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GENETIC VARIABILITY AND TRAIT ASSOCIATIONS FOR YIELD AND FIBER QUALITY IN UPLAND COTTON (GOSSYPIUM HIRSUTUM L.)

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Abstract

The genetic advance of upland cotton requires a synchronized focus on both yield and fiber quality traits, as these features collectively conclude the crop's economic value. The current study was piloted at the Cotton Research Section (CRS), Ayub Agricultural Research Institute (AARI), Faisalabad, to gauge 18 cotton genotypes for their agronomic performance and fiber quality. Yield components such as per plant bolls, boll mass, per plant seed cotton yield, seed index and ginning outturn (GOT %) displayed wide variability, with genotypes G6 and G16 recording the highest outcome traits. Traits of fiber excellence i.e., length, strength, micronaire, and uniformity ratio, also exhibited marked genotypic variation. Genotypes G6, G2, and G16 were superior in length (≥32 mm), strength (>30 g tex^{-1}), and uniformity (>85%), while maintaining acceptable micronaire values. The findings emphasize the role of genetic variability and trait associations in guiding cotton improvement strategies.

Keywords: Upland Cotton, Genetic Variability, Yield Components, Fiber Quality, Trait Associations, Gossypium Hirsutum

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INTRODUCTION

Cotton is amongst the most imperative fiber-producing crops globally, cultivated in more than 80 countries for its economic and industrial value (Basra A), (Han Z), (Harshitha AG). Among the agriculturally opted species, *Gossypium hirsutum* L. the upland cotton accounts for nearly 90% of total cotton produce worldwide due to its wide adaptability, higher potential and suitability for diverse agro-climatic conditions (Bitew Y), (Viot CR). Besides serving as a textile industry's primary source of natural fiber (Zhang J), cottonseed contributes to edible oil, protein meal, and other by-products (Anwar M), making it a multipurpose crop of global significance (Orken A). In countries such as Pakistan, India, China, and the United States, cotton not only supports the textile industry (Sadaf T) but also plays a crucial role in the incomes of masses of farmers (Arshad MU) and in national economies (Abdullah K).

Yield improvement and fiber quality enhancement are the twin objectives of modern cotton breeding programs (Naoumkina M), (Zhang X). Seed cotton yield, a complex quantitative trait, is influenced by several morphological and physiological attributes such as bolls per plant, boll weight, lint percentage, and seed index (Kumar R), (Shahzad K). Similarly, fiber quality traits including staple length, fiber strength, micronaire value, and uniformity ratio are decisive in determining market acceptability and spinning efficiency (Tesema GB), (Hossain MA). However, simultaneous improvement in yield and fiber quality has remained a major challenge for cotton breeders, as these traits are often governed by polygenic inheritance and subject to genotype × environment interactions (Zardari MA), (Korra CG). Therefore, a comprehensive understanding of genetic variability and the relationships among yield and fiber quality traits is essential to design effective selection strategies [20].

Genetic variability forms the foundation of any successful breeding program [21]. The presence of significant variability within a population ensures that breeders can exploit desirable traits and improve crop performance through hybridization and selection [22,23]. Measures like genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance serve as important indicators for assessing the degree and type of variability present in different traits [24,25]. High heritability coupled with high genetic advance, for instance, suggests additive gene action and allows breeders to make effective selections in early generations [26]. Conversely, traits with low heritability often require population improvement methods or molecular approaches for effective enhancement [27].

Another critical aspect in cotton improvement is the study of trait associations. Correlation analysis helps to determine the degree and direction of relationships between yield and its contributing characters [28,29]. Positive and significant correlations among yield components such as number of bolls, boll weight, and lint percentage are desirable, as they facilitate indirect selection for higher yield [30]. On the other hand, negative correlations between yield and fiber quality traits have often been reported, posing a challenge to breeders [31]. Path coefficient analysis further partitions these correlations into direct and indirect effects, providing a deeper understanding of the causal relationships among traits and helping breeders prioritize traits for simultaneous improvement [32,33].

