Unravelling the complexity of cold acclimation in plants

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Abstract

Many plants respond to low non-freezing temperatures by increasing their freezing tolerance in a process known as cold acclimation. Microarray studies have shown that hundreds of genes are differentially expressed during the cold acclimation process in *Arabidopsis*. To predict the gene regulatory interactions amongst these differentially expressed genes a rule based bioinformatics model was developed. The inferred regulatory network correctly identified several previously characterized interactions and predicted several new interactions under combinatorial control of many TF families (Chapter 3.1, Paper I). As a continuation of this work, detailed combinatorial studies on promoters were done to understand weather the key regulon DREB1/CBFs in turn is regulated by several other TFs in *Arabidopsis* and rice (*Oryza Sativa L.*). The results showed that bioinformatics can correctly predict combinatorial regulation and can be used to identify previously known promoters motifs and predict new ones involved in co-regulated genes (Chapter 3.1, Paper II).

In Sweden, cultivated oat (*Avena sativa L.*) is grown only as a spring crop as no suitable winter oat exists. To develop such a cultivar, a model system to detect differences between spring and winter oats on the molecular level is required. To this end 294 winter oat lines from throughout the world were collected, tested in the field in Sweden and rated based on their survival and vigor. The best performing lines were further characterized in the laboratory by physiological, biochemical and molecular analysis. The tests showed that while the German cultivar LPWH992209 performed best in the field, the American cultivar Win/Nor-1 outperformed the others in the controlled tests. Six cultivars including two spring, two intermediate and two winter cultivars were finally selected to make up the winter oat model system. Metabolic analysis revealed several metabolites such as sugars, amino acids as well as unknown metabolites that were differentially expressed in the winter oat model lines (Chapter 3.2, Paper III).

Finally, an EMS mutagenized oat TILLING (Target Induced Local Lesions In Genomes) population consisting of 2,500 different mutated lines was generated. The genetic variation of the library was verified by various molecular analysis and proven by the identification of mutations in the *AsPAL1* and *AsCslF6* genes. Several mutants producing low levels of lignin in their husk were identified by biochemical analysis. This TILLING population will now be used to identify mutants with increased freezing tolerance (Chapter 3.3).

Akademisk avhandling

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