DR IQRAR AHMAD RANA, **CNIC: 33100-0607796-5**
Contact:
E.mail: iqrar_rana@uaf.edu.pk
Cell: 0333 6627846, 041-9200161-69 ext.2925, Home.041-2573485.

Professional Objectives:

1. Generate useful knowledge for next generation of learners
2. Understand the basics of biotic and abiotic stress tolerance in crop plants

Employment Track:

ASSOCIATE PROFESSOR (Tenured)

Centre of Agricultural Biochemistry and Biotechnology (CABB), University of Agriculture Faisalabad
(August 31, 2019 till todate)

Official Responsibilities:

i. Teaching of Molecular Genetics and Biotechnology to M.S and PhD students
ii. Supervision of MS and PhD dissertations.
iii. Main area of research under focus is the application of Molecular Biology techniques including genetic transformation to improve the agronomic performance of cotton and other important crops.
iv. Biosafety analysis of the transgenic plants.

ASSISTANT PROFESSOR:

Centre of Agricultural Biochemistry and Biotechnology (CABB), University of Agriculture Faisalabad
(October, 2009 to August 30, 2019)

Official Responsibilities:

v. Teaching of Molecular Genetics and Biotechnology to M.S and PhD students
vi. Supervision of MS and PhD dissertations.
vii. Main area of research under focus is the application of Molecular Biology techniques including genetic transformation to improve the agronomic performance of cotton and other important crops.
viii. Biosafety analysis of the transgenic plants.

Assistant Research Officer:

Cotton Research Institute, AARI, Faisalabad.
(September 10, 2003 to October 31, 2004)

i. Taking care of filial generations
ii. Wide crosses b/w *hirsutum* and *arboreium*

ACADEMIC QUALIFICATION

Doctor of Philosophy (PhD) **(2005-2009)**

Department of Botany, University of Hamburg, Germany
Thesis Title: Reverse and Forward Genetic Approaches for the Development of Disease Resistant Wheat (*Triticum aestivum* L.)

M.Sc (Hons.) Plant Breeding and Genetics **(2001-2003)**

University of Agriculture, Faisalabad-Pakistan

Thesis: Induction of Somaclonal Variation for Red Rot and Sugarcane Mosaic Virus in Sugarcane (*Sacchuram officinarum* L.)
1st Division (3.59/4.00)

B. Sc (Hons.) Agriculture-Plant Breeding & Genetics (1997-2001)
University of Agriculture, Faisalabad-Pakistan
1st Division (3.34/4.00)

Recent Projects:

1. Preservation and propagation of healthy Shisham (Dalbergia sissoo) through cloning of resistant germplasm against dieback disease
   Role: Team Leader Biotechnology Funding Agency: PARB
   Component Budget: Rs. 12.05 Million for 3 Years (June 2019- June 2024)
2. Gene editing of Biological agents for nutritional, biochemical and therapeutic purposes (establishment of National Center for genome editing for crop improvement and human health, NCGE), (Principal Investigator Fruit and Forest Trees); Funding Agency; Ministry of Science and Technology. Pakistan (July-1, 2022 to June 30, 2025)

3. Developing salt tolerant cotton germplasm. Role: CoPI/Principal Investigator. Funding agency. Higher Education Commission of Pakistan. (June 2019 to July 2023). Final Report Submitted.

4. Expression analysis of haplotypes of TaWRKY transcription Factors and salt responsive genes to enhance salinity tolerance in wheat germplasm. Role: CoPI. Fubmitted by HEC. (July1, 2019 to June 30, 2022) Final Report submitted.

5. Development and genetic characterization of grapefruit haploids and mutants for hybridization and germplasm enhancement. Role: CoPI. Fubmitted by HEC. (July1, 2019 to June 30, 2022) Final Report submitted.

PUBLICATIONS:

1. **T**AYYAB M, TAJ MH, AHMAD AI, RANA FR, SHAHZAIB M, ATIF RM, AZHAR MT, KHAN SH, KAKAKHEL IAM, HE S, RANA IA (2025) Phylogenomic analysis of Bromodomain genes in Cotton (*Gossypium spp*.) and their potential roles in abiotic stress tolerance. Journal of Cotton Research. Accepted. **IF: 3.1**
2. Zafar UB, IA Rana, SH Khan, RM Atif (2025) Molecular characterization of shisham dieback-associated fungal isolates across the Punjab Province, Pakistan.Asian Journal of Agriculture and Biology. https://doi.org/10.35495/ajab.2024.153 **IF: 1.6**
3. Saleem MS, SH Khan, A Ahmad, IA Rana, ZA Naveed and AI Khan. 2024. The 4Fs of cotton: genome editing of cotton for fiber, food, feed, and fuel to achieve zero hunger. 10.3389/fgeed.2024.1401088. **IF:4.9**
4. Jamil S, S Ahmad, R Shahzad, N Umer, S Kanwal, HM Rehman, IA Rana, RM Atif**. 2024.** Leveraging Multiomics Insights and Exploiting Wild Relatives' Potential for Drought and

Heat Tolerance in Maize. *J. Plant Protect. Res.* 2021, 243–253. doi: 10.24425/jppr.2021.137950. **IF: 5.80**

