

Closure Report

File Number : SRG/2019/001924

Project Title : Big data and Machine learning based approach to understand combined stress response signatures in multiple cultivating crop plants

Principal Investigator : [Dr. Pankaj Barah](#)
Tezpur University
Distt. sonitpur p.b.no.72 napaam, tezpur, Tezpur, Assam-784011

Total Sanctioned Amount : 23,24,102 (INR)

Total Released Amount : 18,63,000 (INR)

Start Date of the Project: 19 Nov, 2019

Date of completion: 18 Feb, 2022 (26 months & 31 days)

Approved Objectives :

- What are the available genomic, transcriptomic, epigenomic, metabolomic and phenomic dataset generated in diverse crop plants during combined biotic and abiotic stresses?
- Is the combined stress response signature is unique and independent of the single stress conditions, or additive of both individual stresses?
- What are the common and unique pathways and processes differentially regulated during single and double stresses?
- Is there any novel signal cross talk mechanism in crop plants during the combined exposure the biotic and abiotic stress signals?
- How the single and concurrent stresses affect the phenotype?
- How does the topological connectivity of the gene co-expression network changes between single and combined stresses?
- Can we predict the molecular and phenotypic response behavior of the crop plants during combine stress using machine-learning algorithms?
- What is the role of non-coding RNAs in single and combined plant stress responses?

Deviation made from original objectives (If Any) :

The effect of single and concurrent stresses on the phenotype of a plant couldn't be completed on time due to the lockdown for the COVID-19 outbreak and non availability of relevant data.

Ph.D. Produced/ Likely to be : 1

Technical Personnel Trained : 2

Total Expenditure : 16,85,016 (INR)

Concise Research Accomplishment :

1.CroPCS: We have developed Combined Stress Knowledgebase in Crop Plants (CroPCS) The first of its kind knowledgebase on combined stress in crop plants. CroPCS was developed by collecting, correlating, and organizing all available OMICS (Genomic, Transcriptomic, Proteomic, Metabolomic, and Phenomic) scale data generated on important crop plants under various combined biotic and/or abiotic stress conditions. CroPCS contains data from 13 different combined stress conditions in 13 crop plant species. Manuscript under preparation. YRL: <http://www.tezu.ernet.in/cropcs>

2.RNA-Seq data analysis pipeline: Using open-source software, we have developed our in-house modular and scalable RNA-Seq data analysis pipeline. [Roy et al., 2020 (<https://doi.org/10.1007/s12031-020-01738-x>), Sahu et al., 2020 (<https://doi.org/10.1016/j.ygeno.2020.08.028>)].

3. Lnc-RNA identification pipeline: Using publicly available software, tools, and databases, we have developed an end-to-end computational pipeline that takes raw transcriptomic data as input and identifies and quantifies all known as well as novel lncRNAs. LINK: <https://github.com/PranganNath/LncRNA-identification-pipeline>.

4.Rice plants respond to low and high temperatures during Xoo infection: We performed RNA-Seq data analysis on rice plants using public datasets generated under high heat, low heat, and Xoo (*Xanthomonas oryzae* pv. *oryzae*) infection, and found that rice plants initiate conventional transcriptome expression under low temperature and while focusing on growth and development under high heat and Xoo through crucial signal crosstalk events. Published manuscript (<https://doi.org/10.1016/j.ygeno.2020.08.028>).

5.Transcriptome analysis reveals signal crosstalk mechanism in Maize plants under combined salinity and boron stress: Integrative systems-level analysis of transcriptome data I maize under combined salinity and boron stress identified important hub proteins like GOLS2, ALDH, pmpm4, mlg3 and COR410 transcription factors like HSFs, NAC, ATAF 1-2, CUC2, play a crucial role in combined stress tolerance. Manuscript published (<https://doi.org/10.1155/2022/1027288>).

6.Transcriptome response of Barley to combined biotic and abiotic stress: Transcriptomic data analysis on barley under combined drought and spidermite stress was conducted and it was found that under combined stress and single spidermite stress barley synthesizes defense-related compounds while under drought stress focuses more on nucleotide and fatty acid synthesis. Manuscript under preparation.

