



Development of a Disease Forecasting Model for Rhizoctonia Aerial Blight (AG1-1A) of Soybean in the Central Agroclimatic Zone of India

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10.18805/LR-5538

ABSTRACT

Background: Rhizoctonia aerial blight (RAB), incited by *Rhizoctonia solani*, poses a significant risk to soybean production, reducing yield and grain quality. No single or multivariate predictive models employing subset or stepwise regression analysis currently exist for RAB for central zone of India's principal soybean growing regions using susceptible soybean genotypes.

Methods: Weekly RAB incidence data from six susceptible genotypes, including JS 95-60, were correlated with weekly weather variables using Pearson's analysis. Significant variables were used to develop single and multivariate regression models. Models with superior performance metrics were validated using cross-validation and evaluated for predictive accuracy through case-control classification and ROC analysis.

Result: Disease was initiated during pod formation stage and gradually progressed up to harvest. Disease development was favoured by conducive microclimatic conditions, including dense canopy, warm temperatures (28–30°C), high relative humidity (>85%) and well-distributed rainfall. Significant variation in area under the disease progress curve (AUDPC) values across genotypes, years and their interaction was observed in the current study. Two single-variable models and one multivariable model were developed using stepwise and subset regression. These models identified minimum temperature, rainfall and the number of rainy days as key factors influencing the development of RAB disease. Multivariable regression model outperformed single-variable models with higher accuracy (85.90%), area under the curve (AUC=0.860) and better performance indicators based on cross-validation and ROC analysis. These models show promise for quantitative risk assessment of RAB epidemics up to 15 days in advance.

Key words: Model, Regression analysis, Rhizoctonia aerial blight, Soybean, Weather variable.

INTRODUCTION

Soybean has swiftly emerged as the predominant oilseed crop in India, with nearly 11 million hectares currently under cultivation (Prashnani *et al.*, 2024). This expansion has occurred in new regions, especially the central zone of India and within established soybean-growing areas, leading to shortened crop rotation cycles or continuous soybean cultivation. As a result, the prevalence of the soilborne pathogen *R. solani* has risen, particularly impacting soybean crops in India (Bhamra *et al.*, 2022; Amrate *et al.*, 2021; Amrate *et al.*, 2023).

R. solani, a necrotrophic soilborne fungus, is a primary cause of soybean RAB, particularly during central India's pod formation stage (Amrate *et al.*, 2018). The disease thriving in high humidity (>95%), warm temperatures (25–35°C) and heavy rainfall during canopy closure favour rapid disease development (Rodriguez-Herrera *et al.*, 2023). It survives *via* sclerotia in soil, debris and seed, initiating foliar blight characterized by rapidly spreading lesions and eventual defoliation (Rupe and Spurlock, 2015). Globally, RAB has been linked to an estimated 2.56% reduction in overall soybean yield (Wrather *et al.*, 2010). In India, yield losses can exceed 35% under favourable conditions, with up to 80% reported during severe epidemics (Bhamra *et al.*, 2022).

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How to cite this article: Yadav, A., Rajput, L.S., Kumar, S., Singh, R.K., Aggarwal, S.K., Rajesh, V. and Dhaka, P. (2025). Development of a Disease Forecasting Model for Rhizoctonia Aerial Blight (AG1-1A) of Soybean in the Central Agroclimatic Zone of India. *Legume Research*. 1-6. doi: 10.18805/LR-5538.

Submitted: 30-06-2025 **Accepted:** 10-09-2025 **Online:** 06-10-2025

No commercially available soybean cultivars offer complete resistance to RAB, due to broad host range and high genetic diversity (Rupe and Spurlock, 2015). A major outbreak occurred during rainy season of 2020 in central zone of India with >90% disease severity (Annual Report, ICAR-NSRI, 2020). This emphasizes the critical importance

of implementing integrated disease management strategies at the right time.

Despite controlled environment studies establishing the roles of temperature, rainfall and humidity in RAB development (Harikrishnan and Yang, 2004), field-based predictive models remain underdeveloped. Previous models, limited to the Tarai zone (<1% of India's soybean area) and not validated for central India, which contributes ~90% of national production (Surbhi and Singh, 2020; Nainwal *et al.*, 2024). In central India, no validated single- or multivariate model exists for forecasting RAB in the highly susceptible and widely grown soybean cultivar JS 95-60 (Amrate *et al.*, 2021).

