

PATRICK X. ZHAO, Ph.D.

December 2010

Associate Professor

Plant Biology Division
The Samuel Roberts Noble Foundation
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SUMMARY

Patrick X. Zhao is an Associate Professor of Bioinformatics in the Plant Biology Division, Samuel Roberts Noble Foundation. He also holds an Adjunct Assistant Professor appointment in the Department of Computer Science, Oklahoma State University. Dr. Zhao received his Ph.D. degree in Communications and Information Systems from Shanghai Jiao Tong University in 2000. After his graduation, he joined Dr. Eugenia Wang's Lab in the School of Medicine, University of Louisville, as a bioinformatics research associate developing bioinformatics technologies to discover genes and biological networks that are essential to the determination of the normal aging process, in particular those related to successful aging in centenarians. In 2004, he joined the Samuel Robert Noble Foundation as a faculty member. Dr. Zhao's current research centers on Plant Bioinformatics and Plant and Soil Microbe Functional Genomics. His lab develops innovative computational methods to tackle large-scale plant 'omics' data, with specific focus on: 1) gene function, regulation, and networks, 2) comparative 'omics' and genome annotation, 3) functional genomics and metagenomics for understanding plant-microbe interactions, and 4) biological data integration, mining, and knowledge discovery.

PERSONAL

Nationality:	P. R. China/US Permanent Resident
Date of Birth:	February 4, 1969
Place of Birth:	Jiangsu, China
Spouse:	Jie Cai
Children:	Alexander S. Zhao (born 2004) Olivia X. Zhao (born 2008)

CURRENT POSITION

Associate Professor, Bioinformatics, Plant Biology Division, Samuel Roberts Noble Foundation, 2510 Sam Noble Parkway, Ardmore, OK 73401, USA

CURRENT RESEARCH INTERESTS

- Bioinformatics and functional genomics for understanding plant gene function, regulation, and interactive networks
- comprehensive and *de novo* annotation methods for function-specific genes, proteins, and metabolites in plants, fungi, and bacteria
- Bioinformatics and metagenomics for understanding plant-microbe interactions
- Machine learning for biological data integration, mining, and knowledge discovery

PROFESSIONAL EXPERIENCE

- Assistant Professor then Associate Professor, Plant Biology Division, Samuel Roberts Noble Foundation, Ardmore, Oklahoma, 2004-present

- Research Associate, University of Louisville, School of Medicine, Louisville Kentucky, 2001-2004
- Systems Engineer, Guoxin Lucent Technologies, Shanghai, China, 1999-2000
- Application Engineer and Project Manager, CASCO Signal Co. Ltd., Shanghai China, 1995-1997
- Lecturer then Assistant Professor in Electrical Engineering, Tong Ji University, Shanghai China, 1993-1996

EDUCATION & TRAINING

- Tong Ji University, China, Electrical Engineering specializing in Telecommunication Engineering, B.S. 1990
- Tong Ji University, China, Electrical Engineering specializing in Automation Control, M.S. 1993
- Shanghai Jiao Tong University, China, Communication & Information Systems, Ph.D. 2000
- University of Louisville, Postdoctoral Fellow in Bioinformatics, 2000

SCIENTIFIC SERVICES

A) Scientific Review panels

- PLANT-KBBE, jointly launched by the Spanish Ministry of Science and Innovation (MICINN), the German Ministry of Education and Research (BMBF), the French Ministry of Research (MdR), and the French National Agency for Research (ANR)
- GABI (Genome Analysis of the Plant Biological System) - FUTURE Program, by the German Federal Ministry of Education and Research (BMBF)
- Ohio Plant Biotechnology Consortium (OPBC)

B) Editorial Board

- *The Int. J. of Data Mining Modeling and Management (IJDMMM)*

C) Reviewing

- Reviewer of manuscripts for: *Briefing in Bioinformatics, Bioinformatics, BMC Bioinformatics, BMC Plant Biology, BMC genomics, Evolutionary Bioinformatics, Bioinformatics Track of BIONETICS*

D) Organized International Conferences

- Program Committee Member of *the IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2010)*, December 19-22, 2010, Hong Kong.
- Program Committee Member of *the IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2009)*, November 1 - 4, 2009, Washington D.C., USA.
- Co-Chair of the special session on bioinformatics and computational biology, *the IEEE Symposium on Signal Processing and Information Technology (ISSPIT 2008)*, December 16-19, 2008, Sarajevo, Bosnia, and Herzegovina

E) Postdoctoral/Research Associates Supervised (with current or recent employer information)

- Haiquan Li (2006-2010)- Assistant Research Professor, University of Chicago, IL
- Yuanji Zhang (2004-2005)- Monsanto Company, Chesterfield, MO
- Indira Reddy (2004-2006)- Mayo Clinic, Rochester, MN
- Ji He (2004-2008)- The Noble Foundation, Ardmore, OK

F) Visiting Scientist

- Dr. Yuan Harmonie Zhong, Biology Department, Millersville University of Pennsylvania, Sabbatical 2008.

