

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
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Keyword 1	: Pre-breeding
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Title of Entry	: Bioinformatics inference of badh2 Gene in South Asian Rice Varieties
Presenting author	: Nisha Kottearachchi
Presenting author email	: kottearachchins@yahoo.com
Co author 1	: W.V.E.WITHANA
Co author 2	: J. WEERASENA
Affiliation presenting author	: Department of Biotechnology, Faculty of Agriculture and Plantation Management,Wayamba University of Sri Lanka,Makandura,Gonawila(NWP),60170,Sri Lanka
Affiliation 1	: Department of Biotechnology, Faculty of Agriculture and Plantation Management,Wayamba University of Sri Lanka,Makandura,Gonawila(NWP),60170,Sri Lanka
Affiliation 2	: Institute of Biochemistry, Molecular Biology and Biotechnology, University of Colombo
Select only one type of presentation	: 15 minute oral presentation
Abstract	: Fragrance of the rice is important quality trait which plays a major role in rice trade market. Aroma of the rice arises due to accumulation of volatile substance called 2-acetylcysteine-1-pyrroline (2AP). The predicted biosynthesis pathway of 2AP was induced by a non-functional BADH2 protein encoded by a mutated badh2 gene. This critical mutation has been reported in many fragrant rice varieties as 3SNPs and 8bp deletion occurred in 7th exon which is referred as badh2.1 allele. Also, few other mutations were discovered in other exon regions of badh2 gene which are designated from badh2.1 to badh2.10 alleles. There are some other exceptions to these mutations reported in intron regions of the badh2 gene. In this study we aimed at identifying such mutations in badh2 gene of different rice varieties in South Asian region using insilico nalysis in order to increase the varietal choice for farmers and breeders of the region. Sequences of 876 rice accession: retrieved from Rice SNP-Seek -Database were analyzed using NCBI blast tool in order to identify mutations in exon regions of badh2 gene. Results revealed that twenty five varieties representing 6 countries carry the badh2.1 allele that cause fragrance, except Bhutan and Sri Lanka. Next to badh2.1 allele, other predominant fragrant allele in this region was badh2.7 which showed a 'G' insertion in 14th exon. This allele was found only in India, Bangladesh, Pakistan and Sri Lanka. Several other substitution mutations were also found in 05th, 06th, 07th, 10th, 12th and 14th exon of badh2 representing throughout the regions. Protein structures were predicted for each type of

mutation and loss of functional activity was found for the proteins encoded by badh2.1 and badh2.7 alleles. According to the results, other mutations were unlikely to cause fragrance because they did not affect any functional domains of amino acid sequence as examined in the predicted protein structures. The phylogenetic analysis showed seven different clusters in which the specific mutation was separately grouped. The results of this study would be useful to identify all the fragrant rice varieties of South Asian region that are available in Rice SNP-Seek -Database.

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