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Title:	Genotyping-by-sequencing based QTL mapping identified a novel waxy allele contributing to high amylose starch in wheat
Authors:	Sharma, Vinita (/jspui/browse?type=author&value=Sharma%2C+Vinita)
Keywords:	Genotyping-by-sequencing QTL mapping novel waxy starch
Issue Date:	2021
Publisher:	Springer Link
Citation:	Euphytica, 217(6)
Abstract:	Health benefits associated with high amylose starch have drawn scientific interest to elevate amylose content in wheat. Despite of several attempts, the elucidation of genetic factors behind high amylose biosynthesis remains unclear. We identified variation for amylose content in a bi-parental population (F2:3), developed by crossing of high amylose donor 'TAC 75' and high yielding variety 'WH 1105' and report the first QTL map by Genotyping-by-sequencing. A stable QTL qhams7A.1 among 12 major effect QTLs was identified. Gene Ontology identified GBSSI, within qhams7A.1. High amylose donor carrying a novel missense mutation g.35767184 T > C in GBSSI led to mutant GBSSI_L539P. Subsequent analysis of mutant allele in a backcross population suggests the contribution of mutant allele to phenotype. The identified QTLs and GBSSI allele provide a useful resource for marker development and pre-breeding material for the trait.
Description:	Only IISER Mohali authors are available in the record.
URI:	<a href="https://doi.org/10.1007/s10681-021-02861-5">https://doi.org/10.1007/s10681-021-02861-5</a> ( <a href="https://doi.org/10.1007/s10681-021-02861-5">https://doi.org/10.1007/s10681-021-02861-5</a> ) <a href="http://hdl.handle.net/123456789/4422">http://hdl.handle.net/123456789/4422</a> ( <a href="http://hdl.handle.net/123456789/4422">http://hdl.handle.net/123456789/4422</a> )
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