

# Transcriptome Dynamics During Stem Elongation in Rice



Manu Kandpal<sup>1</sup>, Chandrapal Vishwakarma<sup>2</sup>, Viswanathan Chinnusamy<sup>2</sup>, Manoj K. Sharma<sup>3</sup> and Rita Sharma<sup>1</sup>

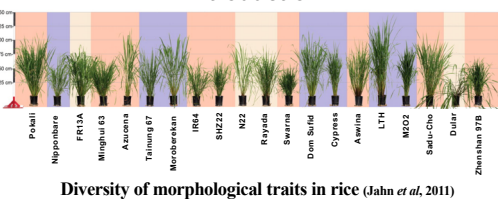
<sup>1</sup>School of Computational & Integrative Sciences, Jawaharlal Nehru University; <sup>2</sup>Division of Plant Physiology, Indian Agricultural Research Institute, New Delhi; <sup>3</sup>School of Biotechnology, Jawaharlal Nehru University, New Delhi

Email : rita.genomics@gmail.com

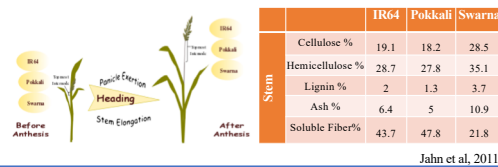
## ABSTRACT

Rice is a major staple food crop, worldwide. Elongation of internode in rice is an important developmental process that not only plays pivotal role in plant height and panicle exertion but also dramatically affects grain and biomass yield. Although a handful of genes have been characterized using forward genetic studies, the genetic basis of internode elongation in rice remains unexplored. Our study aims at exploiting the genetic diversity in rice to identify genes and genetic pathways implicated in stem elongation at the heading stage. We selected three widely grown Indica rice cultivars with contrasting cell wall composition and plant height to study the transcriptional dynamics regulating internode elongation in rice. Transcriptomic profiles of topmost internodes collected before and immediately after anthesis, from all three cultivars were generated using RNA sequencing. A total of 978.8 million high quality reads with an average read length of 100 bp were generated. Differential expression analysis revealed 2030 genes upregulated and 1589 genes downregulated in at least two of the cultivars. The results indicate positive role of brassinosteroid and auxin biosynthesis genes in promoting stem elongation, whereas, JA and ABA-related genes likely inhibit it. The contrasting patterns of gene expression of some of the key transcription factor genes highlight genetic basis of variation in plant height and biomass composition among different cultivars..

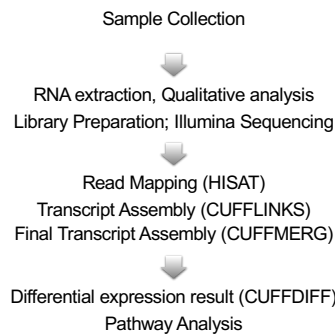
## Introduction



Diversity of morphological traits in rice (Jahn et al., 2011)