5. Shahzaib M., U.M. Khan, M.T. Azhar, R.M. Atif, S.H. Khan, Q.U. Zaman, I.A. Rana. 2024. Phylogenomic curation of Ovate Family Proteins (OFPs) in the U's Triangle of *Brassica* L. indicates stress-induced growth modulation. Plos one 19 (1), e0297473. **IF: 2.9**
6. Majeed S., M.T. Chaudhary, M.S. Mubarik, I.A. Rana, M. Shaban, D.K.Y. Tan, Y. Jia, X. Du, L. Hinze, M.T. Azhar. 2024. Genetics of biochemical attributes regulating morpho-physiology of upland cotton under high temperature conditions. J.C.R 7 (1), 3. **IF: 3.1**
7. Ali I.A., A.I. KHAN, M.A. Negm, R. Iqbal, M.T. AZHAR, S.H. KHAN, and I.A. RANA. 2024. Enhancing cotton resilience to challenging climates through genetic modifications. JCR. 7:10. **IF: 3.1**
8. Shaban M., T. Riaz2, I.A. Rana, R.M. ATIF, A.M. Abubakkar, I. Zubair, M. Sajid and M.T. Azhar. 2024. Comparative analysis of SIMILAR to RCD ONE (SRO) family from tetraploid cotton species and their diploid progenitors depict their significance in cotton growth and development. JCR. 7:5. **IF: 3.1**
9. Chaudhary, M.T., Majeed, S., Rana, I.A. *et al.* 2023. Impact of salinity stress on cotton and opportunities for improvement through conventional and biotechnological approaches. *BMC Plant Biol* 24, 20 (2024). https://doi.org/10.1186/s12870-023-04558-4. **IF:5.26**
10. Arif T, MT Chaudhary, S Majeed, IA Rana, Z Ali, HO Elansary, IM Mousa, S Sun, MT Azhar. 2023. Exploitation of various physio-morphological and biochemical traits for the identification of drought tolerant genotypes in cotton. *BMC Plant Biol* **23**, 508. **IF:5.26**
11. Zafar U.B., M Shahzaib, RM Atif, SH Khan, MZ Niaz, K Shahzad, N Chughtai, FS Awan, MT Azhar, **IA Rana**. 2023. De novo transcriptome assembly of *Dalbergia sissoo* Roxb. (*Fabaceae*) under *Botryodiplodia theobromae*-induced dieback disease. *Scientific Reports*, *13*(1), 1-17. **IF: 4.60**
12. Q Raza, MAR Rashid, M Waqas, Z Ali, IA Rana, SH Khan, IA Khan, and RM Atif (2023) Genomic diversity of aquaporins across genus *Oryza* provides a rich genetic resource for development of climate resilient rice cultivars. BMC Plant Biology 23 (1), 172. **IF:5.26**

13. Shaheen N., Khan U.M., Farooq A., Zafar U.B., Khan S.H., Ahmad S., Azhar M.T., Atif R.M., Rana I.A., Seo H. (2023). Comparative transcriptomic and evolutionary analysis of FAD-like genes of Brassica species revealed their role in fatty acid biosynthesis and stress tolerance. BMC Plant Biology 23 (1), 1-13 **IF:5.26**
14. UM Khan, IA Rana, N Shaheen, Q Raza, HM Rehman, R Maqbool, IA Khan, RM Atif (2023) Comparative phylogenomic insights of *KCS* and *ELO* gene families in *Brassica* species indicate their role in seed development and stress responsiveness. Scientific Reports 13 (1), 3577 **IF:4.9**
15. Q Raza, MAR Rashid, M Waqas, Z Ali, IA Rana, SH Khan, IA Khan,and RM Atif (2023) Genomic diversity of aquaporins across genus *Oryza* provides a rich genetic resource for development of climate resilient rice cultivars. BMC Plant Biology 23 (1), 172 **IF:5.26**
16. Almas HI, MT Azhar, RM Atif, MA Iqbal, AI Khan, IA Rana. (2023) Adaptation of genetically modified crops in Pakistan. GMOs and Political Stance, 93-114
17. UM Khan, N Shaheen, A Farooq, R Maqbool, SH Khan, MT Azhar, IA Rana, H Seo (2022) Optimization of Regeneration and *Agrobacterium*-Mediated Transformation Protocols for Bi and Multilocular Varieties of *Brassica rapa*. Plants 12 (1), 161. **IF: 4.5**

