SNPs Based Genetic Diversity Analysis of Elite Wheat Germplasm to Identify High Resistant Starch Genotypes for Type-2 Diabetic Patients

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Abstract (300 word limit)

Statement of the Problem:

Starch provides more than 70% daily caloric intake worldwide. This starch is readily digested to glucose leading to rapid increase in glycaemic index (GI), rendering an individual susceptible to type-2 diabetes. In contrast, resistant starch (RS), exhibits naturally or artificially modified structure. Increased RS uptake in daily food can significantly help in preventing colon cancer, early occurrence of type-2 diabetes and improves cardiovascular health.

Methodology and Theoretical Orientation:

Synthesis of RS is genetically controlled. Therefore, present study was designed to determine the genetic diversity in 250 elite wheat lines originated from CIMMYT and USDA to understand the mechanism of RS synthesis to identify suitable variants for the development of RS enriched wheat lines. SNPs targeting starch synthesizing enzymes were used to determine the genetic diversity among genotypes.

Findings and Conclusion:

Results indicated that genotypes exhibited variations for suitability to breeding program aimed at increasing RS content. However, this genetic diversity was narrow due to more emphasis on selection for yield. Increased, RS content was associated with altered physico-chemical starch properties. It was found that proportion of B-granules and altered granule morphology was highly correlated with increased RS. Our results also indicated that granule bound starch synthase (GBSS) and starch branching enzymes (SBEs) play major role in increasing RS content but genetic diversity targeting SBEs was found more effective. Alteration in protein complexes compared to wild type also added in increased RS content. This study first of its kind, shows that CIMMYT-originated Pakistani wheat germplasm exhibits genetic diversity which can be significantly used to develop wheat material with increased RS content.

Recent Publications (minimum 5)

1. Mushtaq R, Shahzad K, Shah ZH, Alsamadany H, Mujtaba T, Al-Zahrani Y, Alzahrani HAS, **Ahmed Z,** MansoorS, Bashir A, 2019. Development of expressed sequenced tags (EST) to identify some pathogen resistance genes expressed in Gossypium arboreum, Gene Reports,15. https://doi.org/10.1016/j.genrep.2019.100397.
2. Fatima M, **Ahmed Z,** Aslam M, Zaynab M. 2018. Drought effect and tolerance potential of wheat: a minireview. International Journal of Nanotechnology and Allied Sciences, 2(2), 16-21. https://journals.psmpublishers.org/index.php/ijnas/article/view/240.
3. •Fatima M, Abbas S, **Ahmed Z,** Sharif Y, Umair M, Bahadar K, Zaynab M. 2018. Plants Defense System Resist against the Pathogen Attack: Transcription Factors in Focus. International Journal of Nanotechnology and Allied Sciences.
4. **Ahmed Z,** Shah ZH, Rehman HM, Shahzad K, Daur I, Al-feel AA, Hassan MU, Elsafori AK, Yang SH, Chung G. 2017. Genomics: A hallmark to monitor molecular and biochemical processes leading toward a better perceptive of seed aging and ex-situ conservation. Current Issues in Molecular Biology, 22: 89-112.
5. **Ahmed Z,** Yang H, Fu YB. 2016. The associative changes in scutellum nuclear content and morphology with viability loss of naturally aged and accelerated ageing wheat (Triticum aestivum) seeds. Frontiers in Plant Science. http://dx.doi.org/10.3389/fpls.2016.01474.



Biography:

I am Dr. Zaheer Ahmed, currently working as an Assistant Professor, in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. I have completed PhD from the University of Guelph, Canada and Post-doctorate from the Agriculture and Agri-Food Canada (AAFC), Saskatoon, Canada. My research is focused on improving wheat quality using advanced molecular plant breeding techniques and genomics approaches.

Thank you.

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Notes/Comments: