Legume Research - An International Journal

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CONTENT **Page No.**

REVIEW

PLANT GENETICS AND BREEDING

PLANT PROTECTION

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Message

Transforming Legume Research through Genomics, Microbiomes, and Artificial Intelligence

Legumes have always held a pivotal place in global agriculture, serving as a vital source of dietary protein while simultaneously enriching soil fertility through biological nitrogen fixation. Beyond their nutritional and ecological significance, legumes are central to the sustainability of farming systems. In recent years, advances in molecular breeding, genomic selection, and precision agronomy have remarkably accelerated the development of climate-resilient and nutrient-dense legume cultivars. The integration of biotechnology with conventional breeding has broadened resistance against pests, diseases, and abiotic stresses, while ecological approaches such as intercropping and rhizobial inoculation continue to enhance resource-use efficiency and ecosystem services.

Looking ahead, cutting-edge innovations are redefining the future of legume research. Gene editing tools such as CRISPR are enabling precise trait improvement, while microbiome engineering is unlocking new pathways for plant–microbe symbiosis and stress adaptation. Digital agriculture, supported by artificial intelligence (AI) and machine learning, is transforming crop monitoring, predictive modelling, and decision-making in legume production systems. By integrating multi-omics data with AI-driven analytics, researchers can now accelerate breeding pipelines and optimize management practices with unprecedented accuracy.

Collectively, these advancements will contribute to global food and nutritional security while fostering resilient, sustainable, and climate-smart legume-based systems.

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Message

It is indeed a privilege to acknowledge the remarkable contributions of the Agricultural Research Communication Centre (ARCC) and its flagship journals, particularly Legume Research, in advancing agricultural science at the global level. Over the years, ARCC has created a vibrant platform that not only disseminates high-quality scientific findings but also connects researchers, practitioners, and policymakers in addressing the most pressing challenges in agriculture and food security.

Agricultural research today stands at a critical juncture, where sustainable production, climate resilience, and nutritional security must be achieved together. In this context, the role of communication and knowledge sharing becomes indispensable. The Legume Research journal continues to serve as a trusted repository of innovative studies, methodologies, and practical insights that benefit both academia, researchers, policymakers and farming communities.

As we look ahead, I, as a member of Editorial Board, strongly encourage our research community to share more impactful findings and innovative solutions through this journal. By contributing cutting-edge research, we collectively strengthen the mission of ARCC to empower agriculture for a sustainable future. Together, let us continue to expand the frontiers of knowledge and inspire the next generation of agricultural scientists.

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Message

Legume Research is a peer-reviewed international agricultural journal, proudly celebrating a special issue at GARCX 2025, a global conference hosted at Dusit Thani, Dubai. The journal has established itself as a respected platform for advancing legume science and promoting sustainable agricultural practices with over 50 years of continuous publication. Its indexing in SCOPUS reflects the dedication and collaborative efforts of researchers, editors, reviewers, and authors who have contributed to its growth and global recognition.

Agricultural research plays a pivotal role in ensuring food security, rural development and environmental sustainability. Amid climate change and resource limitations, it drives science-based innovations. In legumes, research has produced resilient, high-yielding, nutrient-rich varieties that support soil health and food systems. Technologies like gene editing, precision farming, and digital tools are revolutionizing agriculture, boosting productivity while minimizingenvironmental impact.

My vision for agriculture is sustainable, inclusive, and innovation-driven. I envision systems where all farmers, regardless of scale, can access the tools and knowledge needed to thrive. As an editorial board member, I am dedicated to promoting impactful research that shapes the future of global agriculture.

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Message

Agricultural research should prioritize sustainable and climate-resilient farming, effective water management, economic and livelihood diversification, strengthening community-based disaster risk management institutions, and assisting communities to adapt to the negative impacts of a growing population. By studying traditional cropping systems, plant genetics, soil science, and pest management, researchers can develop innovative solutions to address challenges posed by increasing population pressures. Therefore, it is essential to utilize all available agricultural resources to enhance productivity and sustainability to meet the rising demands of a global population. Moreover, collaboration among researchers, farmers, and policymakers is vital to ensure that advancements in agricultural research are effectively implemented on a broad scale. One key challenge is balancing increased food production with conservation efforts to safeguard natural resources and biodiversity through innovations in cropping systems. This calls for a holistic approach that recognizes the interconnectedness of agriculture, ecosystems, and human well-being. Intercropping legumes with other crops (including new cultivated varieties) offers an innovative way to improve soil health, reduce reliance on synthetic fertilizers, and boost crop yields. By diversifying cropping systems in this manner, farmers can promote sustainable practices while also addressing food security concerns.

