

## **XIAOHAN YANG**

Biosciences Division

Oak Ridge National Laboratory

1 Bethel Valley Road

Building 1507, Room 208

Oak Ridge, TN 37831-6407, USA

Phone: 865-241-6895

E-mail: [yangx@ornl.gov](mailto:yangx@ornl.gov)

Website: <https://www.ornl.gov/staff-profile/xiaohan-yang>

Google Scholar: <https://scholar.google.com/citations?user=DYH7aqAAAAAJ&hl=en>

### ***Education and Training***

- 2006 – 2008 Oak Ridge National Laboratory (ORNL), Postdoc in *Populus* genomics
- 2005 – 2006 University of Tennessee, Postdoc in *Populus* genomics
- 2002 – 2005 Cornell University, Postdoc in molecular genetics of Arabidopsis
- 2003 Cornell University, Ph.D. Floriculture & Ornamental Horticulture/Plant Molecular Biology/Plant Breeding
- 1989 Huazhong Agricultural University, China M.S. Ornamental Botany
- 1986 Huazhong Agricultural University, China B.Sc. Forest Science

### ***Research and Professional Experience***

- 2017 – present Joint Faculty, Department of Plant Sciences, University of Tennessee, Knoxville
- 2017 – present Senior Staff Scientist, Biosciences Division, Oak Ridge National Laboratory
- 2015 – present Faculty Member, Bredesen Center for Interdisciplinary Research and Graduate Education, University of Tennessee, Knoxville
- 2014 – present Joint Faculty, Graduate School of Genome Science and Technology (GST), University of Tennessee, Knoxville
- 2012 – present Joint Faculty, Department of Biochemistry & Cellular and Molecular Biology, University of Tennessee, Knoxville
- 2011 – 2016 Staff Scientist, Biosciences Division, Oak Ridge National Laboratory
- 2009 – 2017 Adjunct Faculty, Department of Plant Sciences, University of Tennessee, Knoxville
- 2008 – 2011 Associate Staff Scientist, Biosciences Division, Oak Ridge National Laboratory
- 1989 – 1997 Assistant Research Scientist, Chinese Academy of Agricultural Sciences, Beijing, China.

### ***Honors and Awards***

- 2018 The R&D 100 Award (TNT Cloning System)
- 2008 Distinguished Achievement Award for Post-Graduate Research in Environmental Science (In recognition of outstanding early career productivity, ability to collaborate effectively in a team setting, and ability to integrate bioinformatics and molecular biology to gain novel insights into evolutionary genomics).

- 2000 Liu Memorial Award in recognition of his excellent progress and high potential for a successful academic career.
- 1995 Israeli Foreign Ministry Fellowship for training at the Volcani Center.

***Other Professional Activities***

US National Science Foundation (NSF) review panel.

Reviewer for USDA National Research Initiative Competitive Grants Program, Biotechnology and Biological Sciences Research Council (BBSRC), Research Foundation – Flanders (FWO), and USDA Internal Project.

Reviewer for Biotechnology Progress, BMC Bioinformatics, BMC Biotechnology, Critical Reviews in Plant Sciences, Environmental Management, International Journal of Plant Genomics, Journal of Experimental Botany, Journal of Plant Biotechnology, Journal of Proteomic Research, Nature Biotechnology, Nature Plants, New Phytologist, Physiologia Plantarum, Planta, Plant Methods, Plos Computational Biology

Member of American Association for the Advancement of Science (2018 - present)

Organizer of the 34th New Phytologist Symposium: Systems biology and ecology of CAM plants. Tahoe City, CA, USA, 15–18 July 2014.  
(<http://www.newphytologist.org/symposiums/view/5>)

Leader of the ORNL CAM research team, a key component of the \$14.3 million multi-institutional DOE project to engineer crassulacean acid metabolism (CAM) into C<sub>3</sub> plants to enhance water-use efficiency for sustainable biofuels production on marginal land.