In recent years, advances in molecular breeding and biotechnology have expanded the opportunities to improve cotton [34,35], yet conventional breeding approaches based on the assessment of genetic variability and trait associations remain fundamental [36]. Particularly in developing countries, where access to advanced genomic tools may be limited, morphological and fiber quality evaluations provide practical and cost-effective means for varietal improvement [37,38]. Evaluating a diverse set of genotypes for yield and fiber quality traits not only helps in identifying superior lines for direct cultivation but also provides a valuable genetic resource for hybridization programs [39].

Despite the global significance of cotton, yield stagnation and declining fiber quality are major concerns in many cotton-growing regions [40]. Biotic stresses such as bollworms and whitefly, abiotic challenges like drought and heat stress, and the narrowing of genetic diversity due to overdependence on a few elite varieties have further complicated cotton improvement efforts [41,42]. Therefore, systematic evaluation of available germplasm to estimate the extent of genetic variability, heritability, and trait associations is crucial for sustaining cotton productivity and quality under changing climatic and production environments [43,44].

This study was conducted to evaluate genetic variability, heritability, and genetic advance for yield and fiber quality traits in upland cotton, as well as to examine the correlations and path coefficients among these traits.

MATERIALS AND METHODS

Trial Site and Plant Material

The field research was conducted during the kharif 2024 season at the exploration farm of Lasbella University Uthal, Baluchistan. The investigational site is described by sub-tropical climate with hot summers and mild winters.

A total of 18 upland cotton genotypes, including advanced breeding lines and commercially released varieties, were the experimental material being used. These genotypes were selected based on their variation in the traits of yield and fiber quality to ensure adequate genetic diversity for the study.

Investigational Design and Crop Supervision

The research was laid out in a triplicated RCBD. Each genotype was sown in a plot consisting offour rows of 5 m length each with 75 cm and 30 cm row-to-row and plant-to-plant distances. Standard agronomic practices, including land preparation, seedbed fertilization, irrigation scheduling, and weed control, were uniformly applied to all plots. Pest and disease control measures were taken as required to ensure healthy crop growth.

Data Recording

Observations were recorded on arbitrarily selected plants from the central rows of every plot to avoid border effects. The following traits were measured:

- **Yield components:** bolls per plant, boll mass (g), yield per plant (g), seed index (g), and ginning outturn (GOT %).
- **Fiber quality traits:** Length (mm) & strength of fiber (g tex^{-1}), micronaire value, and fiber uniformity ratio (%).

Quality traits were assessed using High Volume Instrument (HVI) Central Cotton Research Institute.

Statistical Analysis

Data collected from all genotypes were subjected to ANOVA to test the statistical differences among genotypes. GCV and PCV were estimated and broad-sense heritability (h^2) was calculated and genetic advance as %age of mean was determined to assess the scope of selection.

RESULTS AND DISCUSSION

Yield Components

Bolls per plant

Substantial differences were experiential among genotypes for the bolls per plant (Table 1). The highest bolls count was recorded in G6 (43) and G16 (42), while the lowest was noted in G9 (25). Genotypes G2, G4, G10, and G13 also performed well with >37 bolls per plant. These results highlight the genetic variability for boll bearing capacity among tested genotypes, which is a key determinant of seed cotton yield. Previous studies also demonstrated that higher boll numbers are strongly correlated with yield potential in upland cotton [6,9].

Boll weight (g)

Boll weight varied significantly among genotypes, ranging from 3.12 g in G9 to 5.21 g in G6 (Table 1). Genotypes G2, G6, G10, and G16 exhibited superior boll weight (>5.0 g), indicating their potential for contributing to higher seed cotton yield. Comparable variation in boll weight has been reported in cotton breeding populations, where boll size was shown to be an important trait under additive genetic control [34,39].

Seed cotton yield per plant (g)

Seed cotton yield per plant ranged between 82 g (G9) and 146 g (G6), with G16 (144 g) and G2 (140 g) also performing well (Table 1). The lowermost yield was observed in G9 and G14, which also had fewer bolls and lighter boll weight. Yield superiority of G6 and G16 may thus be attributed to the combined effect of higher boll numbers and greater boll weight. These findings corroborate earlier reports that genotypes combining favorable boll traits produce higher yield [15,28,35].

Seed index (g)

Seed index varied between 8.24 g in G14 and 11.43 g in G2 (Table 1). Genotypes G2, G10, and G16 showed higher seed index values (>11 g), which are desirable for seed weight and processing quality. Variation in seed index among cotton genotypes has also been highlighted in previous studies, where it contributed significantly to overall yield differences [34,37,39].

