Contents lists available at SciVerse ScienceDirect

**Plant Science** 

journal homepage: www.elsevier.com/locate/plantsci

## Editorial Bioenergy plants in the United States and China

The emerging bio-economies of the US and China hinge on the development of dedicated bioenergy feedstocks that will increase the production of next-generation biofuels and bioproducts. While biofuels might have less eventual importance than bioproducts, transportation needs for both countries require increasingly more biofuels to be produced in the coming decades. The US Renewable Fuels Standard mandate 136 billion litres of biofuels by 2022. Nearly 80 billion litres are required to be "advanced biofuels," generally regarded as fuels from non-corn and soybean feedstocks. Because of food security concerns and the limited cultivated land for food production, China plans to develop bioenergy forestry which will provide 6 billion litres of biodiesel oil by the end of 2020. Generally speaking, the only way to reach these governmental mandates is to rapidly develop new feedstocks and also new fuels. The new feedstocks-bioenergy plants-might be new crops, crop residues, or existing wild or cultivated plants that can be modified for new uses. Certainly genetics-breeding, genomics, and biotechnologywill be important tools to develop these new bioenergy plants.

The papers in this special issue had their origins from a topical workshop, "Biotechnology of Bioenergy Plants" that was held in November 2009 in Knoxville, TN, USA that was originated and sponsored by the China–U.S. Joint Research Center for Ecosystem and Environmental Change. There have been subsequent meetings held by the center that bring researchers together with a common cause. The papers found in this special issue of *Plant Science* represent some of the exciting science that is aimed towards creating new sources of renewable and sustainable fuels and products.

Stress tolerance is an important suite of traits that will be required for a number of plants to be grown on the marginal lands that would not compete with existing fuel and fibre crops. Tang et al. [1] investigated the effect of over-expression of a Jatropha curcas transcription factor gene for enhanced salt and freezing tolerance in this emerging oil-producing feedstock. Indeed, because of its potential as a dedicated bioenergy woody biomass crop in warm-marginal regions Jatropha was the subject of a number of papers. Another example was the identification and characterization of heat shock proteins in Jatropha [2]. Switchgrass (Panicum virgatum) was also a popular feedstock in this special issue. Ma et al. [3] studied the adaptability of switchgrass to the degraded and semi-arid Loess Plateau of China, and showed that there is much diversity for multiple stress tolerance in this species. Another group of researchers studied water use efficiency and stress tolerance of two native plants from the Loess Plateau, the C4 herbaceous grass (Bothriochloa ischaemum) and a C3 leguminous subshrub (Lespedeza davurica) [4]. Finally, Sorghum bicolor is another bioenergy plant that has stress-tolerance characteristics Liu and co-workers [5] characterized sorghum two pyrroline-5carboxylate synthetase genes and promoters and their expression characteristics in response to water and salt stress.Plant development emerged as another important theme. The endosperm and embryo proteomes from Jatropha were characterized [6]. Control of flowering time in the same species was also investigated by the characterization of a dof transcription factor where Circadian rhythms were found to be important [7].Since dedicated bioenergy feedstocks will likely be an important factor of the global bioenergy solution, a crucial problem to solve is the recalcitrance of cell walls to saccharification. Details of plant cell wall biosynthesis are still not well known. Many genes and pathways have not been elucidated. Therefore, an important task is to perform comparative bioinformatic analysis among species, which is what Yang et al. [8] did for Populus and Arabidopsis. Another comparative analysis was performed by the same group, but focusing on the glyosyltransferase family 14 subfamily of genes from a number of diverse plant species [9]. Xu and co-workers [10] performed a study to characterize expressed sequence tags from Jatropha seeds to analyze and identify the key genes involved in oil synthesis. Taken together, these studies demonstrate the depth of "omics" knowledge being added about new bioenergy feedstocks. There are two papers that focused on biotechnology tools for feedstocks. Zhang and co-workers [11] described a tissue culture and transformation method for sweet potato (Ipomoea batatas), and Mazarei et al. [12] described a new fine cell culture type from switchgrass.Taken all together, these papers show the breadth of plant science that is being undertaken in China and the US towards making new sources of bioenergy a reality. This no small task has numerous constraints that go beyond science, including policy, economics and engineering. Nonetheless, the environmental quality and economic success of these two large countries hinge on the success of agricultural and plant science towards the implementation of solutions, namely the growth and success of bioenergy feedstocks, many of which are grown on few hectares today. We have a long way to go, but such scientific exchange of ideas and materials are crucial if we are to have any hope of attaining the solutions.