Co-Editor-in-Chief of BioDesign Research (<https://spj.sciencemag.org/bdr/>) (2019 - present)

Editorial Board of Scientific Reports (2018 - present)

Lead guest editor for Special Issue "Genetics, genomics, and evolution of CAM photosynthesis" in Genes.

[http://www.mdpi.com/journal/genes/special\\_issues/cam\\_photosynth](http://www.mdpi.com/journal/genes/special_issues/cam_photosynth)

Lead guest editor for Research Topic entitled “Systems Biology and Synthetic Biology in Relation to Drought Tolerance or Avoidance in Plants” in Frontiers in Plant Science.

<http://journal.frontiersin.org/researchtopic/6651/systems-biology-and-synthetic-biology-in-relation-to-drought-tolerance-or-avoidance-in-plants>

Lead guest editor for a special issue entitled “Plant Comparative and Functional Genomics”. International Journal of Genomics.

<http://www.hindawi.com/journals/ijg/si/825361/>

### ***Media Coverage***

“Does Agave Hold the Secret to Drought-Resistant Farming?” (July 13, 2015)

<http://www.scientificamerican.com/article/does-agave-hold-the-secret-to-drought-resistant-farming/>

“Can genetic engineering help quench crops’ thirst?” (January 4, 2016)

<http://ensia.com/features/can-genetic-engineering-help-quench-crops-thirst/>

“New study of water-saving plants advances efforts to develop drought-resistant crops” (December 5, 2016)

<https://www.ornl.gov/news/new-study-water-saving-plants-advances-efforts-develop-drought-resistant-crops>

“Small Proteins Secreted by Poplar Roots Form Communication Route with Associated Fungal Communities” (May 10, 2017)

<http://genomicscience.energy.gov/program/berhighlights.shtml>

“SimPath licenses novel ORNL system for enhanced synthetic biology” (October 16, 2017)

<https://www.ornl.gov/news/simpath-licenses-novel-ornl-system-enhanced-synthetic-biology>

“Genes found in drought-resistant plants could accelerate evolution of water-use efficient crops” (December 1, 2017)

<https://www.ornl.gov/news/genes-found-drought-resistant-plants-could-accelerate-evolution-water-use-efficient-crops>

“Researchers Discover Genes That Make Plants Drought-Resistant” (June 21, 2018)

<https://www.rdmag.com/article/2018/06/researchers-discover-genes-make-plants-drought-resistant>

<https://www.rdmag.com/article/2018/07/r-d-special-focus-plant-science>

### ***Invention***

#### ***Patent***

US Patent No.: 10,017,770 B2 (Issued: July 10, 2018) “TNT Cloning System”. Inventors: Tuskan GA, Yang X, De Paoli HC.

U.S. patent No. US 10,227,601 B2 (Issued: March 12, 2019): “PtDUF266 Gene Regulating Cell Wall Biosynthesis and Recalcitrance in *Populus*”. Inventors: Jin-Gui Chen, Sara Jawdy, Xiaohan Yang, Gerald A. Tuskan, Yongil Yang, Lee E. Gunter

U.S. patent No. US 10,246,719 B2 (Issued: April 2, 2019): “Modulating Laccase Enzyme to Regulate Cell Wall Biosynthesis and Recalcitrance in Plants”. Inventors: Jin-Gui

Chen, Lee E. Gunter, Sara S. Jawdy, Xiaohan Yang, Gerald A. Tuskan, Anthony C. Bryan

Pending patent

Yang et al. “Genes for enhancing drought and heat tolerance in plants, and methods of use” (2018) US Patent App. 16/015,732

Provisional patent application

Yang et al. “Gene for enhancing salt and drought tolerance in plants” (2019)

Invention disclosures

Invention Disclosure 201303169, DOE S-124,759, “A Lectin-Like Receptor Kinase Leads to Enhanced Mycorrhization in Plants” (elected for patent application)

Invention Disclosure 201403422, DOE S-138,049, “A PtDUF231 Gene Regulating Cell Wall Biosynthesis and Recalcitrance in *Populus*”. (elected for patent application)

Invention Disclosure 201403416 DOE S-138,043, “A Laccase Enzyme Regulating Cell Wall Biosynthesis and Recalcitrance in *Populus*”.

