and ripe fruit are controlled by a major dominant cluster of QTLs on chromosome P5. *Scientia Horticulturae,* **181**, 81–88.

Than, P. P., Jeewon, R., Hyde, K. D., Pongsupasamit, S., Mongkolporn, O. and Taylor, P. W.J. (2008). Characterization and pathogenicity of *Colletotrichum* species associated with anthracnose on chilli (*Capsicum* spp.) in Thailand. *Plant Pathology* **57**(3), 562–572.

Voorrips, R. E., Finkers, R., Sanjaya, L. and Groenwold, R. (2004). QTL mapping of anthracnose (*Colletotrichum* spp.) resistance in a cross between *Capsicum annuum* and *C. chinense*. *Theoretical and Applied Genetics* **109**(6), 1275–1282.

Xue-xiao Zou, F. Z. (2022). Origin, evolution and cultivation history of the pepper. *Acta Horticulturae Sinica,* **49**(6), 1371–1381.