18. Raza Q., A. Riaz, R.M. Atif, B. Hussaın, **I.A. Rana,** Z. Ali, H. Budak, I. A Alaraidh (2022) Genome-Wide Diversity of MADS-Box Genes in Bread Wheat is Associated with its Rapid Global Adaptability. Frontiers in Genetics. Vol. 12 No. 818880. **IF:3.789**
19. Riaz A, Kanwal F, Ahmad I, Ahmad S, Farooq A, Madsen CK, Brinch-Pedersen H, Bekalu ZE, Dai F, Zhang G and Alqudah AM (2022) New Hope for Genome Editing in Cultivated Grasses: CRISPR Variants and Application. *Front. Genet.* 13:866121. **IF:3.789**
20. Ahmed, S., M.AR. Rashid, S.A. Zafar, M.T. Azhar, M. Waqas, M. Uzair, **I.A. Rana,** F. Azeem, G. Chung, Z. Ali, et al. (2021) Genomewide investigation and expression analysis of APETALA-2 transcription factor subfamily reveals its evolution, expansion and regulatory role in abiotic stress responses in Indica Rice (Oryza sativa L. ssp. indica). Genomics, 113, 1029–1043. **IF:5.736**
21. Majeed S., **I. A. Rana**, M. S. Mubarik, R. M. Atif, S. H. Yang, G. C., Y. Jia, X. Du, L. Hinze, M. T. Azhar (2021) Heat stress in cotton: a review on predicted and unpredicted growth-yield anomalies and mitigating breeding strategies. Agronomy, 11, 1825 **IF: 3.949**
22. Rehman A.U., **I. A Rana**,, S. Majeed , M. T. Chaudhary, M. Zulfiqar, S. H. Yang, G. Chung , Y. Jia , X. Du , L. Hinze and M. T. Azhar (2021) Intra-Plant Variability for Heat Tolerance Related Attributes in Upland Cotton. Agronomy, 11, 2375 **IF:3.949**

23. Arsh Q. A., M. T. Azhar, R. M. Atif, M. Israr, A. I. KHAN, S. Khalid, **I. A. Rana** (2021) A discussion on cotton transformation during the last decade (2010–2021); an update on present trends and future prospects. J Cotton Res 4:29, 2-14. **IF: 2.6**

24. Shaheen N., U. M. Khan, M. T. Azhar, D. K. Y. Tan, R. M. Atif, M. Israr, S. H. Yang, G. Chung, and **I. A. Rana** (2021) Genetics and Genomics of Fusarium Wilt of Chilies: A Review. Agronomy, 11, 2162 **IF:3.949**

25. Usman M, B. Fatima, M. Usman, and **I. A. Rana**. 2021. MORPHOLOGICAL AND STOMATAL DIVERSITY IN COLCHIPLOID GERMPLASM OF GRAPEFRUIT. Pak. J. Agri. Sci., Vol. 58(2), 555-560. **IF:0.856**

26. Chaudhary MT, Shakeel A, **Rana IA**, et al. Evaluation of morpho-physiological and biochemical attributes of cotton under salt stress. Int J Agric Biol. 2020;24:1061–9 **IF:0.81**

27. Rana, M.A., M. Usman, B. Fatima, A. Fatima, **I.A. Rana**, W. Rehman and D. Shoukat. 2020. Prospects of Mutation Breeding in Grapefruit (Citrus paradisi Macf.). J. Hort. Sci. Tech. 3:31-35.

28. Ahmed, S.; Rashid, M.A.R.; Zafar, S.A.; Azhar, M.T.; Waqas, M.; Uzair, M.; **Rana, I.A**.; Azeem, F.; Chung, G.; Ali, Z.; et al. 2020. Genome-wide investigation and expression analysis of APETALA-2 transcription factor subfamily reveals its evolution, expansion and regulatory role in abiotic stress responses in Indica rice (Oryza sativa L. ssp. indica). Genomics , 113, 1029–1043 **IF:5.736**

29. Babar, U., M. A. Nawaz, U. Arshad, M. T. Azhar, R. M. Atif, K. S. Golokhvast, A. M. Tsatsakis, C. Sherbakova, G. Chung, and **I. A. Rana**. 2020. Transgenic crops for the agricultural improvement in Pakistan: A perspective of environmental stresses and the current status of genetically modified crops. GM Crops & Food 11 (1):1–29. **IF:3.076**

30. Majeed S, Malik TA, **Rana IA**, Azhar MT (2019) Antioxidant and physiological responses of upland cotton accessions grown under high-temperature regimes. Iranian J Sci Tech Trans: A Sci 43(6):1–10 . **IF: 1.194**

31. Majeed, S., **I. A. Rana,** R. M. Atif, Z. Ali, L. Hinze, M. T. Azhar (2019) Role of SNPs in determining QTLs for major traits in cotton. Journal of Cotton Research, A BMC recognize Journal. doi.org/10.1186/s42397-019-0022-5. eISSN: 2523-3254. **IF: 2.6**

32. Salman, M., Z. U. Zia, **I. A. Rana**, R. H. Maqsood, S. Ahmad, A. Bukhsh and M. T. Azhar (2019) Genetic effects conferring heat tolerance in upland cotton (*Gossypium hirsutum* L). Journal of Cotton Research, A BMC recognize Journal. doi.org/10.1186/s42397-019-0025-2.eISSN: 2523-3254. **IF: 2.6**

33. Waqas M., M.T. Azhar, **I.A. Rana**, F. Azeem, M.A. Ali, M.A. Nawaz, G. Chung, R.M. Atif, 2019. Genome-wide identification and expression analyses of WRKY transcription factor family members from chickpea (Cicer arietinum L.) reveal their role in abiotic stress-responses. Genes & genomics.DOI: 10.1007/s13258-018-00780-9. **IF: 1.625**