Invention Disclosure 201403419, DOE S-138,046, “PtCAD2359 Knockdown Affects the Lignin Biosynthetic Pathway in *Populus*”.

Invention Disclosure 201403421, DOE S-138,048, “A PtVND6 Gene Regulating Cell Wall Biosynthesis and Recalcitrance in *Populus*.”

Invention Disclosure 201403424, DOE S-138,051, “A Prolyl 4-Hydroxylase Alpha Subunit Enzyme Regulates Cell Wall Biosynthesis and Recalcitrance in *Populus*”.

Invention Disclosure 201403434, DOE S-138,061, “A Serine Hydroxymethyltransferase Regulates Cell Wall Biosynthesis and Recalcitrance in *Populus*”.

Invention Disclosure 201403435, DOE S-138,062, “A Prefoldin-Like Protein Regulates Cell Wall Biosynthesis and Recalcitrance in *Populus*”.

Invention disclosure 201804142 “Gene for enhancing photosynthetic performance and biomass production in plants”

***Invited Talk***

“Application of Genome-Editing in Crassulacean Acid Metabolism (CAM) Plants”  
aBIOTECH board meeting and the First aBIOTECH International Conference. June 13 – 14, 2019. Beijing, China

“Expanding the Capabilities for Plant Genome-Editing and Synthetic Biology”. International Plant & Animal Genome XXVII; January 12-16, 2019, San Diego, CA

“Plant Systems Biology and Biotechnology in Relation to Crassulacean Acid Metabolism”. October 18, 2018, Morgan State University in Baltimore, Maryland

“Implementation of drought avoidance mechanisms for sustainable crop production”. July 20-24, 2018. The Fifth International Horticulture Research Conference. Beijing, China.

“An integrative approach to understanding the function of crassulacean acid metabolism (CAM)-related genes in *Agave* and *Kalanchoe*”. April 9-13, 2018. An international symposium entitled “Biology of CAM Plants”. Phoenix, Arizona, USA

“Unravelling the Molecular Basis of Plant Water-use Efficiency and Plant-microbe Symbiosis”. February 16, 2018. Clemson University.

“Molecular signatures of crassulacean acid metabolism”. July 23-29, 2017. The XIX International Botanical Congress (IBC2017). Shenzhen, China.

“Toolbox for plant synthetic biology”. February 16-17, 2017. BBSRC-funded Global Challenges Research Fund (GCRF) Workshop titled “Exploring synthetic biology for enhanced plant production”, University of Liverpool, UK

“Systems Biology and Synthetic Biology of Crassulacean Acid Metabolism”. April 13, 2016. BCMB 615 Seminar Series, University of Tennessee, Knoxville, TN

“Comparative Evolution of Crassulacean Acid Metabolism (CAM)”. The Plant and Animal Genome Conference; January 2016 in San Diego, CA.

“Discovery of effector-like proteins in *Populus* during symbiosis formation”. IUFRO Tree Biotechnology Conference. 8-12 June 2015, Florence, Italy.

“Genome-wide discovery of non-coding RNAs in willow (*Salix purpurea*)”. The Plant and Animal Genome Conference XXIII. 10-14 January 2015, San Diego, CA, USA.

“Comparative genomics of CAM plants” The 34th New Phytologist Symposium: Systems biology and ecology of CAM plants; Tahoe City, CA, USA 15–18 July 2014

“Comparative genomics of CAM species” The Plant and Animal Genome XXII Conference; January 11-15, 2014 in San Diego, CA

“*Agave* genomics in support of CAM engineering”. International Symposium on C<sub>4</sub> and CAM Plant Biology (6-9th August, 2013, Champaign, IL).

