Indian Journal of Agricultural Sciences **95** (11): 1359–1365, November 2025/Article
https://doi.org/10.56093/ijas.v95i11.169149

Mineral dynamics in cauliflower (*Brassica oleracea* var. *botrytis*) genotypes under *Alternaria brassicicola* infection: A multivariate approach

VARUN B H[1], SHRAWAN SINGH[1]* and NAVINDER SAINI[1]

ICAR-Indian Agricultural Research Institute, New Delhi 110 012, India

Received: 18 July 2025; Accepted: 07 November 2025

ABSTRACT

Among many diseases effecting cauliflower (*Brassica oleracea* var. *botrytis* L.), *Alternaria* leaf spot (ALS) disease caused by *Alternaria brassicicola* (Schw.) impacts the most, with yield reduction upto 50% under favourable condition. The present study was carried out during 2024 at ICAR-Indian Agricultural Research Institute, New Delhi to evaluate the role of mineral nutrients in disease resistance. Six genotypes [DCF-14, DC-309, VV, Pusa Meghna (PM), Pusa Kartiki (PK) and Pusa Deepali (PD)] were assessed pre- and post-infection conditions artificially challenged by pathogen. The disease severity-index (DSI) showed that genotypes DCF14 and VV were resistant (6.67%), while Pusa Kartiki and Pusa Deepali as moderately resistant (20%), and Pusa Meghna and DC309 as susceptible (33.33%) at 9th day. ANOVA revealed significant genotypic interactions for essential macro- (N, P, K), secondary- (Ca, Mg, S), and micro- (Fe, Cu) nutrients. Resistant genotypes exhibited substantial post-inoculation increase in K, Ca, S, and Fe nutrients compared to others. Principal Component Analysis (PCA) explained 92.56% of total phenotypic variance (PC1-71.99%, PC2-20.57%), with minerals N, P, K, S and Ca aligning negatively with DSI. PCA-biplot distinguished susceptible, moderate and resistant genotypes based on nutrient profile. Heatmap showed distinct clustering of genotypes where resistant genotypes having higher nutrients with lower DSI and susceptible genotypes grouped with lower nutrient profile and higher DSI. Partial correlation network (PCN) identified P, Mg, and Cu are negatively correlated with DSI, highlighting their potential roles in resistance against ALS. These outcomes revealed that coordinated mobilization of key nutrients K, Ca, S, and Fe, is pivotal for resistance against *A. brassicicola*, which provides solid foundation for genotype improvement and integrated nutrient management strategies in cauliflower.

Keywords: *Alternaria* leaf spot, Cauliflower, Heatmap, PCA, Minerals

Cauliflower (*Brassica oleracea* var. *botrytis* L.) is a widely cultivated brassica vegetable for its economical and nutritional value throughout the globe. The edible curd is rich in nutrients, vitamins, glucosinolates and dietary fibers (Singh *et al*. 2022) and according to FAOSTAT (2024), the combined global production of cauliflower and broccoli reached approximately 26.5 million tonnes in 2023, with India and China contributing more than 72% of the total output. Despite its importance to human nutrition and food security, cauliflower production is frequently hindered by biotic stresses, particularly *Alternaria* leaf spot (ALS) caused by *Alternaria brassicicola* (Schw.). This necrotrophic fungal pathogen produces dark necrotic lesions on leaves, induces premature senescence, and reduces curd quality, especially under warm and humid environmental conditions (Meena *et al*. 2017, Sharma *et al*. 2020).

Although conventional breeding and chemical management strategies are employed, increasing focus is being placed on mineral nutrition as a sustainable and complementary approach to combat disease. Macro-nutrients (nitrogen, phosphorus, and potassium), secondary nutrient (calcium, magnesium and sulfur) along with micronutrients (iron, copper, and zinc) are vital for plant growth and development. They also play central roles in modulating plant defense mechanisms (Datnoff *et al*. 2007, Marschner 2012, Pandey *et al*. 2002). These nutrients enhance disease resistance in plants, by influencing defense signaling, enzyme activities, cell wall integrity, and increase synthesis of secondary metabolites (Broadley *et al*. 2007, Cakmak and Kirkby 2008).

Potassium not only strengthens cell walls, it also promotes polyphenol synthesis, deterring pathogen invasion in *Brassica* (Wang *et al*. 2013), while calcium is involved in cell wall stability and functions as a secondary messenger during defense responses (Hepler 2005). Sulfur is crucial for biosynthesis of glucosinolates, important for antimicrobial activity in all *Brassicas* (Rausch and Wachter 2005). Iron and copper support redox homeostasis and oxidative burst key mechanisms against necrotrophs like *A. brassicicola* (Verma *et al*. 2018). Genotypes that sustained nutrient

[1]ICAR-Indian Agricultural Research Institute, New Delhi.
*Corresponding author email: singhshrawan@rediffmail.com

homeostasis under infection often show greater disease tolerance (Mandal *et al*. 2019, Bharti *et al*. 2021).

