

then used to determine the identity of 133 differentially expressed proteins. A putative identification has been assigned to greater than 90% of the proteins by searching the NCBI nonredundant protein database and a translated petunia database developed at OSU. The programmed senescence of flower petals allows the plant to remobilize nutrients from dying to developing tissues. In support of this recycling function most of the senescence up-regulated proteins were found to be involved in catabolic processes including the degradation of nucleic acids, proteins, lipids and cell walls. Some of the genes encoding senescence up-regulated proteins have been identified from Petunia EST database searches (TIGR and SGN) and others have been cloned using degenerate primers and RT-PCR. The functional analysis of selected senescence up-regulated proteins using virus-induced gene silencing (VIGS) will be presented.

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2:45–3:00 pm

Glutaredoxin-mediated Oxidative Stress Protection to Improve Stress Tolerance in Vegetable Crops

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Glutaredoxins are glutathione-dependent oxidoreductases known to protect cellular proteins against damage by oxidative stress. Plants contain many glutaredoxins whose functions are not well understood. We analyzed expression profiles of glutaredoxins in the genome of *Arabidopsis thaliana* using publicly-available Microarray data. This study identified that 11 out of 33 glutaredoxins are modulated at the transcriptional level by one or more abiotic stress factors, implying roles in stress tolerance. To test whether transgenic expression of a glutaredoxin could be a tool to improve stress tolerance, a fern cDNA for a glutaredoxin PvGrx5, previously implicated in arsenic resistance, was overexpressed in *Arabidopsis thaliana*. Homozygous lines expressing PvGrx5 were significantly more tolerant than vector control lines when container-grown plants were stressed at supraoptimal temperatures. Compared to vector control lines, PvGrx5-transgenic lines were characterized by significantly greater growth and photosynthesis under stress conditions and significantly less tissue damage as measured by ion leakage and the amount of oxidized proteins. Our work indicates for the first time the potential of using genes for plant glutaredoxins for improving vegetable crops for high temperature stress tolerance.

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3:00–3:15 pm

Clone S-RNase cDNAs and Establish CSP-PCR-RFLP System for Cultivars S-genotyping in Chinese Sand Pear [*Pyrus pyrifolia* (Burm.) Nak.]

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Chinese sand pear is closely related to Japanese pear. Both of them belong to [*Pyrus pyrifolia* (Burm.) Nak.] that exhibits gametophytic self-incompatibility. Knowledge of self-incompatibility genotypes (S-genotypes) of cultivars is essential for improving pear production and cross-breeding. Recently, new S-alleles in Chinese sand pear were discovered and the JP-PCR-RFLP (Japanese pear-PCR-restriction fragment length polymorphism) system did not work for Chinese sand pear cultivars S-genotyping. We cloned eight cDNAs of S-RNases from Styler RNA of Chinese sand pear cultivars by RT-PCR and RACE and two (S15 and S16) of them were new S-RNase alleles. Based on sequence analysis, a novel CSP-PCR-RFLP (Chinese sand pear-PCR-RFLP) system was established that consists of genomic PCR amplification with a pair of consensus primers followed by digestion of the PCR fragments with S-RNase allele specific restriction endonucleases. Using this system, a total of 13 S-RNase alleles in Chinese sand pear were efficiently discriminated and 15 cultivars were rapidly and accurately S-genotyped. The CSP-PCR-RFLP will be applied for further studies of Chinese sand pear. These results will ensure the higher and stable yields in the orchards and a more efficient breeding program.

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3:15–3:30 pm

Probing the *Vitis* Genome—Opportunities and Pitfalls

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Over the past decade an enormous number of ESTs and genomic sequences of *Vitis* have been made available in various databases and the Pinot Noir genome was sequenced in 2007. This data provides vital information for analysis of genes and proteins associated with important biological functions and processes, further enhancing the efficacy of genetic manipulation of grapevine. Using several sequence analysis tools, we have identified genes and their products related to disease resistance and other agronomic traits. For example, up to 438 putative translated sequences harboring the NBS-LRR domain similar to that found in the Run1 disease resistance gene of grape have been identified. Phylogenetic analysis has established the evolutionary profile of such gene superfamilies in grape. In addition, new found genomics data has revealed that a unique gene, previously cloned and suggested to play a vital role in powdery mildew resistance in a wild *Vitis* species, actually exists in the *Vitis vinifera* genome as well. Based on SCAR markers, candidate genes closely associated with the seedless trait have also been identified. Analysis of their complex genomic structure suggests highly regulated control of gene expression. The implication of sequence-based genomics analysis and the effectiveness of current strategies for the molecular improvement of grapevine will be discussed.