**Publications** (95 in total)

1. J. Zhang *et al.*, Overexpression of a Prefoldin  $\beta$  subunit gene reduces biomass recalcitrance in the bioenergy crop *Populus*. *Plant Biotechnology Journal*, <https://doi.org/10.1111/pbi.13254>, (2019).
2. J. Zhang *et al.*, Overexpression of a serine hydroxymethyltransferase increases biomass production and reduces recalcitrance in the bioenergy crop *Populus*. *Sustainable Energy & Fuels* **3**, 195-207 (2019).
3. X. Yang, D. Liu, T. J. Tschaplinski, G. A. Tuskan, Comparative genomics can provide new insights into the evolutionary mechanisms and gene function in CAM plants. *Journal of Experimental Botany*, <https://doi.org/10.1093/jxb/erz408>, (2019).
4. X. Wang *et al.*, *Agrobacterium*-mediated transformation of *Kalanchoe laxiflora*. *Horticultural Plant Journal* **5**, 221-228 (2019).
5. T. J. Tschaplinski *et al.*, The nature of the progression of drought stress drives differential metabolomic responses in *Populus deltoides*. *Annals of Botany*, *mcz002*, <https://doi.org/10.1093/aob/mcz002>, (2019).
6. R. C. Moseley, G. A. Tuskan, X. Yang, Comparative genomics analysis provides new insight into molecular basis of stomatal movement in *Kalanchoë fedtschenkoi*. *Frontiers in Plant Science*, <https://doi.org/10.3389/fpls.2019.00292>, (2019).
7. R. Mewalal *et al.*, Identification of *Populus* small RNAs responsive to mutualistic interactions with mycorrhizal fungi, *Laccaria bicolor* and *Rhizophagus irregularis*. *Frontiers in Microbiology*, doi: 10.3389/fmicb.2019.00515 (2019).
8. D. Liu *et al.*, CRISPR/Cas9-mediated targeted mutagenesis for functional genomics research of crassulacean acid metabolism plants. *Journal of Experimental Botany*, <https://doi.org/10.1093/jxb/erz415>, (2019).
9. J. Labbé *et al.*, Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. *Nature Plants* **5**, 676-680 (2019).
10. H.-B. Guo *et al.*, A suggestion of converting protein intrinsic disorder to structural entropy using shannon's information theory. *Entropy* **21**, 591 (2019).
11. H. B. Chhetri *et al.*, Multitrait genome-wide association analysis of *Populus trichocarpa* identifies key polymorphisms controlling morphological and physiological traits. *New Phytologist* **223**, 293-309 (2019).
12. H. Yin *et al.*, Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in Agave. *BMC Genomics* **19**, 588 (2018).
13. R. C. Moseley *et al.*, Conservation and diversification of circadian rhythmicity between a model crassulacean acid metabolism plant *Kalanchoë fedtschenkoi* and a model C<sub>3</sub> photosynthesis plant *Arabidopsis thaliana*. *Frontiers in Plant Science* **9**, 1757 (2018).
14. D. Liu *et al.*, Perspectives on the basic and applied aspects of crassulacean acid metabolism (CAM) research. *Plant Science* **274**, 394-401 (2018).
15. S. D. Lim *et al.*, A *Vitis vinifera* basic helix-loop-helix transcription factor enhances plant cell size, vegetative biomass and reproductive yield. *Plant Biotechnology Journal* **16**, 1595-1615 (2018).

