

Identification of Superior UCB-1 Rootstocks Using DNA Markers

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INTRODUCTION

There is now a variety of biotechnology and genomic approaches available for crop improvement. We are developing and adapting such approaches for pistachio to ensure that pistachio does not lag behind in benefitting from these technological advances. Pistachio has a small genome, and application of these approaches provides several opportunities for rapid and significant improvement of the crop, particularly with regard to determining the basis of the stunting problem and increasing the reliability of the performance of the UCB-1 rootstock.

RESULTS

We are using high-throughput DNA sequencing and genotyping technologies to identify and manipulate natural genetic variation that influence the performance of the UCB-1 rootstock and stunting of scions. In the first two years of this project, libraries of many genes transcribed (expressed) in leaves of pistachio were generated, sequenced, assembled, and analyzed to determine the level of variation within and between each of the parents of UCB-1 (*Pistacia atlantica* female x *P. integerrima* male). Genotyping by sequencing of a random set of 95 UCB-1 trees plus the parental trees was made, as well as reduced representation sequencing of 957 UCB-1 trees growing in Davis. This is the foundation for generating ultra-dense, gene-based genetic maps of both parental species that is currently underway. This will assign many genes to genetic bins ordered along each chromosome of pistachio. Measurements of phenotypes, including height and trunk caliper, have been made every year to provide data on the performance of UCB-1 trees. The genetic basis of the phenotypic variation will be analyzed to reveal the number and positions of chromosomal regions responsible for each trait as well as markers for them. The data will be displayed on a website to make genetic and horticultural information publicly accessible over the internet. This year, additionally, DNA was extracted from 1032 grafted UCB-1 trees, from commercial orchards in Central Valley, and GBS libraries were sequenced. Performance in commercial orchards will be further analyzed in subsequent years to dissect the genetic and environmental basis of the stunting phenomenon.

CONCLUSION AND APPLICATIONS

The genomics data and the phenotypic data will be combined to find molecular markers for growth. This will enable early detection of UCB-1 seedlings that will grow into low-vigor trees so that they can be rogued and not used in orchards.