

Personal Data Sheet (PDS)

1. **Name** : **Dr. Md. Wali Ullah**
2. **Father's name** : Md. Yasin Ali
3. **Mother's name** : Mrs. Rahima Khatun
4. **Husband's name (if applicable)** : Not Applicable
5. **Gender** : Male
6. **Present Address** : Senior Scientific Officer, Molecular Biology
Department, Genetic Resources and Seed
Division, Bangladesh Jute Research Institute,
Manik Mia Avenue, Dhaka-1207
7. **Permanent Address** : Village- Parulia, Post Office- Parulia,
Upazila- Debhata, District- Satkhira
8. **Date of birth** : 26-10-1979
9. **Age (as on 01-01-2023)** : 43 years 02 months 06 days
10. **Educational Qualification** :

Degree/Diploma/ Certificate	Board/University	Year of Passing	Division/Class/Grade
S.S.C	Jessore	1995	First Division*
H.S.C	Jessore	1997	First Division
B.Sc.Ag/M.Sc./Equiv.	Sher-e-Bangla Agricultural University, Dhaka-1207	2001 (Held 2004)	First Class
M.Sc.Ag/Equiv.	Sher-e-Bangla Agricultural University, Dhaka-1207	2006	Grade A (CGPA-3.65 out of 4.00)
M.Sc.Ag/Equiv.	Kochi University Faculty of Agriculture, Japan	2010	Satisfactory
Ph.D.	Ehime University, Faculty of Agriculture, Japan	2014	Awarded

11. Field of Specialization:

- (a) Knowledge and working experience on host-pathogen interactions at the physiological and molecular level which makes aware about the plant-microbe interactions.
- (b) Experience of work in the microbial pathogenicity mechanisms and virulence diversity whose elucidation will have the most far-reaching effect in explaining and controlling disease development.
- (c) Acquainted and working experience in next generation genome sequencing, DNA fragment sequencing and manually sequenced data analysis.
- (d) Expertise and working experience on different molecular techniques, such as:
 - i. Site-directed/ Knock out/ Transposon mutagenesis, Recombinant expression vector construction, Phylogenetic tree construction, Cloning (eg. TA, Blunt ended, Seamless, Gateway, In-Fusion), Real Time-PCR, Reverse Transcription-PCR, Primer designing, PCR, DNA, RNA isolation.
 - ii. Transformation system in bacteria, fungi and plant (Tissue culture depended and independent).
- (e) Acquainted and working experience with different bioinformatic tools, such as: Augustus, geneid, GeneMark, CAP3, Batch web CD search / Domain search, seqMassager, reverse-complement, Uniprot, InterProScan, SMART, Pfam, Expasy, HMMER, ORF Finder, CodonCode Aligner, MEGA, Clustal W/omega/X, GenScript, Oligos 6.2, Oligo Analyzer Version 3.1 (IDT), Oligonucleotide Properties Calculator, BioEdit, SnapGene, TreeView, BLAST.
- (f) Well versed in bacterial phenotypical characterization (Motility, siderophores production, biofilm formation, pigmentation, multi-drug tolerance, bio-surfactants).
- (g) Expertise in different machine handling, such as:
PacBio Sequel (Third generation genome sequencing machine), PFGE (Pulsed-field gel electrophoresis), BluePippin (DNA size selection for next generation sequencing with Pulsed-Field), Megaruptor (Fragmentation/shearing of genomic DNA for next generation sequencing), and Microscope (Laser Scanning Microscope, compound and simple).

