Curriculum Vitae

Full Name: **Dr. Mehboob-ur-Rahman, *PoP, ICAC Researcher of the Yr-2014 Laureate***

Professional Experience

Dec 01, 2019—present: Deputy Chief Scientist & Professor
Dec 01, 2009—Nov 30, 2019: Principal Scientist & Associate Professor
Sept 20, 2002—Nov 30, 2009: Senior Scientist
Date of birth: 01-03-1972
Postal Address: Agricultural Biotechnology Division, National Institute for Biotechnology and Genetic Engineering (NIBGE), PO Box577, Jhang Road, Faisalabad, PAKISTAN.
Phone: 92-41-2554378 or 0300-7675801
Fax: 92-41-2651472
E-mail Address: mehboob_pbd@yahoo.com
ormehboob@nibge.org
Field of research: Plant Breeding & Genetics (specialization, Genomic-assisted breeding)

Educational Qualifications:

Degree	**Year**	**University/Board**	**Div / %age**	**Subject**
Borlaug Fellowship	2012	Stoneville, FAS, USDA		Cotton Genomics
Postdoc	2008	Univ Georgia USA		Cotton Genomics
PhD	2002	Univ. pf Agric Fsd	Ist/ 83	Plant Breeding & Genetics
M.Sc (Hons)	1997	Univ. of Agric. Fsd	Ist / 82.12	Plant Breeding & Genetics
B.Sc (Hons)	1995	Univ. of Agric. Fsd	Ist / 80.56	Plant Breeding & Genetics
F.Sc	1990	Govt. College, Fsd	Ist / 65.63	Pre-Medical
Matriculation	1987	Sargodha Board	Ist / 76.35	Science

Awards/Honours:

A- International AWRDS:

1. International Cotton Advisory Committee (ICAC, Washington DC) "Cotton Researcher of the Year Award-2014
2. Third World Academy of Sciences Award in Applied Science-Technology in Agriculture (under 40 in Agriculture)—2011

B- National

1. PAS Gold Medal in Agricultutre-2021
2. Stood first in "Agriculture Sciences" for Research Productivity Award 2017, and ranked 3rd in Productive Scientists of Pakistan-2017
3. ***Letter of Recognition from Seed Association of Pakistan March 18, 2017.***
4. ***Shield of Recognition bestowed by the Govt of Pakistan, for recognising my services rendered for cotton research and development, June 11, 2014.***
5. **Civil Award**: ***Presidential Award for Pride of Performance—2012, presented by the President of Pakistan***

6. Farmer Associate of Pakistan Award in Agriculture 2012.
7. ***LCCI Research Scientist Award-2010 along with Rs. 0.50 million, presented by Prime Minister of Pakistan on 18 Sept 2010.***
8. Letter of Appreciation by Seed Association of Pakistan, 2011
9. ***Outstanding Scientist: Biotechnology (1st Position) Award-2009***
10. Pakistan Atomic Energy Performance **GOLD MEDAL-2009**
11. Won five research productivity awards. **Stood first in "Agriculture Sciences" for Research Productivity Award 2013-14**
12. Presidential Young Innovator Award-HEC, 2007

Member of Committee

- i. **Nominated as Eminent cotton scientist in PCCC by the Prime Minister of Pakistan**
- ii. **Nominated as Member of Green Revolution 2.0 committee for transforming agriculture in Punjab**
- iii. **Nominated as Member Board of Punjab seed Corporation**

List of Projects:

1. Functional Genomics for quality traits in crop plants, Ministry of Science and Technology, (MoST), Pakistan Pak. (29.3475) Million, 2003-2005….Co-P.I. (completed)
2. Marker assisted selection for fiber quality improvement in mutation breeding programme of cotton (PI-International Atomic Energy Agency, Vienna Austria)
3. Development of farm facilities for biotechnology Faisalabad for NIBGE" Ministry for Food Agriculture and Livestock, MinFAL. (Rs. 13 Million) 2003-2005…. one of the P.Is. (Completed)
4. Development of genetic linkage map for quality traits in cotton (*Gossypium hirsutum* L.). Pak-China project (Rs. 4.48 million)….2003-2005 One of the PIs.
5. Application of DNA fingerprinting technology for drought tolerance in wheat. ALP competitive research grant (Rs. 4.0732 million)…PI (Completed)
6. DNA-based genetic characterization of cotton. ALP competitive research grant (Rs 4.078 million)….. Co-PI. (Completed)
7. DNA Fingerprinting approaches to study drought tolerance in cotton. (Rs. 0.993 million)….PI (Completed)
8. Development of high-tech Fibre Testing facilities at NIBGE (Rs. 18.86 million)…. One of the PIs. MinFAL (Completed)
9. Finding single nucleotide polymorphisms (SNPs) in cotton genome under Presidential Young Innovator (PYI) program. PI, Rs. 6.00 million.
10. Exploration of cotton germplasm potential against drought stress using genomic approaches. NSLP-PSF. PI. Rs 2.00 million (completed).
11. Integrated genetic/physical mapping of Gossypium. Pak-US Project (140,000 US$), PI from Pak side. 2008-2010—PI of the project
12. Identification of DNA markers linked with resistance to cotton leaf curl disease (Approved, ~400,000 US$; Pak-US through Kary-Loger Bill—completed)—PI of the project (2012-2016)

13. Enriching the genetic base of cotton resources for combating cotton leaf curl disease as a step towards sustaining the income of small farmer community disease (Completed, ~200,000 US$; Pak-US through Kary-Loger Bill—completed) –PI of the project (2012-2016)

14. Development and characterization of TILLING populations in crop plants using genomic approaches (Euro, 280,000—completed)—PI of the project

15. Development of cotton leaf curl virus (CLCuV) resistant germplasm for Pakistan using tranditional and non-conventional breedign approaches, Pak-US Phase-2, (13,000 US$, completed) PI of the project. July 2016-march 17

16. Identification of DNA markers (gene mapping) linked with resistance to cotton leaf curl virus (CLCuV) for production of CLCuV resistant cotton, Pak-US phase-2, (26,000 US$, completed)—PI of the project July 2016-march 17

17. Mining Of Elite Genes For High Yield, Super Fiber Qualities and Heat Tolerance and their Usages in Improving Pak and China Cotton Cultivars (completed, 7.76 million, Pak-China) —PI of the project.

18. Identification of disease and insect resistant mutants using SSRs and NextGen sequencing tools for improved wheat yield in Pakistan (Ongoing, Rs. 3.7 million HEC) —PI of the project

19. Identification of DNA markers (Gene Mapping) linked with resistance to cotton leaf curl virus (CLCuV) for production of CLCuV resistant cotton, Pak-US phase-3, 2018-jan 2019, (12000$)

20. Characterization of mutants derived from EMS-derived Gandum-1 for rust and drought tolerance for sustaining wheat yield in Pakistan (CS049). (Approved 9.953 million, ALP) —PI of the project

21. Identification of DNA markers (Gene Mapping, A/C 1965-7) linked with resistance to cotton leaf curl virus (CLCuV) for production of CLCuV resistant cotton, Pak-US phase-4, March 2019- Feb 2020 (14000$)

22. Development of Resilient Cotton through Bridging Conventional and Biotechnological Approaches (ongoing Rs. 59.54 million; PARB)—PI of the project,

23. Application of genomic assays for the development of improved wheat genotypes—varieties with improved amylose content, Pak-China (approved in 2023, Rs 4.00 million)—PI of the project

24. Deployment of genomic assays upon the selected heat tolerant elite cotton lines for future breeding work, PSF-NSLP (approved Rs. 6.96 million)—PI of the project (approved in 2023)

Teaching and thesis supervision

Faculty Member

- Ph.D. Coordinator of Ph.D course "Comparative Genomics" (100% teaching laoding)
- Faculty Member: Advances in Molecular Genetics (30% teaching load)
- M.Phil. (Biotechnology) course at NIBGE (10% teaching load)

Thesis completed under Supervision

PhD: 14 (8 as supervisor-I + 03 as supervisor-II+ 03 as o-supervisor)
Mentored PhD student in my Lab: 08 (mentor)
MPhil: 13 (as supervisor) 04 (co-supervisor) 06 (as mentor)
Trainee fellow: >15

Professional Affiliation and Appointments:

Expert Visits supported by IAEA:

1. Sokoine University of Agriculture, Morogoro Tanzania, 2016, IAEA
2. Baqa, Amman, Jordan, China, 2016, IAEA

Fellowships

1. Borlaug Fellowship for 2-months, Stoneville, Mississippi, USA (Sept 2012 to Nov 2012).

Visiting Professor/Scientist

3. Henan Institute of Sceince & Technology (HIST) Sept 15-Oct06, 2024
4. Hebei Agricultural University, China (Nov 19 to Dec 10, 2023)
5. **Visiting scientist**, Nanjing Agriculture University, China, 2017.
6. **Visiting scientist**, Seibersdorf, Vienna, Austria, 2015.
7. **Visiting Scientist,** Seibersdorf, Vienna, Austria, 2012.
8. **Visiting Scientist,** University of Arkansas, 2005
9. **Visiting Scientist**, Nanjing, Agriculture University of 2004.
10. **Visiting Scientist,** Institute of Developmental Bio. & Genet., Beijing, China, 2004