In the present study, six cauliflower genotypes were evaluated under *Alternaria brassicicola* pre- and post-infection conditions. Multivariate tools PCA, heatmap clustering, and partial-correlation network, were used to investigate the role of relationship between mineral dynamics and ALS resistance. This study provides a novel insight into nutrient-mediated defense response and direct future breeding programmes with integrated nutrient strategies aimed at enhancing sustainable resilience in cauliflower for ALS.

MATERIALS AND METHODS

Plant material: The present study was carried out during 2024 at ICAR-Indian Agricultural Research Institute (28.6377°N, 77.1571°E; at an elevation of 228.61 m amsl), New Delhi. Six genotypes used in this study were DCF-14, DC-309, VV, Pusa Meghna (PM), Pusa Kartiki (PK), Pusa Deepali (PD) which were developed and maintained by ICAR-Indian Agricultural Research Institute, New Delhi. The experiment was conducted in months of July to September 2024 (due to congenial climatic conditions for pathogen). The seeds were sown in the 12-inch pots filled with soil as media in three replication per genotype. Three healthy seedlings were retained/genotype and taken regular care by following standard practices recommended by ICAR-Indian Agricultural Research Institute, New Delhi.

Pathogen culture, inoculation and disease monitoring: Pure culture of *Alternaria brassicicola* was obtained from the Indian Type Culture Collection (ITCC) No. 1707, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi. Sub-culturing was conducted aseptically by transferring a portion of the culture onto sterile Potato Dextrose Agar (PDA) plates in a laminar airflow chamber, followed by incubation at 25°C under a 12 h light/dark cycle for 6–10 days to promote growth and sporulation. For inoculum preparation, the sporulated mycelial mat was suspended in sterile distilled water and filtered through muslin cloth to eliminate agar debris. Spore concentration was determined using a hemocytometer (Avni Scientific Co. India) and adjusted to 1×10^5 spores/mL for drop inoculation and $2–4 \times 10^5$ spores/mL for foliar spray, following the procedure of Singh *et al*. (2022).

Plants with 45 days of age, were screened via two methods *in planta* foliar spray and detached leaf assay (DLA) methods. The foliar spray method involves uniform spray of the spore suspension until entire plants are covered, followed by covering the plants with polyethylene sheets to maintain high humidity and promote spore germination (Chakrabarty *et al*. 2012). Parallel to this DLA was performed to validate the robustness of the foliar spray and to eliminate the chances of disease escape due to environmental variation. Healthy leaves were collected before spray inoculation. The collected leaves were placed on moist germination paper, and their petioles were cut slantly and the cut petiolar ends were wrapped in moist cotton to reduce the transpiration and prolong the viability of leaves. Ten microliter inoculum was placed at 4 different spots using micropipette (Singh *et al*. 2022) (Supplementary Fig. 1).

Disease progression was monitored at regular intervals, and final scoring was conducted on the 9th day post-inoculation. Disease severity (DS) was assessed using a 0–5 rating scale based on lesion diameter: 0, No infection or germination in the 0.3 cm inoculated area; 1, Lesion diameter up to 0.5 cm; 2, 0.51–1.0 cm; 3, 1.1–1.5 cm; 4, 1.51–2.0 cm; 5, >2.0 cm (Singh *et al*. 2022). The disease severity index was calculated using the formula (Meena *et al*. 2016) given below:

$$\text{Disease severity index (DSI)} = \frac{\text{Total sum of numerical ratings} \times 100}{\text{Max. rating} \times \text{No. of samples observed}}$$

Estimation minerals

Sample preparation: The samples were collected before inoculation at 45 days and at the grand growth stage (10th day after inoculation) days of the genotypes at and oven dried at 65 ± 2°C until a constant weight was achieved. One gram of sample was digested using di-acid mixture of nitric acid and perchloric acid. The digested samples were diluted using distilled water and filtered using Whatman no.1 filter paper and volume was made up to 100 mL and stored for further estimation of phosphorus, potassium, sulfur, calcium (Ca), copper (Cu), magnesium (Mg) and iron (Fe) (Tandon 2009).

Estimation of macronutrients: Phosphorus (P) content was estimated using vanadomolybdate yellow colour method developed by Jackson (1973). The absorbance was read at 420 nm using UV-Vis spectrophotometer. Potassium (K) content was estimated by using flame photometer and calibrated against KCl standards (Jackson 1973). Sulfur (S) content in the samples was estimated using turbidometry method given by Chesnin and Yien (1950). The sample was reacted with barium chloride ($BaCl_2$) along with gum acacia to form a turbid complex which was read at 420 nm. Nitrogen (N) was estimated using Kjeldhal method suggested by Jackson (1973). One gram dried sample was digested using conc. sulfuric acid along with catalytic mixture (K_2SO_4: Cu SO_4: Se 10:1:1). The digest was distilled with 40% NaOH and the ammonia generated is trapped in boric acid and titrated against 0.01 N HCl. The nitrogen content was expressed as % nitrogen 100/g.