Closure Details

Experimental/ Theoretical Investigation carried out

1. Mining Publicly Available Datasets for OMICS experiments and creation of CroPCS knowledgebase: All publicly available OMICS scale datasets and literature related to crop plants under various combined stress were mined in different repositories like Google scholar, PubMed, Scopus, NCBI, GEO, ENA, DDBJ etc. OMICS studies related to combined stress in various crop plants were listed and considered for further analysis. Collected literature was carefully examined and supporting data like differentially expressed genes (DEGs), differentially expressed proteins (DEPs), differentially expressed metabolites (DEMs), lncRNA, and miRNA were downloaded, analyzed, and organized in a systematic manner. Additional information like nucleotide FASTA, protein FASTA, nucleotide accession number, protein accession number, description, Uniprot ID, and PubChem ID were collected from databases like NCBI, ENA, UniprotKB, STRING, PubChem, Phytozome. Using HTTP, SQL servers, PHP, JavaScripts, HTML markup language, and integrating all the collected data, first of its kind knowledgebase on combined stress in crop plants called CroPCS (Combined Stress Knowledgebase in Plants) has been developed. 2. Transcriptomic data analysis on rice plants exposed to low and high temperatures under bacterial blight pathogen infection: A RNA-Seq dataset on an IR24 rice variety, under combined low temperature 29/21 °C (day/night), high temperature 35/31 °C (day/night), and bacterial blight pathogen *Xanthomonas oryzae* pv. *oryzae* at 3 time points i.e. 3 hpi, 72 hpi and 120 hpi was considered for the study. Raw transcriptomic data was downloaded from the NCBI SRA database (PRJNA314700) and analyzed using our in-house data analysis pipeline. After differential expression (DE) analysis, obtained DEGs (with p-adjusted value 0.05) were processed for downstream analysis like Gene Set Enrichment Analysis (GSEA) using AgriGO, Transcriptional Regulatory Network (TRN) analysis using MEME suite of FIMO tools with PWMs (position weight matrix) and upstream sequence datasets from CIS-BP and RSAT Plants respectively. Networks were created using Cytoscape v3.8.2. 3. Transcriptomic data analysis on Maize plants under combined salinity and boron stress: Raw transcriptomic data on combined salinity (150mM NaCl) and boron stress on Maize plants were retrieved from the NCBI-SRA database (PRJNA327501) and analyzed using our in-house data analysis pipeline. The plants were first grown under normal conditions for two weeks and then subjected to combined salinity (150mM NaCl) and boron stress for 3 and 96 hours. Similarly, After differential expression (DE) analysis, obtained DEGs (with p-adjusted value 0.05) were used for Gene Set Enrichment Analysis (GSEA) using AgriGO, Transcriptional Regulatory Network (TRN) analysis using MEME suite of FIMO tools with PWMs and upstream sequence datasets from CIS-BP and RSAT Plants respectively. Networks were created using Cytoscape v3.8.2. 4. Transcriptomic data analysis on Barley plants under combined abiotic (drought) and biotic (spider mite) stress: For this study we have used a publicly available transcriptomic dataset generated on barley plants under drought (initiated by water deprivation) and spidermite infestation. The RNA-Seq data were first retrieved from the ENA database (PRJEB25386) and analyzed using our in-house RNA-Seq data analysis pipeline. Differential expression analysis resulted with the DEGs (with p-value 0.05). Gene Ontology analysis for the biological processes was performed using g:Profiller, pathway enrichment analysis performed using Phytozome v13 and transcriptional regulatory network analysis using MEME suite of FIMO tools with PWMs and upstream sequence datasets from CIS-BP and RSAT Plants respectively. Networks were created using Cytoscape v3.8.2. 5. Transcriptomic data analysis on Soybean plants under combined heat and drought stress: To investigate time specific response of plants to combined stress, we used a publicly available transcriptomic dataset generated on drought-resistant soybean cultivar 'Heinong44' which was first grown at optimal conditions till V3 stage and then exposed to heat (40 °C) and drought (PEG-6000) stress. Tri-foliolate leaves were collected at 8 h and 24 h and sequenced, The RNA-Seq data were retrieved from the NCBI SRA database (SRP115717) and analyzed using our in-house RNA-Seq data analysis pipeline. Obtained DEGs were then further analyzed with gene ontology analysis using g:Profiller, pathway enrichment analysis was performed using KEGG database and transcriptional regulatory network analysis with PWMs and upstream sequence datasets from CIS-BP and RSAT Plants respectively using MEME suite of FIMO tools. Networks were created using Cytoscape v3.8.2. ** All experimental procedures are explained in Figure 1.

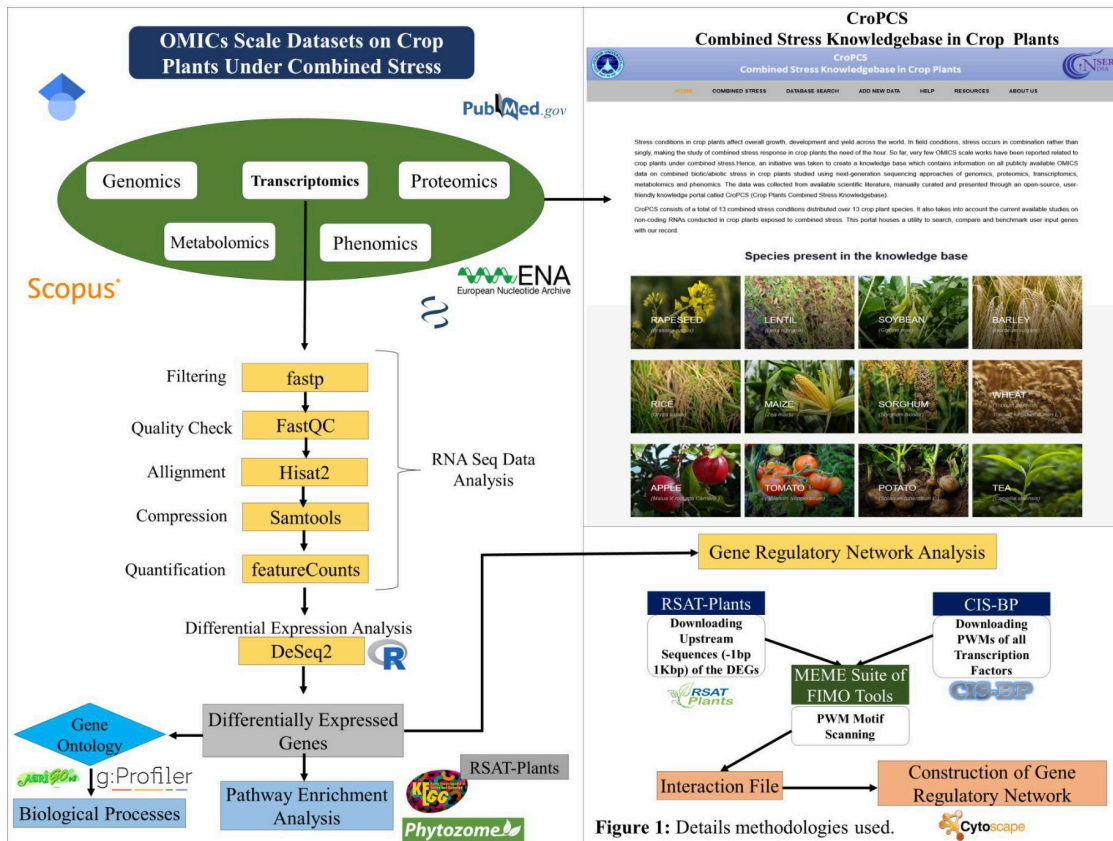


Figure 1: Details methodologies used.