Membership of International Scientific Societies:

1. International Cotton Genome Initiative
2. International Wheat Genome Sequencing Consortium

Editorships of National and International Journals:

1. Journal of Cotton Research (BMC)
2. Crop Design (Elsevier)
3. Frontier in Genetics
4. Frontier in Plant Sciences
5. Discover Agriculture (springer)
6. Functional & Integrative Genomics (springer)

Reviewer of National and International Journals:

1. Scientific Reports, (Nature publishing group)
2. Plant Registration Journal
3. International Journal of Agriculture & Biology
4. Journal of Integrative Agriculture
5. GM crops and Foods
6. Euphytica
7. Molecular Biology Reports
8. Frontier in Plant Sciences

Publications

Books edited

1. Rahman M, Y. Zafar and Tianzhen Zhang (Eds). 2021. Cotton Precision Breeding. Springer Publisher, Cham. https://doi.org/10.1007/978-3-030-64504-5_1

2. Rahman M and Y. Zafar (Eds). 2018. Past, Present and Future Trends in Cotton Breeding. Intech Publisher, ISBN : 9 78-1 -789 23 -077-2; Print ISBN : 978-1-78923-076-5, DOI: 1 0. 5772/Intech open. 69672

Book Chapters (Foreign Publishers, In Total: 27)

1. Ahmad, N., Fatima, S., Hundleby, P., Rahman, M. 2024. Genome Editing in Brassica juncea Using CRISPR/Cas9 Technology. Fatemeh Maghuly (ed.),Plant Functional Genomics: Methods and Protocols, Volume 2, Methods in Molecular Biology, vol. 2788, https://doi.org/10.1007/978-1-0716-3782-1_20,

2. Rahman, S., Ikram, AR., Azeem, F., Qamar, MT., Shaheen, T., Rahman M. 2024. Precision Genome Editing with CRISPR-Cas9. In: Fatemeh Maghuly (ed.), Plant Functional Genomics: Methods and Protocols, Volume 2, Methods in Molecular Biology, vol. 2788, https://doi.org/10.1007/978-1-0716-3782-1_21,
3. Aslam S., Mehmood MA., Mehboob-ur Rahman, Noor F., and Ahmad N. (2022). Bioinformatics-assisted multiomics approaches to improve the agronomic traits in cotton. In. Bioinformatics in Agriculture. DOI: https://doi.org/10.1016/B978-0-323-89778-5.00037-4.
4. Rahman, M, A. Majeed, S. Zulfiqar, S. Ishfaq, M. Mohsan and N. Ahmad. 2021. Genomic assisted breeding for stress tolerance. **In:** Rahman et al. (Eds) Cotton Precision Breeding. Springer Publisher https://doi.org/10.1007/978-3-030-64504-5_6
5. Rahman M., Zulfiqar S., Mahmood A., Zafar Y., Zhang T. (2021) Historical Perspectives: From Conventional to Precision Breeding in Cotton. In: Rahman M., Zafar Y., Zhang T. (eds) Cotton Precision Breeding. Springer, Cham. https://doi.org/10.1007/978-3-030-64504-5_1
6. Malik, W, N. Anjum, M Usman, MS Abid, J. Ashraf, R. Zhang, C. Liang, M. Hanif, A. Qayyum and M. Rahman. 2021. Genomics of naturally colored cotton: a way forward to initiate precision breeding**.** Rahman et al. (Eds) Cotton Precision Breeding. Springer Publisher, https://doi.org/10.1007/978-3-030-64504-5_8
7. Rahman, M, S. Zafar, M. Hussain, H. Abbas and B. Till. 2021. Mutagenesis for targeted breeding in cotton. Rahman et al. (Eds) Cotton Precision Breeding. Springer Publisher, https://doi.org/10.1007/978-3-030-64504-5_9
8. Ahmad. A, MZ. Ghouri, A. Jamil, SH. Khan, N. Ahmad and M. Rahman. 2021. First Generation transgenic cotton crops**.** Rahman et al. (Eds) Cotton Precision Breeding. Springer Publisher, https://doi.org/10.1007/978-3-030-64504-5_10
9. Zaidi, SS, N. Ahmad and M. Rahman. Second and third generations of transgenic cotton**.** Rahman et al. (Eds) Cotton Precision Breeding. Springer Publisher, https://doi.org/10.1007/978-3-030-64504-5_13

10. Zhang B., Rahman M. (2021) Targeted Breeding in Cotton Using CRISPR/Cas9 Genome Editing. In: Rahman M., Zafar Y., Zhang T. (eds) Cotton Precision Breeding. Springer, Cham. https://doi.org/10.1007/978-3-030-64504-5_14
11. Khezir Hayat, Adem Bardak, Mehboob-ur-Rahman, Hafiz Muhammad Imran, Furqan Ahmad, Donay Parlak, Muhammad Azam, Muhammad Usmaan, Muhammad Adnan, Sidra Anjum and Rao Sohail Ahmad Khan (May 5th 2021). Association Mapping for Improving Fiber Quality in Upland Cottons, Plant Breeding - Current and Future Views, Ibrokhim Y. Abdurakhmonov, IntechOpen, DOI: 10.5772/intechopen.94405.
12. **Rahman, M**. and Y. Zafar. 2018. Introductory chapter: Updates on achieving sustainable cotton production. In: M. Rahman and Y. Zafar (Eds) Past, Present and Future Trends in Cotton Breeding. Intech Publisher, pp 3-10. http://dx.doi.org/10.5772/intechopen.74410
13. Zafar, SA., MA Noor, MA Waqas, X Wang, T Shaheen, M Raza and **M. Rahman**. 2018. Temperature extremes in cotton production and mitigation strategies. In: M. Rahman and Y. Zafar (Eds) Past, Present and Future Trends in Cotton Breeding. Intech Publisher, pp 65-91. http://dx.doi.org/10.5772/intechopen.74648
14. Bardak, A., K Hayat, O Erdogan, Z Mahmood, N Khan, MA Iqbal, H Tekerek and **M. Rahman**. 2018. Genetic mapping in cotton. In: M. Rahman and Y. Zafar (Eds) Past, Present and Future Trends in Cotton Breeding. Intech Publisher, pp 93-122. http://dx.doi.org/10.5772/intechopen.74513
15. **Rahman, M**., Z. Rahmat, M. Gul and Y. Zafar. 2016. Plant Functional Genomics: Approaches and Applications. In Khan et al. (Eds) Applied Molecular Biotechnology: The Next Generation of Genetic Engineering. CRC Press (Taylor & Francsis), pp 157-186.
16. **Rahman M, T**. Shaheen, M. Rahman, M.S. Riaz and Y. Zafar. 2016. Bioinformatics: a way forward to explore “plant omics”. In: A. Abdurakhmonov (Ed) In Bioinformatics: Updated features and applications. Intech Publisher

17. Raza G, N. Ahmad, M. Hussain, Y. Zafar and M. Rahman. 2016. Role of genetic and genomics in mitigating abiotic stresses in soybean. In Miransari (Ed) Environmental stresses in soybean production. Elsevier Publisher
18. Shaheen, T., Mehmood-ur-Rahman, M.S. Riaz, Y. Zafar and **M. Rahman**. 2015. Soybean production and drought stress. In: Miransari (Ed.) Abiotic and biotic stresses in soybean production. Elsevier Publisher
19. Ahmed, N., M. Zeshan, S. Gill, M. A. Mehmood & **M. Rahman**. 2015. Functional genomic studies of chloroplast genome in Arabidopsis. In: A. Sofo (Ed.). Arabidopsis thaliana Cultivation, Life Cycle and Functional Genomics. Pp 51-76. Nova Publisher, New York, USA
20. Rahman, M., T. Shaheen, S. Irem and Y. Zafar. 2015. Biosafety risk assessment of genetically modified crops containing *Cry* genes. In: Lichetfouse et al. (Eds) CO2 sequestration, biofuels and depollution. Pp 307-334
21. Rahman, M., Z. Rahmat, A. Mahmood, K. Abdullah and Y. Zafar. 2014. Cotton germplasm of Pakistan. In: A. Abdurakhmonov (Ed) World Cotton Germplasm Resources. Intech Publisher. http://dx.doi.org/10.5772/58620
22. Rahman M., M.A. Iqbal, N. Shaheen, Y. Zafar. 2014. Microsatellites: Methods & Protocols. In: M. Miransari (Ed) Stress and Plant Biotechnology. Stadium Press LLC.
23. Rahman M., T. Shaheen, M. Ashraf and Y. Zafar. 2012. Bridging Genomic and Classical breeding approaches for improving crop productivity. Crop Production for Agricultural Improvement. Springer Publisher. DOI 10.1007/978-94-007-4116-4_2. pp 19-41.
24. Ashraf, M., N. A. Akram, M. Rahman and M. R. Foolad. 2012. Marker-assisted selection in plant breeding for salinity tolerance. Springer Publisher. Methods Mol Biology 913:305-333.
25. Rahman, M., and A. H. Paterson. 2010. Comparative Genomics in Crop Plants. In: S.M. Jains & D.S. Brar (Eds). Springer Publisher, pp23-60.
26. Rahman M., M. Asif, T. Shaheen, N. Tabbasam, Y. Zafar and A.H. Paterson. 2011. Marker-assisted breeding in Higher Plants. Sustainable Agriculture Reviews. In: Eric Lichtfouse (Ed) Alternative Farming Systems, Biotechnology, Drought Stress and Ecological Fertilization. Springer Publisher.
27. Rahman, M., Yusuf Zafar and Andrew. H. Paterson. 2009. Gossypium DNA markers types, number and uses. In: Andrew H Paterson (Ed) Genomics of Cotton. Springer, Dordrecht.

