Producing and (epi)genotyping a large collection of intravarietal diversity for grapevine improvement

Lizamore, Darrell[1*]; Bicknell, Ross[2], Winefield, Chris[3]; Barrell, Philippa[2]

[1]Bragato Research Institute, Grapevine Improvement Team, Lincoln, New Zealand
[2]Plant and Food Research Limited, Lincoln, New Zealand
[1]Lincoln University, Dept. Wine, Food & Molecular Biosciences, Lincoln, New Zealand
*Darrell.Lizamore@bri.co.nz

Abstract

In New Zealand, wine production depends on a very limited amount of genetic diversity, with approximately 75% of all export revenue coming from the sale of Sauvignon Blanc. Only a small number of clones are used, and strict national biosecurity regulations make importing collections of new genetics impractical. However, the industry's largest research programme aims to generate new intravarietal diversity from which to select and propagate material for future plantings. This involves two approaches. The first is a grower-led identification and tagging of atypical vines using a mobile web app, supported by industry members working in vineyards across the country. The second is the production of somaclonal variation by exposing grapevine somatic embryos to calibrated stress treatments. Vines recovered from these cultures display diverse novel phenotypes. Using a target-enriched sequencing approach, combined with a multi-dimensional pooling strategy, we have identified genetic variation caused by transposable element activity. This same method can also distinguish among existing clones of the same variety. More recently, we have also characterised stable epigenetic changes in mature vines regenerated from somatic embryos. Some of these epigenetic changes persist after 3-4 years in the field. To date, we have trialled the use of tissue culture to trigger transposition events in three varieties. Based on these experiments, we are now working to produce a population of 12,000 – 20,000 Sauvignon Blanc vines displaying the maximum scope of intravarietal diversity possible. These will be used to select clones showing improved characteristics related to productivity, disease resistance and climate change. By cataloguing the genetic and epigenetic diversity of each vine, we hope to provide a repository of information that can be cross-referenced with phenotypic data, thereby creating a resource for functional genomics research.

Keywords: genotyping, epigenetics, transposable elements, somaclones, intravarietal diversity, sequencing