



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(6): 1355-1357
© 2021 TPI

www.thepharmajournal.com

Received: 02-04-2021

Accepted: 06-05-2021

Raveendran Muthurajan
Professor and Head, 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

Rohit Kambale
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

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

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

Surveying allelic diversity of *ONAC129* in Aus rice germplasm

Raveendran Muthurajan, Veera Ranjani Rajagopalan, Rohit Kambale, Bharathi Ayyenar and Vignesh Mohanavel

Abstract

Heat stress, one of the severe hazard to global food security as a result of a rapidly warming climate. Even though, rice being the most important staple food crop for more than half of the world's population, heat stress often reduces the quantity and quality of rice. In the view of rapidly increasing world's population there is an urgent need to increase grain yield under drastic varying climatic conditions, especially to breed heat tolerant rice cultivars. Rice production is extremely sensitive to heat stress, since its yield is reduced by increasing temperature. Many genes have been reported for heat tolerance in rice, but their novel allelic variation for breeding heat tolerant rice varieties remain unclear. Therefore, in the present study, attempts were made to identify the allelic variation for the heat responsive *ONAC129* in 3K RG (Rice genome) panel subset. A set of 201 *aus* accessions from 3K rice genome project were accessed for the allelic variation. *ONAC129* (LOC_Os11g31380), a heat stress responsive NAC transcription factor which play a significant role in rice grain filling. Allelic diversity analysis identified 74 SNPs and 30 INDELS in *ONAC129* gene. In this study, four haplotypes (H1, H2, H3 and H4) were identified for *ONAC129* based on 18 non synonymous SNPs.

Keywords: Heat stress, *ONAC129*, haplotype analysis, rice, grain yield

1. Introduction

Rice is a staple food crop for more than half of the world's population and the most widely grown cereal. One of the most important factors influencing the seasonal growth and geographic distribution of crops is environmental temperature (Li *et al.*, 2018) [3]. Global warming has become a major concern that cannot be ignored as a result of population increase and industrial development (Quint *et al.*, 2016) [2]. Climate change and global warming have a negative impact on food production and are expected to have a greater impact in the coming years (Xu *et al.*, 2021) [4]. Despite the fact that rice is a tropical crop, every 1° C rise in average temperature during rice growing season reduces its yield by 6.2%, total milled rice yield by 7.1%–8.0%, head rice yield by 9.0%–13.8%, and total milling cost by 8.1%–11.0% (Lyman *et al.*, 2013) [1]. High temperature can cause poor germination rate, dead seedlings, reduced tiller number during vegetative stage, also reduced spikelet number, poor pollen viability, impaired pollination and fertilization during reproductive stage and reduced grain weight, increased chalkiness during grain filling stage. High temperatures denature protein and impair enzyme function at the cellular and molecular levels (Hu *et al.*, 2020) [5]. Identification of differentially expressed protein during anthesis were reported with an aim to understand high temperature responsive proteins in rice genotypes during anthesis stage (Jagadish *et al.*, 2010) [6]. Despite the fact that various unique alleles of heat stress related genes have been exploited in breeding to improve rice production (Tabassum *et al.*, 2021) [8], still it lacks a superior haplotype combination of various essential genes. *ONAC129* (LOC_Os11g31380) which is present in chromosome 9, a significant heat stress responsive NAC transcription factor which play a major role in rice grain filling stage. Variation in this gene may lead to alter the grain filling process consequently increases the grain yield. The present study was undertaken to find out the allelic variations of *ONAC129* in relation with grain filling stage in 3K RG panel *aus* subset.

2. Materials and Methods

2.1 Allelic diversity of *ONAC129* in 3K RG panel subset

Allelic diversity of *ONAC129* was extracted from 201 *aus* type rice lines from a 3K rice genome panel using the SNP seek database (<https://snp-seek.irri.org/>).

Allelic variation of *ONAC129* (LOC_Os11g31380) was accessed from the SNP seek database to perform haplotype analysis. The 3K filtered SNP dataset was obtained by adopting default parameters with Calinski criteria for k-group determination and by using the following criteria *viz.*, (i) alternative allele frequency at least 0.01, (ii) missing calls per SNP 0.2 and this was readily available in the database (Mansueto *et al.*, 2016)^[7].