National Publisher (Total= 6)

1. Y. Zafar, S. Mansoor, **M. Rahman**, W. A. Haris and K.A. Malik.Cotton Biotechnology: Contribution of NIBGE Cotton biotechnology conference, Nov, 2000, Univ. of Agric. Faisalabad.
2. **Mehboob-ur-Rahman**. DNA Fingerprinting:. "Modern Techniques in Biotechnology", 2-7 March 2003, at NIBGE, Pakistan.
3. **Mehboob-ur-Rahman.** Development of IR-cotton: a case study. "Capacity building in Biosafety of genetically modified crops GMOs detection", 14-17 June 2004, NIBGE Pakistan.
4. **Mehboob-ur-Rahman**. DNA Fingerprinting:. "Modern Techniques in Biotechnology", 4-8 April 2005, at NIBGE, Pakistan.
5. **Mehboob-ur-Rahman.** DNA Fingerprinting of Crop Plants: Plant Molecular Genomics", 6-10 June, 2005, at National Agricultural Research Center (NARC) Islamabad

Proceedings (international)

1. Yusuf Zafar,S. Mansoor, S. Asad, **M. Rahman**, Z. Mukhtar, M. Asif, A. Bashir and K.A. Malik. 2007. Current Status and Prospectus of Biotech Cotton in Pakistan. Proceeding of the regional consultation on genetically modified cotton for risk assessment and opportunities for small-scale cotton growers (CFC/ICAC/34Ft). pp 87-93.
2. **Rahman, M**. 2015. Role of genetic and genetic engineering in optimizing input use. Enhancing the mechanism of input interaction in cotton production. Proceedings of 73rd ICAC Meeting, Thessaloniki, Greece. pp4-6

Proceedings (National)

1. **Rahman, M**, D Hussain and Y Zafar. "DNA Markers: A review". Proceedings, First SESCOB Biotechnology Conference, January 11, 1996, Univ. of Agric. Faisalabad.
2. Hussain M, M.A. Iqbal and **M. Rahman.** Bridging mutation and genomic approaches for the development of mutant population. 9th National Wheat Conference Proceedings, 12-14 Feb, 2019, College of Agriculture, University of Sargodha, Pakistan. pp19-33

Peer Reviewed Papers (Total publications: 100 including **two in Nature and one in Nature Genetics** as a submitting or co- author; **Impact Factor: ~340 with more than 9400 google citations**)

1. Zengqiang Li , Yanhui Li , Muhammad Haneef Kashif , Xiangjun Kong , Ali Muhammad , Zihao Dong , Wuxian Fu , Mengyao Shao , Lijie Li , Na Bai , Xin Zhang , Mehboob-ur Rahman , Honghong Wu Zhiyong Zhang 2025. CeO2 nanoparticles downregulate the expression of AhRbohB6 and AhRbohC18 to improve salt tolerance in peanut. Plant Physiology and Biochemistry, 223; 109819. https://doi.org/10.1016/j.plaphy.2025.109819
2. Zafar S, Abbas H, Zulfiqar S, Abbas A, Iqbal MA, Till BJ and M. Rahman. 2024. Inducing mutations with EMS are useful in breaking the established correlations among economically important traits in cotton. African Journal of Botany 175: 90-102. https://doi.org/10.1016/j.sajb.2024.09.061
3. Javaid A, Hameed S, Li L, Zhang Z, Zhang B and Rahman M. 2024. Can nanotechnology and genomics innovations trigger agricultural revolution and sustainable development. Functional and Integrative Genomics 24, 216. https://doi.org/10.1007/s10142-024-01485-x
4. Zulfiqar S, **Rahman MU**, Bukhari SAR, Till B, Gu R, Liu D, Dreisigacker S. Genotyping by sequencing; a strategy for identification and mapping of induced mutation in newly developed wheat mutant lines. Functional & Integrative Genomics. 2024 Oct 16;24(6):191. doi: 10.1007/s10142-024-01424-w.
5. Han, Z., Si, Z., Rahman, M. *et al.* 2024. Genomic insights into local adaptation of upland cotton in China and Pakistan. *Theor Appl Genet* **137**, 136 (2024). https://doi.org/10.1007/s00122-024-04624-x
6. Zulfiqar S, Ishfaq S, Bukhari SAR, Sajjad M, Akhtra M, Liu D and Rahman M. 2024. New genetic resources for aphid resistance were identified from a newly developed wheat mutant library. *Heliyon*, 10, e26529.
7. Liu, F., Cai, S., Ma, Z., Yue, H., Xing, L., Wang, Y., Feng, S., Wang, L., Dai, L., Wan, H., Gao, J., Chen, M., Rahman, M. and Zhou, B. (2023) RVE2, a new regulatory factor in jasmonic acid pathway, orchestrates resistance to Verticillium wilt. Plant Biotechnol. J.,https://doi.org/10.1111/pbi.14149.
8. Schoonmaker, AN, Hulse-Kemp, AM, Youngblood, RC, Rahmat, Z, Atif Iqbal, M, Rahman, M.-u, Kochan, KJ, Scheffler, BE, Scheffler JA. 2023. Detecting Cotton Leaf Curl Virus Resistance Quantitative Trait Loci in Gossypium hirsutum and iCottonQTL a New R/Shiny App to Streamline Genetic Mapping. Plants 2023, 12,1153.
9. Zahra S, Shaheen T, Qasim M, Mahmood-ur-Rahman, Hussain M, Zulfiqar S, Shaukat K, Rahman Mu. 2023. Genome-wide survey of HMA gene family and its characterization in wheat (*Triticum aestivum*).PeerJ 11:e14920 DOI 10.7717/peerj.14920.
10. Mahreen N,Yasmin S, Asif M,Yahya M, Ejaz K, Mehboob-ur-Rahman,Yousaf S, Amin I, Zulfiqar S,Imran A, Khaliq S and Arif M (2023) Mitigation of water scarcity with sustained growth of Rice by plant growth promoting bacteria. Front. Plant Sci.14:1081537. doi: 10.3389/fpls.2023.1081537
11. Ahmad N, Fatima S, Mehmood MA, Zaman Q, Atif RA, Zhou W, Rahman Mu, Gill RA. 2023. Targeted genome editing in polyploids:Lessons fro Brassica. Front. Plant Sci. 14:1152468. doi: 10.3389/fpls.2023.1152468
12. Rahman, M.-u.; Zulfiqar, S.; Raza, M.A.; Ahmad, N.; Zhang, B. 2022. Engineering Abiotic Stress Tolerance in Crop Plants through CRISPR Genome Editing. *Cells*, *11*, 3590. https://doi.org/10.3390/cells11223590
13. Khan AH, Akram A, Saeed M, Ur Rahman M, Ur Rehman A, Mansoor S, Amin I. 2023. Establishment of Transcriptional Gene Silencing Targeting the Promoter Regions of GFP, PDS, and PSY Genes in Cotton using Virus-Induced Gene Silencing. Mol Biotechnol. doi: 10.1007/s12033-022-00610-0.
14. Gohar S, Sajjad M, Zulfiqar S, Liu J, Wu J and Rahman M-u (2022), Domestication of newly evolved hexaploid wheat—A journey of wild grass to cultivated wheat. Front. Genet.13:1022931. doi: 10.3389/fgene.2022.1022931
15. Zafar S, Abbas A, Iqbal MA, **Rahman M**. 2022. Mutagenesis with EMS is an alternative to recombinant breeding for inducing allelic diversity in cotton. Pak J Bot. 54 (4) 2022.
16. **Rahman M**. 2022. Fabrication of High-Quality Genome Assembly of Cultivated Alloltetraploid Cottons: A Way Towards Achieving Sustainability in Cotton Production. ICRA, 2022.