G) Current Membership of Scientific Societies

- Full Member of Sigma Xi, The Scientific Research Society
- The American Association for the Advancement of Science (AAAS)
- Intelligent Systems for Molecular Biology (ISMB)
- Institute of Electrical and Electronics Engineers (IEEE)
- American Society of Plant Biologists (ASPB)

INVITED SEMINARS

- *Computational Approaches to Deciphering Plant Gene Regulatory Networks (GRNs)*, Computer Science Department, Oklahoma State University, Stillwater, Oklahoma, February 25, 2010
- Seminar: *Computational Intelligence in Bioinformatics and Plant Genomics*; Guest Lecture: *Comparative genomics of secretory trichomes - A Case Study on Bioinformatics and Plant Genomics*, Botany Department, Miami University, Oxford, Ohio, November 12-13, 2009.
- *Computational Intelligence in Plant Genomics and Bioinformatics*, Computer Engineering and Computer Science Department, University of Louisville, Louisville, KY, November 9, 2007
- *Association Analysis on Microarray Gene Expression Data & Target Prediction of Transcription Factors*, Computer Science Department, University of Missouri – Columbia, November 16, 2006
- *Plant Genomics and Bioinformatics: from Genome to Phoneme*, UC Davis Biotechnology Program, May 18, 2005

CURRENT EXTERNAL GRANT SUPPORT

- **Project title:** ABI: Systems bioinformatics approaches to modeling and deciphering plant transcriptional regulatory networks
Source of support: National Science Foundation Advances in Biological Informatics (ABI)
Investigators: Patrick X. Zhao (PI)
Senior Personnel: Xinbin Dai and Jun Li
Total Noble Foundation award: \$1,183,305
Duration of award: July 2010-June 2013
Effort: 20%
- **Project title:** Develop graph-based models to stimulate and decipher plant gene regulatory networks
Source of Support: Oklahoma Center for the Advancement of Science & Technology (OCAST)
Investigators: Patrick X. Zhao (PI)
Total Noble Foundation award: \$89,550
Duration of award: August 1, 2009-July 31, 2011
Effort: 15%
- **Project title:** Comparative genomics of secretory trichomes – Biofactories for production of plant secondary metabolites
Source of support: National Science Foundation Plant Genome
Investigators: As Faculty Associate, PI: Dr. Richard A. Dixon, Co-PI: Dr. David. Marks, U. of Minnesota
Total Noble Foundation award: \$1,406,741 (NF \$1,133,074)
Duration of award: August, 2006-July, 2009 (currently, no cost extension)

Effort: 15%

- **Project title:** Development and application of genomic tools for drought tolerance enhancement in Alfalfa (*Medicago sativa* L.)
Source of support: Oklahoma Department of Energy – Oklahoma Bioenergy Center
Investigators: As Co-PI, PI: Dr. Michael Udvardi, Co-PIs: Drs. Yuhong Tang, Maria Monteros, Patrick X. Zhao and Zeng-Yu Wang
Total Noble Foundation award: \$199,850
Duration of award: January, 2008-December, 2010
- **Project title:** Development of genetic resources to dissect the regulatory networks governing nodule development and differentiation in *Medicago truncatula*
Source of support: National Science Foundation Plant Genome
Investigators: As Collaborator, PI: Michael Udvardi, Co-PIs: Dr. Kiran Mysore and Rujin Chen
Total Noble Foundation award: \$3,831,732 (\$~200,000 for Zhao lab)
Duration of award: September 15, 2007-August 31, 2011
- **Project title:** Development and application of genomic tools for drought tolerance enhancement in alfalfa (*Medicago sativa* L.)
Source of support: Oklahoma Bioenergy Center (Pending application)
Investigator: As Co-PI, PI: Maria Monteros, Co-PIs: Michael Udvardi, Yuhong Tang, Patrick X. Zhao and Zeng-yu Wang
Total Noble Foundation award: \$146,480
Duration of award: December, 2010-December, 2011

PENDING EXTERNAL GRANT SUPPORT:

- **Project title:** Advancing Bioinformatics to Understanding Mechanisms of Plant Regulatory Non-coding Small RNA -Target Interactions
Source of Support: Oklahoma Center for the Advancement of Science & Technology (OCAST)
Investigators: Patrick X. Zhao (PI)
Total requested award amount: \$100,000
Requested award period: March, 2010 – February, 2012
- **Project title:** GEPR: A systems approach to understand the interactions of potatoes with their soil microbial environment
Source of support: National Science Foundation Plant Genome Program (Pending application)
Investigators: As collaborator, PI: Drs. Jorge Vivanco, Co-PIs: David Holm, Dr. Dayakar Badri, Colorado State University and Daniel Manter, Colorado State University and USDA-ARS
Total requested award amount: \$924,258 (\$157,428 for Zhao lab)
Requested award period: August, 2010 – July, 2012

RECENT PUBLICATIONS (papers published while affiliated with the Noble Foundation)

Please note: (1) *I have published under three names: “Patrick Xuechun Zhao”, “Patrick Zhao”, and “Xuechun Zhao”* (2) * *Corresponding Author*

1. Marina A. Naoumkina, Qiao Zhao, Lina Gallego-Giraldo, Xinbin Dai, **Patrick X. Zhao** and Richard A. Dixon, Genome-wide analysis of phenylpropanoid defence pathways, *Molecular Plant Pathology*, 2010. doi: 10.1111/j.1364-3703.2010.00648.x.

2. Rakesh Kaundal, Reena Saini and **Patrick X. Zhao**, Combining machine learning and homology-based approaches to accurately predict subcellular localization in *Arabidopsis thaliana*. *Plant Physiology*, 2010: DOI:10.1104/pp.110.156851.
3. Mingyi Wang, Vagner Benedito, **Patrick Xuechun Zhao**, and Michael K. Udvardi, *Inferring Large-scale Gene Regulatory Networks using a Low-Order Constraint-based Algorithm*. *Molecular BioSystems*, 2010: DOI:10.1039/b917571g.
4. Vagner A. Benedito, Haiquan Li, Xinbin Dai, Maren Wandrey, Ji He, Rakesh Kaundal, Ivone Torres-Jerez, S. Karen Gomez, Maria J. Harrison, Yuhong Tang, **Patrick X. Zhao**, and Michael K. Udvardi, *Genomic inventory and transcriptional analysis of *Medicago truncatula* transporters*. *Plant Physiol.*, 2009: DOI:10.1104/pp.109.148684.
5. Xinbin Dai, Guodong Wang, Dong Sik Yang, Yuhong Tang, Pierre Broun, M. David Marks, Lloyd W. Sumner, Richard A. Dixon, and **Patrick Xuechun Zhao***, *TrichOME: A Comparative Omics Database for Plant Trichomes*. *Plant Physiol.*, 2009. **152**(1): 44-54.
6. Ji He, Vagner A. Benedito, Mingyi Wang, Jeremy D Murray, **Patrick Xuechun Zhao**, Yuhong Tang, and Michael Udvardi, *The *Medicago truncatula* gene expression atlas web server*. *BMC Bioinformatics*, 2009. **10**: 441.
7. Haiquan Li, Vagner A. Benedito, Michael K. Udvardi, and **Patrick Xuechun Zhao***, *TransportTP: A two-phase classification approach for membrane transporter prediction and characterization*. *BMC Bioinformatics*, 2009. **10**(1): 418.
8. Li Tian, Gregory Peel, Zhentian Lei, Naveed Aziz, Xinbin Dai, Ji He, Bonnie Watson, **Patrick Zhao**, Lloyd Sumner, and Richard Dixon, *Transcript and proteomic analysis of developing white lupin (*Lupinus albus L.*) roots*. *BMC Plant Biology*, 2009. **9**(1): 1.
9. Vagner Benedito, Ivone Tomez-Jerez, Jeremy Murray, Andry Andrianakaja, Stacey Allen, Klementina Kakar, Maren Wandrey, Jerome Verdier, Helene Zuber, Thomas Ott, Sandra Moreau, Andreas Niebel, Tancred Frickey, Georg Weiller, Ji He, Xinbin Dai, **Patrick Xuechun Zhao**, Yuhong Tang, and Michael Udvardi., *A gene expression atlas of the model legume *Medicago truncatula**. *Plant J*, 2008. **55**(3): 504-13.
10. Xinbin Dai and **Patrick Xuechun Zhao***, *pssRNAMiner: a plant short small RNA regulatory cascade analysis server*. *Nucleic Acids Res*, 2008. **36**(Web Server issue): W114-8.
11. Asuka Itaya, Ralf Bundschuh, Anthony J. Archual, Je-Gun Joung, Zhangjun Fei, Xinbin Dai, **Patrick X. Zhao**, Yuhong Tang, Richard S. Nelson, and Biao Ding, *Small RNAs in tomato fruit and leaf development*. *Biochimica et Biophysica Acta (BBA) - Gene Regulatory Mechanisms*, 2008. **1779**(2): 99-107.
12. Haiquan Li, Xinbin Dai, and **Xuechun Zhao***, *A nearest neighbor approach for automated transporter prediction and categorization from protein sequences*. *Bioinformatics*, 2008. **24**(9): 1129-1136.
13. MA Rouf Mian, Yan Zhang, Zeng-Yu Wang, Ji-Yi Zhang, Xiaofei Cheng, Lei Chen, Konstantin Chekhovskiy, Xinbin Dai, Chunhong Mao, Foo Cheung, **Xuechun Zhao**, Ji He, Angela D Scott, Christopher D Town, and Gregory D May, *Analysis of tall fescue ESTs representing different abiotic stresses, tissue types and developmental stages*. *BMC Plant Biol*, 2008. **8**: 27.
14. Million Tadege, Jiangqi Wen, Ji He, Haidi Tu, Younsig Kwak, Alexis Eschstruth, Anne Cayrel, Gabi Endre, **Patrick Xuechun Zhao**, Mireille Chabaud, Pascal Ratet, and Kirankumar Mysore, *Large-scale insertional mutagenesis using the *Tnt1* retrotransposon in the model legume *Medicago truncatula**. *Plant J*, 2008. **54**(2): 335-47.