16. H.-B. Guo, Y. Ma, G. A. Tuskan, X. Yang, H. Guo, Classification of complete proteomes of different organisms and protein sets based on their protein distributions in terms of some key attributes of proteins. *International Journal of Genomics* **2018**, Article ID 9784161. <https://doi.org/9784110.9781155/9782018/9784161> (2018).
17. B. J. Garcia *et al.*, Phytobiome and transcriptional adaptation of *Populus deltoides* to acute progressive drought and cyclic drought. *Phytobiomes*, <https://doi.org/10.1094/PBIOMES-1004-1018-0021-R> (2018).
18. A. M. Borland, A. Leverett, N. Hurtado-Castano, R. Hu, X. Yang, in *The Leaf: A Platform for Performing Photosynthesis*, W. W. Adams III, I. Terashima, Eds. (Springer International Publishing AG, Cham, Switzerland, 2018), pp. 281-305.
19. A. K. Biswal *et al.*, Working towards recalcitrance mechanisms: increased xylan and homogalacturonan production by overexpression of GALactUronosylTransferase12 (GAUT12) causes increased recalcitrance and decreased growth in *Populus*. *Biotechnology for Biofuels* **11**, 9 (2018).
20. A. K. Biswal *et al.*, Sugar release and growth of biofuel crops are improved by downregulation of pectin biosynthesis. *Nature Biotechnology* **36**, 249 (2018).
21. R. Badmi *et al.*, A new calmodulin-binding protein expresses in the context of secondary cell wall biosynthesis and impacts biomass properties in *Populus*. *Frontiers in Plant Science* **9**, 1669 (2018).
22. P. E. Abraham *et al.*, Quantitative proteome profile of water deficit stress responses in eastern cottonwood (*Populus deltoides*) leaves. *PLOS ONE* **13**, e0190019 (2018).
23. Y. Yang *et al.*, Overexpression of a Domain of Unknown Function 231-containing protein increases O-xylan acetylation and cellulose biosynthesis in *Populus*. *Biotechnology for Biofuels* **10**, 311 (2017).
24. Y. Yang *et al.*, Overexpression of a Domain of Unknown Function 266-containing protein results in high cellulose content, reduced recalcitrance, and enhanced plant growth in the bioenergy crop *Populus*. *Biotechnology for Biofuels* **10**, 74 (2017).
25. X. Yang *et al.*, The *Kalanchoë* genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. *Nature Communications* **8**, 1899 (2017).
26. J. M. Plett *et al.*, *Populus trichocarpa* encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. *Scientific Reports* **7**, 382 (2017).
27. D. Liu, R. Mewalal, R. Hu, G. A. Tuskan, X. Yang, New technologies accelerate the exploration of non-coding RNAs in horticultural plants. *Horticulture Research* **4**, 17031 (2017).
28. D. Close, M. Rodriguez, R. Hu, X. Yang, Disposition and bioavailability of inulin and free sugar in untreated and dilute acid pretreated *Agave tequilana* leaves. *Biomass and Bioenergy* **106**, 176-181 (2017).
29. Y. Yang *et al.*, Genome-wide analysis of lectin receptor-like kinases in *Populus*. *BMC Genomics* **17**, 699 (2016).
30. P. Qian *et al.*, Understanding the catalytic mechanism of xanthosine methyltransferase in caffeine biosynthesis from QM/MM molecular dynamics and