17. Hussain M, Gul M, Kamal R, Iqbal MA, Zulfiqar S, Abbas A, Röder MS, Muqaddasi QH, **Mehboob-ur-Rahman.** Prospects of Developing Novel Genetic Resources by Chemical and Physical Mutagenesis to Enlarge the Genetic Window in Bread Wheat Varieties. Agriculture 2021, 11, 621.
18. Rahman M, T Shaheen, P. Zaib , M. Fazal Abbas , **M. Rahman** and A. Arif. Identification, characterization and infection of Di19-2 gene from *Gossypium arboreum*. Pak J Bot , 53(2): 483-492, 2021.
19. Zulfiqar S, Ishfaq S, Ikram M, Nawaz MA, Rahman M. 2021. Characterization of Gamma-Rays-Induced Spring Wheat Mutants for Morphological and Quality Traits through Multivariate and GT Bi-Plot Analysis. *Agronomy*, 11(11):2288.
20. Zahra, S., Hussain, M., Zulfiqar, S. Ishfaq S, Shaheen T, Akhtar M and Rahman M. 2021. EMS-based mutants are useful for enhancing drought tolerance in spring wheat. Cereal Res Comm.
21. Zahra, S., Shaheen, T., Hussain, M., Zulfiqar, S., & Rahman, M (2021). Multivariate analysis of mutant wheat (*Triticum aestivum* L.) lines under drought stress. *Turkish Journal of Agriculture and Forestry*, *45*(5), 617-633.
22. Rahman M. 2020. Cotton Vision 2030. ICAC Recorder Vol 38;4: 21-25.
23. Ali I, NU Khan, S Gul, SU Khan, I Tahir, Z Bibi, IH Khalil, **Mehboob-Ur-Rahman,** S Ahmed, K Aslam, G Shabir, HA Haq, A Din, S Fahad. 2020. Association mapping of QTLs with yield and lint traits in elite upland cotton germplasm. Intl J Agric Biol 24:17–28
24. Rajwana IA, T. Shaheen, AU Malik, AS Khan, Mahmood-ur-Rahman, MA Iqbal, Y Zafar and **M. Rahman**. 2020. A high genetic similarity among the selected mango (*Mangifera indica* L.) genotypes-cultivars demonstrated by SSR fingerprinting assay. JAPS, 30 (4): 895-904.
25. Hu et al.…**M. Rahman**…T. Zhang. 2019. *Gossypium barbadense* and *Gossypium hirsutum* genomes provide insights into the origin and evolution of allotetraploid cotton. Nature Genetics 51 (4):739-748.
26. Ahmad N, **M. Rahman**, Z. Mukhtar, Y. Zafar and B. Zhang. 2019. A critical look on CRISPR-based genome editing in plants. J Cell Physiol. 2019;1–17.
27. Hussain M and **M. Rahman**. 2019. Registration of PGMB-15-30 spring wheat. J Plant Reg 13:245-250. doi:10.3198/jpr2018.03.0015crg.
28. Zainab R, S. Ahmad, Z. Zia and M. Rahman. 2019. Genetic monitoring of introgressed alleles from G. arboreum into G. hirsutum using SSR markers: A potential approach for bringing new alleles under cultivation. Pak J Bot 51(2).
29. Hussain M, MA Iqbal, B. Till and **M. Rahman**. 2018. Identification of induced mutations in hexaploid wheat genome using exome capture assay. PLoS ONE.13 (8).
30. Shaheen, T., Mahmood-ur-Rahman, M.F. Abbas, P. Zaib, **Mehboob-ur-Rahman**, I. Ullah, M.T.U. Qamar and A. Arif, 2018. Identification, characterization, homology modeling and protein-protein interactions of cotton (Gossypium arboreum L.) DREB gene. Int. J. Agric. Biol. 20: 1055–1061
31. Ali, I ., N.U. Khan, **M. Rahman**, R. Gul, Z. Bibi, S. Gul, S. Ahmed, S. Ali, N. Ali, K. Afridi and H.A. Haq, 2018. Genotype by environment and biplot analyses for yield and fiber traits in upland cotton. Int. J. Agric. Biol., 20: 1979-1990
32. Ali, I., NU Khan, F. Muhammad, MA Iqbal, A Abbas, Farhatullah, Z Bibi, S. Ali, IA Khalil, S. Ahmad and **M. Rahman**. 2017. Genotype by environment and GGE-biplot analysis for seed cotton yield in upland cotton. Pak J Bot. 49(6): 2273-2283.
33. Bakhsh, A., S.M. Iqbal, **M. Rahman** and A. Javaid, 2017. Use of RAPD markers in comparison with agro-morphological traits for estimation of diversity among chickpea genotypes. Int. J. Agric. Biol., 19(3): 427-431
34. **Rahman, M**., A.Q.Khan, Z Rahmat, M A Iqbal and Y. Zafar. 2017. Genetics and genomics of cotton leaf curl disease, its viral causal agents and whitefly vector: a way forward to sustain world cotton fiber security. Frontier in Plant Sciences (Virology). doi: 10.3389/fpls.2017.01157
35. Iqbal, M.A. and **M. Rahman**. 2017. Identification of marker-trait associations for lint traits in cotton. Frontier in Plant Sciences. 10.3389/fpls.2017.00086
36. Zafar SA, A. Hameed, MA Nawaz, MA Wei, MA Noor, M Hussain and **M. Rahman**. 2017. Mechanisms and molecular approaches for heat tolerance in rice (Oryza sativa L.) under climate change scenario. Journal of Integrative Agric. 16(0): 60345-7
37. Manssor S, I. Amin, S. Aftab and M. Rahman. 2016. Recent Developments in Cotton Biotech Research in Pakistan. Vol 3: 15-20
38. Rahman, M. 2016. Cotton improvement for economically stressed economies. ICAC Recorder, Vol 1: 12-13.
39. Shaheen, T., Y. Zafar and M. Rahman. 2016. Phylogenetic analysis of cotton species (diploid genomes) using Single Nucleotide Polymorphisms (SNPs) markers. Pak J Agri Sci 283-290
40. Iqbal, M.A., M. Abbas, Y. Zafar and M. Rahman. 2015. Characterization of *Gossypium arboruem* L. genotypes for various fiber quality traits. Pak J Bot 47(6): 2347-2354, 2015.
41. **Rahman, M.**, M. Zaman, Y. Zafar, Z. Hayder, A. Jamil, A. kikuchi and K.N. Watanabe. 2015. Mammalian Food Safety Risk Assessment of Transgenic Cotton Containing *Cry1Ac* Gene Conducted Independently in Pakistan. Med Safe Glo Heal, 4:2

42. Abbas, M., M. A. Iqbal, **M. Rahman** and A.H. Paterson. 2015. Estimating genetic diversity among selected cotton genotypes and the identification of DNA markers associated with resistance to cotton leaf curl disease. Turk J Bot 39: 1033-1041
43. **Rahman, M.,** M. Zaman, T. Shaheen, S. Irem and Y. Zafar. 2015. Safe use of Cry genes in genetically modified crops. Environmental Chemistry Letter 13:239-249.
44. **Malik S, M.** Rahman and T.A. Malik. 2015. Genetic mapping of potential QTLs associated with drought tolerance in wheat. J Anim Plant Sci 25(4): 1032-1040.
45. Zaman, M., M.S. Mirza, S. Irem, Y. Zafar and **M. Rahman**. 2015. A temporal expression of Cry1Ac protein in cotton plant and its impact on soil health. Int J Agric Biol 17:280-288
46. Shaheen, T., A.A. Khan, Mahmood-ur-Rahman, M.T.U. Qamar. and **M. Rahman**. 2015. Estimation of genetic diversity of plant growth promoting rhizobacteria (PGPR) strains found in different areas of Pakistan using RAPD and 16s rRNA analysis. JAPS, 25:1457-1465
47. Mustafa, G., A. Tahir, M. Ashger, **M. Rahman** and A. Jamil. 2014. Comparative sequence analysis of Citrate synthase gene and 18S rRNA from a wild and mutant strains *Aspergillus* niger with various fungi. Bioinformation. 10(1) 001-007.
48. Tabassam, N., Y. Zafar. And **M. Rahman**. 2014. Pros and cons of using genomic SSRs and EST-SSRs for resolving phylogeny of the genus *Gossypium*. Plant Syst Evol 300: 559-575.
49. Mustafa, G., M. Ashger, **M. Rahman** and A. Jamil. 2014. Citrate synthase gene comparison and use of RAPD genomic fingerprinting to study relatedness among different *Aspergillus* sp. The FASEB Journal vol. 28 no. 1 Supplement 912.1.
50. Shaheen, T., Y. Zafar and **M. Rahman**. 2014. Single nucleotide polymorphism analysis of ubiquitin extension protein genes (UBQ) of Gossypium arboreum and Gossypium herbaceum in comparison with *Arabidopsis thaliana*. Pak J Bot 46(2): 605-608.
51. Shaheen, T., Y. Zafar and **M. Rahman**. 2013. QTL mapping of some productivity and fiber traits in Gossypium arboreum. Turk J bot. 37:802-810.
52. Shaheen, T., Y. Zafar., J.M. Stewart. and **M. Rahman**. 2013. Development of short gSSRs in *G. arboreum* and their utilization in phylogenetic studies. Turk J AGric Fort. 37: 288-299.
53. Iqbal, M.J., **M. Rahman**., M. Ashraf., M.A. Sheikh and A. Jamil. 2012. Trehalose Expression in Hexaploid Wheat (*Triticum aestivum* L.) Germplasm under Drought Stress. Pak. J. Life Soc. Sci. 10(2): 106-110
54. Paterson, A.H., J.F. Wendel,….**M. Rahman**, D.S. Rokhsar, X. Wang and J. Schmutz. 2012. Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. **Nature** 492: 423-428.
55. **Rahman M**., and Y. Zafar. Registration of NN-3. 2012. Journal of Plant Registrations 6:342-347.
56. **Rahman M**., T. Shaheen, N. Tabbasam, M. A. Iqbal., M Ashraf, Y. Zafar and A. H. Paterson. 2012. Genetic resources in cotton and their improvement. Agronomy for Sustainable Development. DOI: 10.1007/s13593-011-0051-z.
57. Sarwar, M.K.S., M. Y. Ashraf, **M. Rahman** and Y. Zafar. 2012. Genetic variability in different biochemical traits and their relationship with yield and yield parameters of cotton cultivars grown under water stress conditions. Pakistan Journal of Botany 44 (2): 515-520.
58. Ali, H., S.S. Alam, R.N. Attanayake, **M. Rahman** and W. Chen. 2012. Population structure and mating type distribution of the chickpea blight pathogen *Ascochyta Rabie* from Pakistan and United States. Journal of Plant Pathology 94 (1): 99-108.
59. Ali, H., M. I. Haq, T.M. Shah, **M. Rahman** and W. Chen. 2012. Validation of molecular markers for resistance among Pakistani chickpea germplasm to races of *Fusarium oxysporum* f. sp. ciceris. Eur J Plant Pathol. DOI 10.1007/s10658-011-9868-1.
60. Saeed, M., W. Guo, I.Ullah, N. Tabbasam, Y. Zafar, **M. Rahman** and T. Zhang. 2011. QTL mapping for physiology, yield and plant architecture traits in cotton (Gossypium hirsutum L.) grown under well-watered versus water-stress conditions" Electronic Journal of Biotechnology DOI: 10.2225/vol14-issue3-fulltext-3
61. Awan, M. S., N. Tabbasam, N. Ayub, M. E. Babar, **M. Rahman**, S. M. Rana and M. I. Rajoka. 2011. Gamma radiation induced mutagenesis in *Aspergillus niger* to enhance its microbial fermentation activity for industrial enzyme production. Molecular Biology Report. DOI 10.1007/s11033-010-0239-3.
62. Khan, S.M., A. Nawaz, W. Malik, N. Javed, T. Yasmin, **M. Rahman**, A. Qayyum, Q. Iqbal, T. Ahmed and A.A. Khan. 2011. Morphological and molecular characterization of Oyster mushroom (Pleurotus spp.). African J Biotechnology 10(14): 2638-2643.
63. Asif, M., **M. Rahman** and Y. Zafar. 2011. Marker-assisted selection for fiber quality improvement in mutation breeding programme of cotton. IAEA-TECDOC. Physical Mapping Technologies for the Identification and Characterization of Mutated Genes Contributing to Crop Quality. PP 27-37.
64. Shaheen, T., Y. Zafar and **M. Rahman.** 2010. Detection of single nucleotide polymorphisms in the conserved ESTs regions of *Gossypium arboreum*. Electronic J Biotechnology: DOI: 10.2225/vol13-issue5-fulltext-3.

