

Developing tools to accelerate plant breeding

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Plant breeding is the art and science of genetic improvement of plants for the benefit of humankind. The agronomic traits for improvement differ with the plant species and the geographical region for cultivation. Breeding programs evaluate thousands of breeding lines every year for the selection of plants with desirable traits using conventional selection methods such as visual inspection or with more advanced selection techniques involving molecular markers (genotypic selection) to automate and accelerate selection. Molecular markers are successfully used for genotypic selection of numerous agronomic traits in various plant species. In the recent years, plant phenotyping with sensors has become popular for phenotypic selection i.e., selection based on the phenotype of a plant. New statistical methods are being developed to increase the accuracy of selection with genotypic and phenotypic data.

The methods used for progeny selection depends on the agronomic trait of interest and the difficulty in evaluating the trait. A selection method should be economical, feasible and precise and should shorten the time for cultivar development. For example, molecular markers for disease resistance allow early selection of resistant plants thus saving both time and resources. Therefore, there is a high interest in the plant breeding community for developing and implementing molecular markers for disease resistance. We evaluated a large panel of winter wheat germplasm for resistance to the disease *Septoria tritici* Blotch (STB) and identified a major resistance locus (molecular marker) for STB. In another project, we developed an approach to identify candidate genes in relatively small bi-parental populations. In this approach, we combined DNA molecular marker analysis with whole genome expression analysis in a winter wheat bi-parental population and successfully identified three candidate genes for yellow rust disease resistance. In a separate project, we also developed an approach to use protein molecular markers for resistance breeding and combined proteomics and machine learning to identify eight protein markers for resistance to late blight disease in potato. These molecular markers enable marker-assisted selection of resistant plants in the breeding programs incorporating disease resistance in new cultivars.

Phenotyping in the field allows further evaluation of key agronomic traits, adaptation to the environment and the overall performance of plants. Manual phenotypic evaluation in the field is laborious and thus methods for automated phenotyping can be more resource efficient. For example, in wheat, early vigour trait which is faster growth in initial plant growth stages is beneficial for weed competition and in utilizing nutrients from the soil in early stages. Early vigour trait can be measured from plant biomass at the seedling stage. We developed a low cost imaging system and evaluated a panel of winter wheat genotypes for early vigour trait under controlled conditions and identified several genotypes with high vigour. In another project, we developed phenotyping methods for disease detection in wheat by utilizing phenotyping sensors and machine learning. These phenotypic selection methods are non-destructive and are thus complementary to other selection methods and automate the selection of superior plants in the breeding programs. These new methods for selection generate a large amount of data and thus efficient data analysis is required to identify molecular markers and phenotypes. We have thus developed open-source software packages to interactively analyze and visualize such high-throughput data.

Further development of new techniques for identifying molecular markers, automated phenotyping in controlled and field conditions and data analysis methods will play a key role in producing superior cultivars for sustainable agriculture and food security in the changing climate.