34. Aslam S., S.H. Khan, I**.A. Rana** and R.M. Atif, 2019. Development of founder lines for recombinase based gene targeting in Nicotiana banthamiana. Intl. J. Agric. Biol., 21: 429–436. **IF: 0.86**
35. Bhatti S.A., **I.A Rana**, 2018. Causes for the refusal of Cottonseed Cake. Zarai Digest. January. 2018. Page 38.
36. Saddique M.A., Z. Ali, A.S. Khan, I.A. Rana, and I.H. Shamsi, 2018. Inoculation with the endophyte Piriformospora indica signifcantly afects mechanisms involved in osmotic stress in rice," Rice.11(1) **IF: 3.039**
37. Raza H, **IA. Rana**, A Shakeel, L Hinze, J Frelichowski, and MT Azhar (2017) Genetic diversity in gossypium hirsutum (L.) for cotton leaf curl disease in association with agronomic and fiber traits. Pak. J. Phytopathol., Vol. 29 (01) 2017. 47-56
38. Shah ZH, HM Rehman, T Akhtar, I Daura, MA Nawaz, MQ Ahmad.,**IA Rana**, RM Atif, SH Yang and G Chung (2017) Redox and Ionic Homeostasis Regulations against Oxidative, Salinity and Drought Stress in Wheat (A Systems Biology Approach). Vol. 8 No. 141 **IF: 4.151**
39. Kanwal M, FA Joyia, G Mustafa, MA Zia, **IA Rana**, MS Khan (2017) Direct in vitro Regeneration of Nicotiana plumbaginifolia L. and the Potential for Genetic Transformation. International Journal of Horticulture 7 (6)
40. Yaqub MS, IA Khan, M Usman, and **IA Rana**(2017) Molecular detection of *CandidatusliberibacterA*siaticus, the causal organism of Huanglongbing (citrus greening) in Faisalabad, Pakistan for Huanglongbing management. *Pak. J. Agri. Sci.* 54(1): 21-26. **IF: 0.89**
41. Saeed U, **IA Rana**, S Ijaz, and Z Ali. (2017) Improving Regeneration from Mature Embryo Derived Callus in Wheat (*Triticum aestivum*L.) by Pre-and Post Callus Induction Treatments. *Int. J. Agric. & Biol.* DOI: 10.17957/IJAB/15.0324. **IF: 0.86**
42. Azmat M., FA. Khan, HA. Sadaqat, and **IA Rana**. 2016. Diversity Analysis of Sesame (SesamumIndicum L.) Genotypes Screened for Different Yield Parameters using SSR Markers. Tran. Rev. XXIV (9), Special Issue.
43. Saba M., F.A. Khan, H.A. Sadaqat and **IA Rana** (2016) Estimation of diversity and combining abilities in Helianthus annuus L. under water stress and normal conditions. *Genet. Mol. Res*. 15 (4): gmr15048670. **IF: 0.78**

44. Ijaz S., A. I. Khan, **IARana**. 2016. Development of Source Independent Micropropagation System in *Dalbergiasissoo*Roxb, as a basis for Germplasm Conservation and Disease Free Plants Production. *Mol. Pl. Breed.* 7(15): 1-12
45. Zafar SA, M Hussain, M Raza, HGM Ahmad, **IA Rana**, B Sadia, RM Atif (2016) Genome wide analysis of heat shock transcription factor (HSF) family in chickpea and its comparison with Arabidopsis. Plant Omics 9(2):136-141
46. Kaleem MN, **IA Rana**, A Shakeel, L Hinze, RM Atif and MT Azhar (2016) Genetic Analysis of some Agronomic and Fiber traits in *Gossypiumhirsutum* L. grown in Field conditions. *Turk. J. Field Crops*. 21(2): 240-245. **IF: 3.00**
47. Cheema HMN, AA Khan, MI Khan, U Aslam, **IA Rana,** and IA Khan (2016) Assessment of Bt cotton genotypes for the Cry1Ac transgene and its expression. *The J. Ag. Sci.* (Cambridge University Press). 154(1): 109-117. **IF:1.186**
48. **Rana IA**, Salomon S, Schaefer W, and Becker D (2014) Downregulation of Glucan Synthase-Like (TaGSL) genes in wheat leads to inhibition of transgenic plant regeneration.*In Vitro Cell. Dev. Bio. Pl.*50(6):696–706 **IF: 2.20**
49. Khan AU, MA Aslam, I Hussain, AG Naz, **IA Rana,** MM Ahmad, M Ali, S Ahmad (2013) Role of Toll-like receptor 2 (-196 to -174) polymorphism in susceptibility to pulmonary tuberculosis in Pakistani population. Int. J. Immunogen. 41(2): 105 –111. **IF:2.30**
50. Jamil M, **IA Rana,** Z Ali, FS Awan, Z Shahzad, A Khan (2013)Estimation of Genetic diversity in Rice (*Oryza sativa* L.) Genotypes using Simple Sequence Repeats. *Mol. Pl. Breed.* 4(36): 36 285-291.
51. Rehman HM, **IA Rana**, SIjaz, GMustafa, FAJoyia, IA Khan, PM Pijut (2012) *In vitro* Regeneration of *Dalbergiasissoo*Roxb. and the Potential for Genetic Transformation. Not Bot HortiAgrobo, 40(2): 140-147. **IF:0.648**
52. Ijaz S, and **IA Rana**(2012) An overview of biotechnological approaches for crop improvement. *Gen. and App. Bio*, 3:1
53. Ijaz S, N Anjum, **IA Rana** and IA Khan (2012) Optimization of Minimal Inhibitory Dose of Selective Agent (Basta) for Selection of Transgenics in Sugarcane. *Mol. Pl. Breed.* Vol.3, No.5 50-56
54. Ijaz S, **IA Rana** and IA Khan (2012) Orange juice, a natural source for enhancing in vitro regeneration in *Saccharum*spp. *Biosci. Meth.*, 3(9): 55-57.
55. Anjum N, S Ijaz, **IA Rana,** IA Khan et al. (2012) Establishment of an *in vitro* regeneration system as a milestone for genetic transformation of sugarcane (*Saccharumofficinarum*) against *Ustilagoscietaminae. Biosci. Meth*. 3(2): 7-20.
56. Ijaz S, **IA Rana**, IA Khan and M Saleem (2012) Establishment of an *in vitro* regeneration system for genetic transformation of selected sugarcane genotypes. Genet. Mol. Res. 11 (1): 512-530. **IF: 0.78**
57. **Rana IA**, H Loerz, W Schaefer and D Becker (2012) Over expression of chitinase and chitosanase genes from *Trichoderma harzianum* under constitutive and inducible promoters in order to increase disease resistance in wheat *(Triticumaestivum* L**),** Molecular Plant Breeding, Vol.3, No.4 37-49 (doi: 10.5376/mpb.2012.03.0004).