65. Azhar, M.T., **M. Rahman**, S. Aftab, Y. Zafar and S. Mansoor. 2010. Utilization of natural and genetically-engineered sources in Gossypium hirsutum for the development of tolerance against cotton leaf curl disease and fiber characteristics. Int J Agric. Biol. 12-744-748
66. Lin, L., G.J. Pierce, J.E. Bowers, J.C. Estill, R.O. Compton, L.K. Rainville, C. Kim, C. Lemke, J. Rong, H. Tang, X. Wang, M. Braidotti, A.H. Chen, K. Chichola, K. Collura, E. Epps, W. Golser, C. Grover, G. Ingles, S. Karunakaran, D. Kudrna, J. Olive**,** N. Tabassum**,** E. Um**,** M. Wissotski**,** Y. Yu**,** A. Zuccolo**, M. Rahman,** D. G. Peterson**,** R. A. Wing**,** J. F. Wendel and A. H. Paterson. 2010. A draft physical map of a D-genome cotton species (*Gossypium raimondii*) BMC Genomics 11: 395.
67. Paterson A.H., J. Rong…..**Mehboob-ur-Rahman**, Y. Zafar…2010. Sequencing and utilization of the Gossypium genomes. Tropical Plant Biology. DOI: 10.1007/s12042-010-9051-4.
68. Paterson, A.H., John E. Bowers, …… **M. Rahman**, Doreen Ware, Peter Westhoff, Klaus F.X. Mayer, Joachim Messing, Daniel S. Rokhsar (2009). The *Sorghum bicolor* genome and the diversification of grasses. **Nature** 457: 551-556.
69. Arshad M, M.I. Khan, C.R. Ali, M. Afzal and **M. Rahman.** 2009. Registration of 'CIM-496' cotton cultivar. (Crop Science Society of America), 3:231-235.
70. Ali I, A Kausar, **M. Rahman**, Y. Zafar, M. Asif, M Ashraf, S. Riaz, S. Zafar, A. Wahid, S. Maqsood, M. Niaz and S. Q. Abbas. 2009. Development of genetic linkage map of hairiness in *Gossypium hirsutum* (cotton) using molecular markers. Pak J Bot 41(4): 1627-1635.
71. Ali I, M Ashraf, **M. Rahman**, Y. Zafar, M. Asif, A. Kauser, S. Riaz, M. Niaz, A. Wahid and S. Q. Abbas. 2009. Development of genetic linkage map of red leaf colour in cotton (Gossypium hirsutum) using DNA markers. Pak J Bot 41(3): 1127-1136.
72. Ali, S., M.E. Baber, P. Akhter, A. Ali, **M. Rahman**, J.I. Sultan and H.L. Shaheen. 2009. Genetic divergence and relationship among five buffalo breeds of Pakistan using random amplified polymorphic DNA (RAPD) analysis. Pak J Zool. 9:303-308.
73. Asif, M. **M. Rahman**, J.I. Mirza and Y. Zafar. 2009. Parentage confirmation of cotton hybrids using molecular markers. Pak J Bot 41 (2): 695-701.
74. Shaheen, T., M. Asif, Y. Zafar and M. Rahman. 2009. Single nucleotide polymorphism analysis of MT-SHSP gene of Gossypium arboreum and its relationship with other diploid cotton genomes, *G. hirsutum* and *Arabidopsis thaliana*. Pak J Bot 41(1): 117-183.
75. Asif, M., **M. Rahman**, J.I. Mirza and Y. Zafar. 2008. High resolution metaphore agarose gel electrophoresis for genotyping with microsatellite markers. Pak J Agric Sci 45(1): 75-79.
76. **Rahman**, **M**., T. Yasmin, N. Tabassum I. Ullah, M. Asif and Y. Zafar. 2008. Studying the extent of genetic diversity among *Gossypium arboreum* L. genotypes/cultivars using DNA fingerprinting. Genetic Resour Crop Evol 55: 331–339.
77. **Rahman, M.**, I. Ullah, M. Ashraf and Y. Zafar. 2008. A study of genotypic variation for drought tolerance in cotton. Agronomy for Sustainable Development, 28:439–447.
78. Rajwana I.A., N. Tabbasam, A.U. Malik, S.A. Malik, **M. Rahman** and Y. Zafar. 2008. Assessment of genetic diversity among mango (Mangifera indica L.) genotypes using RAPD markers. Scientia Horticulturae 117: 297-301.
79. Ullah, I., **M. Rahman**, M. Ashraf and Y. Zafar. 2008. Genotypic Variation for Physiological and Productivity Traits in Cotton (*Gossypium hirsutum L.*) Under two Contrasting Water Regimes. Flora 203: 105-115.
80. Ahmad, S., T. Zhang, Noor-ul-Islam, T. Shaheen and **M. Rahman**. 2007. Identifying genetic variation in Gossypium based on single nucleotide polymorphism. Pak J Bot. 39(4): 1245-1250.
81. Ahmad I, S.A. Malik, **M. Rahman**, A.U. Malik and R. Anwar. 2007. Exploring the potential of new promising mango (Mangifera indica L.) hybrid cv. faiz kareem. HortScience 42 (4): 913-913.
82. **Rahman, M**. and Y. Zafar. 2007. Registration of NIBGE-115. Journal of Plant Registrations (Crop Science Society of America), 1: 51-52.
83. **Rahman, M**. and Y. Zafar. 2007. Registration of NIBGE-2. Crop Science Society of America), 2:113-114.
84. Z. Jeffrey Chen, ….**Mehboob-ur-Rahman**, Yusuf Zafar, John Z. Yu, Russell J. Kohel, Jonathan Wendel and Andrew H. Paterson. 2007. Towards sequencing cotton (*Gossypium*) genomes. Plant Physiology, 145: 1251-1263.
85. Asif, M., **M. Rahman** and Y. Zafar. 2006. Genotyping Analysis of Maize (*Zea mays* L.). Hybrids Using DNA Fingerprinting Technology. *Pak J Bot*. 38 (5): 1425-1430.
86. Fauzia Y. Hafeez, Sumera Yasmin, Dini Ariani, **Mehboob-ur-Rahman,** Yusuf Zafar and Kauser A. Malik. 2006. Characterization of plant growth promoting bacteria (PGPB) from geographically different regions. *Agron. Sustain. Dev*. 26: 143–150.
87. Sarwar, M.K.S., I. Ullah, **M. Rahman**, M.Y. Ashraf and Y. Zafar. 2006 Glycinebetaine accumulation and its relation to yield and yield component in cotton genotypes grown under water deficit condition. *Pak J Bot*. 38 (5): 1449-1456.
88. Shafeeq, S., **M. Rahman**, M. Ashraf and Y. Zafar. 2006. Genetic variability of different wheat (*Triticum aestivum* L.) genotypes/cultivars under induced water stress. *Pak J Bot*. 38 (5): 1671-1678.
89. Shaheen, T., **M. Rahman** and Y. Zafar. 2006. Chloroplast RPS8 gene of cotton reveals the conserved nature through out taxa. *Pak J Bot*. 38 (5): 1467-1476.

