Title
High-throughput approaches to genome-wide analysis of genetic variation in polyploid wheat

Permalink
https://escholarship.org/uc/item/727211fb

Journal
CANADIAN JOURNAL OF PLANT SCIENCE, 92(3)

ISSN
0008-4220

Authors
Akhunov, E
Chao, S
Saintenac, C
et al.

Publication Date
2012-05-01

Peer reviewed
specialized multitrophic pest complexes whose members interact in both positive and negative ways. In this context, management recommendations based on the traditional single-species pest control paradigm may lead to undesirable outcomes. Our goal was to evaluate a modeling framework to make multi-pest management decisions that take into account the existence of direct and indirect interactions among pests belonging to different trophic levels. We adopted a Bayesian decision theory approach in combination with path analysis to evaluate interactions between *Bromus tectorum* (cheatgrass), *Fusarium* crown rot, and *Cephus cinctus* (wheat stem sawfly). We assessed the joint response of these pests to seeding rates, cultivar competitiveness, and cultivar wheat stem sawfly tolerance. Results indicate that yield differences can be more readily explained as a result of the effects of management on pests and multi-pest interactions, rather than just by the direct effect of any particular management scheme on yield. For example, wheat stem sawfly tolerant varieties should be planted at a low seeding rate under high insect pressure. However, this variety should be replaced by a competitive and drought tolerant cultivar at high seeding rates as *B. tectorum* levels increase, despite the persisting wheat stem sawfly infestation. Also, the incidence of *Fusarium* can be explained by the abundance of *B. tectorum*, an alternative host for this disease. Our research suggests a framework for establishing a balance between model simplicity and the complexity of the process being modeled.

High-throughput approaches to genome-wide analysis of genetic variation in polyploid wheat. E. Akhunov1*, S. Chao2, C. Saintenac2, S. Kiani2, D. See3, G. Brown-Guedira4, M. Sorrells5, A. Akhunova6, J. Dubcovsky6, C. Cavanagh8, and M. Hayden9. 1Department of Plant Pathology, Kansas State University, Manhattan, KS 66506, USA; 2USDA-ARS Biosciences Research Laboratory, Fargo, ND, USA; 3USDA Western Region Small Grains Genotyping Lab, Johnson Hall, WSU, Pullman, WA, USA; 4USDA-ARS Eastern Regional Small Grains Genotyping Lab., 4114 Williams Hall, NCSU, Raleigh, NC, USA; 5Plant Breeding & Genetics, Cornell University, NY, USA; 6Integrated Genomics Facility, Kansas State University, Manhattan, KS, USA; 7Department of Plant Sciences, University of California, Davis, CA, USA; 8CSIRO, Food Futures National Research Flagship, Canberra, ACT 2601, Australia; and 9Department of Primary Industries Victoria, Victorian AgriBiosciences Center, 1 Park Drive, Bundooora, VIC 3083, Australia.

Genome-wide analysis of genetic variation is a powerful tool for detecting marker-trait associations in diversity panels and mapping populations. Genome scale genotyping data can be generated using high-throughput assays capable of detecting allelic variation in a predefined set of SNP loci or by direct sequencing. The combined effort of several research groups in collaboration with the International Wheat SNP Working Group developed high-throughput SNP genotyping assays based on the Illumina iSelect platform. The assay was used to genotype 12 000 wheat lines including cultivars, landraces, wild relatives and the progeny of several mapping populations. Out of ~9000 SNP assays 95% produced high-quality genotype calls with up to 70% being polymorphic in a diverse sample of wheat cultivars with a minor allele frequency >0.05. Two high-density genetic maps based on SynOp and 4-way MAGIC populations were developed. An alternative approach to SNP detection relies on next-generation sequencing technologies for direct sequencing of complexity reduced genomic libraries prepared either by restriction digestion or by selective capture of genomic regions of interest. These sequence-based genotyping approaches demonstrated high efficiency for detecting allelic variation in the wheat genome. The applicability of iSelect assay and genotyping-by-sequencing approaches for the analysis of genetic variation and genotype-phenotype relationships in wheat will be presented.

Overview and progress of the CTAG project. C. McCartney1, C. Pozniak2, A. Sharpe3, R. MacLachlan3, P. Hucl3, M. Jordan3, R. Knox4, H. Randhawa5, D. Spaner6, F. Bekkaoui6, V. Galushko7, and R. Gray8. 1AAFC-Cereal Research Centre, 195 Dafoe Road, Winnipeg, Manitoba, Canada; 2Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK; 3Plant Biotechnology Laboratory, Fargo, ND, USA; 4AAFC-Semiarid Prairie Agricultural Research Centre, Box 1030, Swift Current, Saskatchewan, Canada; 5AAFC-Cereal Research Centre, 5403 1st Ave South, Lethbridge, Alberta, Canada; 6Department of Agricultural, Food and Nutritional Science, University of Alberta, 4-16D Agriculture Forestry Ctr, Edmonton, Alberta, Canada; 7Department of Economics, University of Regina, 3737 Wascana Parkway, Regina, Saskatchewan, Canada; and 8Department of Bioresource Policy, Business & Economics, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, Canada.

The Canadian Triticum Advancement through Genomics (CTAG) project aims to provide genetic information and tools for the improvement of molecular breeding in wheat. The project has four major activities: (1) generating the first complete sequence of chromosome 6D, (2) capturing and sequencing genomic coding sequences from Canadian wheat varieties, (3) identifying, validating, and mapping SNP markers in Canadian wheat germplasm, and (4) examination of the role of public-private partnerships in wheat genomics and breeding (GE3LS research). Sequencing of chromosome 6D will be done on a BAC by BAC basis, as agreed