12. Training:

(a) In Country:

Sl. No.	Organization	Year	Duration		Name of Program
			Mos.	Days	
01.	Eppendorf Venue: BARJ, BJRI	2017	-	03	Training on Eppendorf Fermentor Bioflo 415 (SIP)
02.	ESCO Biological Safety Institute Venue: BARJ, BJRI	2017		01	Overview & Safe Use of Laboratory Ventilation Equipment (Laminar Air Flow, Biosafety Cabinets and Fume Hood)

Sl. No.	Organization	Year	Duration		Name of Program
			Mos.	Days	
03.	Pacific Biosciences Venue: Basic and Applied Research on Jute project, Bangladesh Jute Research Institute, Dhaka	2018		05	Pacific Biosciences New SEQUEL Instrument Post Installation Application Training With 30kb SMRTbell Express Libraries Prep.
04.	The Jackson Laboratory (online course)	2020		01	Basics of CRISPR/Cas9
05.	The Jackson Laboratory (online course)	2020		01	CRISPR/Cas9 and Cre-lox Technologies Certificate program
06.	Bangladesh Jute Research Institute, Dhaka	2022		01	Service Commitment (Citizen's Charter)
07.	Bangladesh Jute Research Institute, Dhaka	2022		01	e-Governance and Innovation Action Plan Implementation
08.	Bangladesh Jute Research Institute, Dhaka	2022		01	Office Management and Skill Development
09.	National Agriculture Training Academy, Gazipur	2023		05	Crop improvement through Plant Biotechnology

(b) Abroad:

Sl. No.	Organization	Year	Duration		Name of Program
			Mos.	Days	
01.	Kochi University, Japan	2007-2008	06		Japanese language
02.	Kochi University General Education Center, Japan	2010		05	Basic Course of Teaching Assistant
03.	Kochi University, Japan	2015		05	Laser scanning microscope handling

13. Experience:

Position	Period		
	From	To	Total (Yr./Mo)
Teaching Assistant, Laboratory of Plant Pathology and Biotechnology, Kochi University, Japan	01/04/2008	31/03/2013	Five (05) years
Research Assistant, Laboratory of Plant Pathology and Biotechnology, Kochi University, Japan	01/04/2010	31/03/2013	
Post-doctoral/Rendai Research Fellow, The United Graduate School of Agricultural Sciences, Ehime University, Japan.	01/10/2013	31/03/2016	Two (02) years and Six (06) months

Position	Period		
	From	To	Total (Yr./Mo)
Biotechnologist, Basic and Applied Research on Jute Project, Bangladesh Jute Research Institute,	02/04/2016	30/06/2021	Five (05) years and Three (03) months
Senior Biotechnologist, Basic and Applied Research on Jute Project, Bangladesh Jute Research Institute	01/07/2021	24/01/2022	Seven (07) months
Senior Scientific Officer (SSO) Molecular Biology Department, Genetic Resources and Seed Division, Bangladesh Jute Research Institute (Currently working as a Senior Biotechnologist at BARJ project with office order)	25/01/2022	Till now	

14. Publication:

(a) Full Scientific paper as principal author: 03	
Sl. No.	Published paper
01.	Md. Wali Ullah , Md. Samiul Haque and Md. Shahidul Islam. 2019. First Report of <i>Fusarium oxysporum</i> Causing Fusarium Wilt on Jute (<i>Corchorus olitorius</i>) in Bangladesh. Plant Disease 103 (10):2673-2673. DOI: https://doi.org/10.1094/PDIS-05-19-0945-PDN
02.	Md. Wali Ullah , Yuka Mori, Risa Maenaka, Kenji Kai, Masayuki Tanaka, Kouhei Ohnishi, Akinori Kiba and Yasufumi Hikichi. 2015. The <i>N</i> -acetyltransferase gene-implicated iron acquisition contributes to host specificity of <i>Pseudomonas cichorii</i> strain SPC9018 and its virulence. Physiological and Molecular Plant Pathology 92 :14-21. DOI: https://doi.org/10.1016/j.pmpp.2015.08.008
03.	Md. Wali Ullah , Risa Maenaka, Yuka Mori, Daisei Ueno, Kenji Kai, Kouhei Ohnishi, Akinori Kiba, Hideo Hayashi and Yasufumi Hikichi. 2015. Implication of limited iron acquisition of <i>Pseudomonas cichorii</i> strain SPC9018 in reduction of its virulence on eggplant. Journal of General Plant Pathology 81 (2): 136-141. DOI: https://doi.org/10.1007/s10327-014-0569-4
(b) Full Scientific paper as associate author: 11	
01.	Borhan Ahmed, Mobashwer Alam, Nasima Aktar, Md. Sabbir Hossain, Md. Wali Ullah , Kazi Khayrul Bashar, Shah Md Tamim Kabir, Emdadul Mannan Emdad, Md. Shahidul Islam. 2023. Genome-wide investigation of aquaporin genes in <i>Corchorus</i> spp and their role in organ development and abiotic stress tolerance. Journal of Plant Gene. In press. DOI: https://doi.org/10.1016/j.plgene.2023.100410