90. Tabassam, N., **M. Rahman** and Y. Zafar. 2006. DNA-based genotyping of sorghum hybrids. *Pak J Bot*. 38 (5): 1599-1604.
91. Ullah, I., **M. Rahman**, M. Ashraf and Y.Zafar. 2006. Genotypic variations for drought tolerance in cotton (*Gossypium hirsutum* L.): seed cotton yield responses. *Pak J Bot*. 38 (5): 3679-1687.
92. Zafar I., **M. Rahman,** A. Saleem and Y. Zafar. 2006. Genetic diversity among *Fusarium subglutinans* isolates causing mango Malformation disease in Pakistan. *World J Microbiol. Biotech.* 22: 1161-1167.
93. Asif, M., **M. Rahman** and Y. Zafar. 2005. DNA fingerprinting studies of some wheat (*Triticum aestivum* L.) genotypes using random amplified polymorphic DNA (RAPD) analysis. *Pak J Bot*. 37 (2): 271-277.
94. Tanveer, A., K. Akhtar, M.A. Ghouri, M. A. Anwar, M. Rehman, **Mehboob-ur-Rahman,** Y. Zafar & A.M. Khalid. 2005. Phylogenetic relationship among acidophilic bacteria from diverse environments as determined by random amplified polymorphic DNA analysis (RAPD). *World J Microbiol. Biotech*. 21: 645-648.
95. **Rahman, M**., T.A. Malik, D. Hussain and Y. Zafar. 2005. Genetics of resistance to cotton leaf curl virus disease in *Gossypium hirsutum*. *Plant Pathology (BSPP)* 54: 764-772.
96. Ali, I., M. Ashraf, **M. Rahman**, I. Ullah, M. Niaz, M. Hanif, M. Hassan and Y. Zafar. 2004. Screening of cotton varieties regarding hairiness trait for DNA fingerprinting. J. Nat. Sci 2(1), 91-99.
97. Ali, I., M. Ashraf, **M. Rahman**, I. Ullah, M. Niaz, M. Hassan, Y. Zafar and M. Hanif. 2004. Optimization of PCR conditions for DNA fingerprinting in cotton. J. Nat. Sci 2(2), 47-51.
98. **Rahman, M.,** T. A. Malik, M.J. Iqbal, Y Zafar, and K. A. Malik. 2004. Gene tagging for salinity resistance in wheat by RAPD. *Pak J Bot.* 36 (3): 595-602
99. Amir, A.H., T.A. Malik., H. Raza and **M. Rahman**. 2002. DNA marker studies for leaf nectaries in upland cotton. Asian J Plant Sci. 1(4): 395-396.
100. Amir, A.H., T.A. Malik., M. Rizwan and **M. Rahman**. 2002. Genetics of leaf nectaries in upland cotton. *Asian J Plant Sci*. 1(4): 423-424.
101. **Rahman, M.**, D Hussain and Y Zafar. 2002. Estimation of genetic divergence among elite cotton (*Gossypium hirsutum* L.) cultivars/genotypes by DNA fingerprinting technology. Crop Science 42: 2137-2144.
102. Mukhtar, S., **M. Rahman** and Y Zafar. 2002 Assessment of genetic diversity among wheat cultivars using random amplified polymorphic DNA (RAPD) analysis. *Euphytica* 128: 417-425.
103. **Rahman, M.**, T.A. Malik, N. Aslam, M. Asif, R. Ahmad, I. A. Khan and Y. Zafar. 2002. Optimization of PCR Conditions to Amplify Microsatellite Loci in Cotton (*Gossypium hirsutum* L*.). Int. J. Agric. Biol*. 2(4):282-284.
104. **Rahman, M.** and Y Zafar. 2001. Genotyping of a new strain of lentil (*Lens culinaris* Medik) by DNA fingerprinting. *Pak J Bot.* 33 (4): 423-428.
105. Rehman S, M. S. Shaheen, **M. Rahman** and T. A. Malik. 2000. Evaluation of Excised Leaf Water Loss and Relative Water Content as Screening Techniques for Breeding Drought Resistant Wheat. Pak. J. Biol. Sci. 3 (4): 663-665.
106. **Rahman, M.,** T. A. Malik, M.J. Iqbal, Y Zafar, K. Alam, Z Perveen and S. Rehman. 1998. DNA Marker For salinity Resistance. Rice Biotechnology Quarterly, **USA,** 35:12-13.

Conferences attended, national and international (I don't keep record of conferences/meetings in which I was not invited speaker)

1. **Rahman, M.**, N. Aslam, M. Asif, T.A. Malik, K.A. Malik and Y. Zafar. 2002. Identification of DNA markers for Cotton Leaf Curl Virus Disease (CLCD) in Cotton (*Gossypium hirsutum* L.). *Cotton Science*. 14: 17. (ICGI China)
2. **Rahman, M.,** M. Asif, I. Ali, S.A. Randhawa, T.A. Malik, K.A. Malik and Y. Zafar. 2002. Isolate a Gene for Velvet Hairiness in Cotton (*Gossypium hirsutum* L.) by Map-Based Cloning. *Cotton Science* 14: 25. (ICGI China)
3. **Mehboob-ur-Rahman**, Muhammad Asif, Iftikhar Ali, ZulfiqarHayder, Kausar A Malik and Y. Zafar, (2003). DNA marker studies in cotton. Final meeting of CFC/ICAC 07 project held at ICBA, Dubai 28-30 September 2003.
4. Ghulam Sarwar, ShahidMansoor, Atiq-ur-Rehman, **Mehboob-ur-Rahman**, Iftikhar Ahmed Khan and Y. Zafar, (2003). Mechanism of resistance and diversity in sources of natural resistance against cotton leaf curl disease. Final meeting of CFC/ICAC 07 project held at ICBA, Dubai 28-30 September 2003.
5. **Mehboob-ur-Rahman,** Muhammad Asif, IhsanUllah, Yusuf Zafar and Kausar A Malik. 2004. Cotton genomic studies at NIBGE. International Cotton Genome Initiative (ICGI) Workshop, 10-13 Oct Hayderabad India. PP32.

6. **Rahman, M**., M. Asif, I. Ullah, K.A. Malik and Y. Zafar. 2005. Overview of cotton genomic studies in Pakistan. Plant & Animal Genome Conference XIII. San Diego, CA. USA. PP81.
7. **Rahman, M**., I. Ullah, M. Asif, K.A. Malik and Y. Zafar. 2005. Genomics studies for drought tolerance in cotton. Biotechnology for salinity & drought tolerance in plants. 28-31 March, Islamabad Pakistan. PP48.
8. Malik T.A., S. Rahman, **M. Rahman** and Y Zafar. 2005. Tagging genes for drought resistance by DNA markers in wheat. Biotechnology for salinity & drought tolerance in plants. 28-31 March, Islamabad Pakistan. PP50.
9. **Rahman, M**. and Y. Zafar. 2005. Practical National Biosafety Framework and Institutional Implementation in Agriculture Biotechnology Research. 10th International Congress of SABRAO, 22-23 August, Tsukuba Japan PP S6-3.
10. Rahman, S., T.A. Malik, **M. Rahman** and Y. Zafar. 2005. DNA markers for drought tolerance in wheat. The 2nd International conference on integrated approaches to sustain and improve plant production under drought stress, Univ of Rome La Sapienza Rome Italy.. 24-28 September, 2005
11. **Mehboob-ur-Rahman**, Ali Manan Mohsin& Yusuf Zafar. 2006. Wheat genomic studies in Pakistan. International Wheat Seminar. February 20-21, Wheat Res Inst. Faisalabad Pakistan PP. 80-81.
12. **Mehboob-ur-Rahman**, Ali M Mohsin& Yusuf Zafar. 2006. Development of genetic linkage map for drought tolerance in wheat. International Wheat Seminar. February 20-21, Wheat Res Inst. Faisalabad Pakistan PP. 81-82.
13. Ishtiaq Ahmad, **Mehboob-ur-Rahman**, AmanUllah Malik, Yusuf Zafar. 2006. Application of DNA Fingerprinting Technology to Estimate Genetic Divergence among Mango Cultivars-Genotypes. 27th International Horticultural Congress 13-19 August 2006, Seoul Korea.
14. **Rahman**, M., I. Ullah, M. Ashraf, J.M. Stewart and Y. Zafar. 2006. Genotypic variation for drought tolerance in cotton (*Gossypium hirsutum* L.): Productivity, osmotic adjustment and cellular membrane stability. International symposium on strategies for crop improvement against abiotic stresses. September 18-20, Dept. Bot. UnivAgric Faisalabad Pakistan PP. 14.
15. Ullah, I., **M. Rahman**, M. Ashraf and Y. Zafar. 2006. Genotypic variation for physiological and productivity traits in cotton (*Gossypium hirsutum* L.) under contrasting water regimes. International symposium on strategies for crop improvement against abiotic stresses. September 18-20, Dept. Bot. Univ. Agric Faisalabad Pakistan PP. 14-15.
16. **Rahman**, M., A. Tabassam, M. Kazi and Y Zafar. 2006. A step towards wheat genome initiative studies to combat drought in Pakistan using DNA fingerprinting tool.. International symposium on strategies for crop improvement against abiotic stresses. September 18-20, Dept. Bot. Univ. Agric Faisalabad Pakistan PP. 15.
17. Javed, Y., **M. Rahman**, N. Tabassam, R.W. Briddon and Y. Zafar. 2006. Identification of resistant sources against Burewala virus disease. International Cotton Genome Initiative (ICGI) Workshop, 18-20 Sept Brasilia Brazil. PP 9-10.
18. **Rahman, M., N. Ahmed**, M.Asif and Y. Zafar. 2006. Identification of DNA markers linked with cotton leaf curl disease (CLCD). International Cotton Genome Initiative (ICGI) Workshop, 18-20 Sept Brasilia Brazil. PP 77-78.
19. **Rahman, M.,** M. Nawaz, M.Asif, T.A. Wilkins and Y. Zafar. 2006. A step towards expression profiling of cotton fiber. International Cotton Genome Initiative (ICGI) Workshop, 18-20 Sept Brasilia Brazil. PP 49-50.
20. Saeed, M.; Guo, W.Z.; Ullah, I.; Tabassam, N.; Zafar, Y.; **Rahman, M**. and Zhang T.Z. QTL mapping in cotton (Gossypium hirsutum L.): chromosome 19 containing important genomic regions for stress tolerance. The 3rd International Conference on Integrated Approaches to Improve Crop Production Under Drought-Prone Environments (Oct. 11-16, 2009, Shanghai, China)
21. **Rahman M.** National Seminar on Biodiversity Conservation on Dec 21, 2010 at IABGR, Islamabad
22. **Rahman M.** 2011. Combating cotton leaf curl disease: A way forward. 5th meeting Asian Cotton Research & Development Network, 23-25 Feb 2011, Lahore Pakistan.
23. Beltwide Cotton Conference Jan 3-6, 2012

