

P4–TREE GENOMICS

Organised by G. Taylor for the Plant Environmental Physiology Group and sponsored by The Forestry Research Coordination Committee

P4.1–The Populus sequencing effort: From draft assembly to functional annotation

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Abstract not supplied

P4.2–The Swedish populus genome project

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The Swedish Centre for Tree Functional Genomics, consisting of groups at Umeå Plant Science Centre and the Royal Institute of Technology, Stockholm, have sequenced and annotated over 100 000 ESTs from 19 different cDNA libraries from *Populus tremula x tremuloides*, *Populus tremula* and *Populus trichocarpa*, produced from different tissues in different developmental stages and subjected to different stresses. The assembly of these ESTs indicated that they represent almost 25 000 different genes although the true number might be between 15 and 20 000. About 75% of the *Arabidopsis* have however a very significant hit ($E < 10^{-10}$) in our database. We have produced over 1000 spotted DNA microarrays consisting of 13 488 sequences (verified by 5'- and 3'- resequencing) and are in the process of constructing the second generation of *Populus* arrays, based on the Unigene set of the 100 000 ESTs. These microarrays are currently used for global transcriptomics in diverse tree biology research areas, such as wood formation, leaf development, leaf senescence, dormancy, biotic and abiotic stresses and transgene characterization. Access to the arrays is possible on a collaborative basis. Our global gene profiling approach is linked to protein and metabolite profiling through large-scale proteomics and metabolomics. Our vision is that this genomic approach will allow an unprecedented and comprehensive insight into gene expression correlated with the amounts and types of proteins and metabolites present in specific tissues. A large number of genes involved in wood formation will also be put into a high throughput knockout program.

P4.3–Tree genes in future climates: Global gene expression and long-term adaptation of trees to elevated atmospheric CO₂

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Over half of all global carbon held in vegetation is in forests. The consequences of increasing atmospheric carbon dioxide for the functioning of forest ecosystems remain uncertain although it has been suggested that 'long-term' adaptation to increased CO₂ will negate growth-stimulations that occur in the short-term, limiting the potential of forests to sequester additional carbon in future climates. Given the lifespan of trees, gene-level adaptation to altered environments will determine the potential for such sequestration and will also be central to patterns of development, function and interactions with biotic and abiotic stresses. Here we show that in genome-wide expression of >10 000 EST (expressed sequence tags), representing partially sequenced genes, following long-term exposure of a poplar forest to elevated CO₂ results in approximately 860 (7%) genes being significantly up-regulated, and 480 (4%) genes being significantly down-regulated. In contrast, for genes determining photosynthetic fixation of carbon, 26% of ESTs are down-regulated in elevated CO₂. A large and previously unobserved down-regulation of the light harvesting machinery for photosynthesis was also quantified. Of particular interest was the consistent up-regulation of genes associated with the auxin and ethylene biosynthetic pathway, suggesting these hormones play a key role, previously undocumented, in determining long-term developmental responses to elevated CO₂. We conclude that gene-level adaptations are likely to be important in optimising tree growth in future CO₂ atmospheres and that for fast growing bioenergy trees, continued positive growth responses in future CO₂ climates seem likely.

P4.4–Functional genomic dissection of vascular development in higher plants

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We have exploited the extensive genomic resources in *Arabidopsis* and the model tree, hybrid Aspen to identify