



Lloyd W. Sumner, Ph.D.

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EDUCATION:

Ph.D. in Analytical Chemistry from Oklahoma State University (December, 1993, Stillwater, OK)
B.S. Cameron University (May 1989, Lawton, OK) Major: Chemistry, Minor: Mathematics
Fundamental Electronics Certificate (1984, Lawton, OK) Great Plains Vocational School.
High School Diploma (1983, Lawton, OK) Lawton High School.

HONORS, AWARDS, & APPOINTMENTS

President, Metabolomics Society, Jan. 2009-Sept. 2010
Treasurer, Metabolomics Society, Oct. 2007 to Dec. 2008
Adjunct Assoc. Professor, Oklahoma University, Dept. of Botany and Microbiology, Jan 2008-present
Faculty of 1000, 2008-present
Board of Directors, Metabolomics Society, Oct 2007-2010.
Cameron University Distinguished Alumni 2007 Award
Editorial Board: Plant Physiology (American Society for Plant Biology), appointment Jan 2007-Jan 2012.
Editorial Board Member, The Open Plant Science Journal
Honorary Lifetime membership in The Metabolomics Society awarded June 24, 2006.
Fellow, The American Association for the Advancement of Science (Sept. 2005-present)
Editorial Board: Metabolomics (Kluwer), Oct. 2004 to date.
Scientific Advisory Board, Metabolomics Society, Cambridge, MA (2004-2007)
External Scientific Advisory Committee Member – Colorado State University Metabolomics Consortium (2004-2006)
Scientific Consultant for Sigma-Aldrich Plant Biotech Initiative (2004-2005)
Adjunct Associate Professor, Oklahoma State University, Department of Biochemistry and Molecular Biology, 2004-present.
Co-founding and Current Member of the International Advisory Committee for Plant Metabolomics (2001-present)
Graduate Faculty Appointment, Texas A&M Univ., Department of Chemistry, August 1999
Graduate Research Fellowship, Samuel Roberts Noble Foundation, 1990-1993.
Temple W. Chronister Memorial Scholarship, 1989
Ansley Memorial Scholarship, 1988

EMPLOYMENT EXPERIENCE:

- **The Samuel Roberts Noble Foundation** (Ardmore, OK) Associate Professor, Biological Mass Spectrometry, Plant Biology Division (February, 2005 to present)
- **The Samuel Roberts Noble Foundation** (Ardmore, OK) Assistant Professor, Biological Mass Spectrometry, Plant Biology Division (August, 1999 to February, 2005)
- **Texas A&M University** (College Station, TX) Associate Director of the Laboratory for Biological Mass Spectrometry (September, 1994 to August, 1999).
- **Texas A&M University** (College Station, TX) Manager of The Applied Mass Spectrometry Laboratory (September, 1993 to August, 1999)
- **Oklahoma State University**, Mass Spectrometry Facility Analyst (September, 1991 to September, 1993).
- **Oklahoma State University** (Stillwater, OK) Research Assistant (May, 1990 to September, 1993)
- **Oklahoma State University**, Teaching Assistant (August, 1989 to May, 1990)
- **Home Repair Business Owner** (May, 1987 to May, 1989) These experiences provide a solid electrical and mechanical background that is highly useful in instrumental construction, maintenance, and repair. Profits from this business were used to finance my graduate education.
- **Commercial and Home Rental Maintenance** (June, 1981 to May, 1987)

Synergistic Activities

- Co-chair of The American Society for Mass Spectrometry Metabolomics Interest Group (2010-2012)
- President, The Metabolomics Society, Oct. 1, 2008-Sept 30, 2010
- NSF DBI PGRP Project #701846 Advisory Panel Member & Meeting; An interdisciplinary approach to deciphering the molecular dialogue between the plasma membrane and nucleus of *Medicago truncatula*. June 21-22, 2009 – University of Wisconsin Biotechnology Center, Madison WI, hosts Michael Sussman, Jean-Michel Ane, Josh Coon
- Chair of the chemical analysis working subgroup for the Metabolomic Standardization Initiative (<http://msi-workgroups.sourceforge.net/>).
- Invited participant NIH-sponsored Standards Workshop for Metabolomics, August 1 and 2, 2005, Bethesda, MD.
- Editorial Board: Metabolomics (Kluwer) initiation date, Oct. 2004.
- Scientific Advisory Board, Metabolomics Society, Cambridge, MA (2004-present).
- Program Committee Member and Plant Session Co-chair for the 1st International Conference of Metabolomics Society (June 2005, Tsuroka, Japan).
- Co-organizer of The 2nd International Conference of Metabolomics Society (June 2006, Boston, MA, USA).
- Founding member of the International Advisory Committee for Plant Metabolomics (ICPM; 2001-Present)
- Organizational committee member of the 1st (Wageningen, The Netherlands), 2nd (Golm, Germany), 3rd (Iowa State University, Ames, IA), 4th (Reading, UK) and 5th International Conference on Plant Metabolomics, Yokohama, Japan.
- Organizer of multiple day, hands-on workshop focused on Metabolomics (annually with most recent March 23-27, 2009), Proteomics Workshop (annually and most recent September 22-26, 2008), and Integrated Functional Genomics Workshop. These workshops are hosted in Ardmore, OK and sponsored by the Noble Foundation, and external funding agencies such as the NSF Plant Genome Research Award #010973.
<http://www.noble.org/medicago/NSF/Nsf.main/Workshops.html>.
- Annual contributing instructor including on-site training and demonstration of proteomic and

metabolomic approaches for Instrumental Analysis (Course #CHEM 3525, Southeastern Oklahoma State University) for the last 5 years.