2.2 Haplotype analysis of *ONAC129* in 3K RG panel subset

gPLINK (version 1.07) was used to convert the allelic variation data into a haploview fileset. (Purcell *et al.*, 2007)^[9]. the converted haploview fileset was used to perform haplotype analysis in HaploView (version 4.1), and the significant SNPs were selected using a 0.001 cutoff value (Barrett *et al.*, 2005)^[10].

3. Results and Discussion

3.1 Allelic diversity of *ONAC129* in subset of 3K RG panel

ONAC129 gene contains 114 variations (includes 74 SNPs and 30 INDELS) but only eighteen SNPs were non-synonymous (Table 1). Eighteen non-synonymous variations found in *ONAC129* among 201 aus type rice accessions leads to change of several amino acids (Ala→Thr, Ala→Val, Val→Ile, Pro→Ser, Pro→Ser, Pro→Arg, Asn→Ser,

Val→Met, Phe→Leu, Arg→His, Ala→Val, Leu→Val, Val→Ile, Cys→Phe, Thr→Ala, Ile→Thr, Pro→Leu, Ala→Gly, Gly→Ser) among them only four were significant (Fig. 1).

Table 1: Non synonymous SNP variations in *ONAC129* gene for the 3K RG panel- *Aus* subset

Region	Position	Alleles	Sequence polymorphisms
18311816	Exon 1	1 bp	G/A
18311817	Exon 1	1 bp	C/T
18311921	Exon 1	1 bp	A/G
18311927	Exon 1	1 bp	C/T
18311928	Exon 1	1 bp	C/G
18312287	Exon 2	1 bp	A/G
18312316	Exon 2	1 bp	A/G
18312348	Exon 2	1 bp	A/T
18312398	Exon 2	1 bp	A/G
18312431	Exon 2	1 bp	C/T
18313404	Exon 3	1 bp	C/G
18313410	Exon 3	1 bp	A/G
18313462	Exon 3	1 bp	G/T
18313503	Exon 3	1 bp	A/G
18313534	Exon 3	1 bp	C/T
18313546	Exon 3	1 bp	C/T
18313570	Exon 3	1 bp	C/G
18313644	Exon 3	1 bp	A/G

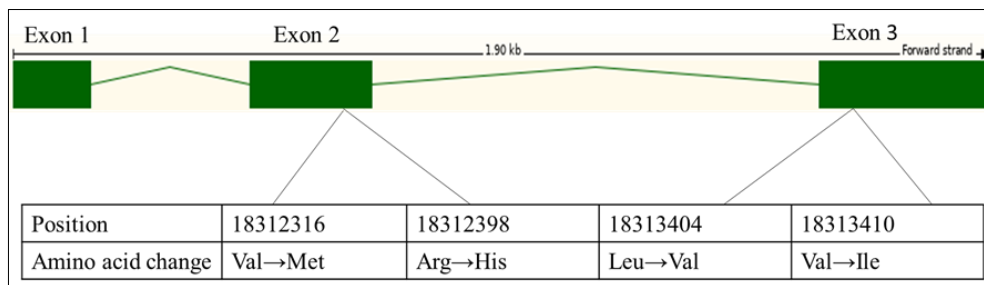


Fig 1: Four significant SNPs and their corresponding amino acid changes. (Solid blocks - exons, lines in between solid blocks – introns)

3.2 Haplotype analysis of 201 aus type genotypes

Among the eighteen significant non-synonymous SNP's found in *ONAC129* gene, four haplotypes namely H1, H2, H3 and H4 were formed which comprises 108, 15, 66 and 13 genotypes respectively based on only four SNP's (18312316, 18312398, 18313404 and 18313410) (Table 2 and Fig 2). The LD plot (Fig 3) showed the correlation of four SNPs involved in haplotype grouping. Previous studies on protein profiling by 2D PAGE during anthesis was evidently showed that upregulation of heat shock protein in N22 rice variety (Heat tolerant genotype). (Jagadish *et al.*, 2010)^[6] In this current

study, N22 has revealed the presence of a five non synonymous SNP in comparison with Nipponbare.

