Dr. Muhammad Tahir ul Qamar

Department of Bioinformatics & Biotechnology, Government College University, Faisalabad, Pakistan
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EDUCATION

Huazhong Agricultural University, Wuhan, China
Ph.D. in Bioinformatics — 2016 – 2019
Dissertation: A novel plant pan-genome construction pipeline based on presence/absence variations and brief insights into the *Citrus* pan-genome
Adviser: Prof. Ling-Ling Chen

University of Agriculture, Faisalabad, Pakistan
M.Phil. in Biotechnology — 2014 – 2016
Thesis: Computational and molecular characterization of wheat DNA sequence encoding plastidic 16S ribosomal RNA
Adviser: Prof. Muhammad Sarwar Khan

Government College University, Faisalabad, Pakistan
BS (Hons.) in Bioinformatics and Biotechnology — 2010 – 2014

PROFESSIONAL EXPERIENCE

Assistant Professor, GC University, Faisalabad, Pakistan	2022 – Present
Postdoctoral Fellow, University of California, Riverside, USA	2022
Postdoctoral Fellow, Guangxi University, Nanning, China	2019 – 2021
PhD Scholar, Huazhong Agricultural University, Wuhan, China	2016 – 2019
MPhil Scholar, University of Agriculture, Faisalabad, Pakistan	2014 – 2016
Research Intern, Ayub Agricultural Research Institute, Faisalabad, Pakistan	2013

RESEARCH INTERESTS

Pan-genomics; Computational Genomics; Computational Biology; Multi-OMICS Data Integration and Analysis using Artificial Intelligence; Bioinformatics Resources & Software Development

FEATURED PUBLICATIONS

(*Publications:* ***±100****, impact factor:* ***±1150****, citations:* ***±5500****, h-index:* ***40*** *– data retrieved from Google Scholar on July 15, 2025*)

1. **Tahir ul Qamar M**, Zhu X, Xing F, Chen LL. ppsPCP: a plant presence/absence variants scanner and pan-genome construction pipeline, ***Bioinformatics*** 2019; doi: 10.1093/bioinformatics/btz168 – [**IF: 6.931**]
2. **Tahir ul Qamar M**, Noor F, Guo YX, Zhu XT, Chen LL. Deep-HPI-pred: An R-Shiny applet for network-based classification and prediction of Host-Pathogen protein-protein interactions, ***Computational and Structural Biotechnology Journal*** 2023; doi: 10.1016/j.csbj.2023.12.010 – [**IF: 6.0**]
3. Fatima K, Hu H, **Tahir ul Qamar M***. PangenePro: an automated pipeline for rapid identification and classification of gene family members, ***Bioinformatics Advances*** 2025; doi: 10.1093/bioadv/vbaf159 – [**IF: 2.8**]
4. Ahmad RS, Sadaqat M, **Tahir ul Qamar M*.** XtractPAV: An Automated Pipeline for Identifying Presence–Absence Variations Across Multiple Genomes, ***bioRxiv*** 2025; doi: 10.1101/2025.06.27.661953
5. Liu H, Wang X, …, **Tahir ul Qamar M**, Xu Q, Chen LL. Citrus Pan-Genome to Breeding Database (CPBD): A comprehensive genome database for citrus breeding, ***Molecular Plant*** 2022; doi: 10.1016/j.molp.2022.08.006 – [**IF: 26.9**]
6. **Tahir ul Qamar M**, Fatima K, Rao MK, ..., Zhu XT. Comparative genomics profiling of Citrus species reveals the diversity and disease responsiveness of the GLP pangenes family, ***BMC Plant Biology*** 2025; doi: 0.1186/s12870-025-06397-x – [**IF: 4.8**]
7. **Tahir ul Qamar M**, Zhu X, Khan MS, Xing F, Chen LL. Pan-genome: A promising resource for noncoding RNA discovery in plants, ***Plant Genome*** 2020; doi: 10.1002/tpg2.20046 – [**IF: 4.219**]
8. Liu Y^{+}, **Tahir ul Qamar M**$^{+}$, Feng JW, Ding Y, Wang S, et al. Comparative analysis of miniature inverted–repeat transposable elements (MITEs) and long terminal repeat (LTR) retrotransposons in six *Citrus* species, ***BMC Plant Biology*** 2019; doi: 10.1186/s12870-019-1757-3 – [**IF: 5.260**]
9. Ding B, Hu H, Liu T, **Tahir ul Qamar M***., ..., Guo X. Pan-genome of pear provides insights into the fruit quality traits differentiation between Asian and European pears, ***Horticultural Plant Journal*** 2024; doi: 10.1101/2023.09.29.560244 – [**IF: 6.2**]