- Local organizing committee member for Molecular Breeding of Forage & Turf, 3rd International Symposium, May 18-22, 2003, Dallas, TX.
 - Panelist NSF Major Research Instrumentation 2002 & 2003.
 - Panelist NIEHS RFA-ES-04-008: Metabolomics: Application to Environmental Health Research. Research Triangle Park, North Carolina, March 3, 2005.
 - Panelist Canadian Foundation for Innovation (CFI), Vancouver, BC, Canada, April 25-26, 2006.
 - Ad-hoc reviewer for BBSRC, NSF 2010, NSF-FIBR, NSF-IOB, NSF-MRI, NSF Plant Genome, NIEHS, Research Corporation, and USDA NRI programs.
 - Peer reviewer for *Analytica Chimica Acta*, *Analytical Biochemistry*, *Analytical Chemistry*, *Bioinformatics*, *BMC Bioinformatics*, *BMC Plant Biology*, *Briefings in Bioinformatics*, *Comparative and Functional Genomics*, *Electrophoresis*, *Genomics*, *John Wiley & Sons Publishing*, *Journal of Agriculture and Food Chemistry*, *Journal of Chromatography B*, *Journal of Experimental Botany*, *Journal of The American Society for Mass Spectrometry*, *Journal of Chemical Ecology*, *Journal of Proteome Research*, *Kluwer/Springer Publishing*, *Mass Spectrometry Reviews*, *Metabolomics*, *Molecular and Cellular Proteomics*, *Molecular Plant Biology*, *Molecular Plant-Microbe Interactions*, *Nature Biotechnology*, *Nature Chemical Biology*, *Nature Methods*, *New Phytologist*, *Nucleic Acid Research*, *Plant Journal*, *Plant Molecular Biology*, *Plant Physiology*, *Planta*, *Physiological & Molecular Plant Pathology*, *Phytochemistry*, *Phytochemistry Reviews*, *Proceedings of The National Academy of Science*, *Proteomics*, *Science*, and *Trends in Plant Science*..
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STUDENTS, POSTDOCS, RESEARCH STAFF, & VISITING SCIENTISTS:

Current:

Zhentian Lei, Ph.D., Research Scientist

Bennie J. Bench, Ph. D., Postdoctoral Research Fellow, Noble Foundation

Dong Sik Tang, Ph.D., Postdoctoral Research Fellow, Noble Foundation

Bonnie S. Watson, MS.c., Sr. Research Associate, Noble Foundation

David V. Huhman, Analytical Chemistry Core Facility Coordinator, Noble Foundation

Mohamed Bedair, Ph.D., Research Associate, Noble Foundation

John H. Snyder, BSc., Graduate Student, Joint Noble Foundation & Cornell University

Shelagh Henson, BSc. Research Technician, Noble Foundation

Former

Victor Asirvatham, PhD., Currently: Florida Atlantic University

Alan Broeckling, summer intern 2002 & 2003

Corey Broeckling, PhD, Research Associate 2004-2006, Currently: Metabolomics Core Colorado State University

Bryna Donnelly-Davis, PhD.

Anthony Duran, MSc. Research Assistant, Currently: Cargill

Aaron Elmer, Ph.D., Currently: Murray State College

Phillip Ershadi, Summer intern 2001, graduate school, OSU

Mohamed Farag, PhD, Asst. Professor, Pharmacognosy Department, University of Cairo

Patrick Fennell, Summer intern 2001 & 2002, Emergency Medical Technician

Mariana Fuego, BSc., Research Technician, Noble Foundation

Aaron Hightower, BSc., Summer Intern 2008, current Oklahoma University Medical School

Karista Hudelston, summer intern 2004

Zhaoyang Liu, Ph.D., Postdoctoral Research Fellow, Current: China

Wensheng Li, PhD., Postdoctoral Research Fellow, Currently Monsanto Company
Satish Nagaraj, Postdoctoral Research Fellow, Current: Research Associate, Mysore Lab, The Noble Foundation
Cesar Moreira, undergraduate Noble Scholar, 2007, Current: Graduate Student, The University of Florida
Ni Pang, MSc., Research Technician, Noble Foundation
Kristy Richardson, MSc. Greenhouse assistant.
Becky Robins-White, BSc., summer intern 2005, Ardmore High School Biology/Chemistry teacher
Guoan Shen, Ph.D., Postdoctoral Research Fellow, 2008-2009, Noble Foundation
Ewa Urbanczyk-Wochniak, PhD., Monsanto Company
Keisha Wood, summer intern 2006 & 2007, Physician Assistant Program Oklahoma Univ.

