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“Marker-Assisted Selection” Makes Efficient Table Grape Breeding

VitisGen2 Identifies 70+ Marker-Trait Associations

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Table grape breeders – both private and public – have an enviable record of success. They have brought the industry a wide range of new cultivars – introduced on a regular basis – that help the industry adapt to changes in the marketplace and new trends. Unlike wine grape breeders, they are not hampered by varietal labels like Chardonnay and Cabernet Sauvignon – names that date back to the 17th century. Consumers readily accept new table grape varieties.

Yet, grape breeders have been flying blind. Unlike corn or soybean breeders that have access to inbred, genetically uniform lines to guide their efforts, grape breeders must use highly heterozygous (genetically variable) parents to make their crosses. Corn breeders can use genetic tools to evaluate 1000s of progeny at the seed stage, select to plant only those individuals with potentially desirable traits, and evaluate them in the field within a few months. With grapevines, the cycle from seed to seed takes a minimum of 2-3 years. And field evaluations of yield and quality generally involve at least 3 annual cropping cycles.

So breeding grapevines has involved a large amount of trial and error – and a limited understanding of the genetics behind important traits. To compensate, breeders make more crosses and produce more progeny to find the proverbial



Figure 1. A ‘poor color’ parent (“01-5024-10”) and a ‘good color’ parent (“Scarlet Red”) were crossed to make a ‘mapping population’ of 300 unique individuals. This mapping population will be used to identify DNA markers for red color.

needle in the haystack: The new variety that combines desirable traits in a novel way. It takes many thousands of seedlings to identify each new variety.

DNA Sequencing Gets Cheaper

New developments in DNA sequencing technology are changing the field. The cost of obtaining DNA sequence information has plummeted – The cost of sequencing each mega-base (that’s 1 million DNA base pairs) now stands at a little more than a penny (1.2 cents), down from \$500 in 2007. Cheap DNA sequencing information is providing breeders with more information to

guide their otherwise ‘conventional’ (Non-GMO) breeding programs.

Note that grape breeders are still making crosses in the same way that plant breeders have done for centuries: They take pollen from one parent and use it to fertilize flowers of another parent. Beyond this natural process, there is no other genetic manipulation happening.

What rapid and inexpensive DNA sequencing allows them to do is to identify DNA markers that are associated with traits. These markers are like mailing addresses specifying locations on a map of the 19 grape chromosomes. Once they

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Breeding

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have these DNA markers, they can then test new vines at the seedling stage, and discard those that don't have the appropriate markers. This technique, called marker-assisted selection, makes the breeding and selection process much more efficient.

This may not sound dramatic, but it really is a big deal. Each seedling that is placed out in the field for evaluation involves an added expense (3-4 years for establishment, and field space) – so if you can find out that a given plant doesn't have the traits you want when it's a seedling, you can toss it early and avoid the time and expense of evaluating it for several years.

Markers for Red Berry Color

A good example is the new effort at the Parlier USDA laboratory to find DNA markers for fruit color. As part of the USDA-funded VitisGen2 project, USDA breeders Craig Ledbetter and Rachel Naegele are working to identify DNA markers for red berry color.

To do this, they have crossed a breeding accession with poor color (01-5024-10) with a variety with great color (Scarlet Royal). The 300 seedlings resulting from this cross – called a 'mapping population' by breeders – are expected to produce vines having a variety of berry colors ranging from very poor to very good when they begin fruiting this season.

For each of these 300 seedlings, researchers will collect tissue samples and amplify and sequence DNA segments that correspond to different locations among the 19 grape chromosomes. Because the parents of these 300 individuals are highly heterozygous (genetically variable), each seedling is a unique combination of genes. By comparing them, using a new testing methodology called AmpSeq, researchers will be able to identify

01-5024-10



Scarlet Royal



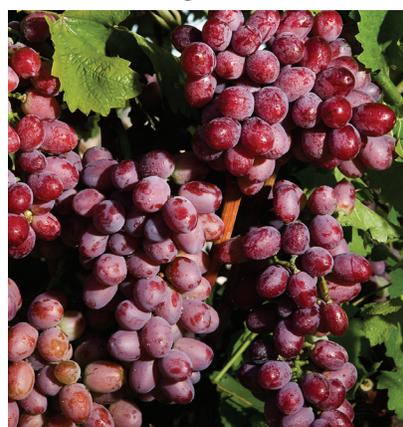
Figure 2. Color samples of berries from '01-5024-10' and 'Scarlet Royal', parents of a 300-vine 'mapping population' at the San Joaquin Valley Agricultural Science Center in Parlier, CA. Numbers indicate the percentage of red color on the berries.

around 7000 short DNA segments that function much like highway 'mile markers' to locate different genetic regions.

At the same time, imaging techniques will allow them to quantify berry skin color in each of the 300 progeny. By matching up color metrics with the DNA 'mile markers', they will be able to identify genetic regions, called 'QTLs' or 'quantitative trait loci' that are associated with genes that influence color.

Once these DNA markers associated with color are identified, breeders will be able to test seedlings shortly after they germinate, and save only the ones that have the desired DNA markers. This is marker-assisted selection.

The savings and increased



efficiency are potentially enormous. Instead of wasting valuable nursery and vineyard space waiting for 2-3 years to see if the grapes are the desired color, breeders will be able to make better decisions about what to toss and what to keep much earlier in the process.

The VitisGen2 project has identified more than 70 marker-trait associations for disease resistance and fruit quality traits. As these markers become available to commercial and public breeding programs, expect a quantum leap in their ability to confidently incorporate useful traits into new varieties – lowering the cost of breeding and helping the table grape industry maintain its competitiveness in years to come.

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