



# Extended Summary



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**1<sup>st</sup> Indian Rice Congress - 2020**  
**RICE RESEARCH AND DEVELOPMENT FOR ACHIEVING SUSTAINABLE  
DEVELOPMENT GOALS**

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## **Extended Summaries**

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## 1<sup>st</sup> Indian Rice Congress - 2020

Rice Research and Development for Achieving Sustainable Development Goals



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## PROTEOMICS APPROACHES OF DIFFERENTIAL GRAIN FILLING IN DIFFERENT SPATIAL LOCATIONS OF PANICLE IN RICE CULTIVARS EXHIBITING VARIATIONS IN THEIR PANICLE COMPACTNESS

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Rice production needs to be increased to at least 800 million tons to feed the World's expected population of approximately 9.6 billion by 2050 (Das et.al,2016). In order to achieve such a higher grain yield, rice breeders have increased the grain numbers within the panicle with no much increase in panicle length which caused more panicle compactness. However, increase in grain number due to more panicle compactness did not improve grain yield proportionately because of poor filling of spikelets which are specifically located in the basal part of the panicle. Grain filling in rice is basically a function of the translocation of photosynthetic assimilates like sucrose from the source leaves to developing endosperm where it is converted to starch by many starch synthesizing enzymes. Our previous work analysed the activities of different starch synthesizing enzymes (Panda et.al,2015) and expression of ethylene receptor and their signal transducer genes (Sekharet.al., 2015) associated with grain filling of rice. Decreased activity of enzymes involved in starch biosynthesis have been found associated with poor grain filling especially in the grains located in the basal part of the panicle and in compact panicle cultivars. Many researchers also studied the involvement of plant hormones like ethylene with inhibitory effect and ABA and Auxin with stimulatory effect on grain filling (Kuanar et.al, 2010) during post anthesis stages of grain development. Similarly, transcriptome analysis revealed differential expression of 623 genes in rice caryopses after 15 days post-flowering in near isogenic lines (NILs) of rice genotypes exhibiting variation in grain chalkiness (Liu et.al., 2010). In this context, a proteomic approach

based on 2-D electrophoresis and mass spectrometric analysis may be an effective tool in analysing differential grain filling in rice and the present work intend to exploit the usefulness of proteomics to unravel the possible reasons for spatial differences in grain filling of lax- and compact-panicle rice cultivars. In the present work, attempt has been made to understand the reasons for differential grain filling in different spatial locations of the panicle by analysing the comparative proteomics in compact-panicle cultivar Mahalaxmi and lax-panicle cultivar Upahar having poor and good grain filling properties respectively.

### MATERIALS AND METHODS

Two rice cultivars namely Mahalaxmi (compact-panicked) and Upahar (lax-panicked) were used in the present experiment. All recommended agronomic practices were followed during the cultivation of the plants in the field. Dry weight, soluble carbohydrate concentrations and ethylene production of apical and basal grains of both the cultivars were measured during post-anthesis period. Proteins from the developing spikelets were also extracted and their differential expression patterns were studied using two-dimensional electrophoresis followed by mass spectrometry. Further, primers were designed to study the spatio-temporal expression of the genes encoding some important proteins that exhibited either higher or lower expression in the basal spikelets compared to the apical ones in Mahalaxmi over Upahar by RT-PCR analysis.

### RESULTS

The results revealed a significant difference in the panicle morphology between the compact panicked



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rice cultivar Mahalaxmi and lax cultivar Upahar. Though the length of panicle was greater (27.7cm) in Upahar compared to Mahalaxmi (25.0cm), panicle weight, total grain number and percentage of unfilled grains was quite higher in Mahalaxmi. Production of ethylene was also higher in the basal grains than the apical ones and also in the corresponding spikelets of Mahalaxmi compared to Upahar. Comparative proteomic analysis showed expression of 391 protein spots in the gel images of the protein extracts from the apical and basal spikelets of Mahalaxmi. Out of these total protein spots, 45 were differentially expressed in the apical and basal spikelets; 34 proteins were more strongly expressed in the apical spikelets compared to basal whereas 11 were more prominently expressed in the basal compared to apical spikelets. On the other hand, 21 proteins were differentially expressed in the apical and basal spikelets of Upahar. Although many proteins were differentially expressed in the 2-DE gel images from the protein extracts of apical and basal spikelets in the compact- and lax-panicle rice cultivars, the most prominent proteins were S-adenosylmethionine synthase, enolase and cell division control protein 48 (CDC48). RT-PCR studies also confirmed greater expression of the gene transcript level of S-adenosylmethionine in the basal spikelets of Mahalaxmi compared to apical spikelets whereas no such difference was observed in lax-panicle cultivar Upahar.

#### DISCUSSION AND CONCLUSION

Although several proteins were up- and down-regulated in the basal spikelets compared to the apical ones of Mahalaxmi, greater expression of the proteins like S-adenosylmethionine synthase and lower expression of CDC48 in the basal spikelets seems more crucial for grain development in rice. S-adenosylmethionine synthase could inhibit grain filling by stimulating more ethylene synthesis in the basal spikelets which in turn is responsible for inhibition of endosperm cell division (Panda et.al., 2009) mediated through lower expression of CDC48 leading to poor

grain filling in the basal spikelets of Mahalaxmi. Higher expression of ethylene synthesis precursor gene like S-adenosylmethionine in the basal spikelets of Mahalaxmi also supports greater ethylene production and hence more inhibition in grain filling. However, only two of these proteins were differentially expressed between the apical and basal spikelets in Upahar indicating more differential metabolic activities in the apical and basal spikelets of Mahalaxmi than that of Upahar. Hence, differential expression of proteins accompanied by variation in ethylene production in the apical and basal grains is the principal factors responsible for variation in grain filling of rice cultivars that contrast for panicle compactness.

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