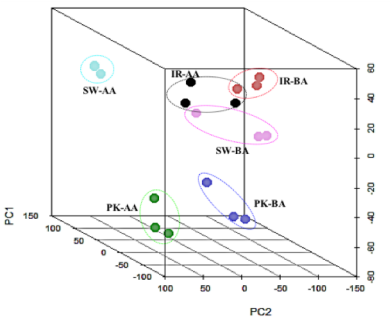
## Methodology



## Read alignment summary

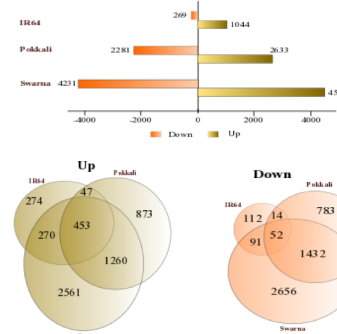
Sample Name	Total Reads	QC Passed	QC Passed%	Aligned Read Count	Aligned %	Unaligned Read Count	Unaligned %
PK3AA	109,179,438	109,059,680	99.00	100,651,179	92.29	8,408,501	7.71
SWAA18	90,146,944	90,104,432	99.00	84,824,312	94.14	5,280,120	5.86
PK3BA	78,209,750	78,176,560	99.00	72,493,124	92.73	5,683,436	7.27
SWAA19	82,120,542	82,073,414	99.00	76,459,992	93.16	5,613,822	6.84
SWAA2	104,028,456	103,962,068	99.00	97,901,079	94.17	6,060,989	5.83
SWAA1	140,348,886	140,023,176	99.00	89,544,821	63.95	50,478,355	36.05
IR6A	131,951,782	131,500,524	99.00	94,114,925	71.57	37,385,599	28.43
IR5A	171,419,842	170,981,666	99.00	124,816,616	73.00	46,165,650	27
IR6A	148,411,428	147,982,242	99.00	107,435,108	72.60	40,547,134	27.40
IR7A	96,108,342	95,963,324	99.00	88,439,799	92.16	7,523,525	7.84
IR8A	144,076,128	143,799,194	99.00	111,214,297	77.34	32,584,897	22.66
IR9A	147,645,788	146,954,118	99.00	98,047,788	66.72	48,906,330	33.28
IR3A	159,614,978	158,739,768	99.00	106,847,738	67.31	51,892,030	32.69
IR4A	98,148,904	97,915,336	99.00	69,617,804	71.10	28,297,532	28.90
PK3AA	145,360,408	145,237,658	99.00	114,955,606	79.15	30,282,852	20.85
PK2BA	166,991,272	166,864,914	99.00	126,583,724	75.86	40,281,190	24.14
SW8A	102,101,768	102,048,156	99.00	95,594,616	93.48	6,653,540	6.52
SW4BA	103,853,666	103,797,708	99.00	97,206,554	93.65	6,591,154	6.35

## Correlation between biological replicates



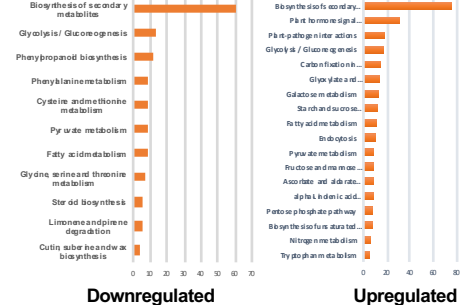
PCA plot showing the RNA-Seq datasets (FPKM values) clustering biological replicates of same development stage of same cultivars

## Differentially expressed genes



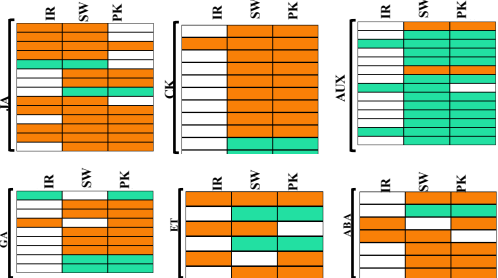
Up & Down regulated genes before/after anthesis in different cultivars

## KEGG pathways



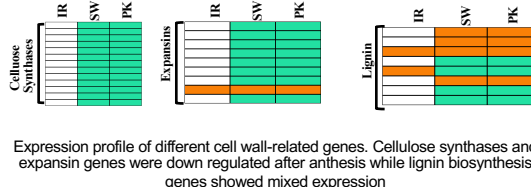
KEGG pathway analysis of significantly up and down regulated genes common in at least cultivars

## Expression profile of hormonal pathways



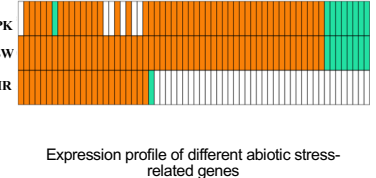
Expression profile of different hormone-related genes important for growth, biotic and abiotic stress tolerance

## Expression profile of cell wall-related genes



Expression profile of different cell wall-related genes. Cellulose synthases and expansin genes were down regulated after anthesis while lignin biosynthesis genes showed mixed expression

## Abiotic stress-related genes



Expression profile of different abiotic stress-related genes

## Conclusions

Genes involved in different pathways and hormonal biosynthesis have been identified in this study. These play an important role in determining the growth and architecture of rice. They can be important targets for genome engineering. Some of these genes have been selected for functional characterization through overexpression and silencing studies, and further work is in progress.

## References:

C.E. Jahn, J.K. Mckay, R. Mauleon, J. Stephens, K.L. McNally, D.R. Bush, H. Leung and J.E. Leach. *Plant Physiology* **155** (2011) 157-168.

## ACKNOWLEDGEMENTS

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