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Allelic diversity analysis of *OsHsp17.7*, a heat tolerance related protein in rice

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Abstract

Rice (*Oryza sativa* L.) is a staple food for more than fifty percent of the world's population. Global food production must increase in order to feed the predicted 9.1 billion people by 2050. Many biotic and abiotic factors reduces the rice yield. One of such factor is reproductive stage heat stress, rice is extremely sensitive to heat stress, and rise in temperature can cause loss of around 10% to 90% of grain production. In the current study we attempted to reveal potential allelic variation in heat shock protein *OsHsp17.7* (LOC_Os03g16040) contains 1 exon with transcript length of 480 bps, through *in silico* analysis based on the sequences available in the Rice SNP-Seek-Database. A set of 201 aus accessions from 3K rice genome project were accessed for analyzing the allelic variation. Allelic diversity analysis identified 1 SNPs in *OsHsp17.7* gene sequence. In this study, two haplotypes (H1 and H2) contributed by 1 SNPs were identified for *OsHsp17.7*.

Keywords: *OsHsp17.7*, SNP, Haplotype analysis, Rice

1. Introduction

Rice (*Oryza sativa* L.) is the principal source of carbohydrates for half of the world's population. Food production must expand to support the world's rising population by 2050 (Carriger and Vallee, 2007) [4]. Global warming and climate change have a detrimental effect on food production and are likely to have a greater influence in the coming years (Xu *et al.*, 2021) [18]. Rising temperature is constantly affecting productivity of agricultural crops worldwide. Although rice is a tropical crop cultivated where the average temperature ranges between 21 to 37^{o} C, rise in temperature just by 1^{o} C can cause >10% loss in yields and quality (Peng *et al.*, 2004) [13]. Increased temperature condition inhibits crop growth and development. High temperatures during vegetative stage damage the photosynthetic organelles (Al-Khatib *et al.*, 1999) [2], decrease photosynthesis, reduces grain number, and increases sterility (Wardlaw *et al.*, 1995; Prasad *et al.*, 2006) [16, 14] resulting in significant grain yield loss (Ferris *et al.*, 1998; Gibson *et al.*, 1999) [7, 8]. Reproductive and grain filling stage are the most susceptible stages for rice productivity (Yoshida, 1981) [17]. High temperatures during reproductive stage result in reduced grain filling duration, grain weight reduction, increased chalky grains (Bao, 2019; Cooper *et al.*, 2006; Ambardekar *et al.*, 2011, Zhou, Yun & He, 2019) [3, 6, 1, 19]. At cellular and molecular level, high temperature damages enzymatic activity and denature protein (Hu *et al.*, 2020) [9]. Protein maintenance in a functional state is critical for cell survival under stress. Precise analysis and identification of differentially expressed protein during anthesis were studied with an aim to understand high-temperature-responsive anther proteins in rice genotypes at anthesis (Jagadish *et al.*, 2010) [10]. Heat-shock proteins function as molecular chaperones to maintain cellular homeostasis under diverse developmental conditions. Heat-shock proteins and their function in heat stress had been studied extensively (Sato *et al.*, 2008; Chen *et al.*, 2014) [15, 5]. Understanding allelic variation in the heat shock protein can help with haplotype breeding as well as developing heat stress tolerant cultivar. For the ever-increasing world's population and limited resources, there is an urgent need to develop heat-tolerant rice cultivars.

2. Materials and Methods

2.1 Allelic diversity analysis of *OsHsp17.7* in an AUS subset of 3K panel

To retrieve data on *OsHsp17.7*, SNPs/INDELs variation among 201 Aus rice lines, the SNP seek database was used. Allelic variation of *OsHsp17.7* (LOC_Os03g16040) was retrieved from the SNP seek database to perform haplotype analysis. SNP seek database was exploited to perform haplotype analysis for *OsHsp17.7* by adopting default parameters with Calinski criteria for k-group determination. Nipponbare was used as the reference genome.

The ‘3kfiltered’ SNP set available in the SNP seek database for the analysis. The filtered dataset was obtained from the Base SNP set with alternative allele frequency of at least 0.01, proportion of missing calls per SNP as 0.2 (Mansueto *et al.*, 2016) and this was available in the SNP seek database. Allele mining was carried out by selecting only the non-synonymous SNPs and INDEL (Insertion deletion).

3. Results and Discussion

3.1 Allelic diversity of *OsHsp17.7* in *Aus*-subset of 3K Rice genome panel

Allelic diversity analysis of heat shock protein gene *OsHsp17.7* revealed that the gene contains only one genetic polymorphism (1 SNP) among the 201 genotypes surveyed (Table 1). The SNP located in the exon 1 of *OsHsp17.7* was found to be non-synonymous leading to V21F (Table 1). The non-synonymous mutations present in the dataset results in the modification of individual amino acids (Valine - Phenylalanine) (Table 2). We identified a novel variation in the first exon of the *OsHsp17.7* allele, consisting of one SNP (C/A) at chr03-8838450 position. This non synonymous SNP formed two haplotypes which comprises 166 and 32 genotypes respectively. Previous studies on heat shock protein *OsHsp17.7* had clearly indicated its role in heat and UV radiation tolerance in rice germplasm (Chen *et al.*, 2014; Murakami *et al.*, 2006) [5, 12]. Studies on protein profiling during anthesis had evidently specified upregulation of heat shock protein in N22 rice variety (Jagadish *et al.*, 2010) [10], in this present study, N22 has shown presence of a SNP in comparison with Nipponabre and shown allelic variation.

Table 1: Allelic variations in *OsHsp17.7* gene for the 3K RG panel-*Aus* subset

Region	Position	Alleles	Sequence polymorphisms	Type
chr03-8838450	Exon 1	1 bp	C/A	SNP

Table 2: SNP Effect of allelic variation of Aus lines in *OsHsp17.7*

Position	Alt (ANN)	Effect (ANN)	Gene Name (ANN)	HGV S.c (ANN)	HGV S.p (ANN)	cDNA position (ANN)
chr03-8838450	A	Missense variant	LOC_Os03g16040	c.61G>T	p.Val21Phe	61/480
	A	Upstream gene variant	LOC_Os03g16020	c.-1G>T	-	
	A	Downstream gene variant	LOC_Os03g16010	c.*2271C>A	-	
	A	Downstream gene variant	LOC_Os03g16030	c.*608C>A	-	
	A	Downstream gene variant	LOC_Os03g16050	c.*1334G>T	-	

4. Conclusion

Insilico analysis of heat shock protein *OsHsp17.7* revealed 1 non synonymous SNP variant among 3K RG subsets (Aus type). Two haplotype clusters were observed by haplotype analysis of *OsHsp17.7*. Phenotypic evaluation of representative lines from the allelic groups will shed more light on the molecular basis of heat tolerance in rice. The findings from this study on allelic variation of *OsHsp17.7* can be a useful resource for generating knowledge on haplotype-based breeding which can lead to the development of heat tolerant rice varieties that meet future food demands.

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