- free energy simulations. *Journal of Chemical Information and Modeling* **56**, 1755-1761 (2016).
31. D. Liu, R. Hu, K. J. Palla, G. A. Tuskan, X. Yang, Advances and perspectives on the use of CRISPR/Cas9 systems in plant genomics research. *Current Opinion in Plant Biology* **30**, 70-77 (2016).
  32. C. E. Hamilton, J. D. Bever, J. Labbé, X. Yang, H. Yin, Mitigating climate change through managing constructed-microbial communities in agriculture. *Agriculture, Ecosystems & Environment* **216**, 304-308 (2016).
  33. H. C. De Paoli, G. A. Tuskan, X. Yang, An innovative platform for quick and flexible joining of assorted DNA fragments. *Scientific Reports* **6**, 19278 (2016).
  34. O. Czarnecki *et al.*, Simultaneous knockdown of six non-family genes using a single synthetic RNAi fragment in *Arabidopsis thaliana*. *Plant Methods* **12**, 16 (2016).
  35. A. C. Bryan *et al.*, Knockdown of a laccase in *Populus deltoides* confers altered cell wall chemistry and increased sugar release. *Plant Biotechnology Journal* **14**, 2010-2020 (2016).
  36. A. M. Borland, H.-B. Guo, X. Yang, J. C. Cushman, Orchestration of carbohydrate processing for crassulacean acid metabolism. *Current Opinion in Plant Biology* **31**, 118-124 (2016).
  37. P. E. Abraham *et al.*, Transcript, protein and metabolite temporal dynamics in the CAM plant *Agave*. *Nature Plants* **2**, 16178 (2016).
  38. J. Yao, H. Guo, X. Yang, PPCM: Combing multiple classifiers to improve protein-protein interaction prediction. *International Journal of Genomics* **2015**, Article ID 608042 (2015).
  39. J. Yao *et al.*, Substrate-assisted catalysis in the reaction catalyzed by salicylic acid binding protein 2 (SABP2), a potential mechanism of substrate discrimination for some promiscuous enzymes. *Biochemistry* **54**, 5366-5375 (2015).
  40. X. Yang, J. Leebens-Mack, F. Chen, Y. Yin, Plant comparative and functional genomics. *International Journal of Genomics* **2015**, Article ID 924369 (2015).
  41. X. Yang *et al.*, A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. *New Phytologist* **207**, 491-504 (2015).
  42. R. Ming *et al.*, The pineapple genome and the evolution of CAM photosynthesis. *Nature Genetics* **47**, 1435 (2015).
  43. J. R. Mielenz, M. Rodriguez, O. A. Thompson, X. Yang, H. Yin, Development of *Agave* as a dedicated biomass source: production of biofuels from whole plants. *Biotechnology for Biofuels* **8**, 79 (2015).
  44. L. Guo *et al.*, A host plant genome (*Zizania latifolia*) after a century-long endophyte infection. *The Plant Journal* **83**, 600-609 (2015).
  45. J. C. Cushman, S. C. Davis, X. Yang, A. M. Borland, Development and use of bioenergy feedstocks for semi-arid and arid lands. *Journal of Experimental Botany* **66**, 4177-4193 (2015).
  46. A. M. Borland *et al.*, Climate-resilient agroforestry: physiological responses to climate change and engineering of crassulacean acid metabolism (CAM) as a mitigation strategy. *Plant, Cell & Environment* **38**, 1833-1849 (2015).



47. A. K. Biswal *et al.*, Downregulation of *GAUT12* in *Populus deltoides* by RNA silencing results in reduced recalcitrance, increased growth and reduced xylan and pectin in a woody biofuel feedstock. *Biotechnology for Biofuels* **8**, 41 (2015).
48. H. Yin *et al.*, Functional genomics of drought tolerance in bioenergy crops. *Critical Reviews in Plant Sciences* **33**, 205-224 (2014).
49. P. Szövényi *et al.*, Efficient purging of deleterious mutations in plants with haploid selfing. *Genome Biology and Evolution* **6**, 1238-1252 (2014).
50. A. A. Myburg *et al.*, The genome of *Eucalyptus grandis*. *Nature* **510**, 356 (2014).
51. U. C. Kalluri, H. Yin, X. Yang, B. H. Davison, Systems and synthetic biology approaches to alter plant cell walls and reduce biomass recalcitrance. *Plant Biotechnology Journal* **12**, 1207-1216 (2014).
52. H. C. De Paoli, A. M. Borland, G. A. Tuskan, J. C. Cushman, X. Yang, Synthetic biology as it relates to CAM photosynthesis: challenges and opportunities. *Journal of Experimental Botany* **65**, 3381-3393 (2014).
53. A. M. Borland *et al.*, Engineering crassulacean acid metabolism to improve water-use efficiency. *Trends in Plant Science* **19**, 327-338 (2014).
54. C.-Y. Ye, X. Yang, X. Xia, W. Yin, Comparative analysis of cation/proton antiporter superfamily in plants. *Gene* **521**, 245-251 (2013).
55. C. Y. Ye *et al.*, Evolutionary analyses of non-family genes in plants. *The Plant Journal* **73**, 788-797 (2013).
56. S. Chen *et al.*, Transcriptome analysis in sheepgrass (*Leymus chinensis*): A dominant perennial grass of the Eurasian Steppe. *PLOS ONE* **8**, e67974 (2013).
57. A. M. Borland, X. Yang, Informing the improvement and biodesign of crassulacean acid metabolism via system dynamics modelling. *New Phytologist* **200**, 946-949 (2013).
58. A. A. Karve *et al.*, Initial characterization of shade avoidance response suggests functional diversity between *Populus* phytochrome B genes. *New Phytologist* **196**, 726-737 (2012).
59. J. L. Bennetzen *et al.*, Reference genome sequence of the model plant *Setaria*. *Nature Biotechnology* **30**, 555 (2012).
60. C.-Y. Ye, T. Li, G. A. Tuskan, T. J. Tschaplinski, X. Yang, Comparative analysis of GT14/GT14-like gene family in *Arabidopsis*, *Oryza*, *Populus*, *Sorghum* and *Vitis*. *Plant Science* **181**, 688-695 (2011).
61. X. Yang *et al.*, Genomic aspects of research involving polyploid plants. *Plant Cell, Tissue and Organ Culture* **104**, 387-397 (2011).
62. X. Yang, C.-Y. Ye, A. Bisaria, G. A. Tuskan, U. C. Kalluri, Identification of candidate genes in *Arabidopsis* and *Populus* cell wall biosynthesis using text-mining, co-expression network analysis and comparative genomics. *Plant Science* **181**, 675-687 (2011).
63. X. Yang, C. M. Winter, X. Xia, S. Gang, Genome-wide analysis of the intergenic regions in *Arabidopsis thaliana* suggests the existence of bidirectional promoters and genetic insulators. *Current Topics in Plant Biology* **12**, 15-33 (2011).
64. X. Yang *et al.*, Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. *Genome Research* **21**, 634-641 (2011).