Visiting Scientists:

Dr. Benkeblia, Visiting Scientist, Hokkaido University, Sapporo, Japan
Prof. Dr. Raoul Bino, Director Plant Research International, Sabatical
MS. Lalita M. Calabria, visiting graduate student, Univ. of Texas at Austin w/ T. Mabry
Clelia de la Pena, visiting graduate student, Colorado State University
Prof. Ken Korth, University of Arkansas, 07Sep10-1Mar11.
Dr. Lanfang Levine, Senior Research Chemist, Dynamic Corporation, NASA, FL.
Prof. Mohammed Meetani, Visiting Professor, Department of Chemistry, College of Science, United Arab Emirates University
Ms. Narumon Sawasdipuksa, Visiting Graduate Student 2007-2008, Dept. of Chemistry, Chulalongkorn Univ., Bangkok, Thailand.
Prof. Joel T. Smith, visiting professor, 2009, Southeastern Oklahoma State University.
Mr. John H. Snyder, Visiting Graduate Student, Department of Plant Biology, Cornell University, Ithaca, NY
Ms. Leepika Tuli, Visiting Graduate Student, Virginia Bioinformatics Institute, Blacksburg, VA
Mr. Chao Zhang, Visiting Graduate Student, Department of Computer Science, University of Missouri, Columbia, MO

PROFESSIONAL ORGANIZATIONS:

President (current), Treasurer (2007-08), and lifetime member The Metabolomics Society
Fellow & Member of The American Association for the Advancement of Science
Member of The American Society for Mass Spectrometry
Member of The American Chemical Society
Member of The Phytochemical Society of North America
Member of The American Society for Plant Biology
Member and former vice-president (1993) of OSU section of Phi Lambda Upsilon, a national chemistry honor society.

PATENTS:

US Provisional Patent Application: Metabolic Engineering for Plant Disease Resistance 14 April 2009.
Wensheng Li, Srinivasa Rao Uppalapati, Kirankumar S. Mysore, Richard A. Dixon, Lloyd W. Sumner.

U.S. Provisional Patent Application No. 61/080,633: Cotton Root Rot Disease Resistant Plants. Srinivasa Rao Uppalapati, Kirankumar S. Mysore, Wensheng Li, Lloyd Sumner, Richard A. Dixon.

PUBLICATIONS:

- xx. Anne Pribat, Alexandre Noiriel, Alison M. Morse, John M. Davis, Romain Fouquet, Karen Loizeau, Stéphane Ravel, Wolfgang Frank, Richard Haas, Ralf Reski, Mohamed Bedair, **Lloyd W. Sumner**, and Andrew D. Hanson, Non-flowering Plants Possess a Unique Folate-dependent Phenylalanine Hydroxylase That Is Localized in Chloroplasts. *Plant Cell*, submitted.
- xx. Moon, Stephanie; He, Kun; Bais, Preeti; Dickerson, Julie; Dixon, Philip; Rhee, Seung; Wohlgemuth, Gert; Fiehn, Oliver; Barkan, Lenore; Lange, Iris; Lange, Bernd; Cortes, Diego; Shuman, Joel; Shulaev, Vladimir; Huhman, David; **Sumner, Lloyd**; Roth, Mary; Welti, Ruth; Ilarslan, Hilal; Wurtele, Eve; Brachova, Libuse; Campbell, Alexis; Perera, Ann; Nikolau, Basil. Metabolomics as a hypothesis-generating functional genomics tool for the annotation of *Arabidopsis thaliana* genes of “unknown function. *Plant Journal*, submitted.
- xx. Zhentian Lei, Fang Chen, Bonnie W. Watson, Satish Nagaraj, Aaron M. Elmer, Richard A. Dixon, and **Lloyd W. Sumner**. Comparative Proteomics of Yeast-Elicited *Medicago truncatula* Cell Suspensions Revealed the Induction of Proteins Associated with Isoflavonoid Biosynthesis and Cell Wall Modifications. *Journal of Proteome Research*. Minor revisions resubmitted.
84. **Lloyd W. Sumner**, Dong Sik Yang, Bennie J Bench, Bonnie S. Watson, and Daniel Jones, Spatially Resolved Metabolomics, *Annual Plant Reviews*, Ed. Robert Hall. In-press.
83. Narumon Sawasdipuksa, Zhentian Lei, **Lloyd W. Sumner**, Polkit Sangvanicha, A lysozyme with antifungal activity from *Pithecellobium dulce* seeds. *Food Technology and Biotechnology*, In-press.
82. Clelia De-la-Peña, Zhentian Lei, Bonnie S. Watson, Dayakar V. Badri, Marcelo M. Brandão, Marcio C. Silva-Filho, **Lloyd W. Sumner**, Jorge M. Vivanco (2010) Root secretion of defense-related proteins is development-dependent and regulated by flowering time. *Journal Biological Chemistry*, Aug 3 [Epub ahead of print].
81. Broz, Amanda; Broeckling, Corey D.; De-la-Peña, Clelia; Lewis, Matthew R.; Greene, Erick; Callaway, Ragan M.; **Sumner, Lloyd W.**; Vivanco, Jorge M. (2010) Plant neighbor identity influences plant biochemistry and physiology related to defense. *BMC Plant Biology* 10:115.
80. Brechenmacher, L., Lei, Z.; Libault, M.; Findley, S.; Sugawara, M.; Sadowsky, M.J.; **Sumner, L.W.**; and Stacey, G. (2010) Soybean metabolites regulated in root hairs in response to the symbiotic bacterium *Bradyrhizobium japonicum*. *Plant Physiol.* 153(4):1808-22.
79. Anna A. Dobritsa, Shuh-Ichi Nishikawa, Ewa Urbanczyk-Wochniak, Daphne Preuss, **Lloyd W. Sumner** (2010) LAP5 and LAP6 encode anther-specific chalcone synthase-like proteins essential for pollen exine development, *Plant Physiology*, 153(3):937-955.
78. Marina A. Naoumkina, Luzia V. Modoloa, David V. Huhman, Ewa Urbanczyk-Wochniak, Yuhong Tang, **Lloyd W. Sumner** and Richard A. Dixon (2010) Genomic and co-expression analyses predict multiple genes involved in triterpene saponin biosynthesis in *Medicago truncatula*. *Plant Cell*, 22(3):850-66.
77. Preeti Bais, Stephanie Moon, Kun He, Ricardo Leitao, Kate Dreher, Tom Walk, Yves Sucaet, Lenore Barkan, Gert Wohlgemuth, Mary R. Roth, Basil Nikolau, Eve Syrkin Wurtele, Philip Dixon, Oliver Fiehn, B. Markus Lange, Seung Y. Rhee, Vladimir Shulaev, **Lloyd W. Sumner**, Ruth Welti, Julie A. Dickerson. (2010) *PlantMetabolomics.org*: A web portal for Plant Metabolomics. *Plant Physiology*, 152(4):1807-16
76. **Sumner, L.W.** (2010) Legume Metabolomics. *Grain Legumes Magazine* (special issue dedicated