Detailed Analysis of result

1. Development of knowledgebase (Figure 2) Databases/knowledgebase related to the stress response of plants are rare. To the best of our knowledge, CroPCS is the first-of-its-kind knowledgebase on combined stress in crop plants. CroPCS houses all OMICS scale (transcriptomics, genomics, proteomics, metabolomics, and phenomics) datasets across 13 different crop species under 13 combined stress conditions. Backend data contains a total of 1,41,415 DEGs, 47 DEPs, 71 metabolites and 19 miRNAs and can be searched using respective gene ID, Uniprot ID, metabolite name, and miRNA ID. Using the search option, users can query their input genes, proteins, metabolites, and miRNA and find out their expression under combined stress conditions. A resource tab is also made available which contains information related to recent databases and literature on combined stress in crop plants.

2. Transcriptomic data analysis on rice plants exposed to low and high temperatures under bacterial blight pathogen infection (Figure 3): Results showed that the highest number of DEGs at 3 hpi in both high-temperature, as well as low-temperature samples and the number of DEGs, were found to be reduced with an increase in time of infection. We also observed that the number of down-regulated DEGs was more as compared to the up-regulated DEGs. Gene Ontology (GO) analysis suggested that the transcriptomic response of rice is more directed toward defense processes during low temperatures rather than growth and development. TFs like ERF3, ERF68, PLT9, and ONAC6 were identified as hub TFs under low temperature at 3 hpi (hour post-infection) under high temperature at 3hpi TFs like ERF19, DREB2A, ERF118, and DUF260 were identified as hub transcription factors. At 72 hpi, under low temperature, unique hub TFs were ERF91, ERF118, bZIP46, R2R3-MYB, and ERF104. No unique hub TFs were found under high temperatures at the same time point. A total of five unique hub TFs viz. SUB1B, WRKY28, WRKY14, WRKY24, and WRKY 62 were found Under low temperatures at 120 hpi. Similarly, a total of unique hub TFs viz. ERF104, ERF83, ERF91, ERF118, and ERF47 have detected at high temperatures Rice plants respond to a combination of high temperature + Xoo pathogen and low temperature + Xoo pathogen differently. It was observed that on combined stress of high temperature + Xoo, rice plants reduced the expression of pathogen-specific genes and pathways and concentrated more on growth and development.

3. Transcriptomic data analysis on Maize plants under combined salinity and boron stress (Figure 4): The transcriptome data analysis on maize under combined salinity and boron stress found a total of 615 and 171 DEGs in leaf and root tissues respectively. Among these, 561 DEGs were found to be up-regulated in the leaf and all 171 DEGs in the root. Out of these, 94 DEGs were found to be

commonly expressed in leaf and root, with varying levels of expression. The processes like 'oxidation-reduction process', 'inorganic substance', 'abscisic acid', 'abiotic stimulus', and 'temperature stimulus' were among the top 5 biological processes in the leaf whereas 'response to chemical', 'organic substance', 'oxygen-containing compound', 'lipid' and 'hormone' were found to be the top 5 biological processes in the root. Proteins in the leaf were found to be LTI65, Pro1, P5CS, ALDH, Glo1, and GOLS2 were found to be hub proteins in the leaf whereas proteins like pmpm4, NAC44, HSP101, BMY1, GOLS2, HSP70, COR410, MLG3, LTI65 were found to be hub proteins in root tissue. Top hub TFs in the leaf was found to be hb41, NAC44, HSF18, HSF1, HSF28, HSF8, MYBR24, and dbf1 while in the case of roots hb41, NAC44 and HSF17 were the hub TFs. Transcription factors contribute to internode development, hypocotyl cell elongation, root elongation, late stamen development, and activation of defense-related genes through a systemic signal crosstalk mechanism, thus helping the plant to cope with the individual as well as combined stresses.

4. Transcriptomic data analysis on Barley plants under combined abiotic (drought) and biotic (spider mite) stress (Figure 5): A total of 603 up-regulated and 255 down-regulated genes were found to be differentially expressed in the combined drought and spider mite stress. Further, 129 and 340 DEGs were found to be up-regulated in single drought and single spider mite stress, respectively. The number of down-regulated DEGs was 63 and 47 for the same. GO analysis suggested that plants coordinatively regulated important biological and metabolic processes like 'organonitrogen compound metabolic process', 'cellular metabolic process', 'organic substance metabolic process' under combined drought and spidermite stress. Under single spider mite stress, biological processes like 'response to stimulus', 'response to stress and similar to single drought stress', 'metabolic process' were found to be highly regulated. Pathway Enrichment Analysis concluded that barley plant advanced with pathway-centric responses like 'jasmonic acid (JA) biosynthesis', 'phospholipases', 'phenylpropanoid biosynthesis', 'triacylglycerol degradation' and 'phosphatidylcholine acyl editing' under combined drought and spider mite stress and almost similar kind of response were observed under single spider mite stress. Whereas during single drought stress conditions a reverse situation was observed. Here the plants focused on synthesizing important molecules like triacylglycerol, sesamin, pyrimidine, cutin, etc by activating pathways such as 'triacylglycerol biosynthesis', 'sesamin biosynthesis', 'pyrimidine deoxyribonucleotide biosynthesis from CTP', 'pyrimidine deoxyribonucleotides de novo biosynthesis I', and 'cutin biosynthesis. A total of 6 hub TFs viz. HAT2, GATA16, SGR5, LBD6, AHL13, and Dof 5.1 are found across all experimental groups (combined drought and spidermite stress, single drought, and single spidermite stress). LEP was present across all down-regulated groups. ERF021 was found as hub TF during single stress conditions whereas not expressed during combined stress conditions while RAX3 was acting as a hub in combined and single drought stress conditions. During single spider mite stress, MYC2 was found to be down-regulated and TCP21 and AGL6 were found to be up-regulated. Barley plants activated more genes during combined stress as compared to single stresses and focused on synthesizing defense-related molecules like jasmonic acid and phospholipases. Similar kinds of responses were observed during single mite stresses. However, during drought stress, triglyceride and nucleotide synthesis was primarily upregulated. Barley plants also focused on ROS (reactive oxygen species) scavenging, floral development, circadian rhythm, etc during single as well as combined stress conditions.

