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Dr. Raveendran Muthurajan
Professor and Head, Department of Plant Biotechnology, Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

Bharathi Ayyenar
Department of Plant Biotechnology, Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

Rohit Kambale
Department of Plant Biotechnology, Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

Veera Ranjani Rajagopalan
Department of Plant Biotechnology, Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

Corresponding Author:

Dr. Raveendran Muthurajan
Professor and Head, Department of Plant Biotechnology, Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

Allelic diversity of *OsSLG1* regulating heat tolerance in rice

Dr. Raveendran Muthurajan, Bharathi Ayyenar, Rohit Kambale and Veera Ranjani Rajagopalan

Abstract

Rice is an important cereal crop in many countries, with majority of Asians eating rice as a staple diet and 70 per cent in South Asia alone. Global warming poses serious threats to global agriculture productivity. As a result of global climate change events, the surface air temperature will rise by 1.4 - 5.8 °C by the end of the twenty-first century. Rice is extremely susceptible to high temperatures and increased exposure to high temperatures will have greater impacts on rice yield. Improved knowledge on the molecular genetic basis of high temperature tolerance, discovery of genes underlying the QTLs and mining elite alleles of these candidate genes will accelerate development of heat resilient rice cultivars. In the present study, allelic diversity of a thermo tolerance gene *SLG1* (*Slender guy1*) was analyzed in a diverse set of *aus* rice germplasm in the 3K genome panel. Bioinformatic analysis of *OsSLG1* (LOC_Os12g39840) sequence among the 201 *aus* rice genotypes revealed the presence of one non-synonymous SNP in the 6th exon. This SNP grouped the 201 *aus* lines into two haplogroups (H1 and H2). Further marker-trait association analysis will identify the elite allele of *OsSLG1*.

Keywords: Rice, *OsSLG1*, allelic variation, haplotype analysis

1. Introduction

Rice (*Oryza sativa* L.) is a major cereal crop of the Poaceae family that is cultivated in diverse ecological conditions, including irrigated, rainfed, upland, and deep water (Cassman *et al.*, 2005). It provides food for over 3 billion people (Rasheed *et al.*, 2020) [11]. Asia consumes more than 80% of the world's rice (Suh *et al.*, 2015) [14], and any shortage in rice production will have major effects for Asia's and Africa's resource-poor farmers (Dawe *et al.*, 2010) [4]. Rice yield reductions have been documented in numerous tropical and subtropical areas due to high temperatures and the effect of high temperatures is increased when it coincides with booting to flowering stage (Satake and Yoshida, 1978) [12]. Despite being a temperature-loving crop, rice is susceptible to heat stress (temperatures above 35°C), especially during gametogenesis and flowering (Jagadish *et al.*, 2010) [5]. During flowering/anthesis, high temperature affects anther dehiscence and pollination, resulting in reduced spikelet fertility (Nakagawa *et al.*, 2003; Jagadish *et al.*, 2010) [8, 5]. Heat-induced spikelet sterility has been linked to yield loss in tropical Asia (Osada *et al.*, 1973) [9] and Africa (Matsushima *et al.*, 1983) [7]. This needs the development of heat-resistant rice varieties that are adapted to the changing temperature in order to achieve a sustained increase in rice output in the face of climate change. Due to a lack of knowledge about the tolerance mechanisms and relevant donors, the development of rice varieties with improved tolerance to high temperature stress has been delayed. Plant introduction (Taichung Native-1 and IR-8), hybridization (CO 51), selection (M-351), and mutation breeding (Binasail) were all used to increase yield in previous decades (Boopathi 2020, Sundaramoorthy *et al.*, 2021) [2, 15]. Transgenic and genome editing will accelerate the yield improvement; however breeding efficiency in these systems requires finding or producing superior alleles over naturally available genotypes (Qaim 2020, Shamsudin *et al.*, 2016) [10, 13]. The re-sequencing of 3K diverse rice germplasm lines allowed for the identification and exploration of allelic/haplotype variants, allowing genetic diversity to be harnessed (Abbai *et al.*, 2019) [1]. This, in turn, paved the path for the discovery of novel donors and novel alleles related with the features of interest, which can then be used to improve crops (Varshney *et al.*, 2018) [16]. Overexpression and natural variation in both the promoter and coding sequences of *slender guy1* (*OsSLG1*) in *indica* varieties showed enhanced thermotolerance, whereas mutations in the cytosolic tRNA 2-thiolation protein *slender guy1* (*OsSLG1*) involved in the post-transcriptional modification of a tRNA showed enhanced sensitivity to high temperature in both vegetative and reproductive development.

In this study, allelic diversity of the gene responsible for the thermotolerance was studied using *aus* type rice germplasm.

2. Materials and Methods

Nucleotide variations present in the thermotolerance gene *OsSLG1* (LOC_Os12g39840) among the 201 *aus* rice germplasms were retrieved from the SNP seek database. The data on SNPs and INDELS were downloaded from the database and filtered by using default parameters. Filtered SNP dataset for the 201 *aus* rice lines were used for the analysis and the Nipponbare was used as the reference genome. The filtered dataset was retrieved from the Base SNP set, which had an alternative allele frequency of at least 0.01, and a proportion of missing calls per SNP of 0.2 (Mansueto *et al.*, 2017) [6].

3. Results and Discussion

The variations present in the thermotolerance gene *OsSLG1* were retrieved from the SNP seek database. This search revealed the presence of one non-synonymous SNP among

the 201 *aus* rice lines for the candidate gene *OsSLG1* (Table 1). This non-synonymous SNP was found to be located in the exon 6 leading to a change at amino acid level (Phenylalanine to Valine) (Table 2). Two haplotype groups were formed among the 201 *aus* rice lines. Out of the total 201 genotypes, 197 genotypes were found to possess C (H1) at 24629075bp on chromosome 12 and four genotypes were found to harbor A (H2) at this position. Xu *et al.*, (2021) previously did the haplotype analysis for the same gene using 4219 rice accessions and reported the presence of two non-synonymous SNPs (out of the total seven SNPs). They suggested that the 98.2% of indica containing Val177-Val362 mutation and 99.1% japonica containing Ala177-Phe 362 and these mutations contribute for the functional divergence of *OsSLG1*.

Table 1: Allelic variations in the *OsSLG1*

Region	Position	Alleles	Sequence polymorphisms	Type
Chr 12- 24629075	Exon 6	1 bp	A/C	SNP

Table 2: Effect of SNP in the *OsSLG1*

Position	Alt (ANN)	Effect (ANN)	Gene Name (ANN)	HGV S.c (ANN)	HGV S.p (ANN)	cDNA position (ANN)
Chr12-24629075	C	Missense variant	LOC_Os12g39840	c.1084T>G	p.Phe362Val	1120/1966
	C	Downstream gene variant	LOC_Os12g39850	c.*915T>G	-	

4. Conclusion

In *silico* analysis of *OsSLG1* identified one non-synonymous SNP among the 201 diverse *aus* rice lines. Haplotype analysis of *OsSLG1* revealed two haplotype clusters. Genotype vs Phenotypes analysis will throw more light on the functional basis of SNP leading to haplotype-based breeding for development of heat-tolerant rice varieties.

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