Manuscripts in Press:

1. Muhammad Shahzaib, Tobias Bruegmann, Muhammad Shakeel, Sultan Habibullah Khan, Muhammad Tehseen Azhar, Rana Muhammad Atif, Matthias Fladung, Iqrar Ahmad Rana. 2023. Development of Climate Smart Fruit Plants via CRISPR/Cas Genome Editing Systems: A Spatiotemporal Review. Under review at Planta. Available on Preprint.

PATENT:

1. Development of Disease Resistance linked SSRs against Dieback disease in Dalbergia sissoo. (In process)

BOOK PUBLISHED

Biofortification of Grain and Vegetable crops; Molecular and Breeding approaches 2023. Academic Press Elsevier UK. Edited by Muhammad Tehseen Azhar, Muhammad Qadir Ahmad, **Iqrar Ahmad Rana**, Rana Muhammad Atif

Book Chapters:

1. Shaheen N., M. Shahzaib, U.M. Khan, H.M. Rehman, R. M. Atif, M.T. Azhar, A.I. Khan and **I.A. Rana**. 2024. Genetically modified organisms for crop biofortification. In: Azhar M.T., M.Q. Ahmad, **I.A. Rana**, and R.M. Atif. BIOFORTIFICATION OF GRAIN AND VEGETABLE CROPS: Molecular and Breeding Approaches. Pages 19-37. Published by Elsevier Academic Press UK. ISBN: 78-0-323-91735-3.
2. Raza Q., M.T. Azhar, **I.A. Rana**, M.Q. Ahmad and R.M. Atif. 2024. Biofortification of crops to achieve food and nutritional security. In: Azhar M.T., M.Q. Ahmad, I.A. Rana, and R.M. Atif. BIOFORTIFICATION OF GRAIN AND VEGETABLE CROPS: Molecular and Breeding Approaches. Pages 1-13. Published by Elsvier Academic Press UK. ISBN: 78-0-323-91735-3
3. Almas HI, MT Azhar, RM Atif, MA Iqbal, AI Khan, **IA Rana**. (2023) Adaptation of genetically modified crops in Pakistan. In: GMOs and Political Stance Global GMO Regulation, Certification, Labeling, and Consumer Preferences. Pages 93-114. Published by Elsvier Academic Press UK. ISBN978-0-12-823903-2.
4. Usman M., **I.A. Rana**, S. U. Rehman, B. Fatima, M. S. Khan. 2022.Citrus Genetic Resources Molecular Characterization, Omics and Conservation Approaches. In Citrus Production: Technological Advancements and Adaptation to Changing Climate. Pages 74-85. CRC Press. UK. ISBN. 9781003119852.
5. **Rana, I.A**., A. Bakhsh, S. Tillaboeva, S. Haihong, M.T. Azhar (2022) Genetically Modified Cotton: Boom or Dust. In: Cotton Breeding and Biotechnology. CRC Press, USA, Page: 271-289.

6. Arsh Q., T. Jabbar, S. Khalid, R.M. Atif, H.M. Rehman, **I.A. Rana**. 2021. Wild Relatives and Modern Plant Breeding Technologies. Book Chapter No. 18, published in Wild Germplasm for Genetic Improvement in Crop Plants. Academic Press, Pages 343-371
7. Waqas M., Azhar M.T., **Rana I.A.,** Arif A., Atif R.M. (2019) Drought Stress in Chickpea: Physiological, Breeding, and Omics Perspectives. In: Wani S. (eds) Recent Approaches in Omics for Plant Resilience to Climate Change. Springer, Cham
8. Zafar S., Iqbal A., Azhar M.T., Atif R.M., **Rana I.A.,** Rehman H.M., Nawaz M.A., Chung G. (2019) GM Maize for Abiotic Stresses: Potentials and Opportunities. In: Wani S. (eds) Recent Approaches in Omics for Plant Resilience to Climate Change. Springer, Cham
9. Salman M., Majeed S., **Rana I.A.**, Atif R.M., Azhar M.T. (2019) Novel Breeding and Biotechnological Approaches to Mitigate the Effects of Heat Stress on Cotton. In: Wani S. (eds) Recent Approaches in Omics for Plant Resilience to Climate Change. Springer, Cham

Practical Manual Developed:

1. Biotechnology Practical Manual Series 01. Plant Transformation. Compiled by Dr. Iqrar Ahmad Rana, Edited by Professor Dr. Muhammad Sarwar Khan, Dean Faculty of Agriculture.