10. Zheng YY, Chen LH, …, **Tahir ul Qamar M**, …, Chen LL. Integrative multi-omics profiling of passion fruits revealed the genetic basis for fruit color and aroma, ***Plant Physiology*** 2023; doi: 10.1093/plphys/kiad640 – [**IF: 7.0**]
11. Wang S, Xiao Y, …, **Tahir ul Qamar M**, …, Chen LL. High-quality reference genome sequences of two coconut cultivars provide insights into evolution of monocot chromosomes and crop differentiation, ***Genome Biology*** 2021; doi: 10.1186/s13059-021-02522-9 – [**IF: 17.906**]
12. Zhu XT, Sanz-Jimenez P, Ning XT, **Tahir ul Qamar M**, Chen LL. Direct RNA sequencing in plants: Practical applications and future perspectives, ***Plant Communications*** 2024; doi: 10.1016/j.xplc.2024.101064 – [**IF: 9.4**]
13. Wang J, Hu H, Liang X, **Tahir ul Qamar M**, Zhang Y, Zhao J, Ren H, Yan X, Ding B, Guo J. High-quality genome assembly and comparative genomic profiling of yellowhorn (*Xanthoceras sorbifolia*) revealed environmental adaptation footprints and seed oil contents variations, ***Frontiers in Plant Science*** 2023; doi: 10.3389/fpls.2023.1147946 – [**IF: 6.625**]
14. Noor F, Asif M, Ashfaq UA, Qasim, **Tahir ul Qamar M***. Machine learning for synergistic network pharmacology: a comprehensive overview, ***Briefings in Bioinformatics*** 2023; doi: 10.1093/bib/bbad120 – [**IF: 13.994**]
15. Fatima K, Sadaqat M, Azeem F, Rao, MJ, Albekairi NA, Alshammari A, Tahir ul Qamar M. Integrated omics and machine learning-assisted profiling of cysteine-rich-receptor-like kinases from three peanut spp. revealed their role in multiple stresses, ***Frontiers in Genetics*** 2022; doi: 10.3389/fgene.2023.1252020 – [**IF: 4.772**]
16. Zia K, Rao MJ, Sadaqat M, Azeem F, Fatima K, **Tahir ul Qamar M***, Alshammari A, Alharbi M. Pangenome-wide analysis of cyclic nucleotide-gated channel (CNGC) gene family in citrus *Spp*. revealed their intraspecies diversity and potential roles in abiotic stress tolerance, ***Frontiers in Genetics*** 2022; doi: 10.3389/fgene.2022.1034921 – [**IF: 4.772**]
17. Zhu X, Run Z, …, **Tahir ul Qamar M**, …, Chen LL. Ribosome profiling reveals the translational landscape and allele-specific translational efficiency in rice, ***Plant Communications*** 2022; doi: 10.1016/j.xplc.2022.100457 – [**IF: 8.625**]
18. **Tahir ul Qamar M**, Mirza MU, Song J-M, Rao MJ, Zhu X, Chen LL. Probing the Structural Basis of Citrus Phytochrome B using Computational Modelling and Molecular Dynamics Simulation Approaches, ***Journal of Molecular Liquids*** 2021; doi: 10.1016/j.molliq.2021.116895 – [**IF: 6.633**]
19. Yang L, Xing F, He Q, **Tahir ul Qamar M**, Chen LL, et al. Conserved Imprinted Genes between Intra-Subspecies and Inter-Subspecies are Involved in Energy Metabolism and Seed Development in Rice, ***International Journal of Molecular Sciences*** 2020; doi: 10.3390/ijms21249618 – [**IF: 6.208**]
20. Song Q, Lv F, **Tahir ul Qamar M**, Xing F, Zhou R, et al. Identification and Analysis of Micro-Exon Genes in the Rice Genome, ***International Journal of Molecular Sciences*** 2019; doi: 10.3390/ijms20112685 – [**IF: 6.208**]
21. Ullah A, **Tahir ul Qamar M**, Nisar M, Hazrat A, Rahim G, et al. Characterization of a novel cotton MYB gene, *GhMYB108-like* responsive to abiotic stresses, ***Molecular Biology Reports*** 2020; doi: 10.1007/s11033-020-05244-6 – [**IF: 2.724**]
22. Chang JW, Ding Y, **Tahir ul Qamar M**, Shen Y, Gao J, et al. A deep learning model based on sparse auto-encoder for prioritizing cancer-related genes and drug target combinations, ***Carcinogenesis*** 2019; 10.1093/carcin/bgz044 – [**IF: 4.944**]
23. Wang L, Guo J, Chang JW, **Tahir ul Qamar M**, Chen LL. Inference of Transcriptional Regulation from Expression Data Using Model Integration, ***Current Bioinformatics*** 2018; doi: 10.2174/1574893612666171006162012 – [**IF: 4.85**]
24. Mumtaz A, Ashfaq UA, **Tahir ul Qamar M***, Anwar F, Gulzar F, et al. MPD3: a useful medicinal plants database for drug designing, ***Natural Product Research*** 2017; doi: 10.1080/14786419.2016.1233409 – [**IF: 2.861**]
25. Chang JW, Zhou YQ, **Tahir ul Qamar M**, Chen LL, Ding Y. Prediction of Protein–Protein Interactions by Evidence Combining Methods, ***International Journal of Molecular Sciences*** 2016; doi: doi.org/10.3390/ijms17111946 – [**IF: 6.208**]