15. Guodong Wang, Li Tian, Naveed Aziz, Pierre Broun, Xinbin Dai, Ji He, Andrew King, **Patrick X. Zhao**, and Richard A. Dixon, *Terpene Biosynthesis in Glandular Trichomes of Hop*. *Plant Physiol.*, 2008. **148**(3): 1254-1266.
16. Yan Zhang, Ji He, **Patrick Zhao**, Joseph Bouton, and Maria Monteros, *Genome-wide identification of microsatellites in white clover (*Trifolium repens* L.) using FIASCO and phpSSRMiner*. *Plant Methods*, 2008. **4**(1): 19.
17. Amanda K. Broz, Corey D. Broeckling, Ji He, Xinbin Dai, Patrick **Xuechun Zhao**, and Jorge M. Vivanco, *A first step in understanding an invasive weed through its genes: an EST analysis of invasive *Centaurea maculosa**. *BMC Plant Biol*, 2007. **7**: 25.
18. Xinbin Dai, Ji He, and **Xuechun Zhao***, *A new systematic computational approach to predicting target genes of transcription factors*. *Nucleic Acids Res*, 2007. **35**(13): 4433-40.
19. Ji He, Xinbin Dai, and **Xuechun Zhao***, *PLAN: a web platform for automating high-throughput BLAST searches and for managing and mining results*. *BMC Bioinformatics*, 2007. **8**(1): 53.
20. Saeed Irian, Ping Xu, Xinbin Dai, **Patrick X. Zhao**, and Marilyn J. Roossinck, *Regulation of a Virus-Induced Lethal Disease in Tomato Revealed by LongSAGE Analysis*. *Molecular Plant-Microbe Interactions*, 2007. **20**(12): 1477-1488.
21. Ji He, Xinbin Dai, and Xuechun Zhao. *Associative Artificial Neural Network for Discovery of Highly Correlated Gene Groups Based on Gene Ontology and Gene Expression*. in *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB)*. April 2007, p17-24.
22. Marina Naoumkina, Ivone Torres-Jerez, Stacy Allen, Ji He, **Patrick Zhao**, Richard Dixon, and Gregory May, *Analysis of cDNA libraries from developing seeds of guar (*Cyamopsis tetragonoloba* (L.) Taub)*. *BMC Plant Biology*, 2007. **7**(1): 62.
23. Vagner A. Benedito, Xinbin Dai, Ji He, **Patrick X. Zhao**, and Michael K. Udvardi, *Functional Genomics of Plant Transporters in Legume Nodules*. *Functional Plant Biology*, 2006. **33** (**8**): 731-736.
24. Corey D. Broeckling, Indira R. Reddy, Anthony L. Duran, **Xuechun Zhao**, and Lloyd W. Sumner, *MET-IDEA: Data Extraction Tool for Mass Spectrometry-Based Metabolomics*. *Analytical Chemistry*, 2006. **78**(13): 4334-4341.
25. Ji He, Xinbin Dai, and Xuechun Zhao. *A Systematic Computational Approach for Transcription Factor Target Gene Prediction*. in *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB)*. September 2006, p385-391.