Estimation of micro-nutrients: The micronutrients (Ca, Mg, Cu and Fe) were estimated using Atomic Absorption Spectrophotometer (AAS) (Shimadzu AA-7800). Standard curve for each element was prepared using respective standard and the micronutrient content was expressed as mg 100/g of sample.

Statistical analysis: All statistical analyses were conducted in R version 4.3.3 (R Core Team 2023). The experiment was laid out in a completely randomized design (CRD) with three replications and one-way analysis of variance (ANOVA) for pre and post conditions was performed using R aov function, and homogeneity of variances was assessed by F-test on residuals. A paired t-test

was performed in R using the t-test function with the paired = TRUE argument to compare mineral concentrations between pre- and post-inoculation conditions for each genotype and trait. Pairwise Pearson correlations were calculated via cor (method = "pearson") and visualized as a clustered heatmap using pheatmap (v1.0.12) with Euclidean distance and complete linkage. Principal component analysis (PCA) on centered and scaled data was carried out using prcomp, and biplots were generated with factoextra (v1.0.7). Partial correlation coefficients controlling for all other variables were computed via ppcor (v1.1) and rendered as a circular network plot in q graph (v1.9.2) using layout = "circle".

RESULTS AND DISCUSSION

Statistically analysed data (Supplementary Table 1) for minerals (N, P, K, Ca, S, Fe) showed highly significant variation among genotypes, especially after disease, indicating their role in stress response. Cu levels showed significance only post-inoculation. Paired t-test showed significant differences between pre- and post-inoculation conditions (Supplementary Table 2). Significant differences were observed among multiple genotypes for key minerals, especially Mg, Ca, S, and Cu. Genotypes DCF14, VV, and PK showed highly significant changes, while DC309 and PD exhibited minimal or non-significant responses across most traits, indicating genotype-specific nutrient modulation.

Screening of cauliflower genotypes against A. brassicicola: Genotypes DCF14 and VV exhibited strong resistance to *A. brassicicola*, with the lowest disease severity (DS) (1) and DSI (6.67), whereas DC309 and PM were highly susceptible (DS = 5, DSI = 33.33). PK and PD showed moderate resistance (DS= 3, DSI= 20.00), distinguishing resistant, moderately resistant and susceptible classes clearly. The classification is strongly in agreement with previous studies in *Brassicas* for *Alternaria* resistance (Meena *et al*. 2017, Singh *et al*. 2022). Consistent results obtained from *in planta* foliar spray and DLA confirmed the reliability of both methods for phenotypic disease screening for ALS in cauliflower and use for further breeding (Chakrabarty *et al*. 2012).

Mineral profiling: Resistant genotypes DCF-14 and VV showed substantial increases in multiple nutrients estimated. Susceptible genotypes DC-309 and PM showed poor responses coupled with higher DSI. PK and PD showed intermediate nutrient profiles and moderate disease resistance (Table 1) **(**Fig. 1).

Macronutrients (N, P, K): Genotype DCF-14 exhibited a marked increase in N content of 5.58–6.27%, P content from 35.6–41.23 ppm, and K content from 208.17–255.33 ppm post inoculation. VV showed similar trends N from 5.27% to 5.82%, P from 33.5–41.77 ppm, K from 203.33 to 238.67 ppm. PK and PD accumulated moderate levels of these nutrients, while DC-309 and PM showed negligible changes. DC-309 showed reduction in P content from 26.87–25.6 ppm, and minimal changes in K and N content. These findings highlighted the critical role of macronutrients in plant defense. N supports biosynthesis of defense-related proteins, yet excessive availability may enhance susceptibility in *Brassica's* depending on form of N source and its availability stage (Huber and Watson 1974). In genotypes DCF-14 and VV, higher and controlled levels of N likely supported enhanced metabolic activity and