5. Transcriptomic data analysis on Soybean plants under combined heat and drought stress: A total of 4867 DEGs were found to be up-regulated and 4292 DEGs were found to be down-regulated at 8 h time points. Similarly, 4604 DEGs were found to be up-regulated and 3780 DEGs were found to be down-regulated at 24 h time points. Interestingly, 1897 DEGs were found to be commonly upregulated while 1917 DEGs were commonly down-regulated. Pathways like 'protein processing in endoplasmic reticulum', 'ribosome biogenesis in eukaryotes, and 'circadian rhythm - plant' were found to be upregulated at 8h time points. Similarly, at 24 h time point, pathways like 'metabolic pathways', 'biosynthesis of secondary metabolites, and 'carbon metabolism' were found to be up-regulated. Also, pathways like 'metabolic pathways', 'biosynthesis of secondary metabolites', and 'plant-pathogen interaction' were found to be the down-regulated pathways at the 8 h time point and pathways like 'metabolic pathways, 'plant-pathogen interaction' and 'photosynthesis' were down-regulated at 24 h time point. A TF Dof5.8 was found to be both up-regulated as well as down-regulated at all time points. SHN3 was specifically up-regulated at 8h. REM19 was uniquely down-regulated at all time points but also found to be up-regulated at 24 h. Dof1.7 was found to be up-regulated at 8h but was down-regulated at 24 h. At the time of early perception of the stress signal, soybean plants focus more on protein synthesis by activating protein processing and ribosome biogenesis pathways. Additionally, plants also activate genes related to the circadian clock in order to control the expression of genes during morning and evening. After 24 hrs or stress perception, the plant activates pathways related to metabolism and also synthesizes secondary metabolites, and reduces the photosynthesis process.



Figure 2: Features of CroPCS (Combined Stress Knowledgebase in Crop Plants)

1. **Home:** Contains direct links to omics scale datasets (species wise and stress wise)
 - **1.1. Plant Page:** Contains brief crop description, link to datasets and list of highly expressed genes, proteins, metabolites under combined stress.
 - **1.2. Browse Stress Wise:** Datasets are clustered based on the stress conditions
2. **Combined Stress Tab:** Contains general information about combined stress, its importance and the need of CroPCS.
3. **Database Search:** Enables users to search with their input gene, protein, metabolites and miRNA and find out their expression under combined stress.
4. **Add New Data:** Allows users to contribute with new types of OMICS scale data.
5. **Help:** Contains detail explanation about using CroPCS.
6. **Resources:** Contains important databases and articles related to combined stress in plants.
7. **About Us:** Contains contact information about our research group.