02.	Md. Abu Sadat, Md. Wali Ullah , Md Sabbir Hossain, Borhan Ahmed and Kazi Khayrul Bashar. 2022. Genome-wide in silico identification of phospholipase D (PLD) gene family from <i>Corchorus capsularis</i> and <i>Corchorus olitorius</i> : reveals their responses to plant stress. <i>Journal of Genetic Engineering and Biotechnology</i> 20 , 28. DOI: https://doi.org/10.1186/s43141-022-00311-w
03.	Rasel Ahmed, Rajnee Hasan, Md. Wali Ullah and Borhan Ahmed. 2021. Molecular evolution and genetic analysis of Mesta yellow vein mosaic virus and associated betasatellites. Preprint at bioRxiv. DOI: https://doi.org/10.1101/2021.09.05.459025
04.	Md Sabbir Hossain, Borhan Ahmed, Md. Wali Ullah , Md Samiul Haque and Md. Shahidul Islam. 2021. Genome-wide Identification and Characterization of Expansin Genes in Jute. <i>Tropical Plant Biology</i> 15 : 40-54. DOI: https://doi.org/10.1007/s12042-021-09296-1
05.	Md. Abu Sadat, Md. Wali Ullah , Kazi Khayrul Bashar, Quazi Md. Mosaddeque Hossen, Md. Zablul Tareq and Md. Shahidul Islam. 2021. Genome-wide identification of F-box proteins in <i>Macrophomina phaseolina</i> and comparison with other fungus. <i>Journal of Genetic Engineering and Biotechnology</i> 19 (46). DOI: https://doi.org/10.1186/s43141-021-00143-0
06.	Md Sabbir Hossain, Borhan Ahmed, Md Wali Ullah , Nasima Aktar, Md Samiul Haque, Md Shahidul Islam. 2020. Genome-wide identification of fasciclin-like arabinogalactan proteins in jute and their expression pattern during fiber formation. <i>Molecular Biology Reports</i> 47 (10): 7815–7829. DOI: https://doi.org/10.1007/s11033-020-05858-w
07.	Md Sabbir Hossain, Md Rasel Ahmed, Md. Wali Ullah , Ummay Honi, Md Zablul Tareq, Mohammad Saiful Alam Sarker, Borhan Ahmed, Md Shahidul Islam. 2020. Phenylalanine ammonia-lyase gene family (PAL): Genome wide characterization and transcriptional expression in jute (<i>Corchorus olitorius</i>). <i>Journal of Bioscience and Agriculture Research</i> , 26 (02), pp. 2185-2191. DOI: https://doi.org/10.18801/jbar.260220.267
08.	Md. Sabbir Hossain, Rasel Ahmed, Md. Wali Ullah , Shah Md Tamim Kabir, Md. Zablul Tareq and Borhan Ahmed. 2020. GENOME WIDE ANALYSIS AND EXPRESSION PROFILING OF HYDROXYCINNAMOYL COA: SHIKIMATE HYDROXYCINNAMOYL TRANSFERASE (HCT) IN JUTE (<i>Corchorus olitorius</i>). <i>INTERNATIONAL JOURNAL OF BUSINESS, SOCIAL AND SCIENTIFIC RESEARCH</i> 8 (3): 92-97. DOI: http://www.ijbssr.com/currentissueview/14013380
09.	Yasufumi Hikichi, Md. Wali Ullah , Kouhei Ohnishi and Akinori Kiba. 2013. Mechanism of disease development caused by a multihost plant bacterium, <i>Pseudomonas cichorii</i> , and its virulence diversity. <i>Journal of General Plant Pathology</i> 79 (6): 379-389. DOI: https://doi.org/10.1007/s10327-013-0461-7
10.	Masayuki Tanaka, Md. Wali Ullah , Hitoshi Nakayashiki, Tatsuya Fukuda, Hiroyuki Mizumoto, Kouhei Ohnishi, Akinori Kiba, Yasufumi Hikichi. 2012. Implication of an Aldehyde Dehydrogenase Gene and a Phosphinothricin N-Acetyltransferase Gene in the Diversity of <i>Pseudomonas cichorii</i> Virulence. <i>Genes</i> 3 (1):62-80. DOI: https://doi.org/10.3390/genes3010062

