Abstract

Water deficit effects important wine flavor and color constituents of grapes (Vitis vinifera). These changes are associated with improved wine quality and human health benefits. Regulation in this irrigation has been shown to increase grape with less water, an important feature in water-scarce regions. We have taken an integrated functional genomics approach to better understand how water stress affects grapevine gene expression and how those changes translate to wine quality improvements. In this study we have analyzed more than 400 ESTs from abnormally stressed cDNA libraries, and selected sequences were used to initiate the development of a EST microarray platform. Here we present results of EST sequencing and expression profiling that are currently in progress to initiate the systematic identification of each of these volunteer vines are irrigated at 85% evaporative tranpotation after reaching a water potential of ~1.5% (drought stress).

Regulated Deficit Irrigation

- Vines are irrigated at 85% evaporative tranpotation after reaching a water potential of ~1.5% (drought stress).
- No reduction of fruit yield, improved fruit quality
- Reduced irrigation by 86% compared to previous practice
- Vineyards use 14% less water than local alfalfa fields

Experimental Approaches

- Use integrated functional genomic approaches to identify genes involved in stress tolerance and fruit (wine) quality.
- Conduct large-scale EST sequencing for rapid gene discovery.
- Conduct high-resolution microarray analysis to identify genes responding to abiotic stress.
- Conduct meta-analysis profiling in both volatile and non-volatile must fractions to identify volatile color, flavor, and aroma characters associated with water deficit stresses.
- Conduct metabolite profiling in both volatile and non-volatile must fractions to identify volatile color, flavor, and aroma characters associated with water deficit stresses.

Table 1: Abiotic stressed treatments used in the construction of cDNA libraries from Vitis vinifera cv. Chardonnay for EST sequencing.

Stress Tolerance of Vitis vinifera

- Mediterranean origin
- Most important crop
- Very drought tolerant
- Moderately salt tolerant

Table 2: Abiotic stressed treatments used in the construction of cDNA libraries from Vitis vinifera cv. Chardonnay for EST sequencing.

Table 3. Total number of peaks identified in gas chromatograms for the wine shown in Figure 5. These replicates of each stress were analyzed.

Table 4. Area of 5 selected peaks common to both treatments that differ significantly (Mean ± SD; n = 5).

Summary

- More than 52,000 ESTs have been sequenced and analyzed
- A 15K probe set GeneChip® will be available in March 2004
- Proteomics analysis indicates small but significant differences between well-watered and stress-treated shoots. Consistent with water potential and shoot length measurements, protein expression is significantly affected by stress treatment after day 8.
- Metabolic analytical methods are developed and initial experiments show that water-deficit stress changes metabolite profiles. We are able to measure up to 251 compounds in a single leaf sample. There are large quantitative and qualitative differences between control and water-deficit stressed leaves.
- The compounds will be identified in the future and correlated to parallel proteome analysis.

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