- to Model Legumes) 53, 17.
75. **Sumner, L.W.** (2010) Recent Advances in Plant Metabolomics and Greener Pastures. Faculty of 1000 Reports, 2010, 2:7.
74. Qingzhen Jiang, Ji-Yi Zhang, Xiulin Guo, Mohamed Bedair, **Lloyd W Sumner**, Joseph Bouton, and Zeng-Yu Z-Y Wang (2010) Improvement of drought tolerance in white clover (*Trifolium repens*) by transgenic expression of a transcription factor gene WXP1, Functional Plant Biology, 2010, 37, 157–165.
73. Dai, X.; Wang, G.; Yang, D.; Tang, Y.; Broun, P.; Marks, M.D.; **Sumner, L.W.**, Dixon, R.A.; Zhao, P.X. (2010) TrichOME: A Comparative Omics Database for Plant Trichomes, Plant Physiol., 152(1) 44-54.
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72. Dobrista, A.A.; Nishikawa, S.; Preuss, D.; Urbanczyk-Wochniak, E.; **Sumner, L.W.**; Hammond, A.; Carlson, A.L.; Swanson, R.J. (2009) LAP3, a novel plant protein required for pollen development, is essential for proper exine formation. Sex Plant Reprod., 22(3)167-177.
71. Pang, Y., Wenger, J.P., Saathoff, K., Peel, G.J., Wen, J., Huhman, D., Allen, S.N., Tang, Y., Cheng, X., Tadege, M., Ratet, P., Mysore, K.S., **Sumner, L.W.**, Marks, M.D., Dixon, R.A. (2009) A WD40 repeat protein from *Medicago truncatula* is necessary for tissue-specific anthocyanin and proanthocyanidin biosynthesis, but not for trichome development, Plant Physiol. 151(3) 1114-1129.
70. Farag, M.A., Deavours, B.E., De-Fatima, A., Naoumkina, M., Dixon, R.A., **Sumner, L.W.** (2009) Integrated metabolite and transcript profiling identify a biosynthetic mechanism for the formation of the aurone hispidol in *Medicago truncatula* cell cultures, Plant Physiol., 151(3) 1096-1113.
69. Sawasdiipuksa, N., Lei, Z., **Sumner, L.W.**, Sangvanich, P. (2009) Proteome Analysis of *Pithecellobium dulce* Seeds Using Two-Dimensional Gel Electrophoresis and Tandem Mass Spectrometry. Journal of the Science of Food and Agriculture, 89(8) 1284-1291.
68. Tian, L., Peel, G.J., Lei, Z., Aziz, N., Dai, X., He, J., Watson, B., Zhao, P.X., **Sumner, L.W.**, Dixon, R.A. (2009) Transcript and proteomic analysis of developing white lupin (*Lupinus albus* L.) roots, BMC Plant Biology, 9:1, doi:10.1186/1471-2229-9-1.
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67. Xu, P., Chen, F., Mannas, J.P., Feldman, T., **Sumner, L.W.**, Roossinck, M.J. (2008) Virus infection improves drought tolerance, New Phytologist, 180 (4) 911-921.
66. De-la-Peña, C., Lei, Z., Watson, B.S., **Sumner, L.W.**, Vivanco, J.M., (2008) Root-microbe communication through protein secretion, Journal of Biological Chemistry, 283(37):25247-25255.
65. Nagaraj, S., Lei, Z., Watson, B.S., **Sumner, L.W.** (2008) Legume Proteomics, in Plant Proteomics: Technologies, Strategies, and Applications, Agrawal, G.K and Rakwal, R. eds, John Wiley & Sons, Hoboken, NJ, USA, ISBN 978-0-470-06976-9.
64. Bedair, M., **Sumner, L.W.**, (2008) Current and Emerging Mass Spectrometry Technologies for Metabolomics, Trends in Analytical Chemistry, 27(3) 238-250.
63. Kaimoyo, E., Farag, M.A., **Sumner, L.W.**, Wasmann, C., Cuello, J., VanEtten, H. (2008) Sublethal levels of electric current elicit the biosynthesis of plant secondary metabolites. Biotechnology Processes, 24(2) 377-84.
62. Badri, D.V., Loyola-Vargas, V.M., Broeckling, C.D., De-la-Pena, C., Jasinski, M., Santelia, D., Martinoia, E., **Sumner, L.W.**, Banta, L.M., Kopynec, A.C., Stermitz, F., Vivanco, J.M. (2008) Altered profile of secondary metabolites in the root exudates of Arabidopsis ATP-binding cassette mutants. Plant Physiology, 146(2):762-71.
61. Farag, M.A., Huhman, D.V., Dixon, R.A., **Sumner, L.W.**, (2008) Metabolomics reveals novel pathways, differential and elicitor-specific responses in phenylpropanoid and isoflavonoid biosynthesis in *Medicago truncatula* cell cultures, Plant Physiology, 146(2):387-402.
