DURUM WHEAT GENOMICS:
FROM SEQUENCING TO BREEDING

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Innovative breeding methods are required to improve the genetic gain of durum wheat (*Triticum turgidum* L. var *durum* Desf.) to meet the global challenges resulting from a growing human population and environmental changes. In our wheat breeding programs at the University of Saskatchewan and AAFC, we are utilizing next-generation sequencing to enhance high density single nucleotide polymorphism (SNP) arrays implemented in marker assisted selection (MAS) and genomic selection (GS) routines. These dense marker data sets, coupled with the recent availability of tetraploid wheat genome assemblies, are paving the way to uncovering the genetic control of important traits in wheat. Furthermore, we are performing low coverage sequencing of multiple breeding lines and cultivars to access the dispensable genome of durum wheat. In addition to identifying physical regions and gene candidates associated with phenotypic targets of selection, we are working to fully characterize complex traits and their underlying cause through transcriptome/exome sequencing. Automated and high-throughput imaging technologies are being developed that will not only support functional annotation and gene discovery, but together with advances in computational biology, will reduce current phenotyping bottlenecks. We anticipate that integration of all these "omic" technologies will be instrumental for determining the underlying control of important traits that when applied to breeding improve our rates of genetic gain, and accelerate release of superior cultivars for wheat growers globally.

ABSTRACT