Ginning outturn (GOT %)

GOT ranged from 32.5% in G9 to 41.8% in G6 (Table 1). Genotypes G6, G10, and G16 recorded superior GOT (>40%), reflecting their potential in producing higher lint yield. Earlier studies in Pakistan and China also reported substantial genotypic variation for GOT, with values between 31–42% [18,27,31]. Higher GOT values are desirable as they directly contribute to lint yield and economic returns.

Table 1. Yield components of 18 cotton genotypes

Genotype	Bolls per plant	Boll mass (g)	Seed cotton yield per plant (g)	Seed index (g)	GOT (%)
G1	34	4.72	128	9.94	36.9
G2	41	5.13	140	11.43	40.1
G3	27	3.56	96	9.12	34.8
G4	38	4.87	122	10.34	39.6
G5	29	3.92	102	8.71	33.7
G6	43	5.21	146	11.12	41.8

G7	32	4.21	110	9.56	35.2
G8	36	4.65	125	10.24	37.4
G9	25	3.12	82	8.53	32.5
G10	39	5.05	136	11.01	40.7
G11	28	3.74	94	9.04	33.8
G12	31	4.32	106	9.78	35.6
G13	37	4.91	130	10.92	38.9
G14	26	3.45	88	8.24	32.8
G15	35	4.67	120	10.12	37.2
G16	42	5.18	144	11.28	41.2
G17	30	3.88	98	9.21	34.4
G18	33	4.51	115	9.88	36.5

Fiber Quality Traits

Fiber length (mm)

Fiber length ranged from 25.6 mm in G9 to 32.8 mm in G6 (Figure 1). Genotypes G6, G2, and G16 were superior, producing longer fibers suitable for high-quality spinning. Fiber length is among the most heritable traits in cotton and a critical factor for textile applications [11,12].

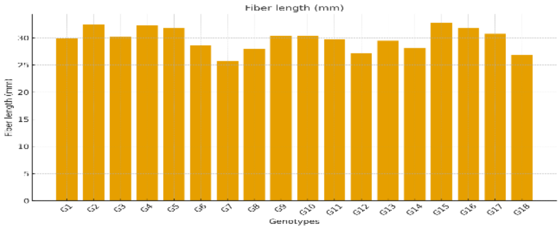

Figure 1: Variation in fibre length of 18 cotton genotypes

Fiber strength (g tex⁻¹)

Fiber strength showed considerable variation, with values ranging from 22.5 g tex⁻¹ in G14 to 31.8 g tex⁻¹ in G6 (Figure 2). Genotypes G6, G10, and G16 exhibited stronger fibers, aligning with industry standards for durable textiles. Strong positive correlations between fiber strength and length have been documented in earlier studies [13,14,2]

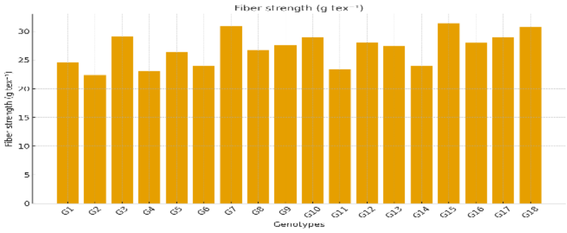

Figure 2: Variation in fibre strength of 18 cotton genotypes

Micronaire

Micronaire values ranged between 3.9 (G11) and 5.1 (G2, G6, and G16) (Figure 3). Most genotypes fell within the acceptable commercial range (3.5–5.0), although excessively high micronaire (>5.0) may negatively affect fiber fineness and spinning quality [26]. Moderate values, as observed in G13 and G15, are preferred. Previous work also emphasized balancing micronaire with fiber length and strength in breeding [12,28,37].