24. ICGI meeting 9-12 Oct 2012
25. **Rahman** et al., 2013. Genetic and Genomic strategies for combating cotton leaf curl disease. Biotechnology: Prospects & Challenges in Agriculture, Industry, Health and Environment. 22-26 April 2013.
26. **I**nternational Conference on Plant Genetics and Breeding Technologies, 18-20 February 2013, Vienna, Austria
27. Key note lecture entitled Exploitation of genomic resources for sustaining crop productivities in Pakistan. The International Conference of Biochemical and Chemical Sciences. 24-26 Feb 2014
28. **Rahman, M.,** A. Ali, A.Q. Khan, A. Abbas, Z. Rahmat, Z. Sarfraz, A. Khalid, F. Rahseed, A. Munir, M.A. Iqbal, J. Scheffler and B. Scheffler. Use of genetic and genomic approaches for combating cotton leaf curl disease in Pakistan. ICGI 25-28 Sept 2014, Wuhan China
29. Tabbasam, N., Y. Zafar, A.H. Paterson and **M. Rahman**. *Gossypium raidomii* derived new gSSRs for linkage map construction and mapping QTLs for fiber quality trait. ICGI 25-28 Sept 2014, Wuhan China
30. Ahmad et al., 2022. Comparative study of 67 cotton cultivars tested in 2021-National Coordinated Varietal Trial (NCVT) conducted at 12 different agro-ecological zones of Pakistan. WCRC-7, 4-9 Oct, 2022, Cairo Egypt
31. Rahman, M. 2023. Genomic-assisted breeding of cotton. Reshaping cotton production in Punjab, Learning from Global Best Practices. June 24, 2023. MANSUA, Multan, Pakistan
32. **Rahman M**. 2024. EMS-based mutagenesis: a way toward creating useful plant mutants. Int conf on Industry University Research Collaboration. Synthetic Biology and Modern Agriculture, Oct 20-21, 2024. HIST, China
33. **Rahman M**, Asad S, Arshad M, Asif M, Amin I, Zulfiqar S and Mukhtar Z. 2024. Use of Modern Genomic Approaches for Developing Resilient Cotton Varieties. 9th Int Conf. Plant Sciences, Capitalizing Plant Diversity for Ensuring Food Security, 2024, BZU, Multan.
34. Zulfiqar S, Bukhari SAR, Till BJ, L Dongcheng, Dreisigacker S and M. Rahman. 2024. Development of useful Genetic and Genomic Resources of Spring Wheat through Bridging Mutational and Next Generation Sequencing Approach. 9th Int Conf. Plant Sciences, Capitalizing Plant Diversity for Ensuring Food Security, 28-30 October, 2024, BZU, Multan.
35. **Rahman M.** 2024. Redesigning wheat genome for improving resilience to achieve sustainability in the changing climate. Two days Int Conf. on Genomic Assisted Breeding in Wheat. Dec 10-11, 2024. NIBGE Faisalabad Pakistan

National Conferences

1. Yasmin, S., D. Ariani, D. Naranchimeg, B. Delgermaa, **M. Rahman,** Y. Zafar and F.Y. Hafeez. 2002. Genetic diversity among plant growth promoting *Rhizobacteria* (PGPR) from geographically different areas using RAPD technique. 9th International Congress of Soil Science. March 18-20, 2002. NIAB, Faisalabad Pakistan. pp 33.
2. ZafarIqbal, **Mehboob-ur-Rahman**, Altaf Ahmad Dasti, Ahmad SaleemAkhtar and Yusuf Zafar (2003). Genetic diversity among Fusariumsubglutinans isolates causing mango malformation disease in Pakistan.. Fourth National Conference of Plant Pathology held on 14-16 October 2003 at University of Arid Agriculture, Rawalpindi, Pakistan.
3. **Rahman, M**., K.A. Malik and Y. Zafar. 2004. Application of DNA fingerprinting for drought tolerance in wheat. First National Conference on Agricultural Biotechnology 16-18 August, 2004 Green Retreat Hotel, Nathiagali, Pakistan.
4. **Rahman, M**., T. Yasmin, H.L. Shaheen, T. Shaheen, N. Tabassum and Y. Zafar. 2006. Harvesting genetic diversity in the cotton genome. National symposium on biotechnology for economic prosperity. July 24-26, 2006 Green Retreat Hotel, Nathiagali, Pakistan.pp.38.
5. Asif, M., H. Mumtaz, J.I. Mirza, **M. Rahman** and Y. Zafar. Development of Genetic Linkage Map for quality traits in cotton. National symposium on biotechnology for economic prosperity. July 24-26, 2006 Green Retreat Hotel, Nathiagali, Pakistan. pp. 134.
6. Ullah, I., **M. Rahman**and Y. Zafar. Development of Genetic Linkage Map for Drought Tolerance in cotton. National symposium on biotechnology for economic prosperity. July 24-26, 2006 Green Retreat Hotel, Nathiagali, Pakistan. pp. 136.

7. Tabbasam N., H.L. Shaheen, M. Rahman and Y. Zafar. 2008. Characterization and genetic diversity analysis of Gossypium hirsutum L. genotypes/cultivars using microsatellites. Genomics for health and prosperity. Dec 20-23, 2008 Univ Karachi Pakistan.

Varieties/cultivars (14 cotton + 01 wheat)

1. We gained insight into the extent of genetic diversity among several crop plants including cotton. This information has been utilized for planning crosses and taking pro-active decisions in routine cotton breeding programs. Our group remained an active part of many international mega projects including physical mapping of D-genome (Lin et al. 2010, BMC Genomics), D-genome sequencing project (Paterson et al. 2012, Nature), etc. All these efforts were appreciated by bestowing me “Gold Medal-2009 by PAEC, Pakistan.
2. Utilized DNA markers associated with cotton leaf curl disease (Multan strain, appeared in 1990s in epidemic form), resulted in the development of three cotton varieties NIBGE-2, NIBGE-115and NN-3.The material developed by my group has been declared the most tolerant to Burewala virus disease by the Ministry of Food Agric Livestock (MinFAL) Islamabad. This material was transferred to other organizations for using in cotton breeding programs. Also share authorship on international registration document of CIM-496 (Arshad et al. 2009, J Plant Reg. Reg. No. CV-125, PI 657627, Pak 024263)). This variety covered up to 43% area of the Punjab in 2006, and remained very popular for four consecutive years (2004—2007). All these efforts towards development of new cotton varieties were appreciated by Ministry of Food and Agriculture by awarding me “Outstanding Award in Biotechnology—first position on 26 May 2009.
3. Dr Rahman has been remained at forefront in generating data for the safe use of Bt cotton containing Cry1Ac gene in local environment (Pakistan) and was submitted to the National Biosafety Committee, EPA, Islamabad Pakistan as a preliminary requirement for getting approval of cultivation of Bt cotton in Pakistan. Presently, Bt cotton varieties developed by us and other public/private entrepreneurs covers ~82% of the total cotton cultivated area of Pakistan. All these efforts toward sustaining cotton production were appreciated by the Prime Minister of Pakistan by awarding me the LCCI Achievement Award 2010.
4. Dr Rahman has also been instrumental in developing four Bt-cotton varieties (IR-NIBGE-3701, IR-NIBGE-1524, IR-NIBGE-3 & IR-NIBGE-901) as a principal breeder. All these varieties covered up to 35%, 25%, 20%, 13% area of Pakistan in 2009, 2010, 2011, 2012 & 2013, respectively. Total increase in production over the control was ~7.39 million bales during these years. President of Pakistan has awarded him “Presidential Award for Pride of Performance in 2012” for sustaining cotton production, and later by TWAS and Farmer Associate of Pakistan.