11.	Md. Abdul Latif, Md. Wali Ullah , Mohd Yusop Rafii and Md. Tajul Islam. 2011. Management of ufra disease of rice caused by <i>Ditylenchus angustus</i> with nematicides and resistance. African Journal of Microbiology Research 5 (13):1660-1667. DOI: https://doi.org/10.5897/AJMR11.265
(c) Popular Artic/Monograph/Bulletin/Book: 01	
01.	Md. Wali Ullah and Md. Shahidul Islam. 2022. Flowering Pathway of Jute Based on Genomic Data. In: Zhang, L., Khan, H., Kole, C. (eds) The Jute Genome. Compendium of Plant Genomes. Springer, Cham. https://doi.org/10.1007/978-3-030-91163-8_20
(d) List of Seminar papers/Workshop/Symposium Proceedings: 11	
01.	Md. Wali Ullah , Md. Samiul Haque and Md. Shahidul Islam. First Report of <i>Fusarium oxysporum</i> Causing Fusarium Wilt on Jute (<i>Corchorus olitorius</i>) in Bangladesh. 9 th International Plant Tissue Culture & Biotechnology Conference, Dhaka, Bangladesh, February 8-10, 2020.
02.	Md. Wali Ullah , Risa Maenaka, Kenji Kai, Hiroyuki Mizumoto, Kouhei Ohnishi, Akinori Kiba, Hideo Hayashi and Yasufumi Hikichi. Implication of <i>pat</i> Encoding Phosphinothricin N-acetyltransferase in Pyoverdine Secretion of <i>Pseudomonas cichorii</i> . Annual Meeting of the Phytopathological Society of Japan, Gifu, Japan, March 27-29, 2013.
03.	Md. Wali Ullah , Masayuki Tanaka, Hiroyuki Mizumoto, Kouhei Ohnishi, Akinori Kiba and Yasufumi Hikichi. Iron acquisition by phosphinothricin <i>N</i> -acetyltransferase-regulated siderophore may be one of determinants for virulence of <i>Pseudomonas cichorii</i> . XV international congress on molecular Plant-Microbe interaction, Koyoto, Japan, July 29-August 2, 2012.
04.	Md. Wali Ullah , Masayuki Tanaka, Hiroyuki Mizumoto, Kouhei Ohnishi, Akinori Kiba and Yasufumi Hikichi. Phosphinothricin <i>N</i> -acetyltransferase gene of <i>Pseudomonas cichorii</i> strain SPC9018 is implicated in its siderophore productivity, relating to its virulence on eggplant. Annual Meeting of the Phytopathological Society of Japan, Fukuoka, Japan, March 28-30, 2012.
05.	Md. Wali Ullah , Masayuki Tanaka, Hiroyuki Mizumoto, Kouhei Ohnishi, Akinori Kiba and Yasufumi Hikichi. Role of phosphinothricin <i>N</i> -acetyltransferase in virulence of <i>Pseudomonas cichorii</i> strain SPC9018 on eggplant. The 2 nd Korea-Japan Joint Symposium, Fukuoka, Japan, March 27-28, 2012. (<i>Awarded</i>)
06.	Md. Wali Ullah , Masayuki Tanaka, Hiroyuki Mizumoto, Kouhei Ohnishi, Akinori Kiba and Yasufumi Hikichi. Involvement of siderophore productivity of <i>Pseudomonas cichorii</i> in its virulence on eggplant but not lettuce. Annual Meeting of the Phytopathological Society of Japan (Kansai sub-committee), Takamatsu, Japan, October 1-2, 2011.
07.	Md. Wali Ullah , Masayuki Tanaka, Makoto Koyanagi , Shigeru Kajihara , Hiroyuki Mizumoto, Kouhei Ohnishi, Akinori Kiba and Yasufumi Hikichi. Involvement of phosphinothricin <i>N</i> -acetyltransferase gene (<i>pat</i>) in virulence diversification of <i>Pseudomonas cichorii</i> . The 5 th Young Bacteriologist Colosseum, Katsurahama, Kochi, Japan, August 8-10, 2011.

