

of these images with vineyard disease occurrence and more precise determinations of real-time severity. The app also calculates the disease incidence, or percentage of bunches affected, logs their GPS coordinates and reports both severity and incidence data via email for later analysis.



Eileen Scott, project leader and professor of plant pathology in University of Adelaide's School of Agriculture, Food and Wine, says the app can help all sizes of growers but may be more powerful for larger operations.

Scott feels PMapp helps all sizes of growers, but recognizes it may be more powerful for larger operations. "The efficiency gains for large growers will be larger because the app should make it easier to manage data collected by multiple assessors, as the results of the in-field assessment can be emailed by the assessor direct to his or her manager," says Scott. "The email cover message would contain the details of vineyard and block, assessment strategy plus any other information required can be added via the notes facility."

Since powdery mildew can be difficult to distinguish from other diseases, spray residue or dust, PMapp has a supporting website (www.pmassessment.com.au) that offers additional resources to help train new staff and refresh the skills of experienced staff. These include a collection of photographs showing powdery mildew symptoms of varying severities on diverse grape bunches to advance users' disease identification skills and a tool for severity estimation training. The website also offers a guide to vineyard assessment.

PMapp was created specifically to aid personnel in identification

and assessment of powdery mildew, but some pilot users have realized its usefulness with other diseases. "Although PMapp was developed for assessing the severity of powdery mildew, we used the app for bunch rot assessment as well," says Ian Macrae, who works as a viticulturist with CCW Cooperative Ltd., based in the Riverland of South Australia, a wine-grape growers' co-op of almost 600 members. "Accurate assessment of severity is required when the patch is facing possible rejection. PMapp was a great tool in making decisions acceptable to both grower and winery."

Scott also says she had inquiries from the United States, Chile, Germany, Italy and New Zealand about global availability soon after the Australian pilot began in December 2015. "Representatives of Accolade Wines and Treasury Wine Estates indicated they're keen to use the app in their U.S. operations. In addition, two members of our project steering group, who are now based in the United States, took part in the early stages of development and can now use it in their current positions." You can find PMapp in Apple's App Store or Google Play.

Sequencing Breakthrough Advances Genome Studies



Bruce Reisch, professor at Cornell University's School of Integrative Plant Science, believes genome sequence data is just the beginning.

A powerhouse partnership of scientists representing nine different institutions has developed two new computer algorithms capable of mapping complex genomes in unprecedented, contiguous detail. Called FALCON and FALCON-unzip, the open-source algorithm was initially tested on several plant species, including Cabernet Sauvignon under the guidance of Dario Cantu, plant geneticist with the UC Davis department of viticulture and enology. "The new [sequencing] process provides rapid access to genetic information that Cabernet Sauvignon has inherited from both its parents, enabling us to identify genetic markers to

use in breeding new vines with improved traits," says Cantu in a UC Davis press release.

A genome of *Vitis vinifera* was previously sequenced in 2007. However, the sequencing technology at the time didn't convey the full details wrapped in the comparatively simple *V. vinifera* genome and hasn't been very effective with complex, diploid genomes, including cultivars like Cabernet Sauvignon. Diploids have duplicate chromosomes, one sourced from each parent. Most sequencing algorithms ignore one chromosome entirely, which can leave out unique genetic details found nowhere else. "Having just one

genome sequence until now was quite a limitation to finding genes related to quality, stress resistance and disease resistance," explains Bruce Reisch, professor in the horticulture section of Cornell University's School of Integrative Plant Science.

Reisch says that, while creation of the FALCON algorithms boosts genome studies, new grape varieties have been under development for some time. "Some have benefited from the genome sequenced and published in 2007, but many others were under development prior to that," he says. "There are Pierce's Disease-resistant grapes being developed in California, disease-resistant and cold hardy grapes at Cornell and highly cold hardy grapes at the University of Minnesota."

Reisch believes genome sequence data is just the beginning. "From here, we'll begin to understand how genes and the control of their expression interact with the environment to produce quality wine and grape products that are unique to each variety,"

Reisch says. "Genome sequencing increases the precision of efforts and is so important that research is underway around the world to sequence additional genomes of *vinifera* grapes and related grape species." Cantu concurs, "Using this new genome sequencing process, we can now develop the genetic markers necessary to combine important traits into new varieties," he says in the press release. "It's been 400 years since that was last done for Cabernet Sauvignon; we can do better."

Just as in the United States, Europe has been breeding and planting more hybrid varieties. In Europe, Reisch observes, motivations seem to revolve around reducing pesticide applications on *V.vinifera* varieties. Reisch recently learned roughly 24,700 and 14,800 acres of hybrid grapes have been planted in Italy and France, respectively. In his opinion, the greatest limitation to acceptance of hybrids developed both before and after creation of the FALCON algorithms will be grower and consumer acceptability.

"In the table grape area, new varieties are rapidly adopted worldwide," he says. "Table and raisin grape breeders are poised to take advantage of genome sequencing and other technologies without the limitation of the wine grape world. Many say it's hard to market new varieties, yet every variety was 'new' at some point. Traminette was introduced 20 years ago and is now widely planted across the eastern United States."

With exponential growth of the U.S. wine market, the expanding geographic range of *V.vinifera* plantings, and global efforts to increase vineyard sustainability and profitability, it seems the wine industry would be eager to adopt genetically adapted varieties. "We have tremendous genetic resources among the 60 species of *Vitis* and we're far from using [their potential] to create well adapted, high quality grapes for different purposes and different regions," says Reisch. He thinks genome sequencing may also educate the wine community "in ways we cannot yet anticipate."

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