Abstracts/Lectures:

1. Usman Baber, Muhammad Tehseen Azhar, Rana Muhammad Atif, Hafiz Mamoon Rehman, and Iqrar Ahmad Rana. 2022. Engineering SHSP17 in Zea mays to develop thermotolerance. Presented and Published in Proceedings of 7th International Conference on Climate Smart Agriculture: Innovations and Adaptations, organized by Faculty of Agriculture, University of Poonch, Rawalakot, Azad Jammu and Kashmir-Pakistan.

2. Ummul Buneen Zafar, Iqrar Ahmad Rana, M. Z. Niaz, K. Shahzad, and N. Chughtai. 2022. Developing dieback disease resistance linked DNA Marker in Dalbergia sissoo. International Conference of the German Society for Plant Sciences 2022. August 28 to September1, 2022. Held in Bonn Germany.

3. Hassan Taj, Rana Muhammad Atif, uzair Muhammad Khan, Iqrar Ahmad Rana. 2022. Genome and transcriptome wide analysis of OFPs in cotton and their possible roles in fiber development. Presented at World Cotton Research Conference-7, held at Cairo, Egypt. 4-7 October 2022.

4. Muhammad Tanees Chaudhry, Iqrar Ahmad Rana, Azeem Iqbal Khan, Muhammad Tehseen Azhar. 2022. Potential of Biochemical assays for identification of salt tolerance in *Gossypium hursutum*. Presented at World Cotton Research Conference-7, held at Cairo, Egypt. 4-7 October 2022.

5. Muhammad Tanees Chaudhry, Iqrar Ahmad Rana, Azeem Iqbal Khan, Muhammad Tehseen Azhar. 2022. Biochemical assays are reliable tools for identification of salt tolerance in *Gossypium hirsutum*. Presented at World Cotton Research Conference-7, held at Cairo, Egypt. 4-7 October 2022.

6. Impact assessment of the transgenic sugarcane over expressing antifungal proteins on endophytic and rhizospheric bacteria. Orally presented at “2nd Annual South Asia Biosafety Conference on 15-16 September, 2014 at Taj Samudra Hotel, Colombo, Sri Lanka (**Oral Presentation**)”

7. Development of Transgenic Plants using agrobacterium mediated transformation. Lecture delivered and training imparted at Hand on training workshop on Biotechnology for crop improvement: “GM Crops Production, Challeneges, and Oppertunities. September 5-7, 2016. **(Resource Person)**

Student Supervision:

Directly Supervised more than 60 MPhil students

PhD Thesis Supervised:

1. **Dr. Siddra Ijaz (2012)**
   Thesis Title: “Engineering sugarcane genome to develop resistance against *Colletotrichum falcatum* to control Red Rot disease.
2. **Usman Saeed (2021)**
   Thesis Title “Hetrologous expression of *stPR*-10 gene in wheat (*Triticum Aestivum*)”

PhD thesis supervised as Member Supervisory Committee.

1.	Muhammad Usman	Member Supervisory Committee
2.	Sajid Majeed	Member Supervisory Committee
3.	Muhammad Zahid Aslam	Member Supervisory Committee
4.	Sabin Aslam	Member Supervisory Committee
5.	Muhammad Tanees Chaudhry	Member Supervisory Committee

PhD Students Under Supervision:

1	Amna Asgher (2017-ag-3629)	Supervisor. (working on transcriptomics of Dalbergia sissoo)
2	Urva Ajmal (2020-ag-1601)	Supervisor (working on transcriptomics of Dalbergia sissoo)
3.	Ummul Buneen Zafar	Supervisor (Developed resistance linked for Dieback disease of Dalbergia sissoo)
4.	Arfa Tanvir	Supervisor (Working on genome editing of citrus)

TEACHING:

Undergraduate:

1. Fundamentals of Biotechnology
2. Recombinant DNA Technology
3. Molecular Cell Biology
4. Fundamentals of Seed Molecular Biology

Postgraduate:

1. Molecular Genetics
2. Molecular Plant Microbe Interaction

Relevant Collequia, Seminars, Conferences, etc.

1. Hand on training workshop on Biotechnology for crop improvement: “GM Crops Production, Challenges, and Opportunities. September 5-7, 2016. (Resource Person).
2. International Seminar on “Transgenic crops: A key to food security”. CABB, UAF. Pakistan. March, 16, 2012. Acted as Focal Person.