ARCC Journals is a leader in the field of agricultural research, providing innovative solutions and cutting-edge technologies to improve crop yields and sustainability. With a team of expert scientists and researchers, ARCC Journals is a leader in advancing the knowledge and practices of agriculture for a more productive and sustainable future. Thank you.

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Molecular Identification of the Groundnut Leaf Miner *Aproaerema modicella* (syn. *Bilobata subsecivella*) (Lepidoptera: Gelechiidae): A Key for Targeted and Accurate Control in Groundnut and Soya Bean

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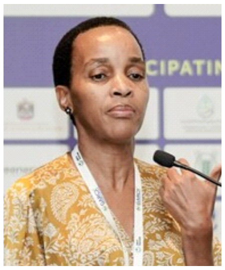

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Abstract

The identity of the African groundnut leaf miner (GLM) (Lepidoptera: Gelechiidae) remains uncertain. Early reports in Africa suggested an invasion of *Aproaerema modicella* species from Indo-Asia. Initial molecular study on mitochondrial DNA (COI) conducted in South Africa linked it to the Australian *Aproaerema simplexella*. Further mtDNA analyses of COII and cytb regions indicated that GLM populations from South Africa, India, Mozambique, and Australia are closely related, suggesting a single species. To clarify this, two nuclear DNA regions 28S rDNA and EF-1 ALPHA were sequenced from 44 South African specimens, four from Mozambique, and three each from India and Australia. Phylogenetic analyses (Maximum Parsimony and Neighbour Joining) showed 28S sequences clustered into a single group, while EF-1 ALPHA sequences revealed some structure, some Australian sequences (*A. simplexella*) formed a distinct clade, with others grouping with African and Indian GLM sequences. Pairwise genetic distances were 0.00% for 28S and 0.48–6.99% for EF-1 ALPHA. These results support mtDNA evidence that GLM populations across Africa, India, and Australia likely represent a single species, with the Australian population showing the greatest diversity. Accurate molecular identification of GLM is therefore critical, as developing effective pest management strategies for groundnut and soya bean depends on correct pest recognition. Future research should expand sampling, include additional DNA markers, and reassess taxonomy to further clarify GLM identity.

Key words: Groundnut leaf miner, Nuclear DNA, Phylogenetics, Pest identification.

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Oviposition and Feeding Preferences of the Groundnut Leaf Miner *Aproaerema modicella* (syn. *Bilobata subsecivella*) (Lepidoptera: Gelechiidae): Current Knowledge and Research Gaps

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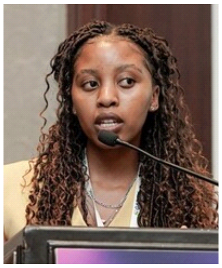

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Abstract

The groundnut leaf miner (GLM), *Aproaerema modicella* (syn. *Bilobata subsecivella*) (Lepidoptera: Gelechiidae) is a significant pest affecting groundnut (*Arachis hypogaea*) and soya bean (*Glycine max*) in Africa and Asia. Since its first record in Africa in 1998, GLM has rapidly expanded its range, caused considerable yield losses and posing a growing threat to food security. Although research has explored its bio-ecology and management, key aspects of its oviposition behaviour and feeding preferences remain poorly understood, limiting the development of targeted pest control strategies. Understanding these traits is crucial for predicting host plant susceptibility, improving IPM strategies, and developing resistant cultivars through approaches such as semiochemical attractants, host resistance breeding, and targeted biological control interventions. This review synthesises current knowledge on the oviposition site selection, host plant preference and feeding behaviour of GLM, incorporating insights from related Gelechiidae species where data are lacking. Furthermore, we identify critical research gaps, particularly in African agroecosystems, emphasizing the need for studies on chemical cues, larval feeding ecology, and environmental factors influencing pest dynamics. Addressing these knowledge gaps will enhance the development of sustainable control strategies and mitigate the impact of GLM on legume production.