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60. Naoumkina, M., Farag, M.A., **Sumner, L.W.**, Tang, Y., Liu, C.J., Dixon, R.A. (2007) Different mechanisms for phytoalexin induction by pathogen and wound signals in *Medicago truncatula*, Proceedings of the National Academy of Sciences, USA, 2007 Nov 13;104(46):17909-15. Epub 2007 Oct 30.
59. Lei, Z., Nagaraj, S., Watson, B., **Sumner, L.W.**, (2007) Proteomics of *Medicago truncatula*. In: Plant Proteomics. Šamaj J, Thelen JJ, eds. Springer-Verlag, Heidelberg, Germany, pp. 121-136. ISBN-13: 978-3540726166.
58. **Sumner, L.W.**, Urbanczyk-Wochniak, E., Broeckling, C.D, Huhman, D.V. (2007) Metabolomics Data Analysis, Visualization, and Integration. in Methods in Molecular Biology: Plant Bioinformatics, Edwards, D. Ed. Humana Press, Totowa, NJ, pps 640. ISBN13: 978-1-58829-653-5.
http://www.humanapress.com/index.php?option=com_bookdetails&task=bookdetails&book_id=2557.
57. Whaley, L., Rummel, J., Zemenu, E., Li, W., Pei, Y., Rodgers, B., Bailey, J., Moody, C., Huhman, D.V., Meier, C., **Sumner, L.W.**, Starnes, S. (2007) Isolation and characterization of osajin and pomiferin: Discovery laboratory exercises for organic chemistry, The Chemical Educator, 12(3) 179-184.
56. Fiehn, O., Robertson, D., Griffin, J., van der Werf, M., Nikolau, B., Morrison, N., **Sumner, L.W.**, Goodacre, R., Hardy, N.W., Taylor, C., Fostel, J., Kristal, B., Kaddurah-Daouk, R., Mendes, P., van Ommen, B., Lindon, J.C., Sansone, S.-A., (2007) The Metabolomics Standards Initiative (MSI), Metabolomics, 3(3) 175-178.
55. **Sumner, L.W.**, Amberg, A., Barret, D., Beale, M., Beger, R., Daykin, C., Fan, T., Fiehn, O., Goodacre, R., Griffin, J., Hardy, N., Higashi, R.M., Lane, A., Lindon, J., Marriott, P., Nicholls, Reily, M., Viant, M., (2007) Proposed minimum reporting standards for chemical analysis, Metabolomics, 3(3) 211-221.
54. Fiehn, O., **Sumner, L.W.**, Ward, J., Dickerson, J., Lange, M.B., Lane, G., Roessner, U., Last, R., Rhee, S.Y., Nikolau, B., (2007) Minimum reporting standards for plant biology context in metabolomics studies, Metabolomics, 3(3) 195-201.
53. Sansone, S.A., Nikolau, B., van Ommen, B., Kristal, B.S., Taylor, C., Robertson, D., Lindon, J., Griffin, J.L., **Sumner, L.W.**, van der Werf, M., Hardy, N.W., Morrison, N., Mendes, P., Kaddurak-Daouk, R., Goodacre, R., Fan, T., Fieh, O. (2007) The Metabolomics Standards Initiative, Nature Biotechnology, 25(7) 846-848.
52. **Sumner, L.W.** (2007) Book review “Metabolome Analysis: An Introduction”, Journal of the American Society for Mass Spectrometry, 18, R1-R2.
51. Williams, B.J., Cameron, C.J., Workman, R., Broeckling, C.D., **Sumner, L.W.**, Smith, J.T., (2007) Amino Acid Profiling in Plant Cell Cultures: An Inter-laboratory Comparison of Capillary Electrophoresis-Mass Spectrometry and Gas Chromatography-Mass Spectrometry, Electrophoresis, 28(9) 1371-1379.
50. Zhang, J.Y., Broeckling, C.D., **Sumner, L.W.**, Wang, Z.Y., (2007) Heterologous Expression of Two *Medicago truncatula* AP2 Domain Transcription Factor Genes, WXP1 and WXP2, in Arabidopsis Led to Increased Leaf Wax Accumulation and Improved Drought Tolerance, but Differential Response in Freezing Tolerance, Plant Molecular Biology, 64(3) 265-278.
49. Urbanczyk-Wochniak, E., **Sumner, L.W.**, (2007) MedicCyc: a biochemical pathway database for *Medicago truncatula*, Bioinformatics, 23, 1418-1423.
48. **Sumner, L.W.**, Huhman, D.V., Urbanczyk-Wochniak, E., Lei, Z. (2007) Methods, Applications, and Concepts of Metabolic Profiling: Secondary metabolism, in Plant Systems Biology, Fernie, A., Baginsky, S. Eds, Bierkenhauser-Verlag, Berlin, Germany, 195-212. (ISBN 13: 978-3-7643-7261-3).
47. Lei, Z., Anand, A., Mysore, K.S., **Sumner, L.W.** (2007) Electroelution of Intact Proteins from SDS-PAGE Gels and Their Subsequent MALDI-TOFMS Analysis. In Plant Proteomics: Methods and Protocols, Methods in Molecular Biology, Humana Press, USA, 355, 353-364.