Therefore, the present study built single and multivariate weather-based models to forecast RAB on the highly susceptible cultivar JS 95-60 and five other susceptible genotypes. All models were validated and their performance was thoroughly evaluated. It draws on two years of RAB disease observations and concurrent meteorological data from Indore, Madhya Pradesh. This was widely regarded as a true representative of India's central soybean zone.

MATERIALS AND METHODS

Multiplication and inoculation of *R. solani*

The pathogen *R. solani* was isolated from soybean roots exhibiting typical symptoms of RAB. The pathogen was identified through detailed morphology and confirmed through molecular analysis of the ITS region (PV536985; AG group AG1-1A) (Rupe and Spurlock, 2015; Rajput *et al.*, 2025).

The pure culture *R. solani* was grown on autoclaved sorghum seeds and the colonized grains were ground into a fine powder. This powder was applied at a standardized rate of 5 g per meter of sowing row length at the planting time for all treatments (Ramteke *et al.*, 2024).

Disease progression and genotypes performance

Five susceptible soybean genotypes were sown along with one mega highly susceptible variety JS 9560 to assess RAB disease incidence. The trial was conducted at the field block of the Plant Pathology Section, ICAR-National Soybean Research Institute (NSRI), Indore (22°40'N, 75°52'E) during the *kharif* seasons of 2021 and 2022. The cultivars were sown in a randomized block design (RBD) with four replications. Each plot had two 5-meter rows, spaced 45 cm between rows and 10 cm between plants. Standard agronomic practices were followed (ICAR, 2009, Rajput *et al.*, 2024).

Weekly assessments of disease incidence were carried out by calculating the percentage of plant mortality in each replication. Data collection commenced at the onset of visible symptoms and was continued through to harvest in the inoculated soybean genotypes. The AUDPC was calculated using the trapezoidal method based on disease incidence percentage (Ramteke *et al.*, 2024).

Meteorological data and weather variables

A set of potential weather predictors for modeling soybean RAB disease epidemics was developed based on previously identified predictors from published studies on various crop diseases (Del Ponte *et al.*, 2006; Aggarwal *et al.*, 2017). Daily weather data during 2020 and 2021 were retrieved from the ICAR-NSRI Indore weather station. Daily weather data for 2020–2021 were obtained from the ICAR-NSRI Indore station, including minimum and maximum temperatures (°C), morning and evening relative humidity (%) and rainfall (mm). These were converted to weekly averages and weekly rainy days were also recorded.

Model development and validation

Weekly disease incidence data, collected from two weeks before symptom onset to harvest, were correlated with weather variables using Pearson's correlation (R package "CAR") (Chaulagain *et al.*, 2020). Pooled disease incidence data from all six genotypes were further correlated with weather variables using Pearson's correlation coefficient (*r*). Variables with $r \geq 0.3$ and a significance level of $p < 0.05$ were selected (Chaulagain *et al.*, 2020).

The pooled disease incidence data used for model development comprised 90 observations recorded during the both cropping season. Disease incidence proportions were logit-transformed and regressed against weather predictors using weighted logistic regression in R. Stepwise and subset regression (via "MASS" and "leaps" packages) were applied for development of single and multiple variable regression models (Chaulagain *et al.*, 2020).

Statistical indicators such as the coefficient of determination (R^2 and adjusted R^2), residual standard error (RSE) and information-based criteria, including the Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC), were used for model comparison. Model selection was guided by the AIC and BIC, with lower values indicating a model closer to the genuine underlying relationship (Chaulagain *et al.*, 2020).

Model validation was performed using the leave-one-out cross-validation (LOOCV) and cross-validated statistics (CVSS) (Del Ponte *et al.*, 2006) techniques. By following the criteria outlined by previous researchers, the most suitable model was identified based on the lowest predicted residual error sum of squares (PRESS) (Chaulagain *et al.*, 2020).

The predictive performance of both single and multiple-variable models was evaluated using a case-control classification approach (Singh *et al.*, 2021). Observations ($n = 48$) were categorized as cases (severity proportion > 0.1) and controls (severity proportion ≤ 0.1) and model predictions were similarly classified. Receiver Operating Characteristic (ROC) curves and AUC values were generated using the 'pROC' package in R was used to assess model discrimination (Singh *et al.*, 2021). Confusion matrices were constructed to compare actual and predicted classifications and standard performance

metrics including accuracy, specificity, recall and F1-score, were calculated (Singh *et al.*, 2021).