PREVIOUS PUBLICATIONS

26. Abdelnaby Khalyfa, Carolyn M. Klinge, William C. Hall, **Xuechun Zhao**, Marilyn M. Miller, and Eugenia Wang, *Transcription profiling of estrogen target genes in young and old mouse uterus*. *Exp Gerontol*, 2003. **38**(10): 1087-99.
27. Eugenia Wang, Chantale Lacelle, Suyin Xu, **Xuechun Zhao**, and Ming Hou, *Designer microarrays: from soup to nuts*. *J Gerontol A Biol Sci Med Sci*, 2002. **57**(11): B400-5.
28. Haiyun Huang, Feihu Qi, and **Xuechun Zhao**, *Active Contour Model Based on Multi-scale Image Analysis*. *Journal of Computer Research and Development*, 2000. **2000-10**.
29. Lei Wang, Feihu Qi, and **Xuechun Zhao**, *BWT and FVQ based algorithm for very low bit rate image coding*. *Chinese Journal of Electronics*, 2000. **22**(4): 667-671.

30. **Xuechun Zhao** and Feihu Qi, *Automatic image segmentation based on deformable models and pixel affinity statistics*. Journal of Infrared and Millimeter Waves, 2000. **19(1)**(1): 33-37.
31. **Xuechun Zhao** and Feihu Qi, *An Overloaded or Unbalanced Freight Wagon License Recognition System Based on Neural Networks*. High-tech Letters, 2000. **10(6)**: 44-47.
32. **Xuechun Zhao** and Feihu Qi, *Content-based image segmentation using deformable template matching*. ACTA ELECTRONICA SINICA, 2000. **28(44)**: 69-72.
33. **Xuechun Zhao**, Feihu Qi, Haiyun Huang, and Jinfeng Zhan. *3-D deformable models for femur shape recovery from volumetric images*. in *IEEE Proceeding of The Fourth International Conference on High-Performance Computing, Beijing, May 2000*. 2000.
34. Jinfeng Zhan, Feihu Qi, and **Xuechun Zhao**, *Automatic Segmentation of Moving Object and Background*. Journal of Infrared and Millimeter Waves, 1999. **18(5)**: 343-350.
35. **Xuechun Zhao**, *Study on the Application of Deformable Models and Templates in image recognition*, Ph.D.Thesis. 1999, Shanghai Jiao Tong University.
36. **Xuechun Zhao**, Feihu Qi, and Lei Wang, *Adaptive Deformable Model for Automatic Vocal Cords Quivering Image Segmentation*. Journal of Infrared and Millimeter Waves, 1999. **18(5)**: 351-357.

INVITED BOOK CHAPTER AND REVIEW ARTICLE

1. Xinbin Dai, Zhaohong Zhuang and **Patrick X. Zhao**, Computational analysis of miRNA targets in plants: current status and challenges, *Briefings in Bioinformatics*, 2010, doi: 10.1093/bib/bbq065.
2. Haiquan Li, Jinyan Li, and **Patrick X. Zhao***, Discovery of Protein Interaction Sites, in *Bioinformatics section, Encyclopedia of Data Warehousing and Mining, Second Edition*. Bioinformatics section, Encyclopedia of Data Warehousing and Mining, Second Edition, ISBN: 978-1-60566-010-3, edited by Dr. John Wang, August, 2008, published under the imprint Information Science Reference, formerly Idea Group Reference.