65. X. Yang *et al.*, in *Biofuel Production-Recent Developments and Prospects*, M. A. D. S. Bernardes, Ed. (Intech, Rijeka, 2011), pp. 375-414.
66. D. J. Weston *et al.*, Comparative physiology and transcriptional networks underlying the heat shock response in *Populus trichocarpa*, *Arabidopsis thaliana* and *Glycine max*. *Plant, Cell & Environment* **34**, 1488-1506 (2011).
67. J. Guo, X. Yang, D. J. Weston, J.-G. Chen, Abscisic acid receptors: Past, present and future. *Journal of Integrative Plant Biology* **53**, 469-479 (2011).
68. J. Guo, Z. Jin, X. Yang, J.-F. Li, J.-G. Chen, Eukaryotic initiation factor 6, an evolutionarily conserved regulator of ribosome biogenesis and protein translation. *Plant Signaling & Behavior* **6**, 766-771 (2011).
69. S. P. DiFazio, X. Yang, G. A. Tuskan, in *Genetics, Genomics and Breeding of Poplar*. (Science Publishers, Enfield, New Hampshire, 2011), pp. 85-111.
70. B. Cai, X. Yang, G. A. Tuskan, Z.-M. Cheng, MicroSyn: A user friendly tool for detection of microsynteny in a gene family. *BMC Bioinformatics* **12**, 79 (2011).
71. L. Tyler *et al.*, Annotation and comparative analysis of the glycoside hydrolase genes in *Brachypodium distachyon*. *BMC Genomics* **11**, 600 (2010).
72. The International Brachypodium Initiative, Genome sequencing and analysis of the model grass *Brachypodium distachyon*. *Nature* **463**, 763 (2010).
73. P. Ranjan *et al.*, Bioinformatics-based identification of candidate genes from QTLs associated with cell wall traits in *Populus*. *BioEnergy Research* **3**, 172-182 (2010).
74. X. Yang *et al.*, Poplar genomics: State of the science. *Critical Reviews in Plant Sciences* **28**, 285-308 (2009).
75. X. Yang, S. Jawdy, T. J. Tschaplinski, G. A. Tuskan, Genome-wide identification of lineage-specific genes in *Arabidopsis*, *Oryza* and *Populus*. *Genomics* **93**, 473-480 (2009).
76. Z. Xu *et al.*, Comparative genome analysis of lignin biosynthesis gene families across the plant kingdom. *BMC Bioinformatics* **10**, S3 (2009).
77. L. D. Osburn, X. Yang, Y. Li, Z.-M. Cheng, Micropropagation of Japanese honeysuckle (*Lonicera japonica*) and Amur honeysuckle (*L. maackii*) by shoot tip culture. *Journal of Environmental Horticulture* **27**, 195-199 (2009).
78. X. Yang *et al.*, The F-Box gene family is expanded in herbaceous annual plants relative to woody perennial plants. *Plant Physiology* **148**, 1189-1200 (2008).
79. J. S. Yuan *et al.*, The endo- $\beta$ -mannanase gene families in *Arabidopsis*, rice, and poplar. *Functional & Integrative Genomics* **7**, 1-16 (2007).
80. X. Yang, G. A. Tuskan, Z.-M. Cheng, Divergence of the Dof gene families in poplar, *Arabidopsis*, and rice suggests multiple modes of gene evolution after duplication. *Plant Physiology* **142**, 820-830 (2006).
81. X. Yang, B. E. Scheffler, L. A. Weston, Recent developments in primer design for DNA polymorphism and mRNA profiling in higher plants. *Plant Methods* **2**, 4 (2006).
82. X. Yang, B. E. Scheffler, L. A. Weston, *SOR1*, a gene associated with bioherbicide production in sorghum root hairs. *Journal of Experimental Botany* **55**, 2251-2259 (2004).

