

Genome-wide investigation of 20S proteasome family genes and their relevance to heat and drought tolerance in common wheat

Sachin Kumar*, Hemant Sharma, Ritu Batra and Sourabh Kumar

Department of Genetics and Plant Breeding, Chaudhary Charan Singh University, Meerut – 250 004 (UP) India

Corresponding author: Sachin Kumar

Department of Genetics and Plant Breeding, Chaudhary Charan Singh University, Meerut – 250 004 (UP) India.

✉ sachinkpsingh@gmail.com

Citation: Kumar S, Singh VP, Saini DK, Sharma H, Saripalli G et al., Genome-wide investigation of 20S proteasome family genes and their relevance to heat and drought tolerance in common wheat. J Plant Breed Agric.2022, 1:S1.

Abstract

The genes encoding α - and β -type subunits of 20S proteasome core protease are integral components of 26S proteasome complex in the ubiquitin-proteasome system (UPS). The 20S proteasome represents a catalytic particle that cleaves cytotoxic, denatured, damaged and unwanted proteins in an ATP/ubiquitin-dependent non-lysosomal pathway and is known to impart thermotolerance in model plants. In the present study, we identified a family of 67 genes (including 34 TaPA and 33 TaPB genes) encoding α - and β -subunits of 20S proteasome in bread wheat (*Triticum aestivum* L.). These genes were distributed on all the 21 wheat chromosomes, majority of them being in triplicate homoeologues. These wheat genes were orthologous to corresponding rice and Arabidopsis genes. The proteins encoded by each of the TaPA and TaPB genes contained 20 different motifs. These 20 motifs were present in corresponding proteins of Arabidopsis and rice. Phylogenetic analysis placed these genes in seven clusters, each with one of the seven α (α 1-7) and one of the seven β (β 1-7) subunits. Expression analysis suggested that 10 of the 67 genes were involved in heat stress response, whereas four genes were involved in drought tolerance at the seedling stage. Nine (9) genes were expressed under both heat and drought suggesting their involvement in response to multiple abiotic stresses. Future research on TaPA/TaPB genes will help in the development of climate-resilient wheat cultivars.

Received: January 27, 2022; **Accepted:** February 03, 2022; **Published:** February 08, 2022

Biography

Sachin Kumar is Assistant Professor of Genetics and Plant Breeding at Chaudhary Charan Singh University, Meerut, India. His research area covers Plant Genomics and Molecular Breeding in cereal crops particularly wheat, which include trait discovery and phenotyping, high-throughput SNP genotyping, construction of high-density genetic maps, physical and radiation hybrid maps, comparative mapping, QTL interval mapping, genome-wide association studies (GWAS), development of molecular markers, marker-assisted selection for biotic and abiotic stress-responsive traits. He has been NSERC Visiting Fellow under Canadian Government Laboratories Program at Agriculture and Agri-food Canada (AAFC), Swift Current, Saskatchewan, Canada.

References

- Kumar S, Singh VP, Saini DK, Sharma H, Saripalli G, Kumar S, et al. (2021) [Meta-QTLs, ortho-MQTLs, and candidate genes for thermo-tolerance in wheat \(*Triticum aestivum* L.\)](#). Mol Breeding 41: 69. [[Crossref](#)] [[Google Scholar](#)] [[Indexed at](#)]
- Gautam T, Kumar K, Agarwal P, Tyagi S, Jaiswal V, Gahlaut V, Kumar S, et al. (2021) [Development of white-grained PHS-tolerant wheats with high grain protein and leaf rust resistance](#). Mol Breeding 41: 42. [[Crossref](#)] [[Google Scholar](#)] [[Indexed at](#)]
- Kumar S, Fetch TG, Knox RE, Singh AK, Clarke JM, DePauw RM, et al. (2021) [Mapping of Ug99 stem rust resistance in Canadian durum wheat](#). Can. J. Plant Pathol. 43 (4): 599–611. [[Crossref](#)] [[Google Scholar](#)] [[Indexed at](#)]
- Kumar J, Kumar S, Kianian SF (2020) The wheat dwarf India virus-betasatellite complex has a wider host range that previously reported. Plant Health Progress 21:119-122. [[Crossref](#)] [[Google Scholar](#)] [[Indexed at](#)]
- Kumar S, Knox RE, Singh AK, DePauw RM, et al. (2018) [High-density genetic mapping of a major QTL for resistance to multiple races of loose smut in a tetraploid wheat cross](#). PLoS ONE 13(2): e0192261. [[Crossref](#)] [[Google Scholar](#)] [[Indexed at](#)]