Table 1 Nutrient profile in cauliflower during pre- and post-inoculation of ALS

Genotype	Macro-nutrients			Secondary nutrients			Micro-nutrients		Disease reaction	
	N	P	K	Ca	Mg	S	Fe	Cu	DS	DSI
Pre-DCF14	5.58	35.60	208.17	38.93	4.41	26.77	2.99	2.45	0	0
Pre-DC309	4.36	26.87	181.83	33.97	3.60	12.97	2.40	2.04	0	0
Pre-VV	5.38	33.50	203.33	44.67	4.37	23.77	2.74	2.19	0	0
Pre-PM	4.20	26.67	179.60	39.17	3.81	16.00	2.41	2.07	0	0
Pre-PK	5.18	31.97	203.33	34.10	4.01	21.43	2.79	2.22	0	0
Pre-PD	5.37	30.77	211.93	33.00	4.03	23.60	2.68	2.30	0	0
Post-DCF14	6.27	41.23	255.33	46.77	5.68	36.27	3.43	2.90	1	6.67
Post-DC309	4.21	25.60	185.10	34.00	4.62	10.9	2.30	2.04	5	33.33
Post-VV	6.12	41.77	238.67	58.10	5.68	32.10	3.38	2.84	1	6.67
Post-PM	4.10	24.80	183.20	33.50	4.82	13.20	2.30	2.06	5	33.33
Post-PK	5.10	30.90	210.60	38.70	5.13	21.50	3.02	2.45	3	20
Post-PD	5.25	31.70	213.10	39.80	5.18	24.10	2.98	2.61	3	20
Mean	5.18	31.85	206.22	39.64	4.61	21.85	2.87	2.45	1.41	9.91
CV	6.99	1.34	0.24	1.22	7.87	1.87	20.35	17.02	35.23	5.50
LSD	0.61	0.72	0.85	0.82	0.61	0.69	0.99	0.71	0.84	0.92

ALS, Alternaria leaf spot.

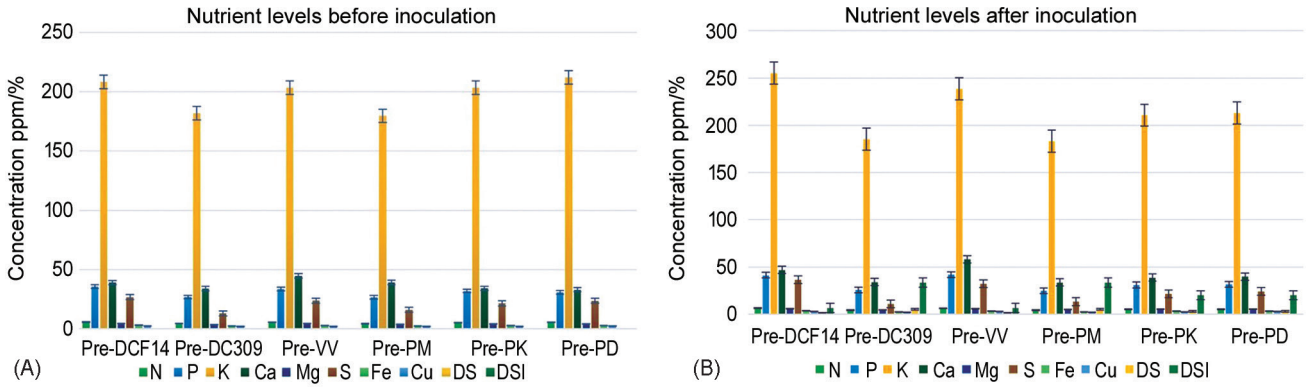

Fig. 1 Comparative nutrient profiles of cauliflower genotypes before (a) and after (b) *A. brassicicola* inoculation, highlighting changes in macro- and micronutrient levels associated with disease response.

increased disease resistance. P facilitates energy metabolism via ATP synthesis and immune signaling (Castrillo *et al*. 2017). Elevated P content in resistant genotypes possibly increase PR-protein synthesis. K is pivotal in activation of enzymes and enrichment of cell wall; it also promotes the production of phenolic compounds that restrict pathogen entry in *Brassicas* (Wang *et al*. 2013).

Secondary nutrients (Ca, Mg, S): DCF14 and VV showed substantial Ca increase (DCF14: 38.93 to 46.77 ppm; VV: 44.67 to 58.1 ppm), along with sulphur (DCF14: 26.77 to 36.27 ppm; VV: 28.87 to 34.33 ppm) but PK and PD followed with moderate rises. Mg content showed consistent but less dramatic increases across genotypes. Ca plays a dual role: strengthening cell walls and also functioning as a secondary messenger in immune signaling cascades against pathogen invasion (Thor 2019). Its accumulation in resistant genotypes helps to facilitate stronger and faster activation of defense response against ALS disease in cauliflower. Elevated S content in resistant genotypes DCF-14 and VV supports the hypothesis of sulfur-induced resistance. Although Mg did not show significant changes, it remains critical for photosynthetic efficiency and increase the vitality of the genotypes. Sulfur is key mineral for glutathione and glucosinolate biosynthesis, also enhances direct antifungal defense, especially in *Brassicaceae* family (Bloem *et al*. 2014).

