Molecular Characterization of Wild Beet in the Imperial Valley's Commercial Sugar Beet Fields

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Wild beet, including Beta macrocarpa and Beta vulgaris ssp. maritima, is a major production constraint on sugar beet throughout the world and especially to the Imperial Valley, California’s only major source of sugar beet production. Gene flow could transfer the glyphosphate resistance gene to the wild beet if crossing were to occur between the wild beet and commercial sugar beet. This would render RoundUp, currently the most effective herbicide for wild beet, ineffective. Thus, weed control would become very difficult for farmers. There is a need to know whether gene flow has occurred. Phylogenetic tree and marker sequences show that the wild beet is Beta macrocarpa and that there exists two distinct populations of this wild beet. One of these populations contains individuals very similar to the commercial sugar beet, suggesting that hybridization has most likely occurred and can occur again in the future. As a result, there was a need to be able to quickly determine whether a given wild population has glyphosphate resistance. To this effect this study developed an effective and inexpensive chemical assay that may be conducted in a greenhouse setting. Finally, wild beet individuals from the Imperial Valley were mapped by location with their corresponding population structure grouping. A correlation was found between the location and group, showing that the accessions that are similar to the sugar beet are found in the southern part of the Valley; therefore, this region requires special care and attention to avoid future hybridization with wild beet and sugar beet.

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