08.	Md. Wali Ullah , Masayuki Tanaka, Kouhei Ohnishi, Hiroyuki Mizumoto, Ayami Kanda, Akinori Kiba and Yasufumi Hikichi. Independent involvement of <i>hrp</i> , Aldehyde Dehydrogenase Gene (<i>aldH</i>) and Phosphinothricin N-acetyltransferase Gene (<i>pat</i>) in Virulence Diversification of <i>Pseudomonas cichorii</i> . Annual Meeting of the Phytopathological Society of Japan, Fuchu, Japan, March 27-29, 2011.
09.	Yasufumi Hikichi, Masayuki Tanaka, Md. Wali Ullah , Hiroyuki Mizumoto, Kouhei Ohnishi and Akinori Kiba. 2011. An aldehyde dehydrogenase gene and a phosphinothricin N-acetyltransferase gene compose of a pathogenicity island with <i>hrp</i> genes of <i>Pseudomonas cichorii</i> . The 4 th ASIAN Conference on Plant Pathology Concurrent with the 18 th Biennial Australasian Plant Pathology Society Conference Darwin, Australia, April 26-29, 2011.
10.	Md. Wali Ullah , Masayuki Tanaka, Kouhei Ohnishi, Akinori Kiba and Yasufumi Hikichi. 2010. Involvement of <i>hrcC</i> and <i>aldH</i> in pathogenicity of <i>Pseudomonas cichorii</i> on <i>Asteraceae</i> plants. Annual Meeting of the Phytopathological Society of Japan, Kyoto, Japan, April 18-20, 2010.

15. Research Achievement

(i) No. of Technology Developed- 08

Sl. No.	Name of Technology Developed	Published	Year
01.	Development of semi-selective media to pure culture of <i>Fusarium oxysporum</i> from infected plant parts by suppression of saprophytic fungi and bacteria.	BARJ Programme	2017
02.	Development of long term (5 to 10 years) preservation method of the fungus using cheap dry filter paper technique for future use at any time.	BARJ Programme	2017
03.	Development of fungal DNA barcoding library with cloning to identify the actual pathogen with more scientific way, and to see any new pathogen or more virulent strain are emerging in future or not.	BARJ Programme	2018-2019
04.	Development of a transformation vector (pH7WG2- <i>CsNDR1</i>) using gateway technology with a reported citrus <i>CsNDR1</i> gene to promote salicylic acid mediated disease resistance in plant.	BARJ Programme	2019
05.	Development of an expression vector (pH7WG2- <i>NtPR5</i>) using gateway technology with a reported tobacco osmotin gene to overproduction of Pathogenesis Related (PR) proteins for disease resistance in plant.	BARJ Programme	2019
06.	Development of a transformation vector (pH7WG2- <i>VvPR2</i>) using gateway technology with a reported grape β -1-3-glucanase gene to increase the expression of PR-proteins for disease resistance in plant.	BARJ Programme	2019

07.	Development of a destination vector (pH7WG2- <i>GhPR5</i>) using gateway technology with a reported cotton TLP (Thaumatococcus-like Protein) gene to overproduction of PR-proteins for disease resistance in plant.	BARJ Programme	2019
08.	Development of a transformation vector (pH7WG2- <i>StPR2</i>) using gateway technology with a reported potato β -1-3-glucanase gene to overproduction of PR-proteins for disease resistance in plant.	BARJ Programme	2020