PRESENTATIONS AT SCIENTIFIC MEETINGS (while affiliated with the Noble Foundation)

1. Haiquan Li, Xibin Dai and **Patrick X. Zhao*** (July 11-13, 2010). *Ciport: A comparative and integrative transporter annotation tool and identification of lignin-related transporters*. 18th Annual International Conference on Intelligent Systems for Molecular Biology, Boston, Massachusetts, USA.
2. Rakesh Kaundal and **Patrick X. Zhao*** (July 11-13, 2010). *A systematic approach to predicting organism-specific subcellular localization suggests species-specific sorting patterns*. 18th Annual International Conference on Intelligent Systems for Molecular Biology, Boston, Massachusetts, USA.
3. Xinbin Dai, Guodong Wang, Dong Sik Yang, Yuhong Tang, Pierre Broun, M. David Marks, Lloyd W. Sumner, Richard A. Dixon, and **Patrick X. Zhao*** (January 9-13, 2010). *Trichome: A Comparative Omics Database for Plant Trichomes*. Plant & Animal Genomes XVIII Conference, San Diego, California, USA.
4. Xinbin Dai and Patrick **Xuechun Zhao*** (January 9-13, 2010). *psRNATarget: A Plant Small RNA Regulator/Target Analysis Server*. Plant & Animal Genomes XVIII Conference, San Diego, California, USA.
5. Yuanhong Han, Yun Kang, Ivone Torres-Jerez, Foo Cheung, Christopher D Town, **Patrick Xuechun Zhao**, Michael K Udvardi, and Maria J Monteros (January 9-13, 2010). *Genome - Wide SNP Discovery In Tetraploid Alfalfa*. Plant & Animal Genomes XVIII Conference, San Diego, California, USA.

6. Ji He, Vagner A. Benedito, Mingyi Wang, Jeremy D. Murray, **Patrick X. Zhao**, Yuhong Tang, and Michael K. Udvardi (January 9-13, 2010). *The Medicago truncatula Gene Expression Atlas: A Web Platform For Integrative Mining Of M. truncatula Gene Expression Data*. *Plant & Animal Genomes XVIII Conference*, San Diego, California, USA.
7. Jun Li and **Patrick Xuechun Zhao*** (January 9-13, 2010). *SeqToPathwayMapper: A RNA-Seq Based Gene Expression And Pathway Analysis Server*. *Plant & Animal Genomes XVIII Conference*, San Diego, California, USA.
8. Rajasekhara Reddy Duvvuru Muni, Xinbin Dai, Yuhui Chen, Guangming Li, **Patrick Xuechun Zhao***, and Rujin Chen* (January 9-13, 2010). *Mt-GOTA: A Genome Tiling Array For Copy Number Variation Detection In Fast Neutron Induced Deletion Mutants And Natural Accessions Of Medicago truncatula*. *Plant & Animal Genomes XVIII Conference*, San Diego, California, USA.
9. Ranamalie Amarasinghe, Uljana Hesse, Haiquan Li, **Patrick Xuechun Zhao**, Christopher Schardl, and Carolyn A Young (January 10-14, 2009). *A Genomic Survey Of Transporters And Their Expression In A Grass-Endophyte Symbiosis Reveals Putative Key Genes In The Nutritional Cross Talk*. *Plant and Animal Genomes XVII Conference*, San Diego, California, USA.
10. Andry Andriankaja, Ivone Torres-Jerez, Mingyi Wang, Jeremy D. Murray, Vagner A. Benedito, Tancred Frickey, Georg Weiller, Shusei Sato, Satoshi Tabata, Karine Gallardo, Richard Thompson, Xinbin Dai, **Patrick Xuechun Zhao**, Yuhong Tang, and Michael K. Udvardi. (January 10-14, 2009). *Unraveling Genetic Regulatory Networks Underlying Seed Storage Metabolism in Model Legume Species*. *Plant and Animal Genomes XVII Conference*, San Diego, California, USA.
11. Xinbin Dai, Guodong Wang, Yuhong Tang, David Marks, Pierre Broun, Lloyd W. Sumner, Richard A. Dixon, and **Patrick Xuechun Zhao*** (July 18-22, 2009). *TrichOME: A Comparative Omics Database for Plant Trichomes*. *Plant Biology 2009*, Hawaii, USA.
12. Xinbin Dai and **Patrick Xuechun Zhao*** (January 10-14, 2009). *pssRNAMiner: A Plant Short Small RNA Regulatory Cascade Analysis Server*. *Plant and Animal Genomes XVII Conference*, San Diego, California, USA.
13. Rakesh Kaundal and **Patrick Xuechun Zhao*** (July 18-22, 2009). *ASLpred: Arabidopsis Subcellular Localization predictor*. *Plant Biology 2009*, Hawaii, USA.
14. Haiquan Li, Vagner A. Benedito, Xinbin Dai, Michael K. Udvardi, and **Patrick Xuechun Zhao*** (May 18-21, 2009). *TransportTP: A Two-phase Classification Approach for Transporter Prediction and Functional Categorization*. *RECOMB 2009*, Tucson, Arizona, USA.
15. Haiquan Li, Vagner A. Benedito, Xinbin Dai, Michael K. Udvardi, and **Patrick Xuechun Zhao*** (July 18-22, 2009). *Saport: A Semi-automatic Transporter Annotation System*. *Plant Biology 2009*, Hawaii, USA.
16. Haiquan Li, Vagner A. Benedito, Xinbin Dai, Michael Udvardi, and **Patrick Xuechun Zhao*** (January 10-14, 2009). *TransportTP: Transporter Prediction And Functional Categorization Using A Two-Stage Classification Approach*. *Plant and Animal Genomes XVII Conference*, San Diego, California, USA.
17. Ranamalie Amarasinghe, Uljana Hesse, Haiquan Li, **Patrick Zhao**, Christopher Schardl, and Carolyn Young (June 26-July 1, 2008). *Transporters Operating at The Plant-Fungal Interface in Tall Fescue-Endophyte Symbiotic Association: Novel Insights From A Nutritional Stand Point*. *Plant Biology 2008*, Mérida, Mexico.
18. Ranamalie Amarasinghe, Uljana Hesse, Haiquan Li, **Patrick X Zhao**, Christopher L Schardl, and Carolyn A Young. (January 12-16, 2008). *Insights into The Life Style Of A Mutualistic*