RESULTS AND DISCUSSION

Disease progression and genotypes performance

RAB onset was observed during the pod formation stage in 2021 (Sept 6–12) and 2022 (Aug 30–Sept 5) (Supp. Fig 1). Earlier studies observed that the disease typically begins at flowering and worsens with crop maturity, progressing of severe blight in the reproductive phase due to canopy-induced humidity (Amrate *et al.*, 2021).

The disease progress was measured in terms of AUDPC. AUDPC values were significantly higher ($F_{cal}=16733.41^{***}$, $P<0.0001$) in 2022 (1488.46) compared to 2021 (416.96), indicating more severe disease progression during the former year (Table 1). In 2021, rainfall was lower (266.40 mm) and more evenly distributed ($SD/ =/ 67.72$; 2.63 rainy days). In contrast, 2022 had higher but more variable rainfall (360.22 mm; $SD = 85.89$; 3.43 rainy days), creating conditions favourable for disease progression. However, excessive rainfall during pod formation may also cause waterlogging, potentially suppressing *R. solani* by inducing anaerobic conditions or hindering sclerotia germination (Kumar *et al.*, 1999).

During the critical phase of RAB development, warm and humid conditions prevailed, with average Tmax of 29.39°C, Tmin of 22.54°C, RHM at 90.01% and RHE at 83.64%. This microclimate favoured RAB progression and sustained *R. solani* activity, aligning with earlier reports that temperatures of 25–30°C and relative humidity of 85–95% promote mycelial growth and sclerotia formation (Harikrishnan and Yang, 2004).

The analysis of AUDPC obtained through percentage disease incidence demonstrated a significant difference among genotypes ($P<0.0001$), year ($P<0.0001$) and genotypes $\times$ year ($P<0.0001$) included in the current study. This result indicated the influence of both genetic and environmental factors on RAB progression. It also reflected

a complex relationship between host resistance and environmental conditions, consistent with earlier findings on genotype–environment effects in RAB development (Rodriguez-Herrera *et al.*, 2023).

Genotypes EC 325098 (959.24), EC 289099 (951.97) and EC 251541 (969.12) showed significantly higher AUDPC than JS 9560 (902.64) and EC 343312 (891.53). The higher AUDPC makes suitable these genotypes suitable candidates for studying disease progression and weather-based modelling. The variation among genotypes suggests differential resistance levels among susceptible genotypes (Surbhi and Singh, 2020).

Weather variables correlation with RAB disease incidence

In 2021, no weather variables significantly correlated with disease incidence ($p<0.05$) in any genotype. However, in 2022, Tmax showed a strong positive correlation (0.76–0.80; $p<0.01$) in every genotypes, indicating its critical role in RAB progression. Elevated temperatures likely enhanced sclerotia germination, infection cushion formation and hyphal spread (Bhamra *et al.*, 2022; Bashya *et al.*, 2022).

Table 1: AUDPC for *Rhizoctonia* aerial blight disease of soybean in six genotypes for 2 years.

Genotypes	Years		
	2021	2022	Mean
EC 281462	446.59 ^d	1636.94 ^a	1041.76 ^a
EC 325098	463.62 ^d	1454.86 ^{bc}	959.24 ^b
JS 95-60	348.55 ^e	1456.73 ^{bc}	902.64 ^c
EC 289099	433.97 ^d	1469.97 ^{bc}	951.97 ^b
EC 251541	456.82 ^d	1481.42 ^b	969.12 ^b
EC 343312	352.21 ^e	1430.84 ^c	891.53 ^c
Mean	416.96 ^b	1488.46 ^a	

The data represents the mean value and standard error. Different superscript letters are statistically different at $p<0.05$ based on Fisher's protected Least Significant Difference test.