Key words: *Aproaerema modicella*, *Bilobata subsecivella*, Feeding behaviour, Host plant selection, Integrated pest management, Oviposition preference.

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Influence of Epidemiological Factors and Survival Studies of Leaf Spot and Stem Canker of Pigeonpea Caused by *Didymella naikii*

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Abstract

The development of leaf spot and stem canker of pigeonpea [*Cajanus cajan* (L.) Mill sp.,] caused by *Didymella naikii* is largely depending on environmental factors such as temperature, precipitation and relative humidity. Understanding its dynamics through mathematical and statistical models will aid in disease forecasting and yield loss prevention. Present study was carried out under natural epiphytotic conditions on pigeonpea cultivar TS-3R during 2021-22 at UAS, Raichur, Karnataka. Weather factors significantly influenced the disease development as revealed by correlation matrix between weekly disease score and weather of preceding one week. Leaf spot and stem canker are positively correlated with rainfall, rainy day and sunshine hour, in addition leaf spot with morning relative humidity also. However, they are negatively correlated with maximum temperature, minimum temperature, evening relative humidity and evaporation whereas stem canker with morning relative humidity also. Apparent rate of infection (r), was recorded maximum (0.030) between 48th and 49th SMW and maximum AUDPC value (437.39) was obtained at 1st SMW. The simple auto regression prediction model for diseases showed accuracy of 88.33 per cent for leaf spot and 86.44 per cent for stem canker. This forewarning model can be useful for efficient management of disease and as well as agro advisory services to farmers. In addition, infected debris such as leaves, stem, petiole, and twig could be an important source of survival for the pathogens and a source of inoculum for the subsequent spreads.The infected samples were buried under 5 and 7.5 cm, and one set was placed on the surface of the soil. These samples were subjected to isolation at 15 days intervals and incubated at 25±2°C. The results revealed that the frequency of recovery of the pathogen decreased over time and the fungus was capable of overwintering for 23 weeks (% reduction was 86.66 6.66) in infected debris buried in sterilized soil. It has survived for 27 weeks (% reduction was 93.33-13.33) in field conditions, 30 weeks (% reduction was 100.0-20.0) on the surface of the soil, 34 weeks (% reduction was 100.0-20.0) in room conditions and 36 weeks (% reduction was 100.00-26.66) in the refrigerated conditions. Hence, the present study indicates the variation in the viability of the pathogen in the infected debris stored at six different conditions.

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Assessment of Genetic Divergence in Mini Core Collection of Peanut (*Arachis hypogaea* L.)

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Abstract

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop where kernel yield is the ultimate economic trait influenced by multiple yield-contributing characters. Due to the narrow genetic base of existing groundnut cultivars, the incorporation of novel gene sources is imperative for enhancing genetic variability and identifying yield-associated alleles. In this context, the present study assessed the genetic divergence among 144 groundnut mini core collections, including five standard checks (K-6, Dh-256, TMV-2, K-9 and ICRC-1), obtained from ICRISAT during *Kharif* 2024. Genetic divergence among the genotypes was quantified using Ward.D^2 method based on Euclidean distance. The genotypes were grouped into eight clusters. Cluster I had the maximum number of genotypes (31) whereas, Cluster VI had the minimum (3). Harvest index contributed the maximum (18.24%) due to wide variation in biomass partitioning and hundred kernel weight the minimum (1.26%) because of its relative stability across genotypes towards genetic divergence. Among clusters, the highest intra-cluster distance in Cluster VI (6.06) indicates the presence of greater genetic variability among its genotypes, arising from wider differences in trait expression. While the lowest intra-cluster distance in Cluster II (2.46) suggests close genetic relatedness, with genotypes exhibiting more uniform trait performance and narrower genetic variation. The maximum inter-cluster distance occurred between Cluster I and Cluster VII (5.82), while minimum inter-cluster distance (1.34) was found between Cluster II and Cluster III, implying a strong genetic resemblance among the genotypes within these clusters. For high pod yield and kernel yield, ICG 76 (Cluster VII) and ICG 14118 (Cluster VIII) were exceptional choices respectively. This study demonstrated considerable genetic divergence among groundnut genotypes, indicating that hybridization between superior lines from distantly related clusters could effectively broaden variability and accelerate yield-oriented genetic improvement.