(ii) No. of Research Programme

(a) Developed – 29

(b) Supervised – 29

Sl No.	Name of Research Programme Developed and Supervised	Published	year
01.	Preparation of semi-selective media to pure culture of <i>Fusarium oxysporum</i> from infected plant parts by suppression of saprophytic fungi and bacteria.	BARJ programme	2016-2017
02.	Development of long term (5 to 10 years) preservation method of the fungus using cheap dry filter paper technique for future use at any time.	BARJ programme	2016-2017
03.	Varietal trial (MLT-Multi-location trial) of BARJ developed advance line (Robi-1) of <i>Corchorus olitorius</i> at different locations in Bangladesh.	BARJ programme	2016-2017
04.	Establishment of fungal DNA barcoding library with cloning to identify the actual pathogen with more scientific way, and to see if any new pathogen or more virulent strain are emerging in future.	BARJ programme	2017-2018
05.	Morphological characterization of <i>Fusarium oxysporum</i> , <i>Fusarium equiseti</i> , <i>Colletotrichum gloeosporioides</i> , <i>Macrophomina phaseolina</i> and <i>Alternaria</i> sp. those are frequently observed in affected jute field.	BARJ programme	2017-2018
06.	First identification of a recently emerging devastating pathogen <i>Fusarium oxysporum</i> causing Fusarium wilt disease on jute.	BARJ programme	2017-2018
07.	Varietal trial (MLT-Multi-location trial) of BARJ developed advance lines (Shoshi-1 and Shoshi-2) of <i>C. capsularis</i> at different locations in Bangladesh.	BARJ programme	2017-2018
08.	To promote Salicylic Acid (SA) associated disease resistance in plant, a transformation vector (pH7WG2- <i>CsNDR1</i>) has been constructed using Gateway technology with a citrus <i>CsNDR1</i> gene.	BARJ programme	2018-2019
09.	Construction of an expression vector (pH7WG2- <i>NtPR5</i>) using gateway technology with a tobacco osmotin gene to overproduction of Pathogenesis Related (PR) proteins for disease resistance in plant.	BARJ programme	2018-2019
10.	Development of a transformation vector (pH7WG2- <i>VvPR2</i>) using gateway technology with a reported grape β -1-3-glucanase gene to increase the expression of PR-proteins for disease resistance in plant.	BARJ programme	2018-2019