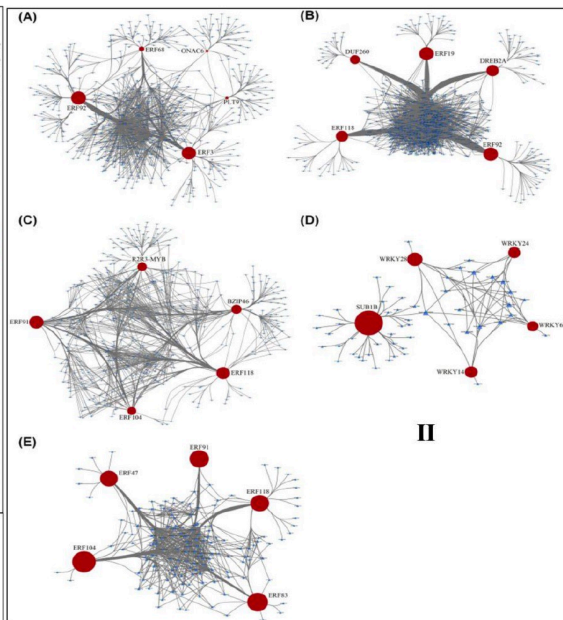
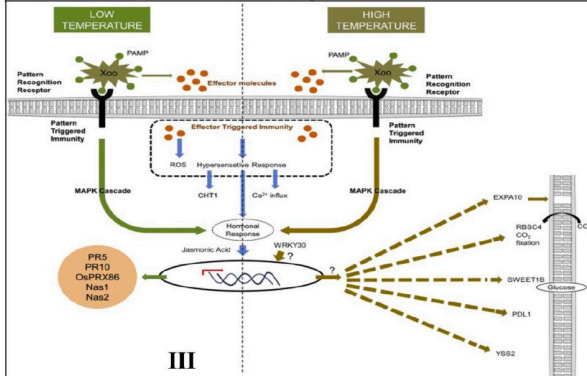
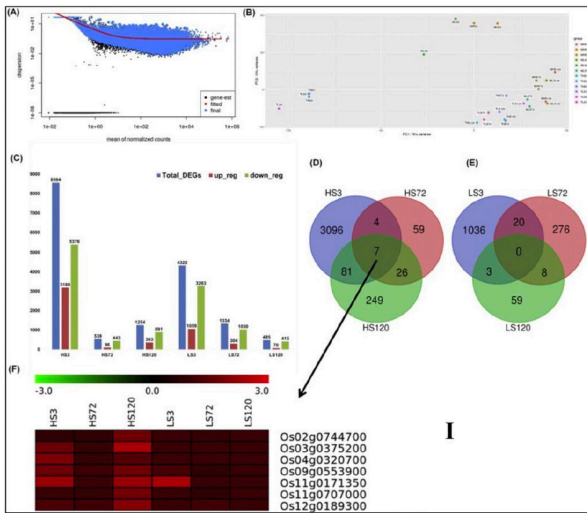
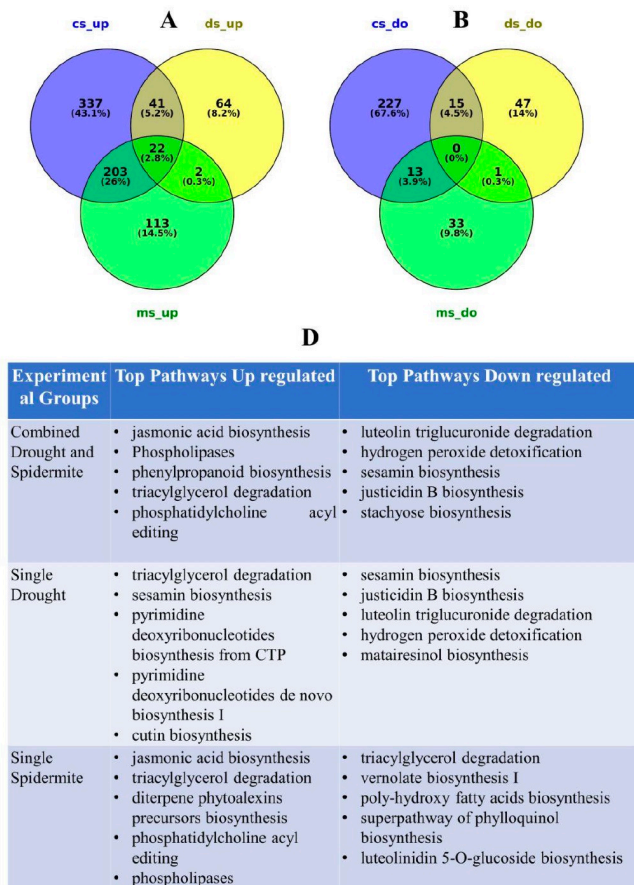


Figure 3: Results from rice transcriptomic data analysis under combined high heat and low heat under bacterial blight pathogen (BB) infection.

- I. Representation of expressed DEGs of rice plant upon exposure to high heat and low heat under BB infection.
- II. Regulatory network of uniquely identified top hub genes
- III. Summary of the crosstalk events among the various responsive genes of low and high temperature condition



Hub Transcription Factors	Present In
HMGGA	cs_do, cs_up, ds_do, ds_up, ms_up
RAX3	cs_do, cs_up, ds_do, ds_up
LEP	cs_do, cs_up, ds_do, ms_do
TCX5	cs_do, cs_up, ds_do
NLP4	ds_up, ms_do, ms_up
ERF021	ds_up, ms_up
MYC2	ms_up
TCP21, AGL6	ms_do
HAT22, GATA16, SGR5 LBD6, AHL13, Dof 5.1	All

Figure 5. Results from Barley transcriptomic data analysis under single and combined drought and spidermite stress

- Venn diagram showing relation between up regulated DEGs of single and combined drought and spidermite stress in barley.
- Venn diagram showing relation between down regulated DEGs of single and combined drought and spidermite stress in barley.
- Table showing hub transcription factors present in different experimental groups
- Table showing up and down regulated pathways under single and combined drought and spidermite stresses.

cs: Combined drought and spidermite stress
 ds: Single drought stress
 ms: Single spidermite stress
 up: Up regulated
 do: Down regulated

Conclusions

Combined stress has been recognized as a real threat to plants. Plants face not single but multiple stress simultaneously in the field condition. Studies have so far focused on studying single stresses on plants. Studies on crop plant response to combined stress are rare. Here, we conducted a transcriptomic analysis of available datasets to understand how crop plants respond to various combinations of stresses. We have built CroPCS which is a first-of-its-kind user-friendly knowledgebase. This knowledgebase houses various multi-OMICS datasets generated on 13 crop plant species under 13 different combined stress conditions. We found that rice plants perceived high-temperature and low-temperature stress differently under bacterial blight pathogen infection. rice plants initiate conventional transcriptome expression under low temperatures while focusing on growth and development under high heat and Xoo through crucial signal crosstalk events. A possible signal crosstalk mechanism between the leaf and root of maize under salinity and boron stress was also proposed. The developed computational tools, methods, and resources will be of benefit for studying and carrying out integrative analysis of plant combined stress OMICs dataset. To study how plants perceive and act on single and combined biotic and abiotic stresses, we have analyzed a transcriptome dataset generated on barley. A conventional transcriptome response was observed under combined stress for example defense and signaling-related genes were activated in this condition. Interestingly, it was found that during single drought stress plants focused on energy storage. Further, the time-specific transcriptome response of soybean under heat and drought stress revealed some important molecular signatures that play a key role during combined stress conditions at different times. Responding to early stress signals, plants elevates protein synthesis by activating protein processing and ribosome biogenesis pathways while responding to late stress signals plants activate metabolism and also synthesize secondary metabolites, and reduce the photosynthesis process. In summary, we have created a first-of-its-kind knowledgebase including omics scale datasets under combined stress. Our study has identified some key molecular signatures, and mechanisms that are involved in the perception and processing of combined stress signals and finally help the plant cope with the stressful environment. We believe that our findings will help the researchers in developing multi-stress resilient crop plants.