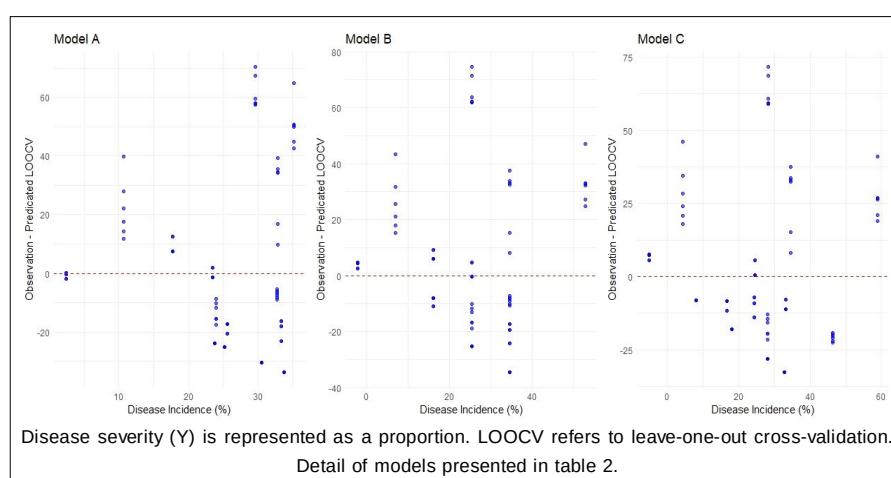


Fig 1: Cross-validated residual plot for model A, model B and model C was generated for the mean RAB disease incidence.

Pooled disease incidence across the tested genotypes showed a strong negative correlation with RF (−0.58, $p<0.0001$) and NRD (−0.62, $p<0.0001$), indicating increased rainfall and number of rainy days are strongly negatively associated with increased virulence of *R. solani* (Amrate *et al.*, 2021). The remaining *weather variables including* Tmax (−0.28, $p<0.01$) and Tmin (0.31, $p<0.01$) were significantly correlated with the pooled disease incidence across the tested genotypes. These associations highlight the role of temperature in enhancing the virulence and epidemic potential of *R. solani* (Spurlock *et al.*, 2016).

Model development

Two single-variable regression models were developed (Table 2). Model A, developed with RF and Model B, based on NRD, both exhibited strong negative associations with RAB progression. Previous studies also highlight rainfall and number of rainy days as a critical factor influencing the onset and progression of the disease, aligning with our findings (Romero *et al.*, 2021). Both models, showing relatively high R^2 and lower AIC, BIC, CVS, RMSE and PRESS values, were prioritized over others for their superior predictive performance (Table 2)

Among the both models, model B demonstrated greater explanatory power, accounting for 38 % (R^2) of the variation in RAB incidence (Table 2). Model B showed superior predictive performance indicator than model A. RF and NRD influence canopy wetness, ambient humidity and leaf surface moisture, thereby creating microclimatic conditions highly favourable

for *R. solani* infection and subsequent disease spread (Rodriguez-Herrera *et al.*, 2023). Earlier studies have demonstrated that epidemic onset and intensity are governed more by the duration and frequency of leaf wetness than by total rainfall, underscoring the pivotal role of rainfall distribution in driving RAB disease outbreaks (Amrate *et al.*, 2021; Surbhi and Singh, 2020; Nainwal *et al.*, 2024).

Model C was developed using stepwise and subset regression based on significantly correlated variables (Table 2). Model C incorporated two independent predictors, Tmin and NRD, which were identified as the key determinants of RAB incidence. It explained 13.63% to 25% more variation in RAB incidence than Models A and B. Additionally, Model C showed improved predictive performance, with lower AIC (225.21), BIC (233.85), RMSE (1.11) and PRESS (120.08) compared to the single-variable models. These results indicate that Model C provided the best fit compared to single-variable models. The improved accuracy highlights the importance of integrating multiple climatic factors for reliable RAB forecasting (Amrate *et al.*, 2021). Similar observations were reported by earlier studies, where multiple regression models effectively captured the variability in RAB disease incidence in soybeans (Amrate *et al.*, 2021; Surbhi and Singh, 2020; Nainwal *et al.*, 2024).

Model validation and predictive power

All regression models were validated using cross-validation statistics calculated from LOOCV and cross-

Table 2: Single-variable and multiple-variable models obtained through stepwise and best-subset regression analyses for predicting RAB disease incidence at in Indore, Madhya Pradesh.