Sl No.	Name of Research Programme Developed and Supervised	Published	year
11.	Construction of a destination vector (pH7WG2- <i>GhPR5</i>) using gateway technology with a reported cotton TLP (Thaumatococcus-like Protein) gene to overproduction of PR-proteins for disease resistance in plant.	BARJ programme	2018-2019
12.	Development of a transformation vector (pH7WG2- <i>StPR2</i>) using gateway technology with a potato β -1,3-glucanase gene to overproduction of PR-proteins for disease resistance in plant.	BARJ programme	2018-2019
13.	Genome-wide identification and characterization of the antifungal <u>Pathogenesis-Related-1</u> (PR-1) genes in both <i>Corchorus olitorius</i> and <i>C. capsularis</i> .	BARJ programme	2018-2019
14.	Genome-wide identification and characterization of the β -1,3-glucanases genes in both <i>Corchorus olitorius</i> and <i>C. capsularis</i> .	BARJ programme	2018-2019
15.	Genome-wide identification and characterization of the Thaumatococcus-like proteins (TLP) in both <i>Corchorus olitorius</i> and <i>C. capsularis</i> .	BARJ programme	2018-2019
16.	Genome-wide identification and characterization of the Class III Chitinase genes in both <i>Corchorus olitorius</i> and <i>C. capsularis</i> .	BARJ programme	2018-2019
17.	Germplasm seed multiplication using 101 accessions from 10 wild <i>Corchorus</i> spp. in Manikgonj and BARJ field.	BARJ programme	2018-2019
18.	Morphological characterization of 101 accessions from 10 wild <i>Corchorus</i> spp.	BARJ programme	2018-2019
19.	Genome-wide identification of fasciclin-like arabinogalactan proteins in jute and their expression pattern during fiber formation.	BARJ programme	2018-2019
20.	Genome-wide identification of expansin genes in jute and their expression patterns in fiber development.	BARJ programme	2018-2019
21.	Development of transgenic jute plants using constructed transformation vector, pH7WG2- <i>CsNDR1</i> using tip infiltration method.	BARJ programme	2019-2020
22.	Screening of disease resistant jute from developed citrus <i>CsNDR1</i> gene inserted transgenic plants.	BARJ programme	2019-2020
23.	Genome wide identification and domain organization of lectin genes in Dhaincha (<i>Sesbania bispinosa</i>).	BARJ programme	2019-2020
24.	Phenylalanine ammonia-lyase gene family (PAL): Genome wide characterization and transcriptional expression in jute (<i>Corchorus olitorius</i>).	BARJ programme	2019-2020
25.	Genome wide analysis and expression profiling of hydroxycinnamoyl CoA: shikimate hydroxycinnamoyl transferase (HCT) in jute (<i>Corchorus olitorius</i>).	BARJ programme	2019-2020
26.	Genome-wide identification of F-box proteins in <i>Macrophomina phaseolina</i> and comparison with other fungus.	BARJ programme	2019-2020
27.	Development of an inexpensive and timesaving efficient DNA isolation protocol from high mucilaginous jute plant without phenol/chloroform extraction, ethanol, or isopropanol precipitation steps.	BARJ programme	2020-2021

Sl No.	Name of Research Programme Developed and Supervised	Published	year
28.	Collection of leaf samples and stored (-80°C) as powder formed using liquid nitrogen for DNA isolation from 93 germplasm accessions of 10 wild jute species.	BARJ programme	2020-2021
29.	Study about evolutionary history of Dhaincha (<i>Sesbania</i>) genome.	BARJ programme	2020-2021

(ii) No. of Research Programme

(c) Executed – 24

Sl. No.	Name of Research Programme Executed	Published	year
01.	Preparation of semi-selective media to pure culture of <i>Fusarium oxysporum</i> from infected plant parts by suppression of saprophytic fungi and bacteria.	BARJ programme	2017-2018
02.	Development of long term (5 to 10 years) preservation method of the fungus using cheap dry filter paper technique for future use at any time.	BARJ programme	2017-2018
03.	Varietal trial (MLT-Multi-location trial) of BARJ developed advance line (Robi-1) of <i>Corchorus olitorius</i> at different locations in Bangladesh.	BARJ programme	2017-2018
04.	Establishment of fungal DNA barcoding library with cloning to identify the actual pathogen with more scientific way, and to see if any new pathogen or more virulent strain are emerging in future.	BARJ programme	2018-2019
05.	Morphological characterization of <i>Fusarium oxysporum</i> , <i>Fusarium equiseti</i> , <i>Colletotrichum gloeosporioides</i> , <i>Macrophomina phaseolina</i> and <i>Alternaria</i> sp. those are frequently observed in affected jute field.	BARJ programme	2018-2019
06.	First identification of a recently emerging devastating pathogen <i>Fusarium oxysporum</i> causing Fusarium wilt disease on jute.	BARJ programme	2018-2019
07.	Varietal trial (MLT-Multi-location trial) of BARJ developed advance lines (Shoshi-1 and Shoshi-2) of <i>C. capsularis</i> at different locations in Bangladesh.	BARJ programme	2018-2019
08.	To promote Salicylic Acid (SA) associated disease resistance in plant, a transformation vector (pH7WG2- <i>CsNDR1</i>) has been constructed using Gateway technology with a citrus <i>CsNDR1</i> gene.	BARJ programme	2019-2020
09.	Construction of an expression vector (pH7WG2- <i>NtPR5</i>) using gateway technology with a tobacco osmotin gene to overproduction of Pathogenesis Related (PR) proteins for disease resistance in plant.	BARJ programme	2019-2020
10.	Development of a transformation vector (pH7WG2- <i>VvPR2</i>) using gateway technology with a grape β -1-3-glucanase gene to increase the expression of PR-proteins for disease resistance in plant.	BARJ programme	2019-2020
11.	Construction of a transformation vector (pH7WG2- <i>GhPR5</i>) using gateway technology with a cotton TLP (Thaumatin-like proteins)	BARJ programme	2019-2020