Scope of future work

The collected uniform datasets will be analyzed to identify the lncRNAs which may be playing important roles in crop plants under combined stress conditions. Data in the field of crop plant research are expanding. The CropCS knowledge base will be updated from time to time with the new type of data generated on crop plants under combined stress. The newly collected datasets will be analyzed and correlated to identify some more important molecular signatures which will be helpful in developing multi-stress-resistant crops. In context with the severe climate change, we will conduct field-level experiments to see the effect of combined biotic and abiotic stress on plant phenotype. Also, we will validate some of the molecular signatures identified using different laboratory methods. The developed computational tools, benchmarked methods, and resources will be of benefit for studying and carrying out integrative analysis of plant combined stress OMICs dataset.

List of Publications (only from SCI indexed journals) :

Title of the Paper	List of Authors	Journal Details	Month & Year	Volume	Status	DOI No	Impact Factor
Identifying Signal-Crosstalk Mechanism in Maize Plants during Combined Salinity and Boron Stress Using Integrative Systems Biology Approaches	Drishtee Barua , Asutosh Mishra , P. B. Kirti and Pankaj Barah	Biomed Research International (International)	Apr-2022	2022 (1-17)	Published	https://doi.org/10.1155/2022/1027288	3.411
Temperature differentially modulates the transcriptome response in <i>Oryza sativa</i> to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> infection,	Ankur Sahu, AkashDas, Katherine Saikia and PankajBarah	GENOMICS (International)	Oct-2022	112 (4842-4852)	Published	https://doi.org/10.1016/j.ygeno.2020.08.028	5.736

List of Papers Published in Conference Proceedings, Popular Journals :

Title of the Paper	List of Authors	Journal Details	Month & Year	Volume	Status	DOI No	Impact Factor
Not Available							

List of Patents filed/ to be filed :

Patent Title	Authors	Patent Type	Country/Agency Name	Patent Status	Application/Grant No.
Not Available					

Equipment Details :

Equipment Name	Cost (INR)	Procured	Make & Model	Utilization %	Amount Spent (INR)	Date of Procurement
Two socket computing server node with 28 Cores and above	4,99,800	Yes	HPE Proliant XL 170r Gen10	100	5,13,030	30 Nov, 2020
Storage Hard disk 8 TB each	1,99,500	Yes	HPE StoreEasy 1660 4LFF, Midplane drive cage	100	1,85,850	30 Nov, 2020

Plans for utilizing the equipment facilities in future:

We have installed the procured hardware as the scaled-out architecture of a High-Performance Computing Facility for Big data analysis developed by the PI. The server and hard drive have been on regular use to analyze in-house multi OMICs data as well as data from collaborative labs.

GFR 12 – A
[(See Rule 238 (1))]
UTILIZATION CERTIFICATE (UC) FOR THE YEAR 2021-2022
in respect of *RECURRING*
as on 18.02.2022 to be submitted to SERB
Is the UC (*Provisional/Audited*)
(To be given separately for each financial year ending on 31st March)

1. Name of the grant receiving Organization : TEZPUR UNIVERSITY
2. Name of Principal Investigator(PI) : Dr. PANKAJ BARAH
3. SERB Sanction order no. & date : SRG/2019/001924, DATE 06/11/2019
4. Title of the Project : *Big data and Machine learning based approach to understand combined stress response signatures in multiple cultivating crop plants*
5. Name of the SERB Scheme : SRG
6. Whether recurring or non-recurring grants : **RECURRING**
7. Grants position at the beginning of the Financial year

(i) Carry forward from previous financial year	4,43,870.00
(ii) Others, If any (Grant received from SERB)	:
(iii) Total	4,43,870.00

8. Details of grants received, expenditure incurred and closing balances: (Actuals)

Unspent Balance of Grants received previous years [figure as at Sl. No. 7(iii)]	Interest Earned thereon	Interest deposited back to the SERB	Grants received during the year			Total Available funds (1+2-3+4)	Expenditure incurred	Closing Balances (5-6)
			Sanction No. (i)	Date (ii)	Amount (iii)			
1	2	3	4			5	6	7
(Rs.)	(Rs.)	(Rs.)	(Rs.)	(Rs.)	(Rs.)	(Rs.)	(Rs.)	(Rs.)
4,43,870.00	4555.00	NIL	SERB/F/2438/2021-2022	19 th August, 2021	2,50,000.00	6,98,425.00	5,11,655.00	1,86,770.00

Component wise utilization of grants:

Grants-in-aid- General	Grant-in-aid-creation for capital assets	Total
5,11,655.00	NIL	5,11,655.00

Details of grants position at the end of the year

(i) Balance available at end of financial year	1,86,770.00
(ii) Unspent balance refunded to SERB (If any)	1,86,770.00
(iii) Balance (Carried forward to next financial year) if applicable	: NIL


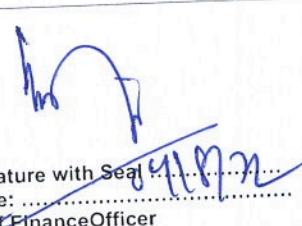
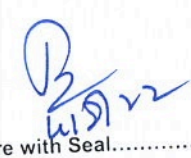
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 in respect of **RECURRING**
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 Is the UC (Provisional/Audited)
 (To be given separately for each financial year ending on 31st March)