Model	Regression equation	R ² value	Adj R ² value	CVS	AICc	BIC	RMSE	Press	P Value
A	Log (Y/1-Y) = -42.63 +1.43 (RF)	0.33	0.32	2.22	234.72	241.20	1.21	142.27	< 0.0001
B	Log (Y/1-Y) = 37.83 -1.67 (NRD)	0.38	0.37	2.03	229.64	236.11	1.17	130.28	< 0.0001
C	Log (Y/1-Y) = -7.60 + 0.40 (Tmin) – 6.85 (NRD)	0.44	0.42	1.87	225.21	233.85	1.11	120.08	< 0.0001

R^2 Value (Coefficient of determination); Adjusted R^2 value (adjusted coefficient of determination); CVS: Cross-validation score, AICc: Corrected akaike information criterion, BIC: Bayesian information criterion; RMSE: Root mean squared error; VIF: Variance inflation factor. and PRESS: Prediction sum of squares.

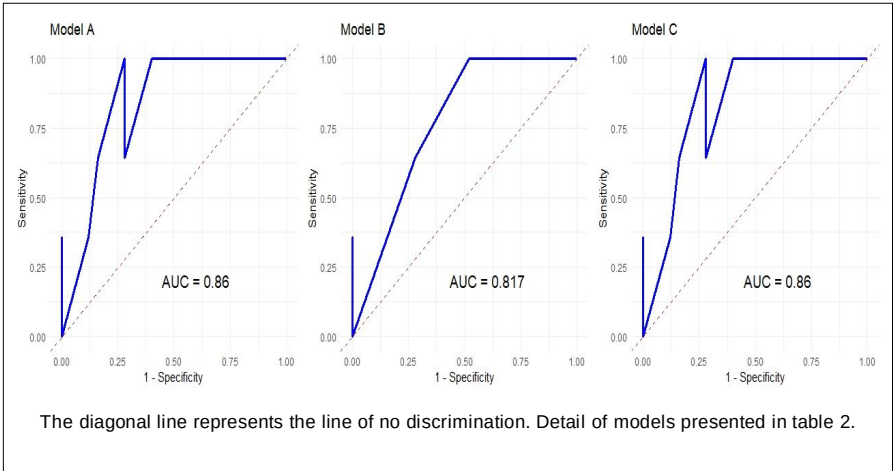


Fig 2: ROC curve for model A, model B and model C predicting RAB disease incidence.

Supp Table 1: Performance parameters of different models for predicting RAB disease incidence.

Performance parameters	Model A	Model B	Model C
Accuracy	76.60	85.90	85.90
Recall	45.50	100.00	100.00
F1-score	39.90	52.60	52.60
Specificity	83.00	84.70	84.70

validated residual distributions (Fig 1 and Table 2). The predictive capacity of each model for future disease incidence was tested using ROC analysis (Fig 1). Lowest prediction error (CVS = 1.87) was observed for multiple-variable regression model C (Table 2), suggesting that integrating multiple environmental predictors substantially enhances model performance (Amrate *et al.*, 2021).

Cross-validated residuals from Model C showed a tighter clustering around the zero line compared to model A and B, indicating a better model fit with minimal deviation between predicted and observed values (Fig 2). Similarly, cross-validated residual distributions have been effectively used to validate weather-based forecasting models for various other plant diseases (Chaulagain *et al.*, 2020; Ali *et al.*, 2022).

Results from the ROC analysis indicated that all models were capable of accurately predicting disease severity at a threshold level of 0.1. Model C achieved the highest predictive accuracy with an AUC of 0.860, indicating excellent discriminatory ability in distinguishing diseased from non-diseased cases. Additionally, both model B and model C demonstrated high accuracy (85.90 %), specificity (84.70%), recall (100.00%) and F1-score (52.60%) (Supp Table 1), indicating strong predictive performance with a good balance between true positives and false positives (Singh *et al.*, 2021).

This study offers key insights for managing RAB in soybeans, especially in India's central zone, which produces ~90% of the country's soybeans and largely grows the susceptible cultivar JS 95-60 (Rajput *et al.*, 2025; Amrate *et al.*, 2018). These models can estimate RAB risk using weather data from the preceding 15 days and support region-specific disease advisories, optimized fungicide scheduling and identification of agroclimatic risk zones. The effectiveness of the proposed prediction models is contingent on the accessibility and precision of localized meteorological data.