*+co-first author, *co-corresponding author*

PATENT

Tahir ul Qamar M, et al. A pan-genome construction method based on presence/absence variations (一种基于存在/缺失变异的泛基因组构建方法), ***China National Intellectual Property Administration*** 2019. Patent no.: CN109698009A, Application no.: CN201910156551A.

Tahir ul Qamar M, et al. PangenePro: an automated pipeline for rapid identification and classification of gene family members, ***IPO Services Pakistan*** 2025. Patent app. no.: 1547/2025.

BOOK CHAPTERS

1. Fatima K, Sadaqat M, Khalil A, **Tahir ul Qamar M**. Role of Circular RNAs (circRNAs) in Environmental Stress Response: Beyond Linear Understanding, ***ncRNAs: Mediated Regulation*** 2024; doi: 10.1007/978-3-031-69354-0_2
2. Fatima K, Sadaqat M, Azeem F, **Tahir ul Qamar M**. Role of integrative omics and bioinformatics approaches in berries research and genetic improvement, ***Berry Bioactive Compound By-Products (vol. I)*** 2023; doi: 10.1016/B978-0-323-95600-0.00005-5
3. **Tahir ul Qamar M**, et al. Pan-proteomics to analyze the functional complexity of organisms, ***Frontiers in Protein and Peptide Sciences (vol. II)*** 2021; doi: 10.2174/9789815036663121020006
4. **Tahir ul Qamar M**, et al. Effectiveness of conventional crop improvement strategies vs. Omics, ***Climate Change, Vegetation and Environment (vol. I)*** 2020; doi: 10.1007/978-3-030-49732-3_11
5. Chen K, Hao L, **Tahir ul Qamar M**, et al. Advances in designing guide RNAs in genome editing of plants, ***Genome editing for precision crop breeding*** 2021; doi: 10.19103/AS.2020.0082.07

RESEARCH GRANTS

General Research Funding (0.59 Million RMBs), National Natural Science Foundation, China — 2019 – 2022

Postdoctoral Research Grant (0.1 Million RMBs), Guangxi Province, China — 2020 – 2022

TUBITAK Research Grant (0.05 Million TLs), Bahcesehir University, Turkey — 2017

AWARDS AND FELLOWSHIPS

Research Contribution Award, GC University, Faisalabad, Pakistan — 2022-2024

PAG Travel Fellowship, Plant and Animal Genome Conference-XXVIII, USA — Jan 2020

Distinguish International PhD Scholar, CSC-MOE, China — Dec 2019

Research Contribution Award, Huazhong Agricultural University, China — Dec 2019

Best Student Paper Award, Huazhong Agricultural University, China — 2018 & 2019

VIB Travel Fellowship, VIBes in Biosciences Symposium, Belgium — Sep 2017

CSC fully funded PhD Scholarship, Huazhong Agricultural University, China — 2016 – 2019

PROFESSIONAL DEVELOPMENT ACTIVITIES

Editor: BMC Bioinformatics, Frontiers in Plant Sciences

Reviewer: Briefings in Bioinformatics, Genome Biology, Bioinformatics, BMC Bioinformatics, Current Bioinformatics, Frontiers in Plant Sciences, BMC Genomics, Bioinformatics and Biology Insights, Journal of Integrative Agriculture, Scientific Reports, PLOS ONE

Member: International Society for Computational Biology (ISCB) — 2019 – Present

Member: American Society for Plant Biologists (ASPB) — 2019 – Present

PROGRAMMING AND OTHER SKILLS

Languages: Perl, Python, R/Bioconductor, Shell scripting, PHP, C++

Tools/Resources: Bowtie, BWA, BLAT, Tophat, Cufflinks, BEDTools, Samtools, DEGseq, Circos, ppsPCP, OrthoMCL, OrthoFinder, Get_Homologues-EST, Genome Browsers, Adobe Suite, etc.