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Meeting Market Demand: New Chickpea Lines for Roasting and Biotic Stress Tolerance

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Abstract

Chickpea is a globally significant pulse crop, with India contributing over 80% of its production. Roasting is a crucial value-addition component for chickpea, significantly enhancing its marketability and consumer appeal. Breeding for market-preferred traits like superior roasting quality can significantly benefit farmers by allowing them to fetch a higher premium in the market. In the state of Karnataka, India, chickpea is primarily grown for this purpose, where consumer preference favours bold seeds with thin seed coats. However, the commonly used roasting variety 'A-1' is now highly susceptible to Fusarium wilt disease, while the wilt-resistant variety Super Annigeri-1 lacks desirable roasting traits due to a rough and wrinkled seed surface. A collaborative study (ICRISAT & UAS-Raichur) was conducted to identify genotypes combining high yield, superior roasting quality, and environmental stability. An initial screening of 58 advanced breeding lines (2019–20 to 2022–23) identified a set of 12 promising lines based on seed yield, seed size, roasting traits and wilt resistance. These lines were evaluated in Rabi 2023–24 across three locations (Bidar, Kalaburagi, and Raichur) in Karnataka state, revealing significant genotype × environment (G×E) interactions for key traits including seed yield, plant height, 100 seed weight, pod number, and grain iron content. Four genotypes (ICCV-191256, ICCV-191156, ICCV-191151, and ICCV-191159) showed both high yield and excellent roasting traits. Further evaluation in Rabi 2024–25 across six locations (Bidar, Kalaburagi, B' Gudi, Raichur, Siruguppa and Hagari) confirmed ICCV-191156 as a consistently superior performer. ICCV-191156 not only received the highest overall acceptability score for roasted chickpea (T9-point hedonic scale) but also claims desirable nutritional qualities (high protein (22.72 % Before roast and 22.39 % after roast), iron (216.66 ppm with seed coat), zinc (49.99 ppm), carbohydrate (59.91 % Before roast and 61.05 % after roast) & low fat (3.79 % Before roast and 3.94 % after roast) and resistance to Fusarium wilt along with pod borer tolerance. These findings highlight the importance of multi-environment selection and the potential of targeted genotypes to enhance both productivity and consumer as well as commercial appeal in chickpea cultivation.

Key words: Chickpea, G x E interaction, Genotype, Roasting, Stability.

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Differential Response of Groundnut Genotypes for Terminal Drought Stress

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Abstract

Groundnut (*Arachis hypogaea* L.) is a self-pollinated allotetraploid, widely grown in tropical and subtropical zones, where the major limiting factor is moisture; moisture stress at the pod developmental stage will predominantly affect the yield. Drought is one of the most important abiotic stresses, estimates of yield losses due to drought range from 15 to 60 percent depending on geographical region, duration of the crop season, and dry spell. The present study was taken to know the response of different groundnuts to the terminal drought stress with the 16 genotypes. The experiment was taken during the summer season with two sets of experiments, one with an unstressed environment and another with a stressed environment. The genotype Dh-293 (0.4) was found to be stable in both the conditions for number of mature pods per plant. The genotype R2018-1 was highest (18) for the trait hundred pod weight and Dh-302(-2) was found better in the stress condition. For the trait shelling percentage Dh-293 found to be highest (20.95) and Dh-245(-25.70) indicating that in the stress condition pod filling was better when compared to the stress free condition. When compare the mean productivity R2018-1 and Dh-245 found to be better performer in the stress condition. Stress tolerance index (STI) is the resilient ability of the plant to maintain the productivity under adverse condition in which Dh-293 is having the less STI and R2018-1 and Dh-257 is having the higher STI, R2018-1 and Dh-257 which can perform better under the moisture stress condition for pod yield per plant. The overall study has given the differential responses of genotypes for the different traits and different factors.

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