Table 2: List of significant SNPs in *ONAC129* for the subset of 3K RG panel

Marker Number	SNP site	Position	HWpval	MAF	Alleles
1	18312316	16411594	1.74E-44	0.415	A:G
2	18312398	16415068	7.83E-50	0.405	A:G
3	18313404	16415203	3.62E-21	0.065	C:G
4	18313410	16415254	1.17E-51	0.065	A:G

HWpval- Hardy Weinberg p value, MAF- Minor Allele Frequency

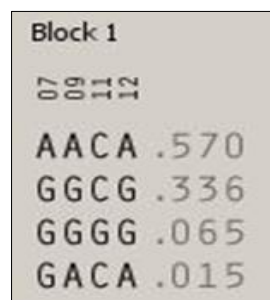


Fig 2: Haplotype block of significant SNPs in *ONAC129* using HaploView (SNP site: 07 – 18312316 (A→G), 09-18312398 (A→G), 11-18313404 (C→G), 12 – 18313410(A→G))



Fig 3: Linkage Disequilibrium plot of significant SNPs in *ONAC129* using HaploView

4. Conclusion

In 3K rice genome panel subset, *insilico* analysis of *ONAC129* revealed 74 SNP and 30 INDELS variants. Based on non-synonymous SNPs, four haplotype groups were identified by haplotype analysis. *ONAC129* with 114 allelic variations in 3K RG *aus* subset, only eighteen were found to be non-synonymous. Identification of novel variation/deletion in *ONAC129* can provide valuable information for deploying haplotype-based breeding to develop next-generation tailor-made better heat tolerant rice cultivars suiting future food demands with dwindling cultivable land and a fast growing population, as well as changing climatic circumstances.

5. References

1. Lyman NB, Jagadish KS, Nalley LL, Dixon BL, Siebenmorgen T. Neglecting rice milling yield and quality underestimates economic losses from high-temperature stress. *PloS one*. 2013;8(8):e72157.
2. Quint M, Delker C, Franklin KA, Wigge PA, Halliday KJ, Van Zanten M. Molecular and genetic control of plant thermomorphogenesis. *Nature plants*. 2016;2(1):1-9.
3. Li B, Gao K, Ren H, Tang W. Molecular mechanisms governing plant responses to high temperatures. *Journal of Integrative Plant Biology*. 2018;60(9):757-779.
4. Xu Y, Chu C, Yao S. The impact of high-temperature stress on rice: challenges and solutions. *The Crop Journal*. 2021;9(5):963-976.
5. Hu Y, Li L, Tian J, Zhang C, Wang J, Yu E, *et al*. Effects of dynamic low temperature during the grain filling stage on starch morphological structure, physicochemical properties, and eating quality of soft japonica rice. *Cereal Chemistry*. 2020;97(2):540-550.
6. Jagadish SVK, Muthurajan R, Oane R, Wheeler TR, Heuer S, Bennett J, *et al*. Physiological and proteomic approaches to address heat tolerance during anthesis in rice (*Oryza sativa* L.). *Journal of experimental botany*. 2010;61(1):143-156.
7. Mansueto L, Fuentes RR, Chebotarov D, Borja FN, Detras J, Abriol-Santos JM, *et al*. SNP-Seek II: A resource for allele mining and analysis of big genomic data in *Oryza sativa*. *Current Plant Biology*. 2016;7:16-25.
8. Tabassum J, Ahmad S, Hussain B, Mawia AM, Zeb A, Ju L. Applications and Potential of Genome-Editing Systems in Rice Improvement: Current and Future Perspectives. *Agronomy*. 2021;11(7):1359.
9. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, *et al*. PLINK: a tool set for whole-genome association and population-based linkage analyses. *The American journal of human genetics*. 2007;81(3):559-75.
10. Barrett JC, Fry B, Maller J, Daly MJ. Haploview: analysis and visualization of LD and haplotype maps. *Bioinformatics*. 2005;21(2):263-5.