Databases/Web development: MySQL, HTML, CSS, JAVA scripting, WordPress, R Shiny

Operating systems: Unix/Linux/Ubuntu, Windows

Biotechnology Approaches: Molecular cloning, Gene transfer and expression analyses, Transgenic lines development and testing etc.

SOFTWARE &

ppsPCP: A plant presence/absence variants scanner and pan-genome construction pipeline

RESOURCES DEVELOPED

CPDB: Citrus Pan-Genome to Breeding Database: A comprehensive genome database for citrus breeding
Deep-HPI-pred: Deep Learning based Host-Pathogen Interaction Prediction
PangenePro: an automated pipeline for rapid identification and classification of gene family members
XtractPAV: An Automated Pipeline for Identifying Presence-Absence Variations Across Multiple Genomes
VirtuDockDL: Deep learning pipeline for accelerating virtual screening in drug discovery
MSAEM: A deep learning model based on sparse auto-encoder for prioritizing cancer-related genes and drug target combinations
MPD3: A useful medicinal plants database for drug designing

VOLUNTEER & SOCIAL WORK

Volunteer: International Student's Volunteer Center, Huazhong Agricultural University, Wuhan, China — 2017 – 2019
Volunteer: Cultural and Character-Building Society, Government College University Faisalabad, Pakistan — 2012 – 2014
Volunteer: ICACBAS 2014, Government College University Faisalabad, Pakistan — Feb 2014
Volunteer: Prospects for a Glorious Pakistan: Role of Emerging Technologies, Government College University Faisalabad, Pakistan — Dec 2013

CONFERENCES, TALKS, AND POSTER PRESENTATIONS

1. The International Conference and Exhibition for Science (ICES2023), Riyadh, Saudi Arabia, February 06-08, 2023. – [**Talk**]
2. Plant and Animal Genome Conference (PAG XXVIII), San Diego, USA, Jan 2020. – [**Poster**]
3. 1st International Forum on Crop Science, Wuhan, China, Jun 2019. – [**Talk & Poster**]
4. European Molecular Biology Organization Workshop: Membrane fusion, Cambridge, UK, Jun 2018.
5. VIBes in Biosciences PhD symposium, Ghent, Belgium, Sep 2017.
6. XIX International Botanical Congress (IBC 2017), Shenzhen, China, Jul 2017. – [**Poster**]
7. International Conference on Structural Biology, Biological Macromolecules: Structure, Catalysis and Regulation, Beijing, China, Apr 2017. – [**Poster**]
8. Computational Biology for Big Data: New Opportunities and Challenges, Shanghai, China, Mar 2017.
9. PACBIO SMRT Technical Update, Wuhan, China, Mar 2017.
10. 1st International conference on Advancements of Biotechnology, Faisalabad, Pakistan, Mar 2016. – [**Talk**]
11. 3rd National Computational Science Conference (NCSC), Islamabad, Pakistan, May 2015. – [**Talk**]
12. 1st International Conference on Applied Chemical, Biological and Life Sciences (ICACBAS 2014), Faisalabad, Pakistan, Feb 2014. – [**Talk & Poster**]
13. Workshop on Research Proposal Writing (Quantitative, Qualitative & Mixed Research Design), Lahore, Pakistan, Sep 2013.
14. 1st International Conference on Application of Molecular Biology in Medicine and Agriculture, Islamabad, Pakistan, Aug 2013. – [**Talk & Poster**]
15. 1st National Conference on Emerging Trends in Bioinformatics and Computational Biology, Islamabad, Pakistan, May 2013. – [**Talk & Poster**]

LANGUAGES

English: Fluent (speaking, reading, writing) | Urdu: Native language | Punjabi: Mother tongue | Chinese: Basic | Arabic: Basic

INTERESTS

Volunteering, Jogging, Sports (cricket), Hiking, Photography, Gardening and Cooking

REFERENCES

Available upon request.