- Endosymbiont: Identification and Classification of The Transporter Gene Complement in The Epichloë festucae Genome. Plant and Animal Genomes XVI Conference, San Diego, California, USA.*
19. Vagner A. Benedito, Ivone Torres-Jerez, Million Tadege, Pascal Ratet, Hong L. Wang, Guangming Li, Haidi Tu, Xinbin Dai, Ji He, Jiangqi Wen, Kirankumar S. Mysore, Rujin Chen, **Patrick Xuechun Zhao**, and Michael K. Udvardi (June 26-July 1, 2008). *Functional Genomics of Legume Nodule Transporters. Plant Biology 2008*, Mérida, Mexico.
 20. Xinbin Dai, Guodong Wang, Yuhong Tang, Wensheng Li, David Marks, Pierre Broun, Lloyd W. Sumner, Richard A. Dixon, and **Patrick X. Zhao*** (December 7-12, 2008). *TrichOME: An Integrated Genomic Database for Comparative Study of Legume Trichomes. IV International legume genetics and genomics conference*, Puerto Vallarta, Mexico.
 21. Xinbin Dai and **Patrick Xuechun Zhao*** (January 12-16, 2008). *miRNAfinder: A Plant MicroRNA Prediction Server. Plant and Animal Genomes XVI Conference, San Diego, California, USA.*
 22. Francis M. Kirigwi, Checovskiy Konstantin, **Xuechun Zhao**, and Malay C. Saha (January 12-16, 2008). *Osmotic-Stress Associated Gene Orthologs in Tall Fescue. Plant and Animal Genomes XVI Conference, San Diego, California, USA.*
 23. Kaundal Rakesh and **Patrick Xuechun Zhao*** (January 12-16, 2008). *An Integrated Prediction System for Protein Subcellular Localization in Arabidopsis. Plant and Animal Genomes XVI Conference, San Diego, California, USA.*
 24. Million Tadege, Jiangqi Wen, Ji He, Hee-Kyung Lee, Erin Hartwell, Janie Gallaway, Xiaofei Cheng, Mingyi Wang, Catalina Pislariu, Jeremy Murray, **Patrick X. Zhao**, Michael K. Udvardi, Pascal Ratet, and Kirankumar S. Mysore (December 7-12, 2008). *Development of Tnt1-insertion mutants in Medicago truncatula for efficient forward and reverse genetic screens. IV International legume genetics and genomics conference*, Puerto Vallarta, Mexico.
 25. Michael Udvardi, Vagner Benedito, Jiyi Zhang, Jeremy Murray, Ivone Torrez-Jerez, Rujin Chen, Million Tadege, Kiran Mysore, Jiangqi Wen, Ji He, **Patrick Zhao**, Yuhong Tang, Christopher D Town, Georg Weiller, Klementina Kakar, Maren Wandrey, Zeng-yu Wang, and Richard A. Dixon (January 12-16, 2008). *Medicago Functional and Translational Genomics. Plant and Animal Genomes XVI Conference, San Diego, California, USA.*
 26. Michael K. Udvardi, Vagner A. Benedito, Jeremy Murray, Catalina Pislariu, Mingyi Wang, Million Tadege, Rajasekhara reddy Duvvuru muni, Ivone Torres-Jerez, Mark Taylor, Shulan Zhang, Xiaofei Chen, Jiangqi Wen, Ji He, Xinbin Dai, **Patrick X. Zhao**, Yuhong Tang, Pascal Ratet, Giles Oldroyd, Rujin Chen, and Kirankumar S. Mysore (December 7-12, 2008). *Functional genomics of nitrogen fixation in Medicago. IV International legume genetics and genomics conference*, Puerto Vallarta, Mexico.
 27. Xinbin Dai, Ji He, and **Patrick Xuechun Zhao*** (January 13-17, 2007). *A Position-Sensitive N-gram Profile Based Computational Approach to Predict Target Genes of Transcription Factors. Plant & Animal Genome XV Conference, San Diego, California, USA.*
 28. Ji He, Xinbin Dai, and **Patrick Xuechun Zhao*** (January 13-17, 2007). *A Novel Adaptive Learning Neural Architecture for Mining Associations between Gene Functional Categorization and Gene Expression Data. Plant & Animal Genome XV Conference, San Diego, California, USA.*
 29. Michael Udvardi, Vagner Benedito, Jiyi Zhang, Jeremy Murray, Ivone Torrez-Jerez, Rujin Chen, Million Tadege, Kiran Mysore, Jiangqi Wen, Ji He, **Patrick Zhao**, Yuhong Tang, Klementina Kakar, Maren Wandrey, Pascal Ratet, Giles Oldroyd, Georg Weiller, Foo Cheung, Hank Wu, and Christopher D. Town (January 13-17, 2007). *New Tools and Resources for Medicago Functional Genomics. Plant & Animal Genome XV Conference, San Diego, California, USA.*