3. One day workshop on "Implementation of Biosafety Protocols" Centre of Agricultural Biochemistry and Biotechnology (CABB), University of Agriculture Faisalabad, Pakistan. May 14, 2011. Oranizer
4. Three days "International Conference on Applied Genetics and Biotechnology". Centre of Agricultural Biochemistry and Biotechnology (CABB), University of Agriculture Faisalabad, Pakistan. December 8-10, 2011. (Conference Secretary)
5. International Training workshop on Biotechnology, Bioinformatics and Biochemistry. April, 2-3, 2019. Organized by CABB, University of Agriculture, Faisalabad (Focal Person)
6. Slow Pace of Agricultural Biotechnology Adaptability: an analysis and way forward, October 10, 2019. University of Agriculture, Faisalabad (Member Organizing Subcommittee)
7. Gene Editing for Agriculture, Society and Sustainable development, prospects and perspectives. 15 December, 2020. (Attended)
8. Webinar on Global Impacts of GM crops: economic and environmental effects, 1996-2018, Focused on Pakistan. In collaboration with International Services for acquisition of agribiotech applications (ISAAA and CropLife Pakistan Association), November 17, 2020 (attended).
9. Did outreach activity at Bhakker and met stakeholders on 15-12 January, 2022
10. Hands on Training on CRISPR/CAS mediated Genome editing held February 21-26, 2022, organized by CAS under NCGE (Member organizing Committee and convenor Communication Committee)
11. Emerging order from Chaos: Alternative splicing in Plants. 17 May 2022 (Member Organizing Committee).
12. Hands on Training on CRISPR/CAS mediated Genome editing held May 23-26 May, 2022. organized by CAS under NCGE (Member organizing Committee and convenor Communication Committee)
13. 7th International Conference on Climate Smart Agriculture: Innovations and adaptations. June 15-17, 2022. (Presented)
14. International Symposium on "Agricultural Network analysis" at CAS-AFS, June 13-18, 2022 (Convenor Communication Committee)
15. Second International Workshop on Biotechnology, Bioinformatics and Biochemistry June 14-15, 2022 (Resource Person)]
16. Public Health seminar at CAS Auditorium on 28th July, 2022. (Member Organizing committee)
17. Annual Departmental Retreat in Balakot/PARAS (KP) on 30-07-22 to 2-8-22 (Member organizing Committee)
18. World cotton research conference-7, held at Cairo, Egypt. 4-7 October, 2022.
19. Outreach activities for irrigated chickpea and soybean at Harappa, District Sahiwal on 13-10-2022 (Member Organizing Committee).
20. International wheat Conference, held at University of Agriculture Faisalabad on 19-20th October, 2022. (Poster evaluation committee)
21. Genetics and Genomics in Forest Tree Improvement. Webinar organized on 3rd November, 2022.

22. International Conference: Food Security Challenges and Opportunities in D-8 Countries. 6-7 March 2023. (Coordinator Communications)
23. 3rd International Training workshop on Biotechnology, Bioinformatics and Biochemistry, 9-10 March, 2023. (Member Organizing Committee)
24. International Seminar on role of Genomics for Soybean adaptation in Pakistan. May2, 2023. (Member Organizing Committee)

Projects Completed along with short Summary:

Project Summary: Establishment of Biomonitoring cell inorder to check Bt cotton efficiency:

We executed this project in 2012-14. I have been Co-PI in it. This was a need based research to address the adulterations made by seed mafia in Bt cotton seed.

The results of this study have been published in an impact factored journal (Journal of Agricultural Sciences, Cambridge University, Press.). Its summery is given below.
SUMMARY Genetically modified (GM) plants expressing Bt toxin provide protection against lepidopteran pests. The only GM crop in Pakistan is Bt cotton, which was illegally imported and adopted rapidly by cotton producers. Farmers gained access to the seed of many unapproved Bt genotypes before the matter was picked up and formal approval granted by the relevant governmental agencies. The present study was conducted to evaluate the samples of Bt cotton, collected from farmers and seed dealer, for transgene integration and expression. Seeds of 52 cotton genotypes, labelledas Bt, were collected from various farmers and seed dealers. Animmunoblot strip test was carried out, which showed that only 0·86 of the samples collected were synthesizing Cry1Ac toxin. According to multiplexed polymerase chain reaction (PCR) results, 0·86 of the genotypes tested were positive for the Mon531 event (an 'event' is a specific genetic modification in a specific species) and 0·14 were negative for any transgene. Transcript analysis of transgenes in positive genotypes by real-time Rt-PCR confirmed the synthesis of mRNA in all genotypes but with significant variation. The concentration of Bt toxin revealed by enzyme linked immunosorbent assay (ELISA) showed that only 0·02 genotypes had the reported optimum level.The real-time PCR and ELISA results further confirmed the attenuation of transgene expression at transcriptional and translational level by various internal and external factors. The same type of event was found in all genotypes, with significant variation in toxin level, revealing the impact of genetic back ground on transgene expression. The findings support the recommendation to improve the existing quality criteria for transgenic cotton variety approval and certification in Pakistan, with the inclusion of toxin concentration in the list of parameters to be considered.

