

## **Comparison of different approaches to estimate linkage disequilibrium extent in crop breeding populations**

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The increasing global concern over crop improvement and agricultural production in the face of continuous population growth and climate change has led to the widespread use of genomic selection as a tool in crop breeding. However, traditional, and non-traditional selection methods can result in a significant loss of genetic diversity in modern varieties, making the maintenance of genetic diversity just as important as genetic gain. One way to achieve this is by understanding and measuring linkage disequilibrium (LD), which refers to the non-random association of alleles at different loci. LD is a valuable tool in population genetics and evolutionary biology, used for mapping quantitative trait loci, estimating effective population size and past founder events, and detecting genomic regions under selection. However, measuring the pattern and extent of LD is influenced by several factors, including mating type, genetic drift, gene flow, selection, mutation, population substructure and relatedness, and the statistical tools used. This talk will compare different approaches commonly used to model LD decay and their impact on estimating the extent of LD, focusing on inbred sunflower lines from a mature breeding program.