Session 4

Genetics and Genomics in Bioenergy and Bioproducts

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There is now widespread acknowledgment that renewable bioresources, as a platform for raw inputs and as a source of powerful biocatalysts, have considerable potential to support sustainable economic growth, increase national energy security, strengthen rural communities, and minimize anthropogenic effects on the environment. Clearly, the transition to renewable resources from fossil fuels must meet certain replacement criteria in the economic arena. However, significant advances are required in science and technology development to help meet such criteria and to ensure sustainable enterprises.

As we enter the 21st century, biotechnology is one such advance that is poised to become a major platform for driving significant progress over the next 20–50 years. The knowledge and understanding of genome sequences, gene function, gene expression, protein interactions, and metabolic control mechanisms, will allow a sound scientific basis for a healthier, more reliable food supply combined with much improved design of renewable resources. The panel participants in this special session provided a state-of-the-art overview of how such advances are being utilized and applied in a range of renewable resource projects.

Tom Jeffries (USDA) discussed the genome-wide expression analysis of *Saccharomyces* metabolically engineered for the fermentation of xylose. *S. cerevisiae* transformed with the *Pichia stipitis* genes for xylose reductase (*XYL1*), xylitol dehydrogenase (*XYL2*), and D-xylulokinase (*XYL3*) will assimilate xylose under aerobic conditions and will produce limited amounts of ethanol. However, they do not metabolize xylose anaerobically and they tend to accumulate xylitol. Affymatrix genechip studies showed that even though these yeasts have the enzymatic machinery necessary for xylose assimilation, they do not possess the regulatory mechanisms to recognize xylose as a fermentable sugar. Metabolism on xylose is oxidative.

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The great strength of genome-wide expression analysis is being able to recognize regulatory patterns.

Frank Larimer (ORNL) covered the role of annotation in microbial genomics, highlighting the important effort required between having a draft sequence and being able to make a function call for individual genes. High-throughput draft sequence information costs were reported at $0.04/base for a 10X coverage, while the cost rises to approx $0.10/base for finished, annotated sequence. Adding important functional information includes assembling inputs from comparative genomics, proteomics, and cross-checking via reconstruction of metabolic activity. The annotated output has implications for designing oligonucleotide arrays, building protein expression constructs, understanding functional clustering, and uncovering metabolic networks.

Sharon Shoemaker (UC-Davis) discussed genomics and proteomics as tools for biocatalysis, including the importance of interrelationships between genomic and proteomic approaches. While the genomics revolution is well underway, the proteomics market is less well developed but is expected to grow to $2.8 billion by 2005. Examples presented included the use of yeast proteome microarrays as screening tools, and the application of exploratory tools to improve the cellulose multienzyme complex for the conversion of cellulose to cellobiose and glucose. A major conclusion was that a combination of approaches may be required to decrease cellulose cost to the economic threshold, including mining natural diversity, gene shuffling, directed evolution, and site-directed mutagenesis.

Jerry Tuskan (ORNL) presented the status of the *Populus* genome project, including plans to add additional shot-gun cloning and BAC-end sequencing to provide up to 6X total coverage. The overall objective is to improve poplar hybrids as renewable sources for bioenergy and bio-based products. Approaches discussed included molecular beam mass spectrometric analysis of lignin, population genetics, microarrays, and comparative genomics for gene identification. The multidisciplinary work integrates the information on tree feedstock quality with map-based cloning in order to improve germplasm stocks for future commercial use.

Jim McLaren (Inverizon) discussed the development of sorghum as a renewable bioresource, through genomics-based tools to enhance starch as a feedstock for a future glucose sugar platform. Initial steps include the application of methyl-filtration to select the genespace for sequencing and the integration of this information with quantitative trait loci, and expression microarrays. Starch-enhanced sorghum hybrids, with elite agronomic characteristics, will be processed via selected biocatalytic technologies in a modified milling system. The integration of these approaches is expected to allow an improved biorefinery design, with an output portfolio that includes biofuels and a selected range of economically acceptable bio-based products.