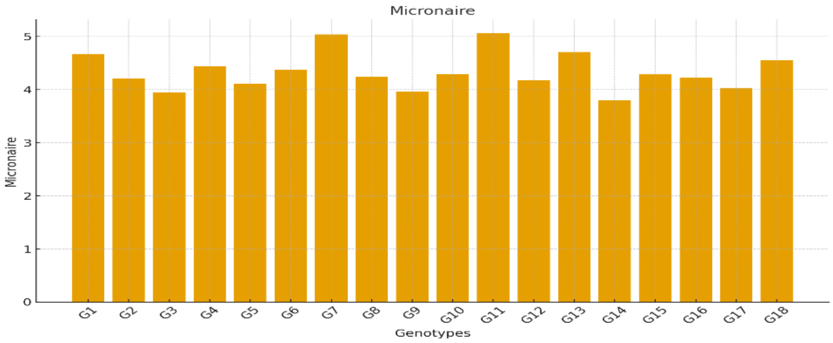

Figure 3: Variation in micronaire of 18 cotton genotypes

Fiber uniformity ratio (%)

Fiber uniformity varied from 78% in G14 to 87% in G6 (Figure 4). Genotypes G6, G2, and G16 had higher uniformity ratios (>85%), enhancing yarn strength and spinning efficiency. Similar genotypic differences in fiber uniformity were reported by highlighting its importance in selecting superior germplasm [36,37,38,40].

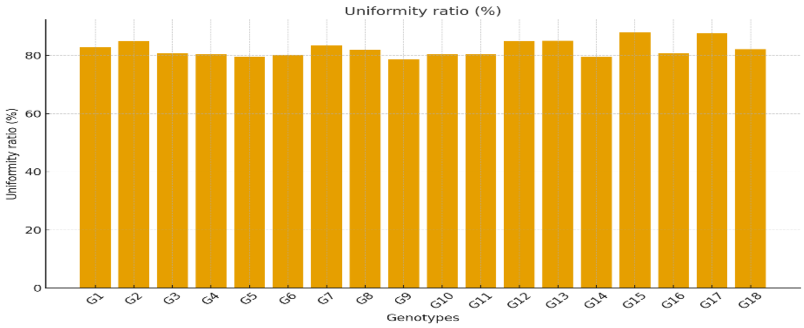

Figure 4: Variation in uniformity ratio of 18 cotton genotypes

CONCLUSION

The present study revealed substantial genetic variability amongst upland cotton genotypes for both yield components and fiber quality traits under the agro-climatic environments of Faisalabad. Genotypes G6 and G16 consistently outperformed others by producing a greater number of bolls per plant, heavier boll weight, higher seed cotton yield, and superior ginning outturn, along with favorable fiber length, strength, and uniformity. These findings suggest that these genotypes possess a desirable balance of agronomic and fiber quality attributes, making them valuable candidates for inclusion in breeding programs aimed at improving lint yield and textile performance. The results also emphasized the importance of considering trait associations in selection, particularly when improving yield and fiber quality simultaneously. Overall, the identified superior genotypes can serve as potential parents in hybridization and population improvement schemes for sustainable cotton productivity.

REFERENCES

Basra A, ed. Cotton fibers: developmental biology, quality improvement, and textile processing. CRC Press; 2024.

Han Z, Chen H, Cao Y, He L, Si Z, Hu Y, Lin H, Ning X, Li J, Ma Q, Liu F. Genomic insights into genetic improvement of upland cotton in the world's largest growing region. Ind Crops Prod. 2022;183:114929.

Harshitha AG, Kumar S, Jain A. A review on organic cotton: various challenges, issues and application for smart agriculture. In: 2021 10th International Conference on System Modeling & Advancement in Research Trends (SMART). IEEE; 2021. p.143-9.

Bitew Y, Abate A. Cotton agronomy and production. In: Cotton Sector Development in Ethiopia: Challenges and Opportunities. Singapore: Springer Nature Singapore; 2024. p.3-17.

Viot CR, Wendel JF. Evolution of the cotton genus, Gossypium, and its domestication in the Americas. Crit Rev Plant Sci. 2023;42(1):1-33.

Zhang J, Wedegaertner T. Genetics and breeding for glandless upland cotton with improved yield potential and disease resistance: a review. Front Plant Sci. 2021;12:753426.

Anwar M, Iqbal MZ, Abro AA, Memon S, Bhutto LA, Memon SA, Peng Y. Inter-specific hybridization in cotton (Gossypium hirsutum) for crop improvement. Agronomy. 2022;12(12):3158.

Orken A, Manabayeva S, Makhmadjanov S, Ramazanova M, Kali B, Rakhimzhanova A, Tussipkan D. Cotton (Gossypium L.) global distribution and adaptation to different geographic region. J Biol Res. 2025;1(1):43-55.