Certified that I have satisfied that the conditions on which grants were sanctioned have been duly fulfilled/are being fulfilled and that I have exercised following checks to see that the money has been actually utilized for the purpose for which it was sanctioned:

- (i) The main accounts and other subsidiary accounts and registers (including assets registers) are maintained as prescribed in the relevant Act/Rules/Standing instructions (mention the Act/Rules) and have been duly audited by designated auditors. The figures depicted above tally with the audited figures mentioned in financial statements/accounts.
- (ii) There exist internal controls for safeguarding public funds/assets, watching outcomes and achievements of physical targets against the financial inputs, ensuring quality in asset creation etc. & the periodic evaluation of internal controls is exercised to ensure their effectiveness.
- (iii) To the best of our knowledge and belief, no transactions have been entered that are in violation of relevant Act/Rules/standing instructions and scheme guidelines.
- (iv) The responsibilities among the key functionaries for execution of the scheme have been assigned in clear terms and are not general in nature.
- (v) The benefits were extended to the intended beneficiaries and only such areas/districts were covered where the scheme was intended to operate.
- (vi) The expenditure on various components of the scheme was in the proportions authorized as per the scheme guidelines and terms and conditions of the grants-in-aid.
- (vii) It has been ensured that the physical and financial performance under SRG (Name of the scheme has been according to the requirements, as prescribed in the guidelines issued by Govt. of India and the performance/targets achieved statement for the year to which the utilization of the fund resulted in outcomes given at Annexure – I duly enclosed.
- (viii) The utilization of the fund resulted in outcomes given at Annexure – II duly enclosed (to be formulated by the Ministry/Department concerned as per their requirements/specifications.)
- (ix) Details of various schemes executed by the agency through grants-in-aid received from the same Ministry or from other Ministries is enclosed at Annexure –II (to be formulated by the Ministry/Department concerned as per their requirements/specifications).

Date: 27.07.2022

Place: TEZPUR, ASSAM

 Signature of Dr. Pankaj Barah PI : Assistant Professor Dept. of Molecular Biology & Biotechnology Tezpur University Tezpur- 784028 (Strike out inapplicable terms)	 Signature with Seal Name: Chief Finance Officer Head of Finance Finance Officer Tezpur University	 Signature with Seal Name: Head of Organisation Registrar Tezpur University
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GFR 12 – A
[(See Rule 238 (1))]
UTILIZATION CERTIFICATE (UC) FOR THE YEAR 2021-2022
in respect of NON-RECURRING
as on 18.02.2022 to be submitted to SERB
Is the UC(Provisional/Audited)

(To be given separately for each financial year ending on 31st March)

1. Name of the grant receiving Organization : TEZPUR UNIVERSITY
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4. Title of the Project : *Big data and Machine learning based approach to understand combined stress response signatures in multiple cultivating crop plants*
5. Name of the SERB Scheme : SRG
6. Whether recurring or non-recurring grants: **NON-RECURRING**

7. Grants position at the beginning of the Financial year

(i) Carry forward from previous financial year	:	7,347.00
(ii) Others, If any (Grant received from SERB)	:	NIL
(iii) Total	:	7,347.00

8. Details of grants received, expenditure incurred and closing balances: (Actuals)

Unspent Balance of Grants received previous years (figure as at Sl. No. 7(iii))	Interest Earned thereon	Interest deposited back to the SERB	Grants received during the year			Total Available funds (1+2+3+4)	Expenditure incurred	Closing Balances (5-6)
			Sanction No. (i)	Date (ii)	Amount (iii)			
1	2	3	4			5	6	7
(Rs.)	(Rs.)	(Rs.)	(i)	(ii)	(iii)	(Rs.)	(Rs.)	(Rs.)
7,347.00	184.00	NA	NIL	NIL	NIL	7,531.00	NIL	7,531.00

Component wise utilization of grants:

Grants-in-aid- General	Grant-in-aid-creation for capital assets	Total
NIL	NIL	NIL

Details of grants position at the end of the year

(i) Balance available at end of financial year	:	7,531.00
(ii) Unspent balance refunded to SERB (If any)	:	7,531.00
(iii) Balance (Carried forward to next financial year) if applicable	:	NIL

GFR 12 – A
 [(See Rule 238 (1))]
UTILIZATION CERTIFICATE (UC) FOR THE YEAR 2021-2022
 in respect of **NON-RECURRING**
 as on 18.02.2022 to be submitted to SERB
 Is the UC *(Provisional/Audited)*

(To be given separately for each financial year ending on 31st March)

Certified that I have satisfied that the conditions on which grants were sanctioned have been duly fulfilled/are being fulfilled and that I have exercised following checks to see that the money has been actually utilized for the purpose for which it was sanctioned:

- (i) The main accounts and other subsidiary accounts and registers (including assets registers) are maintained as prescribed in the relevant Act/Rules/Standing instructions (mention the Act/Rules) and have been duly audited by designated auditors. The figures depicted above tally with the audited figures mentioned in financial statements/accounts.
- (ii) There exist internal controls for safeguarding public funds/assets, watching outcomes and achievements of physical targets against the financial inputs, ensuring quality in asset creation etc. & the periodic evaluation of internal controls is exercised to ensure their effectiveness.
- (iii) To the best of our knowledge and belief, no transactions have been entered that are in violation of relevant Act/Rules/standing instructions and scheme guidelines.
- (iv) The responsibilities among the key functionaries for execution of the scheme have been assigned in clear terms and are not general in nature.
- (v) The benefits were extended to the intended beneficiaries and only such areas/districts were covered where the scheme was intended to operate.
- (vi) The expenditure on various components of the scheme was in the proportions authorized as per the scheme guidelines and terms and conditions of the grants-in-aid.
- (vii) It has been ensured that the physical and financial performance under SRG (Name of the scheme has been according to the requirements, as prescribed in the guidelines issued by Govt. of India and the performance/targets achieved statement for the year to which the utilization of the fund resulted in outcomes given at Annexure – I duly enclosed.
- (viii) The utilization of the fund resulted in outcomes given at Annexure – II duly enclosed (to be formulated by the Ministry/Department concerned as per their requirements/specifications.)
- (ix) Details of various schemes executed by the agency through grants-in-aid received from the same Ministry or from other Ministries is enclosed at Annexure –II (to be formulated by the Ministry/Department concerned as per their requirements/specifications).

