

## **Utilizing Genetic Resources for Prebreeding of Stress Resistant Sugar Beet Germplasm: Using Molecular Tools**

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In the last thirty years, disease pressure has compelled sugar beet breeders to begin utilizing other cultivated beets and wild relatives as genetic resources, despite the reluctance of earlier breeders, who had avoided these sources due to the many undesirable traits introgressed with the resistance genes. In the U.S., public breeders do much of the sugar beet prebreeding. The development of molecular biology has impacted both the methodology and objectives of this germplasm enhancement effort. While introgressing genes, marker development, gene mapping, and gene discovery increasingly are becoming additional goals of the prebreeding effort. For example, the discovery of the vernalization gene in sugar beet, *BvFL1*, was part of a project to use molecular markers to understand the genetic variation present in populations of wild sea beet. Other wild beet populations, used as disease resistant donors, are providing one parent in mapping populations to indentify individual genes or QTLs responsible for that source of resistance. As genetic resources provide new sources of genetic variation in commercial variety development, breeders also are developing the population structure and information necessary to enable genomic and proteomic analyses of the genetic resources available to sugar beet breeders. The identification of major genes within other sections of *Beta*, (or other taxa) facilitates transgenic approaches to disease resistance. This prebreeding effort has increased the use of wild relatives as genetic resources and underscores the need for these populations in our genebank collections.

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