



Elevated Mutation Burdens in Canadian Oat and Wheat Cultivars Released over the Past Century

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Summary:

Deleterious mutations, those that disrupt normal gene functions and negatively impact an individual's fitness or ability to survive and reproduce, are common in plant genomes, including in modern high-yielding crop cultivars. A cultivar carrying more deleterious mutations is expected to have higher vulnerability to environmental changes with lower reproduction success and survival, which can limit plant breeding efficacy. However, little is known about the extent of deleterious genetic variants (or mutation burden) present in different cultivars, particularly in those released over different breeding periods.

This paper describes a study using RNA-Seq to screen for genome-wide deleterious genetic variants in 141 oat and 142 wheat cultivars released through Canadian breeding programs over the past century. Genetic variants characterized by single nucleotide polymorphisms were identified across the genome and the associated genes annotated. Nucleotide substitutions (or genic variants) residing in evolutionarily-conserved chromosomal segments (or genic regions) are predicted to be detrimental to their gene functions or derived proteins. The more conserved a chromosomal segment is, the more detrimental the nucleotide substitution will be. These variant-associated functional predictions revealed 5726 and 3022 deleterious genetic variants across all 21 chromosomes of both the oat and wheat genomes, respectively.

For the most part, the identified deleterious variants were found in only a few cultivars and are predicted to be involved with genes for diverse biological processes, cellular components, and molecular functions. A diverse genetic background of deleterious variants suggests that they may be associated with many traits, some of which could be breeding targets, such as yield and biotic resistance.

At the early seedling stage, different gene expression profiles were observed between oat and wheat cultivars, with none of the top 30 impacted biological processes being the same. This suggests different genetic impacts of Canadian oat and wheat breeding on the genomes of released cultivars, including the accumulated mutations.



There were large variations in mutation burden estimates for each cultivar in both oat and wheat. More interestingly, these mutation burdens were found to be higher in recent cultivars. This finding indicates that existing deleterious mutations accumulated over the different breeding periods, even with multiple cycles of selfing to select genes for increased yield and/or disease resistance. This is expected, as 81% and 98% of the identified deleterious mutations in oat and wheat cultivars were predicted to be weakly or mildly detrimental, respectively. Theoretically, selfing can effectively purge deleterious mutations of large effect such as those resulting in lethal or sub-lethal genes, but those of minor effect are less likely to be eliminated and thus accumulate over time.

Genetic analyses also revealed that broadening the genetic base of both crops by introducing new germplasm (e.g., from related species) has resulted in genetic shifts and expansions over time.

These findings are significant, as they provide the first empirical evidence of elevated mutation burdens in recent Canadian oat and wheat cultivars and the first genomic profiles of deleterious variants in released cultivars, which will be useful for understanding the genetic risk and developing breeding strategies involving the use of gene editing to minimize it in the breeding programs.