CONCLUSION

This study characterizes the progression of RAB in soybean at the pod formation stage under field conditions of the central zone of India. Favourable microclimates, dense canopy, warm temperatures (28-30°C) and high relative humidity (>85%) with well-distributed rainfall in August and September, were key drivers of disease development. AUDPC analysis showed significant genotype, year and genotype × year interaction effects, highlighting the role of

both genetic and environmental factors on RAB disease development. Correlation analyses revealed Tmin as positively associated with RAB, while Tmax, RF and NRD were negatively associated. Multivariable regression (Model C) outperformed single-variable models, demonstrating high accuracy (85.90%), strong discrimination (AUC = 0.860) and superior performance metrics including increased R² and decreased CVS, AIC, BIC, RMSE and PRESS. These findings emphasize the value of integrating multiple climatic predictors for reliable RAB forecasting. These models hold promise for timely and location-specific disease forecasting in the central zone of India. The study also emphasizes the need for robust monitoring and early warning systems based on weather variables. Future research should aim to incorporate biologically relevant factors such as soil moisture, rainfall and microbial activity into predictive models, thereby enhancing their accuracy and supporting proactive, sustainable management of RAB in soybean cultivation.

ACKNOWLEDGEMENT

We are very much thankful to the Director, Indian Council Agricultural Research-Indian Institute of Soybean Research, Indore India, for providing financial assistance.

Conflict of interest

There is no conflict of interest.

REFERENCES

- Aggarwal, S.K., Mali, B.L., Rajput, L.S., Choudhary, M. (2017). Epidemiology of anthracnose of black gram caused by *Colletotrichum lindemuthianum*. *International Journal of Agriculture Sciences*. **9**: 3656-3657.
- Ali, Y., Raza, A., Iqbal, S., Khan, A.A., Aatif, H.M., Hassan, Z., Hanif, C.M.S., Ali, H.M., Mosa, W.F., Mubeen, I., Sas-Paszt, L. (2022). Stepwise regression models-based prediction for leaf rust severity and yield loss in wheat. *Sustainability*. **14**(21): 13893. <https://doi.org/10.3390/su142113893>.
- Amrate, P.K., Pancheshwar, D.K., Shrivastava, M.K. (2018). Evaluation of soybean germplasm against charcoal rot, aerial blight and yellow mosaic virus disease in Madhya Pradesh. *Plant Disease Research*. **33**(2): 185-190.
- Amrate, P.K., Shrivastava, M.K., Pancheshwar, D.K. (2021). Crop-weather-based relation and severity prediction of aerial blight incited by *Rhizoctonia solani* Kuhn in soybean. *Journal of Agrometeorology*. **23**(1): 66-73. <https://doi.org/10.54386/jam.v23i1.90>.
- Amrate, P.K., Shrivastava, M.K., Singh, G. (2023). Identification of sources of resistance and yield loss assessment for aerial blight and anthracnose/pod blight diseases in soybean. *Legume Research*. **46**(11): 1534-1540. doi: 10.18805/LR-4452.
- Annual Report, ICAR-NSRI, (2020). Annual Report 2018-2019. Indore, India: ICAR-Indian Institute of Soybean Research.
- Bhamra, G.K., Borah, M., Borah, P.K. (2022). Rhizoctonia aerial blight of soybean, its prevalence and epidemiology: A review. *Agricultural Reviews*. **43**(4): 463-468. doi: 10.18805/ag.R-2311.