Sadaf T, Kousar R, Mohy Ul Din Z, Abbas Q, Makhdum MSA, Nasir J. Cotton production for the sustainable livelihoods in Punjab Pakistan: a case study of district Muzaffargarh. Int J Ethics Syst. 2022;38(2):191-208.

Arshad MU, Zhao Y, Hanif O, Fatima F. Evolution of overall cotton production and its determinants: implications for developing countries using Pakistan case. Sustainability. 2022;14(2):840.

Abdullah K, Khan Z. Breeding cotton for international trade. In: Cotton Breeding and Biotechnology. CRC Press; 2022. p.323-38.

Naoumkina M, Kim HJ. Bridging molecular genetics and genomics for cotton fiber quality improvement. Crop Sci. 2023;63(4):1794-815.

Zhang X, Wang J, Fu J. Improving cotton yield and fiber quality based on QTL mapping and genomic selection. Cotton Genomics Genet. 2025;16.

Kumar R, Das J, Puttaswamy RK, Kumar M, Balasubramani G, Prasad YG. Targeted genome editing for cotton improvement: prospects and challenges. Nucleus. 2024;67(1):181-203.

Shahzad K, Mubeen I, Zhang M, Zhang X, Wu J, Xing C. Progress and perspective on cotton breeding in Pakistan. J Cotton Res. 2022;5(1):29.

Tesema GB. Cotton quality requirements for spinning. In: Cotton Sector Development in Ethiopia: Challenges and Opportunities. Singapore: Springer Nature Singapore; 2024. p.241-84.

Hossain MA, Srijan SK, Rinaz KR, Khan SQ, Jalal Uddin A. Investigations of the spinning consistency index (SCI) and its impact on yarn quality. Res J Textile Apparel. 2025.

Zardari MA, Mukwana LC, Memon NS, Soomro AA, Shaikh TA, Vistro R, Hanif M. Variability in cotton fiber quality under innovated and traditional farming systems. Res J Soc Aff. 2025;3(2):311-21.

Korra CG, Alemayehu Beyene K, Addis Desta T. Study of Ethiopian genetically modified and organic cotton fiber quality compared with conventional cotton. Cogent Food Agric. 2024;10(1):2301144.

Wan SJ. Fiber quality improvement of upland cotton (Gossypium hirsutum L.) through interspecific introgression [master's thesis]. University of Georgia; 2023.

Singer SD, Laurie JD, Bilichak A, Kumar S, Singh J. Genetic variation and unintended risk in the context of old and new breeding techniques. Crit Rev Plant Sci. 2021;40(1):68-108.

Hoban S, Archer FI, Bertola LD, Bragg JG, Breed MF, Bruford MW, Coleman MA, Ekblom R, Funk WC, Grueber CE, Hand BK. Global genetic diversity status and trends: towards a suite of essential biodiversity variables (EBVs) for genetic composition. Biol Rev Camb Philos Soc. 2022;97(4):1511-38.

Salgotra RK, Chauhan BS. Genetic diversity, conservation, and utilization of plant genetic resources. Genes. 2023;14(1):174.

Barde MA, Mohammed MS, Oyekunle M, Usman IS, Shaahu A. Estimation of genetic variability, heritability and genetic advance in rice (Oryza sativa L.) genotypes. Int J Res Sci Innov Appl Sci. 2021;4:5-90.

Chacko A, Jayalekshmy VG, Shahiba AM. Studies on PCV, GCV, heritability, and genetic advance in rice genotypes for yield and yield components. Int J Plant Soil Sci. 2023;35(16):324-30.

Fufa M, Gedebo A, Leta T, Lule D. Genetic variation, genetic advance, heritability and correlation analysis of phenotypic traits in tetraploid wheat (Triticum turgidum spp.) landraces and some improved cultivars of Ethiopia. Plant Genet Resour. 2024;22(1):8-16.

Mahesh G, Ramesh T, Narendar Reddy S, Meena A, Rathod S, Fiyaz RA, Badri J, Rao LVS, Sundaram RM, Jukanti AK. Genetic variability, heritability, genetic advance and path coefficients for grain protein content, quality traits and grain yield in rice (Oryza sativa L.) germplasm lines. Pharma Innov J. 2022;11(3):1836-9.