Date: 27.07.2022

Place: TEZPUR, ASSAM

 Dr. Pankaj Barah Assistant Professor Dept. of Molecular Biology & Biotechnology Tezpur University Tezpur- 784028	 Signature with Seal..... Name: Chief Finance Officer (Head of Finance) Finance Officer Tezpur University	 Signature with Seal..... Name: Head of Organisation Registrar Tezpur University
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(Strike out inapplicable terms)

REQUEST FOR ANNUAL INSTALLMENT WITH UP-TO-DATE STATEMENT OF EXPENDITURE

1. SERB Sanction Order No and date : SRG/2019/001924, DATE 21.09.2021
 2. Name of the PI : Dr. PANKAJ BARAH
 3. Total Project Cost : Rs. 23,24,102.00
 4. Revised Project Cost : NA
 5. Date of Commencement : 19.11.2019
 6. Statement of Expenditure :
- (Month wise expenditure incurred during current financial year)

Month & year	Expenditure incurred/ committed
April, 2021	20,000.00 (Manpower Fellowship) 1,38,932.00 (Consumables) 31,215.00 (Overhead)
May 2021	20,000.00 (Manpower Fellowship)
June, 2021	20,000.00 (Manpower Fellowship)
July, 2021	20,000.00 (Manpower Fellowship)
August, 2021	20,000.00 (Manpower Fellowship)
September, 2021	20,000.00 (Manpower Fellowship) 22,182.00 (Consumables) 24,500.00 (Contingency)
October, 2021	20,000.00 (Manpower Fellowship)
November, 2021	20,000.00 (Manpower Fellowship)
December, 2021	20,000.00 (Manpower Fellowship)
January, 2022	20,000.00 (Manpower Fellowship)
February, 2022	13,571.00 (Manpower Fellowship) 21,068.00 (Contingency) 6,170.00 (Travel) 10,000.00 (SSR) 44,017.00 (Overhead)

1. Grant received in each year:
 - a. 1st Year : INR 11,13,000.00
 - b. 2nd Year : INR 5,00,000.00
 - c. 3rd Year : INR 2,50,000.00
 - d. Interest, if any : INR 8,775.00 (1st year) + INR 2,803.00 (2nd year)+ INR 4,739.00 (3rd Year) = 16,317.00
 - e. Total (a + b + c + d) : INR 18,79,317.00

Statement of Expenditure
(1st April 2021 to 18th February 2022)

Sl. No.	Sanctioned Heads (II)	Total Funds Allocated (indicate sanctioned or revised) (III)	Released amount (1 st release) (IV)	Released amount (2 nd release) (V)	Released amount (3 rd release) (VI)	Expenditure Incurred			Total Expenditure till 18 th Feb 2022 (X = VII+VIII+IX)	Balance as on 18 th Feb 2022 (XI = IV+V+VI-X)	Requirement of Funds upto 31 st March 2023	Remarks (if any)
						1 st Year (19 th Nov 2019 to 31 st March 2020) (VII)	2 nd Year (1 st April 2020 to 31 st March 2021) (VIII)	3 rd Year (1 st April 2021 to 18 th Feb 2022) (IX)				
1.	Manpower costs	8,03,520.00	4,13,700.00	5,00,000.00	2,50,000	26,400.00	1,86,000.00	2,13,571.00	4,25,971.00	1,77,564.00	NA	
2.	Consumables	4,00,000.00				1,48,897.00	NA	1,61,114.00	3,10,011.00		NA	
3.	Travel	1,00,000.00				NIL	9,616.00	6,170.00	15,786.00		NA	
4.	Contingencies	1,00,000.00				NIL	39,380.00	45,568.00	84,948.00		NA	
5.	Others (SSR)	10,000				NIL	NIL	10,000.00	10,000.00		NA	
6.	Overhead expenses	2,11,282.00				32,938.00	31,250.00	75,232.00	1,39,420.00		NA	
7.	Equipment	6,99,300.00	6,99,300.00	NIL	NIL	NIL	6,98,880.00	NIL	6,98,880.00	420.00	NA	
8.	Interest accrued	NA	8,775.00	2,803.00	4,739.00	NA	NA	NA	NA	16,317.00	NA	
9.	Total	23,24,102.00	11,13,000.00	5,00,000.00	2,50,000.00	2,08,235.00	9,65,126.00	5,11,655.00	16,85,016.00	1,94,301.00	NA	

Name and Signature of Principal Investigator: 

Date: 28.02.2022

Dr. Pankaj Barah
Assistant Professor
Dept. of Molecular Biology & Biotechnology
Tezpur University
Tezpur- 784028

Signature of Competent financial authority:
(with seal)

Date: 04.02.22

Finance Officer
Tezpur University

Note:

- Expenditure under the sanctioned heads, at any point of time, should not exceed funds allocated under that head, without prior approval of SERB i.e. Figures in Column (VIII) should not exceed corresponding figures in Column (III)
- Utilization Certificate (Annexure III) for each financial year ending 31st March has to be enclosed along with request for carry-forward permission to the next financial year.