46. Watson, B.S., **Sumner, L.W.** (2007) Isolation of Cell Wall Proteins from *Medicago sativa* Stems. In Plant Proteomics: Methods and Protocols, Methods in Molecular Biology, Humana Press, USA. 355, 79-92.
45. Farag, M., Huhman, D.V., Lei, Z., **Sumner, L.W.** (2007) Metabolic profiling and systematic identification of flavonoids and isoflavonoids in roots and cell suspension cultures of *Medicago truncatula* using HPLC-UV-ESI-MS and GC-MS. *Phytochemistry*, 68, 342-354.
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44. Nagaraj, S., Lei, Z., Watson, B.S., **Sumner, L.W.**, Gallardo, K., Dumas-Gaudot, E., Recorbet, G., Robert, F., Thiery, O., Valot, B., Mathesius, U. (2006) Proteomics of *Medicago truncatula*, in *Medicago truncatula* Handbook, eds The *Medicago truncatula* Steering Committee, <http://www.noble.org/MedicagoHandbook/>. ISBN 0-9754303-1-9
43. Zhou, L., Hopkins, A.A., Huhman, D.V., **Sumner, L.W.**, (2006) A simple, rapid, and sensitive method for quantitative analysis of alkaloids in Hardinggrass (*Phalaris aquatica*), *Journal of Agriculture and Food Chemistry*, 54(25), 9287-9291.
42. Farag, M.A. Ryu, C.M., **Sumner, L.W.**, Pare, P.W. (2006) GC-MS SPME profiling of rhizobacterial volatiles reveals prospective inducers of growth promotion and induced systemic resistance in plants, *Phytochemistry*, 67(20):2262-2268.
41. Deavours, B.E., Liu, C.-J., Farag, M., **Sumner, L.W.**, Noel, J.P., Dixon, R.A. (2006) Functional analysis of members of the isoflavone- and isoflavanone- *O*-methyltransferase gene families from the model legume *Medicago truncatula*, *Plant Molecular Biology*, 67(20):2262-2268.
40. Fiehn, O., Kristal, B., van Ommen, B., **Sumner, L.W.**, Assunta-Sansone, S., Taylor, C., Hardy, N., Kaddurah-Daouk, R. (2006) Establishing Reporting Standards for Metabolomic and Metabonomic Studies: A Call for Participation. *Omics*, 10 (2):158-63.
39. Broeckling, C.D., Reddy, I.R., Duran, A.L., Zhao, X., **Sumner, L.W.** (2006) MET-IDEA: a data extraction tool for mass spectrometry-based metabolomics, *Analytical Chemistry*, 78(13)4334-4341.
38. **Sumner, L.W.** (2006). Current Status and Forward Looking Thoughts on LC/MS Metabolomics in Biotechnology in Agriculture and Forestry: Plant Metabolomics, K. Saito, R. Dixon, L. Willmitzer Eds. Springer, New York, ISBN-10 3-540-29781-2.
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37. Frydman, A., Weisshaus, O., Huhman, D., **Sumner, L.**, Bar-Peled, M., Lewinsohn, E., Fluhr, R., Gressel, J. and Eyal Y. (2005). Metabolic engineering of plant cells for biotransformation of hesperedin into neohesperidin, a substrate for production of the low-calorie sweetener and flavor enhancer NHDC. *Journal of Agriculture and Food Chemistry*, 53(25):9708-9712.
36. Tarpley, L., Duran, A.L., Kebrom, T.H. and **Sumner, L.W.** (2005). Biomarker metabolites capturing the metabolite variance present in a rice plant developmental period. *BMC Plant Biology*, *BMC Plant Biology* May 31;5(1):8.
35. Lei, Z.; Elmer, A.; Watson, B.; Dixon, R.A.; Mendes, P.; **Sumner, L.W.**; (2005) A 2-DE Proteomics Reference Map and Systematic Identification of 1377 Proteins from a Cell Suspension Culture of the Model Legume *Medicago truncatula*, *Molecular and Cellular Proteomics* 4(11) 1812-1825.
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Current and Prior External Research Support:

Project title: Metabolomics and Genome Wide Association Mapping for the Elucidation of Triterpene Saponin Molecular Biochemistry in Medicago

Source of support: National Science Foundation, Molecular and Cellular Biosciences #1024976

Investigators: Lloyd W. Sumner (PI) and Nevin D. Young (CoPI)

Total (RECOMMENDED) award amount: \$692,394

Total award period: 09/01/10 – 8/31/13

Effort: Cal: 1.3

Project title: Development of Plant Metabolite Tandem Mass Spectral Libraries for a Triple-quadrupole Mass Spectrometer

Source of support: Agilent Corp. Instrumentation Award

Investigators: Lloyd W. Sumner (PI)

Total award amount: \$250,000

Total award period: 9/1/2010 – 8/30/12

Effort: 5%

Project title: Metabolomics 2010 Conference Support

Source of support: National Institutes of Health, NIH Support for Conferences and Scientific Meetings (Parent R13/U13), NIGMS and NIEHS #GM095229-01

Investigators: Lloyd W. Sumner (PI) and Oliver Fiehn (CoPI)

Total award amount: \$7,000

Total award period: 06/27/2010 – 6/26/11

Effort: Cal: 0

Project title: A Joint NSF and JST Workshop: Identifying Potential Collaborative Research Opportunities in Metabolomics

Source of support: National Science Foundation, Molecular and Cellular Biosciences #1038679

Investigators: Lloyd W. Sumner (PI) and Oliver Fiehn (CoPI)

Total award amount: \$35,157

Total award period: 05/05/10 – 05/05/11

Effort: Cal: 0

Project title: Elucidation of Medicago triterpene saponin biosynthesis

Source of support: Oklahoma Center for the Advancement of Science and Technology (OCAST; #PSB10-027; graduate student support and seed grant)

Investigators: Lloyd W. Sumner (PI)

Total award amount: \$88,833

Total award period: 03/01/10 – 02/28/12

Effort: 8%

Project title: Metabolomics: A functional genomic tool for deciphering functions of Arabidopsis genes

Source of support: National Science Foundation 2010, MCB #0520140

Investigators: Basil Nikolau (PI), Bernd M. Lange (CoPI), Oliver Fiehn (CoPI), Seung Rhee (CoPI), Lloyd W. Sumner (CoPI), and Ruth Welti (CoPI)

Total award amount: \$5,886,429 (\$433,811 Sumner Lab)

Total award period: 3/01/09 – 08/30/13

Effort: Cal: 1

Project title: Functional Analysis of Pollen Exine Assembly
Source of support: National Science Foundation 2010, Molecular and Cellular Biosciences #520283
Investigators: Daphne Preuss, Anna Edlund, Robert J. Swanson and Lloyd W. Sumner
Total award amount: \$1,685,616 (\$345,682 Sumner Lab)
Total award period: 09/01/05 – 08/30/09 (no cost extension until 8/30/10)
Effort: Cal: 1

Project title: Development of an Ultra-high Resolution Liquid Chromatography Time-of-flight Mass Spectrometer Platform for Metabolomics
Source of support: LECO Instrumentation Award
Investigators: Lloyd W. Sumner (PI)
Total award amount: \$200,000
Total award period: 09/01/05 – 4/31/10
Effort: 5%

Project title: GEPR: Comparative genomics of secretory trichomes – biofactories for production of plant secondary metabolites
Source of support: National Science Foundation Plant Genome Research Program #0605033
Investigators: Richard Dixon, David Marks, Pierre Broun,
Collaborators: Lloyd W. Sumner and Xuechun (Patrick) Zhao
Total award amount: \$1,406,599 (~\$384,899 Sumner Lab)
Total award period: 05/01/06 – 04/30/09
Effort: 10%

Project title: The Consortium for Legume Research: An integrated approach to cotton root rot disease of alfalfa
Source of support: The State of Oklahoma
Investigators: Richard A. Dixon, Joe Bouton, Bruce Roe, Steve Marek, Kiran Mysore, Mary Sledge and Lloyd Sumner
Total award amount: \$1,400,000 (\$136,612 Sumner Lab)
Total award period: 09/01/05 – 08/30/09
Effort: Cal: 1

Project title: Metabolomics: A functional genomic tool for deciphering functions of Arabidopsis genes
Source of support: National Science Foundation 2010, MCB 0520140
Investigators: Basil Nikolau, Bernd M. Lange, Oliver Fiehn, Seung Rhee, Lloyd W. Sumner and Ruth Welti
Total award amount: \$1,000,000 (\$63,337 Sumner Lab)
Total award period: 09/01/05 – 08/30/07
Effort: Cal: 1

Project title: An integrated approach to functional genomics and bioinformatics in a model legume
Source of support: National Science Foundation (Award DBI#0109732)
Investigators: Pedro-Mendes (PI), Richard Dixon (Co-PI), Lloyd Sumner, Greg May and Tim Smith (Collaborators)
Total award amount: \$3,587,432 (\$1,130,845 Sumner lab)
Total award period: 08/01/02-07/31/05
Effort: Cal: 3
Two year extension of \$99,000 recently approved until 7/31/07