83. X. Yang, T. G. Owens, B. E. Scheffler, L. A. Weston, Manipulation of root hair development and sorgoleone production in sorghum seedlings. *Journal of Chemical Ecology* **30**, 199-213 (2004).
84. C. Bertin, X. Yang, L. A. Weston, The role of root exudates and allelochemicals in the rhizosphere. *Plant and Soil* **256**, 67-83 (2003).
85. D. Mu, X. Yang, Y. Zhang, The proportional fertilization in pot *Cordyline fruticosa* and *Rosa chinensis*. *Acta Horticulturae Sinica* **24**, 71-74 (1997).
86. A. Hagiladi, N. Umiel, X. Yang, in *Flower Bulbs - Seventh International Symposium, Vols 1 and 2*, H. LilienKipnis, A. Borochoy, A. H. Halevy, Eds. (1997), pp. 755-761.
87. A. Hagiladi, N. Umiel, Z. Gilad, X. Yang, in *Flower Bulbs - Seventh International Symposium, Vols 1 and 2*, H. LilienKipnis, A. Borochoy, A. H. Halevy, Eds. (1997), pp. 747-753.
88. X. Yang, B. Jin, Y. Zhang, D. Mu, X. Tang, Enhancement of direct shoot regeneration from internode segments of chrysanthemum by silver nitrate. *Acta Horticulturae* **404**, 68-73 (1995).
89. B. Jin, H. Dong, X. Yang, Shortening hybridization breeding cycle of rose - a study on mechanisms controlling achene dormancy. *Acta Horticulturae* **404**, 40-47 (1995).
90. X. Yang, B. Jin, *The Camellias*. (China Agricultural Sciencetech Press, Beijing, 1994).
91. B. Jin, H. Dong, X. Yang, Influence of gaseous environment and light on growth of tissue-cultured carnation plants. *Acta Horticulturae Sinica* **20**, 389-393 (1993).
92. D. Mu, B. Jin, X. Yang, Studies on the effect of IBA and nutrient- mist on the rooting of chrysanthemum cuttings. *Acta Horticulturae Sinica* **19**, 89-90 (1992).
93. B. Jin *et al.*, Studies on the mechanism of action of B9 in reducing stem elongation of chrysanthemum. *Acta Horticulturae Sinica* **19**, 171-174 (1992).
94. X. Yang, W. Hu, X. Sun, Changes in biomacromolecules in *Magnolia denudata* seed during dormancy breaking. *Acta Horticulturae Sinica* **18**, 75-80 (1991).
95. X. Yang, W. Hu, Studies on the removal of seed dormancy in *Magnolia denudata* Desr. *Journal of Chinese Landscape Architecture* **6**, 49-51 (1990).