30. Michael Udvardi, Vagner Benedito, Jiyi Zhang, Jeremy Murray, Ivone Torres-Jerez, Rujin Chen, Million Tadege, Kiran Mysore, Jiangqi Wen, Ji He, **Patrick Zhao**, Yuhong Tang, Christopher D. Town, Georg Weiller, Klementina Kakar, Maren Wandrey, Zeng-yu Wang, and Rick Dixon (January 13-17, 2007). *Medicago Functional and Translational Genomics. Plant & Animal Genome XV Conference*, San Diego, California, USA.
31. **Patrick Xuechun Zhao***, Ji He, Xinbin Dai, and Haiquan Li (January 13-17, 2007). *A Property Signature Suffix-Tree Based Algorithm for Transporter Annotation and Categorization. Plant & Animal Genome XV Conference*, San Diego, California, USA.
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PUBLISHED BIOINFORMATICS WEB SERVERS & DATABASES

- pssRNAMiner: A Plant Short Small RNA Regulatory Cascade Analysis Server
<http://bioinfo3.noble.org/pssRNAMiner/>
- psRNATarget: A Plant Small RNA Regulator Target Analysis Server
<http://bioinfo3.noble.org/psRNATarget/>
- TransportTP: A Two-phase Membrane Transport Protein Prediction and Characterization Server System
<http://bioinfo3.noble.org/transporter/>

- AtSubP: Arabidopsis Subcellular Localization predictor
<http://bioinfo3.noble.org/AtSubP/>
- PLAN: Personal BLAST Navigator
<http://bioinfo.noble.org/plan/>
- MtGEA: The Medicago truncatula gene expression atlas web server
<http://bioinfo.noble.org/gene-atlas/>
- TrichOME: A Comparative Omics Database for Plant Trichomes
<http://www.plantrichome.org/>

PUBLISHED STAND-ALONE SOFTWARE

- Met-idea: A data extraction and alignment tool for mass spectra. The software is freely available at
<http://bioinfo.noble.org/>.