



Category: Plant Genomics

The impact of natural selection on gene associated with panicle number formation in *Oryza sativa*

Manoj Kumar Gupta¹, Ramakrishna Vadde¹, Gayatri Gouda², Ravindra Donde², Jitendra Kumar², Subhashree Nayak² and Lambodar Behera^{2*}

¹Department of Biotechnology & Bioinformatics, Yogi Vemana University, Kadapa 516003, Andhra Pradesh, INDIA

²ICAR-National Rice Research Institute, Cuttack (Odisha) 753006, INDIA

*Corresponding author: lambodarjamujhadi@gmail.com

Abstract

Panicle number is directly associated with grain number in rice. As the panicle number increases, it affects the total yield of rice. We examined the evolution of genes associated with panicle number formation in *Oryza sativa*. Intramural program written in JAVA script and fastPHASE software used for the generation of genotype and haplotype file of SNPs of 11 individual genes associated with panicle number formation utilizing VCF file obtained from RiceCAP project (USDA/CSREES <http://www.uark.edu/ua/ricecap/>). Tests for natural selection executed on these genes using the Haplotype data. Tajima's D and Fu Li's D* analysis were performed using DNASP v4.0. Rates of non-synonymous Vs synonymous changes were calculated according to the dN/dS algorithm of Nei and Gojobori. dN/dS calculation compared with the ancestral (*Oryza meridionalis*) sequence individually showed that out of 11, almost all genes responsible for grain number formation, Os01g0746400, Os03g0203200, Os03g0706500, Os04g0550600, Os06g0127800, Os06g0154200, Os06g0610350, Os06g0660200, Os08g0162100 and Os11g0528700 are negatively selected throughout evolution., Although Tajima's D was not found significant, the negative value for 8 genes, Os01g0746400, Os03g0123300, Os03g0706500, Os06g0127800, Os06g0610350, Os06g0660200, Os08g0162100 and Os11g0528700 indicated that low frequency variants are more in number than high frequency variants. For Fu Li's D*, the significantly negative values in most of the genes, Os01g0746400, Os03g0123300, Os03g0706500, Os06g0127800, Os06g0610350, Os08g0162100 and Os11g0528700, indicated that the high frequency variants detected through Tajima's D are predominantly singletons. Thus, result from dN/dS, Tajima's D and Fu Li indicated that negative (purifying) selection acts on genes responsible for panicle number formation. These results will be useful for further investigation on how the genes associated with panicle number and how purifying selection result in stabilizing selection through the purging of deleterious variations that arise.

Citation: Gupta, M.K., Vadde, R., Gouda, G., Donde, R., Kumar, J., Nayak, S. and Behera, L. The impact of natural selection on gene associated with panicle number formation in *Oryza sativa* [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 198. <https://doi.org/10.24870/cjb.2017-a184>