Refusal of Cottonseedcake by ruminents! Is Bt Cotton the culprit (PI):

Cottonseed cakes have been a favorite feed for livestock. However, over the past few years there are complaints about the acceptability of cottonseed cakes by livestock. Animal either totally refuses to eat cottonseed cakes (CSC) or eats it reluctantly. Objective the project is to identify the reason of refusal of cotton seedcake by lactating animals. According to prevailing myth, either Bt toxin which is present in cotton seed or the toxins generated by microbiota established on the surface of seed are responsible for refusal of CSC. If both of them are not responsible then CSC preparing protocols or storage may have some fault that results in refusal. Approved Bt-cotton variety along with a non Bt variety were sown in the field. First picking was done in September and immediately ginned. The ginned seed of Bt and non Bt varieties were fed to group of buffaloes. They ate both Bt and non Bt seeds, the impact of seed stay time in the field was studied by picking and ginning second pick in early Mid October. The cottonseeds from later picking were fed to animals to see their acceptance or refusal. This cotton seed was also eaten by both groups of animals. Further the seed microbiota was studied which revealed most of the air born fungi in the samples with some of plant pathogens like Fusarium solani. The concentration of aflatoxins present in both pickings was seen in Bt and Non Bt seeds and it was observed that the seed which was kept in the field for longer period of time resulted in little bit elevated aflatoxin levels but still the animals ate both seeds. The same procedure was repeated by making seedcake and offering it to animals. The same results were obtained. From the mentioned experiments we could infer that it is neither Bt nor delayed picking. It might be the inappropriate conditions which bring some sort of bad smell and may imitate the animal to refuse cottonseed cake. The project report was submitted and accepted by the funding agency.

Engineering maize with heat shock proteins (PI)

Project Summary:
Temperature is among the most critical factors in the life of field crops. It affects the growth and development of the plant at every stage. The crop yield (reproductive or vegetative) is directly affected by abrupt changes in temperature. Cereals are the most important food crops in the world and fulfill 43% of the calories requirements of the population. Rice, maize and wheat are the main cereal crops and are being used as the staple food in most parts of the world. Most of the cereals grow in way that there is weather shift between vegetative and reproductive growth stages. If the temperature changes are abrupt or immediate the yield is affected badly. Maize is grown throughout Pakistan as spring and autumn crops. The spring crop is sown mainly in January and harvested in May-June. March and April are very critical months for this crop. Mild temperatures in these months ensure good yield but it does not happen on regular basis. Most of the times temperature goes high in April which leads to less seed set and grain cannot acquire proper weight. The other important stress is drought which can reduce the maize yield many times and heat stress coupled with drought can bring the catastrophic situation. Pakistan is facing severe drought conditions due to water shortage and less rainfall. This project is aimed to work for the development of heat and drought resistant maize genotypes. The strategy is to transform maize with the genes of heat shock proteins (hsps). Hsps were initially identified as proteins which help the plant to protect under heat stress. It is now known that hsps are basically stress coping proteins and help the cell to maintain homeostasis by refolding the stress affected proteins into functional form. In the present project the role of these proteins is being be seen for heat and drought tolerance in maize.

This project was awarded to me by PSF, through NSLP. We successfully transformed maize with promised genes, seen their expression, characterized them phenotypically and at molecular level. When we compared our transgenic plants with non transgenics, at the early phase of the life stress did not look to harm even the non transgenic plants. When we increased the stress both transgenic and non transgenic died. We provided stress which was tolerable by both transgenic and non transgenics and then let them grow normally. By the end of life cycle we could observe that the non transgenic could bolt early and did not develop normal cobs while the transgenic plants kept on growing normally, developed normal flowers and cobs and yielded normal. This tells that transgenics could recover from the stress and gave normal yield while non transgenics not. This was the target of said project which is duly achieved.

Summary of the Project: Impact Assessment of transgenic sugarcane expressing antifungal proteins on endophytic and rhizospheric microorganisms

Pakistan is the 5th largest grower of sugarcane worldwide but lags behind in production from many, mainly because traditional breeding is not available in our region as natural sugarcane flowering is not possible (Ijaz et al., 2012). Under the circumstances, non traditional breeding such as genetic engineering with genes targeted to improve agronomic traits is one of the serious options. Two antifungal proteins “Chitinase” and “Chitosanase” from *Trichoderma harzianum* were expressed into a disease susceptible sugarcane genotype. The transgenics achieved showed enhanced resistance against *Colletotrichum falcatum* which is causal organism Red Rot disease. This disease is a serious threat to sugarcane production in subcontinent.

We have been targeting to check the impact of transgenic sugarcane on the rhizospheric and endophytic microrganisms. The logic behind this activity is that the said protein are anti microbial and may prove harmful to beneficial endophytes and rhizospheric microorganisms due to the exudates released through the roots or upon decomposition of the plant material in soil. Transgenic plants along with the non transgenics and control genotypes were grown in fresh silt mixed with 25% of farm yard manure. Soil samples were taken from the root zone of sugarcane plants at 6” depth with an interval of 3 months for one year. The samples from the four replicates were used to isolate soil metagenomic DNA using commercial kits. These DNA were used to amplify rDNA using universal primers for bacteria and fungi. Same soil samples were dissolved in double distilled water and plated on LB and PDA media for bacteria and fungi respectively. Our results indicate that rDNA showed identical amplification whether taken from transgenic or non transgenic plant pots or control genotypes. Sometimes the pattern looked different but that was due to experimental variation in the soil samples, not due to transgene. The major amplificates were cloned and sequenced. The sequences were BLASTed which showed either novelty or similarity to non culturable microorganisms. The cultured organisms showed similar pattern for all the samples. In conclusion the transgenic do not have an impact on microrganisms.

Key Words: Transgenics; Metagenomics; sugarcane; rDNA
Presented at second South Asia Biosafety Conferesnce, Held in Coloumbo Sri Lanka, September 14-16, 2014.