Micronutrients (Fe, Cu): Resistant genotypes showed the highest post-inoculation levels of Fe and Cu contrary to susceptible genotypes. Fe increased from 2.994–3.43 ppm and Cu from 2.45–2.9 ppm in DCF-14. Genotype VV also showed a comparable Fe raised from 2.74–3.38 ppm. PK and PD exhibited moderate increase, while PM and DC-309 displayed minor changes in micro-nutrient levels. Fe plays a crucial part in oxidative response and cell wall lignification during pathogen invasion in cauliflower. It also enhances the production of reactive oxygen species (ROS), which are crucial for limiting pathogen spread by protecting from oxidative damage after ALS infection. Cu functions in redox reactions and acts as a cofactor in many enzymes which are responsible for detoxifying ROS. The higher profile of Fe and Cu in resistant genotypes DCF-14 and VV, thus contributes to enhanced ROS signaling and systemic acquired resistance (SAR) in cauliflower (Thor 2019).

Principal Component Analysis (PCA): The principal components (PCs) having more than 1 eigen values, explaining the maximum significant variations were retained from the analysis (Table 2). PC1 (71.99%) and PC2 (20.57%) explained 92.56% of the total variance for the mineral changes during pre- and post- inoculation. Dim1 accounting for 71.99% and Dim 2 for 20.57%, indicated that PCA model effectively captured mineral-related defense dynamics in cauliflower. The PCA-scree plot (Fig. 2a)

Table 2 Variance explained by PCA and PCA loading for mineral traits for ALS resistance

Component	eigen value	variance %	variance (C.P)	Mineral	Dim1	Dim2
1	7.06	70.57	70.57	N	0.97	-0.12
2	2.36	23.61	94.19	P	0.98	-0.09
3	0.41	4.09	98.27	K	0.97	0.11
4	0.08	0.79	99.06	Ca	0.82	0.08
5	0.04	0.42	99.48	Mg	0.70	0.70
6	0.02	0.23	99.71	S	0.98	-0.09
7	0.02	0.16	99.86	Fe	0.98	0.05
8	0.01	0.13	99.99	Cu	0.96	0.20
9	0.00	0.01	100.00	DS	-0.33	0.94
10	0.00	0.00	100.00	DSI	-0.33	0.94

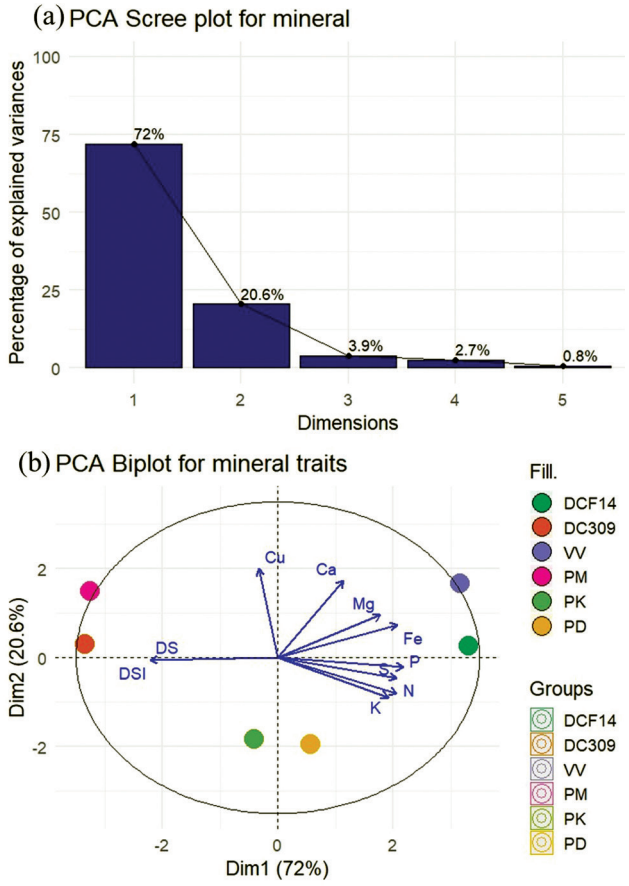

Fig. 2 (a) PCA-Scree plot showing the variance (%) explained by each principal component (b) PCA-biplot for major contributors to total variance among nutrients across genotypes, showing key patterns and nutrient association with DSI.
Genotypes: DCF-14, DC-309, VV, Pusa Meghna (PM), Pusa Kartiki (PK), Pusa Deepali (PD).

validated the contribution of the first two PCs, while the PCA-biplot (Fig. 2b) provided visual interpretation of mineral-trait loadings and genotype grouping based on disease reaction. Dim1, explaining majority of variance (71.99%), was positively associated with S (0.92), P (0.97), K (0.86), N (0.92), and Ca (0.50) nutrients. These nutrients showed strong and significantly negative correlations with the DSI (-0.99), indicating their key role in enhancing disease resistance against ALS. Contrarily, Cu (-0.14) showed a negligible variation, suggesting its limited role in the defense against ALS in cauliflower.

