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Record 1 of 1**Title:** SNP Discovery for mapping alien introgressions in wheat**Author(s):** Tiwari, VK (Tiwari, Vijay K.); Wang, SC (Wang, Shichen); Sehgal, S (Sehgal, Sunish); Vrana, J (Vrana, Jan); Friebe, B (Friebe, Bernd); Kubalaková, M (Kubalaková, Marie); Chhuneja, P (Chhuneja, Praveen); Dolezel, J (Dolezel, Jaroslav); Akhunov, E (Akhunov, Eduard); Kalia, B (Kalia, Bhanu); Sabir, J (Sabir, Jamal); Gill, BS (Gill, Bikram S.)**Source:** BMC GENOMICS **Volume:** 15 **Article Number:** 273 **DOI:** 10.1186/1471-2164-15-273 **Published:** APR 10 2014**Times Cited in Web of Science Core Collection:** 21**Total Times Cited:** 21**Usage Count (Last 180 days):** 1**Usage Count (Since 2013):** 51**Cited Reference Count:** 69**Abstract:** Background: Monitoring alien introgressions in crop plants is difficult due to the lack of genetic and molecular mapping information on the wild crop relatives. The tertiary gene pool of wheat is a very important source of genetic variability for wheat improvement against biotic and abiotic stresses. By exploring the 5M(g) short arm (5M(g)S) of *Aegilops geniculata*, we can apply chromosome genomics for the discovery of SNP markers and their use for monitoring alien introgressions in wheat (*Triticum aestivum* L.).Results: The short arm of chromosome 5M(g) of *Ae. geniculata* Roth (syn. *Ae. ovata* L.; $2n = 4x = 28$, (UUMMg)-U-g-M-g-M-g) was flow-sorted from a wheat line in which it is maintained as a telocentric chromosome. DNA of the sorted arm was amplified and sequenced using an Illumina HiSeq 2000 with similar to 45x coverage. The sequence data was used for SNP discovery against wheat homoeologous group-5 assemblies. A total of 2,178 unique, 5M(g)S-specific SNPs were discovered. Randomly selected samples of 59 5M(g)S-specific SNPs were tested (44 by KASPar assay and 15 by Sanger sequencing) and 84% were validated. Of the selected SNPs, 97% mapped to a chromosome 5M(g) addition to wheat (the source of t5M(g)S), and 94% to 5M(g) introgressed from a different accession of *Ae. geniculata* substituting for chromosome 5D of wheat. The validated SNPs also identified chromosome segments of 5M(g)S origin in a set of T5D-5M(g) translocation lines; eight SNPs (25%) mapped to TA5601 [T5DL . 5DS-5M(g)S(0.75)] and three (8%) to TA5602 [T5DL . 5DS-5M(g)S (0.95)]. SNPs (gsnp_5ms83 and gsnp_5ms94), tagging chromosome T5DL . 5DS-5M(g)S(0.95) with the smallest introgression carrying resistance to leaf rust (Lr57) and stripe rust (Yr40), were validated in two released germplasm lines with Lr57 and Yr40 genes.

Conclusion: This approach should be widely applicable for the identification of species/genome-specific SNPs. The development of a large number of SNP markers will facilitate the precise introgression and monitoring of alien segments in crop breeding programs and further enable mapping and cloning novel genes from the wild relatives of crop plants.

Accession Number: WOS:000334958900001**PubMed ID:** 24716476**Language:** English**Document Type:** Article**KeyWords Plus:** RUST-RESISTANCE GENES; TRITICUM-AESTIVUM L.; SINGLE-NUCLEOTIDE POLYMORPHISMS; IN-SITU HYBRIDIZATION; HEXAPLOID WHEAT; BREAD WHEAT; AEGILOPS-GENICULATA; POLYPLOID WHEAT; COMMON WHEAT; STEM RUST**Addresses:** [Tiwari, Vijay K.; Sehgal, Sunish; Friebe, Bernd; Kalia, Bhanu; Gill, Bikram S.] Kansas State Univ, Dept Plant Pathol, Wheat Genet Resource Ctr, Manhattan, KS 66506 USA.

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Publisher: BIOMED CENTRAL LTD**Publisher Address:** 236 GRAYS INN RD, FLOOR 6, LONDON WC1X 8HL, ENGLAND**Web of Science Categories:** Biotechnology & Applied Microbiology; Genetics & Heredity**Research Areas:** Biotechnology & Applied Microbiology; Genetics & Heredity**IDS Number:** AF8IK**ISSN:** 1471-2164**29-char Source Abbrev.:** BMC GENOMICS**ISO Source Abbrev.:** BMC Genomics**Source Item Page Count:** 11**Funding:**

| Funding Agency | Grant Number |
|---|--|
| Czech Science Foundation | P501/12/G090 |
| Ministry of Education, Youth and Sports of the Czech Republic | |
| European Regional Development Fund (Operational Programme Research and Development for Innovations) | ED0007/01/01 |
| Kansas State University | |
| King Abdulaziz University | |
| Kansas Wheat Commission | |
| Heartland Plant Innovations | |
| NSF | CNS-1006860 EPS-1006860 EPS-0919443 IIP-1338897 |

We thank the International Wheat Genome Sequencing Consortium (Bethesda, USA) for providing pre-publication access to the shotgun sequence assemblies of wheat chromosomes 5AS, 5BS and 5DS. We thank our colleagues Jarmila Cihalikova, Romana Sperkova and Zdenka Dubska for assistance with chromosome sorting and DNA amplification. We thank Jon W. Raupp and Nidhi Rawat, WGRC, for critical reading of the manuscript. JD, JV and MK were supported by the Czech Science Foundation (award no. P501/12/G090) and by the Ministry of Education, Youth and Sports of the Czech Republic and the European Regional Development Fund (Operational Programme Research and Development for Innovations No. ED0007/01/01). VKT was supported by a research agreement grant between Kansas State University and King Abdulaziz University. Part of the research in BSG lab was supported by grants from Kansas Wheat Commission and Heartland Plant Innovations. The computing for this project was performed on the Beocat Research Cluster at Kansas State

University, which is funded in part by NSF grants CNS-1006860, EPS-1006860, and EPS-0919443. This is the contribution number 14-319-J from Kansas Agricultural Experiment Station, Kansas State University, Manhattan KS 66506-502, USA. Work was done under the auspices of WGRC I/UCRC partially funded by NSF grant contract (IIP-1338897).

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Output Date: 2017-07-31

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