- Bashyal, M.B., Kharayat, S.B., Parmar, P., Gupta, A.K., Dubey, S.C., Aggarwal, R. (2022). Influence of temperature on the pathogenesis and gene expression of *Rhizoctonia solani* causing web blight/wet root rot disease in mungbean. *Legume Research*. **45(1)**: 104-109. doi: 10.18805/LR-4342.
- Chaulagain, B., Small, I.M., Shine Jr, J.M., Fraisse, C.W., Raid, R.N., Rott, P. (2020). Weather-based predictive modeling of orange rust of sugarcane in Florida. *Phytopathology*. **110(3)**: 626-632.
- Del Ponte, E.M., Godoy, C.V., Li, X., Yang, X.B. (2006). Predicting severity of Asian soybean rust epidemics with empirical rainfall models. *Phytopathol*. **96**: 797-803.
- Harikrishnan, R. and Yang, X.B. (2004). Recovery of anastomosis groups of *Rhizoctonia solani* from different latitudinal positions and influence of temperatures on their growth and survival. *Plant Diseases*. **88(8)**: 817-823.
- ICAR (2009). Handbook of Agriculture. Indian Council of Agricultural Research, New Delhi, India, pp. 1143-1150.
- Kumar, S., Sivasithamparam, K., Gill, J.S., Sweetingham, M.W. (1999). Temperature and water potential effects on growth and pathogenicity of *Rhizoctonia solani* AG-11 to lupin. *Canadian Journal of Microbiology*. **45(5)**: 389-395.
- Nainwal, M., Satpathi, A., Ranjan, R., Nain, A.S. (2024). Development of weather-based statistical models for RAB disease of soybean in Tarai region of Uttarakhand. *Journal of Agrometeorology*. **26(2)**: 268-270. <https://doi.org/10.54386/jam.v26i2.2530>.
- Prashnani, M., Dupare, B., Vadrevu, K.P., Justice, C. (2024). Towards food security: Exploring the spatio-temporal dynamics of soybean in India. *PLoS ONE*. **19(5)**: e0292005. <https://doi.org/10.1371/journal.pone.0292005>.
- Rajput, L.S., Kumar, S., Nataraj, V., Shivakumar, M., Maheshwari, H.S., Ghodki, B.S. (2022). Evaluation of novel fungicide for the management of soybean anthracnose disease and yield loss estimation. *Legume Research*. **47(11)**: 1998-2004. doi: 10.18805/LR-4783.
- Rajput, L.S., Kumar, S., Pathak, K., Acharya, P., Goswami, D., Nataraj, V., Shivakumar, M., Maheshwari, H.S., Mandloi, S., Jaiswal, S., Yadav, A., Vishwakarma, R. (2025). Morpho-cultural, pathogenic and genetic characterization of Indian isolates of *Macrophomina phaseolina* causing charcoal rot in soybean. *Heliyon*. **11(2)**: 42035. doi: 10.1016/j.heliyon.2025.e42035.
- Ramteke, R., Rajput, L.S., Nataraj, V., Tiwari, S., Borah, M., Kumar, S., Maranna, S., Ratnaparkhe, M.B., Mandloi, S., Jaiswal, S., Maheshwari, H.S. (2024). Evaluation of soybean genotypes for resistance to collar rot (*Sclerotium rolfsii*) under field and glasshouse condition. *Tropical Plant Pathology*. **49(5)**: 714-725.
- Rodriguez-Herrera, K.D., Doyle, V.P., Price, P.P., Padgett, G.B., Thomas-Sharma, S. (2023). Aerial blight of soybean caused by *Rhizoctonia solani* AG1-1A: A diagnostic guide. *Plant Health Progress*. **24(2)**: 234-241.
- Romero, F., Cazzato, S., Walder, F., Vogelgsang, S., Bender, S.F., van der Heijden, M.G.A. (2021). Humidity and high temperature are important for predicting fungal disease outbreaks worldwide. *New Phytologist*. **234(5)**: 1553-1556. <https://doi.org/10.1111/nph.17340>.
- Rupe, J.C. and Spurlock, T.N. (2015). *Rhizoctonia* Aerial Blight and Web Blight. Compendium of Soybean Diseases, 5th Edition. GL Hartman, JC Rupe, EJ Sikora, LL Domier, JA Davis and KL Steffy, eds. American Phytopathological Society St. Paul, MN. 55-56.
- Singh, P., Chatterjee, A., Rajput, L.S., Rana, S., Kumar, S., Nataraj, V., Bhatia, V., Prakash, S. (2021). Development of an intelligent laser biospeckle system for early detection and classification of soybean seeds infected with seed-borne fungal pathogen (*Colletotrichum truncatum*). *Biosystems Engineering*. **212**: 442-457.
- Spurlock, T.N., Rothrock, C.S., Monfort, W.S., Griffin, T.W. (2016). The distribution and colonization of soybean by *Rhizoctonia solani* AG11 in fields rotated with rice. *Soil Biology and Biochemistry*. **94**: 29-36.
- Surbhi, K. and Singh, K.P. (2020). Influence of weather factors on severity of aerial blight of soybean. *Indian Phytopathology*. **73(3)**: 493-497. <https://doi.org/10.1007/s42360-020-00235-w>
- Wrather, A., Shannon, G., Balardin, R., Carregal, L., Escobar, R., Gupta, G.K., Ma, Z., Morel, W., Ploper, D., Tenuta, A. (2010). Effect of diseases on soybean yield in the top eight producing countries in 2006. *Plant Health Progress*. **11(1)**: 29. doi:10.1094/PHP-2010-0125-01-RS.