The biplot further supported the pathogen-mineral interaction in cauliflower. Resistant genotypes DCF-14 and VV were grouped positively with Dim 1, characterized by higher concentrations of defense-related minerals (N, K, P, S, Ca, Fe, and Mg), and aligned negatively with DS and DSI, indicating efficient defense response. Conversely, susceptible genotypes DC-309 and PM were clustered on the negative side of Dim 1, along with low mineral accumulation and higher DS and DSI. Genotypes PK and PD were placed at intermediate positions between Dim 1 and Dim 2, indicating moderate nutrient accumulation and partial defense response for ALS. The PCA results highlighted the importance of balanced nutrient accumulation especially N, P, K, S, and Ca in strengthening cauliflower resistance to *A. brassicicola*. These findings are in agreement with previous studies suggesting that balanced mineral nutrition is crucial for plant defense. K is known to increase phenolic compound biosynthesis, strengthening cell walls and inhibiting pathogen penetration. P plays dual role in structural importance and also essential for ATP synthesis and defense signaling pathways (Tripathi *et al*. 2022). N enhances protein synthesis and regulates redox homeostasis at optimal levels (Huber and Watson 1974).

Heatmap analysis for mineral-pathogen interaction: The heatmap for nutrient-pathogen (Fig. 3) revealed distinct clustering patterns that distinguished resistant and susceptible genotypes responses to *A. brassicicola* infection. Resistant genotypes DCF-14 and VV showed enhanced post-inoculation levels of N, P, K, Ca and S, indicated by warm colour red-orange intensity. These enriched nutrient levels indicated the active mineral mobilization during the defense response against ALS. These genotypes grouped together, indicating a shared nutrient derived defense response. Conversely, DC-309 and PM showed significantly lower levels of the nutrients post-inoculation, indicated by cooler green to blue shades, and clustered with higher values of DS and DSI. The DS and DSI grouped as separate cluster, indicating strong negative associations with most minerals, highlighting the negative association between nutrient and pathogen interaction. Pre-inoculation nutrient levels across all the genotypes exhibited a moderate and balanced mineral profiles indicated by yellow to light green shades. Resistant genotypes retained or enhanced the levels of majority of nutrients post-inoculation. This pattern underscores the essentiality of mineral retention or enhanced uptake during pathogen invasion and development, as a key element of defense response against ALS in cauliflower. These results are in agreement positively with earlier reports emphasizing the role of nutrient enrichment in pathogen defense in cauliflower. S and N, act synergistically in regulating resistance-related metabolic pathways in cauliflower. Karthika *et al*. (2020) reported that, optimal N:S ratio enhances *Brassica* resilience against pathogens, while Rathi *et al*. (2015) demonstrated that, reduced *Alternaria* leaf spot disease severity with sulfur, calcium, and magnesium enrichment in *Brassica*.

Partial-correlation network analysis for nutrient-disease interrelationship: The partial correlation network plot (Fig. 4) highlights the direct and indirect associations between nutrients and DSI while controlling for confounding variables. DS was negatively associated with nutrients P, Mg, and Cu indicating that elevated levels of these nutrients may reduce disease susceptibility for ALS in cauliflower. P emerged as a central node with robust negative correlations, underscoring its potent role in defense via energy transfer of adenosine tri phosphate (ATP), signaling, and membrane stability (Castrillo *et al*. 2017). Mg also exhibited positive

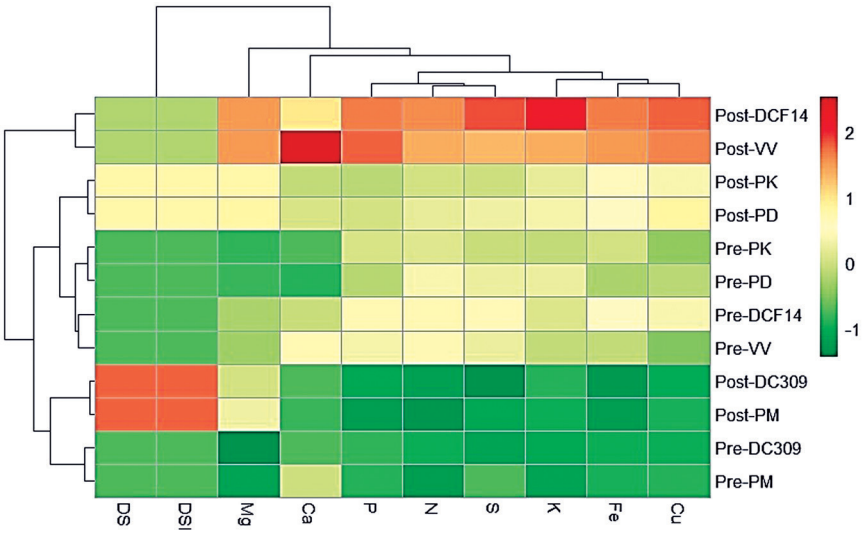

Fig. 3 Heatmap illustrating nutrient-disease interaction in cauliflower genotypes.
Cells shows Z-score values of nutrients and DSI across cauliflower genotypes under pre- and post-inoculation conditions. Colour intensity represents the relative magnitude of association: red shade indicates higher values, green shades indicate lower values, and yellow shades represents intermediate levels. Dendrograms shows hierarchical clustering based on euclidean distance and complete linkage, clustering genotypes and traits with similar nutrient levels.

