

## APPLYING THE TOOLS OF GENOMICS TO SUNFLOWER BREEDING ISSUES

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### ABSTRACT

The last four years have been an illuminating time in the history of sunflower genomics. We have seen the release of the first draft of a public sunflower genome. This reference has been wrought with complexity that is still being investigated, but has presented opportunities to understand our favorite species in ways that we have only dreamed of before. From the perspective of the evolutionary biologist, we can obtain greater understanding of how selection has changed this crop, in both expected and unexpected ways. We are beginning to understand how our inbred lines and hybrids are different in terms of genome size and organization, and not simply on their phenotypic trait structure. In this plenary, I will discuss some of the practical tools that arise out of the sequenced genome. At the USDA in Fargo, together with collaborators at University of Colorado, we have used our historical breeding records complete with phenotypic data to develop a Genomic Selection system. Genomic Selection takes sequence information from parents and progeny in the breeding program, trains a model that assigns breeding values to each polymorphic site in the genomic dataset, and uses the model to make informed selection decisions, fully utilizing the historical phenotypic data that is pertinent to the environments of interest. This should improve accuracy and balance in selection in early generations of progeny, resulting in optimized genetic gain compared to previous inefficient, unbalanced methods. A more familiar model is the GWAS or association mapping model. Community resources have been developed around this system, and can result in greater understanding of quantitative traits of large importance (e.g. fatty acid variation in oilseed sunflower). Genomics has also allowed us to better understand the importance of mutation in breeding programs, allowing us to see for the first time the variety in mutations found in mutagenesis experiments. These advances allow the sunflower community to enter a new age of informed breeding, which could lead to acceleration of genetic gain in the future.

**Key Words :** genomics, breeding, quantitative genetics, genomic selection, GWAS