

GENES TO PHENOTYPE, FUNCTION TO APPLICATIONS: NEAR-TERM POTENTIAL OF LARGE-SCALE GENOMICS

Jerry Tuskan

Oak Ridge National Laboratory, Oak Ridge, TN

The availability of information related to genetic diversity among individuals within natural populations, breeding populations and pedigrees is rapidly becoming affordably abundant. Utilizing such information to related genetic variation to phenotypic variation requires adequate computational infrastructure, reliable phenotypic data from relevant environmental settings and a defined economic target. The application of large-scale genomics approaches and genomic selection to forest tree species improvement comes with many benefits and costs. Although the cost of generating useful data is declining, there is still a substantial investment required to generate the data, including the cost of creating a high-quality reference genome. Moreover, the undomesticated nature of most forest tree species requires the generation of a large marker library to cope with linkage disequilibrium. However if these obstacles can be overcome then the direct use of DNA markers [e.g., single nucleotide polymorphisms (SNPs)] as selectable markers is fairly straightforward. Examples of this approach using *Populus trichocarpa* will be presented for genes controlling cell wall related traits and sugar yield data.