associations, due to its key role in ribosome stabilisation and chlorophyll-mediated oxidative stress reduction. N, Ca and Fe showed partial positive correlations with DSI, indicating a vital association with enhanced susceptibility under certain conditions. N is vital for growth, accumulation in plants in excess, especially in ammoniacal form

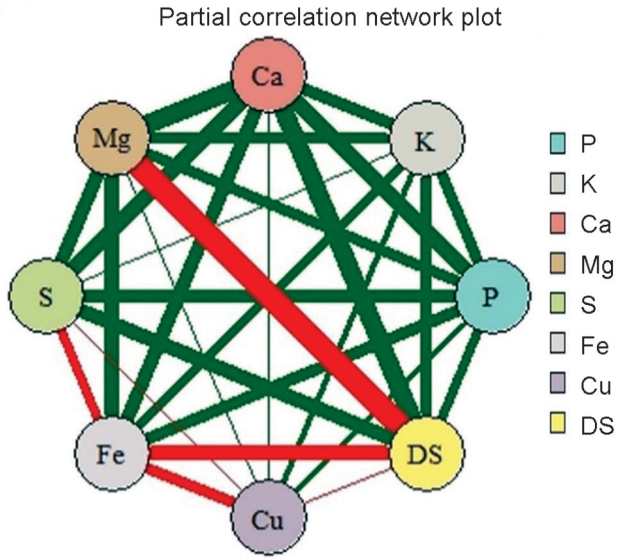

Fig. 4 Partial correlation network plot for nutrient-disease interaction in cauliflower**.**
Circles represent individual nutrients, lines represent the correlations between traits after controlling for all variables. Green lines represent positive correlations; Red lines indicate negative correlations. The line thickness shows the level of association of the nutrient with DSI.

can increase palatability of tissues, promoting pathogen proliferation and increased susceptibility (Huber and Watson 1974). The network topology marked P, Mg, and Cu as key minerals for suppressing disease severity in cauliflower against ALS, which is in alignment with heatmap observations. Contrarily, positively correlated nutrients may require careful management to balance their benefits with susceptibility risks. Rathi *et al*. (2015) reported enhanced *Alternaria* resistance in mustard following S, Ca and Mg application.

This study underscored a clear and key relationship between mineral dynamics and resistance to *A. brassicicola*. DCF-14 and VV were resistant to ALS and showed marked post-inoculation increase in macro-and micro-nutrients nutrients particularly K, Ca, S, and Fe supporting enhanced biochemical, enzymatic and structural defense activation. In contrast, susceptible genotypes DC-309 and PM showed negligible nutrient variation and higher disease susceptibility. These findings highlight the role of nutrient mobilization in defense response and provide us a valuable insight for breeding and nutrient fortification strategies directed at improving plant health and sustainable resilience.

ACKNOWLEDGEMENT

The first author sincerely acknowledges the ICAR-Indian Agricultural Research Institute, Government of India, for the financial support provided through the Senior Research Fellowship during this study.

REFERENCES

Bharti P, Jaiswal S, Sahu S K and Singh A K. 2021. Physiological and biochemical-responses in cauliflower genotypes under *A. brassicicola* stress. *Journal of Plant Stress Physiology* **2**(1): 50–60.

Bloem E, Haneklaus S and Schnug E. 2014. Milestones in plant sulfur-research on sulfur-induced-resistance (SIR) in Europe. *Frontiers in Plant Science* **5**: 779.

Broadley M R, White P J, Hammond J P, Zelko I and Lux A. 2007. Zinc in plants. *New Phytologist* **173**(4): 677–702.

Cakmak I and Kirkby E A. 2008. Role of magnesium in carbon-partitioning and alleviating photooxidative damage. *Physiologia Plantarum* **133**(4): 692–704.

Castrillo G, Teixeira P J P L, Paredes S H, Law T F, de Lorenzo L, Feltcher M E and Dangl J L 2017. Root-microbiota drive direct integration of phosphate stress and immunity. *Nature* **543**(7646): 513–18.