Khan MMH, Rafii MY, Ramlee SI, Jusoh M, Al Mamun M. Genetic analysis and selection of Bambara groundnut (Vigna subterranea [L.] Verdc.) landraces for high yield revealed by qualitative and quantitative traits. Sci Rep. 2021;11(1):7597.

Emon MMH, Khan T, Siam SAJ. Quantifying the influence of supplier relationship management and supply chain performance: an investigation of

Bangladesh's manufacturing and service sectors. Braz J Oper Prod Manag. 2024;21(2):2015.

Gorzelany J, Gorzelany–Dziadkowiec M, Luty L, Firlej K, Gaisch M, Dudziak O, Scott C. Finding links between organisation's culture and innovation: the impact of organisational culture on university innovativeness. PLoS One. 2021;16(10):e0257962.

Lin J, Qiu S, Tan X, Zhuang Y. Measuring the relationship between morphological spatial pattern of green space and urban heat island using machine learning methods. Build Environ. 2023;228:109910.

Thorson JT, Maureaud AA, Frelat R, Mérigot B, Bigman JS, Friedman ST, Palomares MLD, Pinsky ML, Price SA, Wainwright P. Identifying direct and indirect associations among traits by merging phylogenetic comparative methods and structural equation models. Methods Ecol Evol. 2023;14(5):1259-75.

Abdulhamed ZA, Abood NM, Noaman AH. Genetic path analysis and correlation studies of yield and its components of some bread wheat varieties. IOP Conf Ser Earth Environ Sci. 2021;761:012066.

Degefu DT, Gebregiorgis ZD. Cotton biotechnology. In: Cotton Sector Development in Ethiopia: Challenges and Opportunities. Singapore: Springer Nature Singapore; 2024. p.65-88.

Verma K, Sharma P, Tripathi K, Yadav R, Singh SP. Recent advances in genetic improvement of cotton. In: Genetic Engineering of Crop Plants for Food and Health Security: Volume 1. Springer; 2024. p.69-99.

Yang Z, Gao C, Zhang Y, Yan Q, Hu W, Yang L, Wang Z, Li F. Recent progression and future perspectives in cotton genomic breeding. J Integr Plant Biol. 2023;65(2):548-69.

Liang C, Jin S. Editorial–Three decades and beyond: breeding, biotech breakthroughs and future of China's GM insect-resistant cotton. J Integr Agric. 2024;23(10).

Rasheed A, Zhao L, Raza A, Mahmood A, Xing H, Lv X, Saeed H, Alqahtani FM, Hashem M, Hassan MU, Gillani SFA. Role of molecular breeding tools in enhancing the breeding of drought-resilient cotton genotypes: an updated review. Water. 2023;15(7):1377.

Conaty WC, Broughton KJ, Egan LM, Li X, Li Z, Liu S, Llewellyn DJ, MacMillan CP, Moncuquet P, Rolland V, Ross B. Cotton breeding in Australia: meeting the challenges of the 21st century. Front Plant Sci. 2022;13:904131.

Khan Z, Ali Z, Khan AA. Role of breeding and biotechnology in sustainable cotton production. In: Cotton Breeding and Biotechnology. CRC Press; 2022. p.1-14.

Kamburova V, Salakhutdinov I, Abdurakhmonov IY. Cotton breeding in the view of abiotic and biotic stresses: challenges and perspectives. IntechOpen; 2022.

Hussain M, Gao X, Qin D, Qin X, Wu G. Role of biotic and abiotic factors for sustainable cotton production. In: Best Crop Management and Processing Practices for Sustainable Cotton Production. IntechOpen; 2023.

Shelake RM, Wagh SG, Patil AM, Červený J, Waghunde RR, Kim JY. Heat stress and plant–biotic interactions: advances and perspectives. Plants. 2024;13(15):2022.

Kumar J, Murali-Baskaran RK, Jain SK, Sivalingam PN, Mallikarjuna J, Kumar V, Sharma KC, Sridhar J, Mooventhan P, Dixit A, Ghosh PK. Emerging and re-emerging biotic stresses of agricultural crops in India and novel tools for their better management. Curr Sci. 2021;121(1):26-36.