Other relevant information related to cotton varieties

1- NIBGE-2: approved on 14 Dec 2006 for general cultivation; and also got international Registration (Reg. No. CV-124, PI 647088, Pak 022845). (Dr Rahman is the Principal Breeder)
2- NIBGE-115: Approved on Feb 16, 2012 for general cultivation; and also got international registration **as germplasm** (Reg. No GP-880, PI 643972). (Dr Rahman is the Principal Breeder)
3- CIM-496—approved in 2005. Reg. No. CV-125, PI 657627, Pak 024263).

Breeders: M Arshad, M.I. Khan, C.R. Ali, M. Afzal and **M.Rahman**

- Covered 12.15% area of Punjab in 2004

- Covered 32.03% area of Punjab in 2005
- Covered 42.90% area of Punjab in 2006
- Covered 33.30% area of Punjab in 2007
- Covered ~20% area of Punjab in 2008
- Covered ~20% area of Punjab in 2009

4- IR-NIBGE-3701 (Approved on 31 March 2010, Dr. Rahman is the Principal Breeder)

- Covered less than 2% area of Punjab Province in 2008
- Covered ~15% area of Punjab Province in 2009
- Covered around 30% area of Punjab in 2010
- Covered around 13% area of Punjab in 2011
- Covered around 3% area of Punjab in 2012
- Covered around ~2% area of Punjab in 2013

Sindh Province

- Covered less than 2% area of Sindh Province in 2008
- Covered ~2% area of Sindh Province in 2009
- Covered ~10% area of Sindh in 2010
- Covered ~ 15% in Sindh Province of Pakistan in 2011
- Covered ~ 20% in Sindh Province of Pakistan in 2012
- Covered ~20% in Sindh Province of Pakistan in 2013
- Covered ~20% in Sindh Province of Pakistan in 2014
- Covered ~15% in Sindh Province of Pakistan in 2015
- Covered ~10% in Sindh Province of Pakistan in 2016
- Covered ~10% in Sindh Province of Pakistan in 2017
- Covered ~5% in Sindh Province of Pakistan in 2018
- Covered ~4% in Sindh Province of Pakistan in 2019
-

5- IR-NIBGE-1524 (Approved on 31 March 2010, Dr Rahman is the Principal Breeder)

- Covered ~5% area in 2006
- Every year it keeps ~2-4% area of Pakistan particularly in Virus infected areas

Sindh Province

- Covered ~2% area of Sindh Province in 2009
- Covered ~4% area of Sindh in 2010
- Covered ~ 8% in Sindh Province of Pakistan in 2011
- Covered ~ 10% in Sindh Province of Pakistan in 2012
- Covered ~2% in Sindh Province of Pakistan in 2014
- Covered ~2% in Sindh Province of Pakistan in 2015
- Covered ~2% in Sindh Province of Pakistan in 2016
- Covered ~4% in Sindh Province of Pakistan in 2017
- Covered ~4% in Sindh Province of Pakistan in 2018
- Covered ~8% in Sindh Province of Pakistan in 2019

6- IR-NIBGE-901: (Approved on 07-05-2011 for Sindh, Dr Rahman is the Principal Breeder)

- Covered ~1-2% area of Punjab from 2005 to 2011
- Covered ~5% area in Sindh Province of Pakistan in 2005

- Covered ~ 5% in Sindh Province of Pakistan in 2006
- Covered ~ 10% in Sindh Province of Pakistan in 2007
- Covered ~ 12% in Sindh Province of Pakistan in 2008
- Covered ~15% in Sindh Province of Pakistan in 2009
- Covered ~15% in Sindh Province of Pakistan in 2010
- Covered ~ 25% in Sindh Province of Pakistan in 2011
- Covered ~ 20% in Sindh Province of Pakistan in 2012
- Covered ~20% area in Sindh Province in 2013
- Covered ~20% area in Sindh Province in 2014
- Covered ~15% area in Sindh Province in 2015
- Covered ~10% area in Sindh Province in 2016
- Covered ~10% area in Sindh province in 2017
- Covered ~4% area in Sindh province in 2018
- Covered ~2% area in Sindh province in 2019

7- IR-NIBGE-3 (Approved on 16-02-2012 for Punjab; , Dr Rahman is the Principal Breeder)

- Suitable for early sowing.

8- **NN-3:** Approved in May 2013 for general cultivation; and also got international registration as a germplasm (Reg. No. GP-955, PI 665058, Pak 027493). **Dr Rahman is the Principal Breeder**

9- IR-NIBGE-4 (Approved provisionally on July 15, 2016 for Punjab; Dr Rahman is the Principal Breeder)

10- IR-NIBGE-6 (Approved provisionally on July 15, 2016 for Punjab; Dr Rahman is the Principal Breeder)

11- Gandum-1 (Approved on July 15, 2016 , Dr. Rahman is the Principal Breeder).

- Covered ~0.5% area in Punjab Province in 2015
- Covered ~1.5 area in Punjab Province in 2016
- Covered ~2% area in Punjab province in 2017
- Covered ~6% area in Punjab province in 2018
- Covered ~ 6.5% area in Punjab province in 2019

12- IR-NIBGE-11 Approved in 2021, Dr Rahman is the principal breeder

13- IR-NIBGE-15 Approved in 2022, Dr Rahman is the principal breeder

14- IR-NIBGE-13 approved in 2023, Dr Rahman is the principal breeder

15- IR-NIBGE-16 approved in 2023, Dr Rahman is the principal breeder

16- IR-NIBGE-17 approved in 2023, Dr Rahman is the principal breeder

17- IR-NIBGE-17 approved in 2025, Dr Rahman is the principal breeder

18- NIBGE-PF-1 approved in 2025, Dr Rahman is the principal breeder

Short summaries of the nominee’s best research papers.

Establishment and Application of DNA marker in cotton improvement programme.

Dr Rahman’s lab is pioneer in initiating DNA fingerprinting assays in Pakistan. Various DNA marker assays such as RAPDs, SSRs, AFLPs and presently now SNPs have been utilized for the estimation of genetic diversity among cotton varieties/genotypes of *G. hirsutum* (published in 2002). One of the important findings was that conical crosses should be made as one of the important tool to widen the genetic base of the new cultivated cotton varieties for combating the most important menace of cotton leaf curl disease. His group has also demonstrated that there were two center of origin of various G. arboreum accessions in this Pakistan (published in 2008). Similarly, the frequency of SNPs has been identified in various cotton species and their possible usage in the cotton improvement programs. His group has identified DNA markers associated with resistance to cotton leaf curl disease (Multan strain), and identified two SSRs which were later utilized for the improvement of cotton—resulted in the development of NIBGE-2, NIBGE-115 and NN-3 cotton cultivars. Our group has also characterized the G. hirsutum germplasm under water limited conditions (published in 2008), and identified two cotton lines FH-901 (drought sensitive) and RH-510 (drought tolerant). These genotypes were used in developing mapping population, and QTLs associated with drought tolerance have been identified (published in 2010) using intraspecific cross (*G. hirsutum*). We have also identified QTLs associated with various traits (fiber, leaf morphology etc.) using intraspecific crosses (*G. arboreum*, published in 2013).

Genetics of cotton leaf curl disease

Cotton leaf curl, a disease of viral origin, has substantially depressed cotton production in Pakistan. The disease is threatening the other important cotton growing neighboring countries like India and China. We have taken lead in demonstrating that the resistance to the disease is conferred by three genes including one suppressor gene (published in 2005). Another strain called Burewala appeared in epidemic form in 2006 and then in 2010. We first time described the most suitable and user friendly method of scoring the cotton leaf curl disease (0-4) which is being practiced through the country for scoring the disease.

Collaborative efforts towards cotton genome sequencing project.

Dr Rahman as one of the collaborators of Pak-US project entitled “Integrated genetic/physical mapping of Gossypium” has contributed in developing the D-genome physical map (published in 2010). Similarly, he has been the part of the cotton genome sequencing project (Prof Paterson, UGA, was the lead PI). The sequence was made public in 2012. This information has been published in 2012 in Nature. I am too the co-author in this paper. We have surveyed the released D-genome sequence and identified more than 1200 SSRs. These were surveyed on interspecific population, and identified two QTLs conferring tolerance to the cotton leaf curl disease.