Sl. No.	Name of Research Programme Executed	Published	year
	gene to overproduction of PR-proteins for disease resistance in plant.		
12.	Development of a transformation vector (pH7WG2- <i>StPR2</i>) using gateway technology with a potato β -1-3-glucanase gene to overproduction of PR-proteins for disease resistance in plant.	BARJ programme	2019-2020
13.	Genome-wide identification and characterization of the β -1,3-glucanases genes in both <i>Corchorus olitorius</i> and <i>C. capsularis</i> .	BARJ programme	2019-2020
14.	Genome-wide identification and characterization of the Thaumatin-like proteins (TLP) in both <i>Corchorus olitorius</i> and <i>C. capsularis</i> .	BARJ programme	2019-2020
15.	Genome-wide identification and characterization of the Class III Chitinase genes in both <i>Corchorus olitorius</i> and <i>C. capsularis</i> .	BARJ programme	2019-2020
16.	Germplasm seed multiplication using 101 accessions from 10 wild <i>Corchorus</i> spp. in Manikgonj and BARJ field.	BARJ programme	2019-2020
17.	Morphological characterization of 101 accessions from 10 wild <i>Corchorus</i> spp.	BARJ programme	2019-2020
18.	Genome-wide identification of fasciclin-like arabinogalactan proteins in jute and their expression pattern during fiber formation.	BARJ programme	2019-2020
19.	Genome-wide identification of expansin genes in jute and their expression patterns in fiber development.	BARJ programme	2019-2020
20.	Development of transgenic plants using constructed transformation vector, pH7WG2- <i>CsNDR1</i> using tip infiltration method.	BARJ programme	2019-2020
21.	Phenylalanine ammonia-lyase gene family (PAL): Genome wide characterization and transcriptional expression in jute (<i>Corchorus olitorius</i>).	BARJ programme	2019-2020
22.	Genome wide analysis and expression profiling of hydroxycinnamoyl CoA: shikimate hydroxycinnamoyl transferase (HCT) in jute (<i>Corchorus olitorius</i>).	BARJ programme	2019-2020
23.	Genome-wide identification of F-box proteins in <i>Macrophomina phaseolina</i> and comparison with other fungus.	BARJ programme	2020-2021
24.	Collection of leaf samples and stored (-80°C) as powder formed using liquid nitrogen for DNA isolation from 93 germplasm accessions of 10 wild jute species.	BARJ programme	2020-2021

16. Outstanding Achievement

- (i) **Variety development (Group work):** New jute variety development (BJRI Tossa pat 8)
- (ii) **Genome Sequencing (Group work):** Genome sequence of Dhaincha (*Sesbania bispinosa*).
- (iii) **Award received:** Excellent Poster Presentation Award in the 2nd Korea-Japan Joint Symposium held at Fukuoka International Congress Center, Fukuoka, Japan on March 27-28, 2012.
- (iv) **Scholarship received:**
 - a) Japanese Government (Monbukagakusho, MEXT) Scholarship (ID No.- 114187) in PhD. (April, 2011-March, 2013).
 - b) Rotary Yoneyama Memorial Foundation (Japan) Scholarship (ID No.-15055) during MS (April, 2009-March, 2010).
 - c) Nankoku City Foundation Scholarship (Japan) during Ph. D. (April, 2010- March, 2011).
 - d) Japan Student Service Organization (JASSO) Scholarship (Japan) during MS (April, 2008- March, 2009).
 - e) Academic Merit Scholarship from Satkhira District Commission during HSC (1996).



Signature of Applicant:08/02/2023.....

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