Chakrabarty R, Kalita H, Chakravarty M, Basumutary M, Bhattacharyya B and Medhi B. 2022. Integrated management of *Alternaria* blight caused by *Alternaria* in rapeseed (*Brassica rapa* var. *toria*) under field conditions. *Journal of Crop and*

Weed **18**(3): 128–35.

Chesnin L and Yien C H. 1950. Turbidimetric determination of available sulfates. *Soil Science Society of America Journal* **15**(3): 149–51.

Datnoff L E, Elmer W H and Huber D M. 2007. *Mineral-nutrition and plant disease*. APS Press. The American Phytopathological Society, St. Paul, Minnesota, USA.

FAOSTAT. 2024. *Cauliflowers and Broccoli,Production Quantity and Area Harvested*. Food and Agriculture Organization of the United Nations. https: //www.fao.org/faostat/, 22 January 2024

Hepler P K. 2005. Calcium: A central regulator of plant growth and development. *The Plant Cell* **17**(8): 2142–55.

Huber D M and Watson R D. 1974. Nitrogen form and plant-disease. *Annual review Phytopathology* **12**(1): 139–65.

Jackson M L. 1973. *Soil Chemical Analysis*. Prentice-Hall of India Pvt. Ltd., New Delhi.

Karthika K S, Prabha Susan Philip and S Neenu. 2020. Brassicaceae plants response tolerance to nutrient deficiencies. *Plant Family Brassicaceae: Biology and Physiological Responses to Environmental Stresses* **20**: 337–62.

Mandal J, Kumar S and Padbhushan R. 2019. Estimation of suitable extractant and critical level of B in cauliflower (*Brassica oleracea* var. *botrytis*, cv. Sabour Agrim) for the soils of Indo-Gangetic plain of Bihar, India. *The Indian Journal of Agricultural Sciences* **89**(4): 701–07.

Marschner P. 2012. *Marschner's Mineral Nutrition of Higher Plants*, 3rd edn. Academic Press.

Meena P D, Awasthi R P, Chattopadhyay C and Kumar A. 2017. *Alternaria* blight: A chronic disease in rapeseed-mustard. *Journal of Oilseed Brassica* **8**(1): 1–14.

Meena M C, Meena P D, Shukla A K, Mandira Barman M B, Meena M K, Pooja Singh P S and Arvind Kumar K. 2016. Role of plant nutrients in enhancing productivity and managing diseases of oilseed *Brassica*. *Journal of Oilseed Brassica* **7**(1): 1–20.

Meena P D, Rathi A S and Prasad R. 2016. Management of *Alternaria* blight of mustard with fungicides, botanicals, and biocontrol agents. *Journal of Mycology and Plant Pathology* **46**(1): 30–36.

Pandey K K, Pandey P K and Singh B. 2002. Slow blight response of early group of cauliflower (*Brassica oleracea* var *botrytis*) to *Alternaria* blight (*Alternaria brassicae*) under artificial inoculation conditions. *The Indian Journal of Agricultural Sciences* **72**(11): 682–84.

R Core Team. 2023. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria. Accessed 11 March 2025 from https: //www.R-project.org/

Rathi A S, Singh D, Avtar R and Kumar P. 2015. Role of micronutrients defense to white rust and *Alternaria* blight infecting Indian mustard. *Journal of Environmental Biology* **36**(2): 467.

Rausch T and Wachter A. 2005. Sulfur metabolism: A versatile platform for launching defense operations. *Trends in Plant Science* **10**(10): 503–09.

Sharma P, Thakur K and Kumar A. 2020. Management of *Alternaria* leaf spot disease in cauliflower through integrated approaches. *Vegetable Science* **47**(1): 70–75.

Singh A, Singh M and Singh V. 2022. Nutritional and phytochemical properties of cauliflower. *Journal of Food Biochemistry* **46**(4): e14100.

Tandon H L S. 2009. *Methods of Analysis Soils-Plants, Waters, Fertilisers, Organic-Manures*, 2nd edn. Fertiliser Development and Consultation Organization (FDCO), New Delhi.

Thor K. 2019. Calcium-nutrient and messenger. *Frontiers in Plant-Science* **10**: 440.

Tripathi D K, Tewari R K, Singh S, Keswani C, Minkina T, Srivastava A K and Sansinenea E. 2022. Plant mineral nutrition and disease resistance: Significant linkage for sustainable crop protection. *Frontiers in Plant Science* **13**: 1023456.

Verma V Ravindran P and Kumar P P. 2018. Plant hormone–mediated regulation stress responses. *BMC Plant Biology* **18**(1): 1–13.

Wang M, Zheng Q, Shen Q and Guo S. 2013. The critical role of potassium in plant-stress response. *International Journal Molecular Sciences* **14**(4): 7370–90.

Yruela I. 2005. Copper in plants: Acquisition, transport and interactions. *Functional Plant Biology* **32**(11): 409–30.