## References

[1] M. Tang, X. Liu, H. Deng, S. Shen, Over-expression of JcDREB, a putative AP2/EREBP domain-containing transcription factor gene in woody biodiesel plant Jatropha curcas, enhances salt and freezing tolerance in transgenic Arabidopsis thaliana, Plant Science XX (2011) X–Y.





- [2] S. Omar, Q. Fu, M. Chen, G. Wang, S. Song, N. Elsheery, Z. Xu, Identification and expression analysis of two small heat shock protein cDNAs from developing seeds of biodiesel feedstock plant *Jatropha curcas*, Plant Science XX (2011) X–Y.
- [3] Y. Ma, Y. An, J. Shui, Z. Sun, Adaptability and evaluation of *Panicum virgatum* L. cultivars on the Loess Plateau of China, Plant Science XX (2011) X–Y.
- [4] B. Xu, W. Xu, J. Huang, L. Shan, F. Li, Biomass allocation, relative competitive ability and water use efficiency of two dominant species in semiarid Loess Plateau under water stress, Plant Science XX (2011) X–Y.
- [5] M. Su, X. Li, X. Ma, X. Peng, A. Zhao, L. Cheng, S. Chen, G. Liu, Cloning two P5CS genes from bioenergy sorghum and their expression profiles under abiotic stresses and MeJA treatment, Plant Science XX (2011) X-Y.
- [6] H. Liu, Z. Yang, M. Yang, S. Shen, The differential proteome of endosperm and embryo from mature seed of *Jatropha curcas*, Plant Science XX (2011) X–Y.
- [7] J. Yang, M. Yang, W. Zhang, F. Chen, S. Shen, A putative flowering-time-related Dof transcription factor gene, *JcDof3*, is controlled by the circadian clock in *Jatropha curcas*, Plant Science XX (2011) X–Y.
- [8] X. Yang, C. Ye, A. Bisaria, G. Tuskan, U. Kalluri, Identification of candidate genes in *Arabidopsis* and *Populus* cell wall biosynthesis using text-mining, co-expression network analysis and comparative genomics, Plant Science XX (2011) X–Y.
- [9] C. Ye, T. Li, G. Tuskan, T. Tschaplinski, X. Yang, Comparative analysis of GT14/GT14-like gene family in Arabidopsis, Oryza, Populus, Sorghum and Vitis, Plant Science XX (2011) X-Y.
- [10] M. Chen, G. Wang, R. Wang, J. Wang, S. Song, Z. Xu, Analysis of expressed sequence tags from biodiesel plant *Jatropha curcas* embryos at different developmental stages, Plant Science XX (2011) X–Y.

- [11] J. Yang, H. Bi, W. Fan, M. Zhang, H. Wang, P. Zhang, Efficient embryogenic suspension culturing and rapid transformation of a range of elite genotypes of sweet potato (*Ipomoea batatas* [L.] Lam.), Plant Science XX (2011) X–Y.
- [12] M. Mazarei, H. Al-Ahmad, M. Rudis, B. Joyce, C.N. Stewart Jr., Switchgrass (Panicum virgatum L.) cell suspension cultures: establishment, characterization, and application, Plant Science XX (2011) X–Y.

C. Neal Stewart Jr.<sup>a,b,\*</sup>

<sup>a</sup> Department of Plant Sciences, University of Tennessee, Knoxville, TN USA <sup>b</sup> BioEnergy Science Center, Oak Ridge National Laboratory, Oak Ridge, TN, USA

Gong-She Liu

R&D Laboratory of Plant Resources, Institute of Botany, Chinese Academy of Sciences, Xiangshan Nanxincun 20, Beijing, China

> \* Corresponding author. E-mail address: nealstewart@utk.edu (C.N. Stewart Jr.)

Available online 6 September 2011