Agency	Division	Proposal #	Proposal Title	PI	Award Date	End Date	Awarded Amount	To Sumner lab
NSF	MCB	1038679	A Joint NSF and JST Workshop: Identifying Potential Collaborative Research Oppor	Sumner	5/5/2010	5/5/2011	\$ 35,733.00	\$ 35,733.00
NSF	MCB	1024976	Metabolomics and Genome Wide Association Mapping for the Elucidation of Triter	Sumner	9/1/2010	8/31/2013	recommended	\$ 516,814.00
NSF	MCB	820823	Arabidopsis 2010: Metabolomics: A Functional Genomics Tool for Deciphering Fun	Nikolau	3/2/2009	8/30/2013	\$ 5,886,429.00	\$ 433,811.00
NSF	MCB	520283	Arabidopsis 2010: Functional Analysis of Pollen Exine Assembly	Preuss	9/1/2005	8/30/2010	\$ 1,685,616.00	\$ 345,682.00
NSF	MCB	520140	Arabidopsis 2010: Metabolomics: A Functional Genomics Tool for Deciphering Func	Nikolau	8/26/2005	8/30/2007	\$ 1,000,000.00	\$ 63,337.00
NSF	GEPR	605033	Comparative genomics of secretory trichomes – biofactories for production of plan	Dixon	5/1/2006	4/30/2009	\$ 1,406,599.00	\$ 384,899.00
NSF	PGRP	DBI#0109732	An integrated approach to functional genomics and bioinformatics in a model legume	Dio			\$ 3,587,432.00	\$ 1,130,845.00
NIH	NIGMS	GM095229-01	Metabolomics 2010 Conference Support	Sumner	6/27/2010	6/26/2011	\$ 7,000.00	\$ 7,000.00
OCAST	Plant Biol	PSB10-027	Elucidation of Medicago triterpene saponin biosynthesis	Sumner	3/1/2010	2/28/2012	\$ 88,833.00	\$ 88,833.00
State of OK	Special		The Consortium for Legume Research: An integrated approach to cotton root rot di	Dixon	9/1/2005	8/30/2009	\$ 1,400,000.00	\$ 136,612.00
Agilent Inc.	Special		Development of Tandem Mass Spectrometry Libraries on a QQQ-MS	Sumner	9/1/2010	8/30/2013	\$ 250,000.00	\$ 250,000.00
LECO Corp.	Special		Development of an Ultra-high Resolution Liquid Chromatography Time-of-flight M	Sumner	9/1/2005	4/31/10	\$ 200,000.00	\$ 200,000.00
						TOTAL	\$ 15,547,642.00	\$ 3,593,566.00

NSF MCB #1024976 Metabolomics and Genome Wide Association Mapping for the Elucidation of Triterpene Saponin Molecular Biochemistry in Medicago

Intellectual Merit: The fundamental goal of this project is to identify and characterize novel genes responsible for triterpene saponin biosynthesis in *Medicago truncatula* using revolutionary technologies. Triterpene saponins are a class of structurally diverse plant natural products with a wide range of demonstrated bioactivities including allelopathic, antifungal, antibacterial, antiinsect, anticancer, antinutritive activities. The antinutritive properties of triterpene saponins in legume forages such as alfalfa and soybean are of particular and substantial economic importance. However, the biosynthesis of triterpene saponins is poorly characterized and this pathway is absent from most textbooks. This project will use cutting-edge metabolomics, genome wide association mapping, correlated gene expression profiling, and traditional molecular validation approaches for gene discovery and characterization related to triterpene saponin biosynthesis in *M. truncatula*. The goal of this project will be accomplished through the following specific aims: 1) Metabolome analyses of a large and diverse *M. truncatula* germplasm collection to identify hyper- (high) and hypo- (low) saponin accumulating lines and to enable genome-wide association mapping between specific loci with saponin content 2) Comparative gene expression analyses of hyper and hypo saponin accumulating lines to identify putative genes involved in triterpene saponin biosynthesis and regulation, and 3) Molecular and biochemical confirmation of select targeted saponin biosynthetic genes prioritized based upon multiple levels of evidence. Preliminary data document substantial metabolic diversity in saponin accumulation which is a necessary prerequisite for successful association mapping and comparative microarray analyses.

Broader Impacts: This project will identify and characterize specific genes involved in legume triterpenoid saponin biosynthesis. Specific genes identified in this project have the potential for future metabolic-engineering of crop varieties with: 1) improved fitness and defense, 2) decreased bloat and antinutritive properties resulting in optimized livestock weight gain performance, and 3) potential plant neutraceuticals and adjuvants related to human and animal health. High resolution biochemical phenotype data generated for a large number of *M. truncatula* accessions core collection will be generated and will be made publicly available via an anonymous FTP server (<ftp://summerftp.noble.org/pub>). This data will highlight specific germplasm critical for further molecular and biochemical dissection of saponin biosynthesis. More importantly, the copious metabolomics data generated will provide substantial community value in that it will enable association mapping with a wealth of other metabolites (both known and unknown) and related fitness traits including, but not limited, to symbiosis (flavonoids, isoflavonoids, dicarboxylic acids), drought/salinity tolerance (proline, manitol, and other osmoprotectants), and/or aluminum tolerance (malate). Funding of this project will provide multi-disciplinary training for two postdoctoral researchers and one undergraduate summer intern/hourly worker in advanced technologies, plant molecular biology, large-scale integrated systems biology, and large-scale analytical biochemistry. During the three year tenure, the postdoctoral researcher will be mentored in scientific writing, scientific presentations, publishing, grant applications, constructive peer review, project management, time management, and personnel management to further mold a great scientific mind more towards the realistic and professional expectations of modern academic and commercial research. A series of enrichment workshops focused upon local high school students will be provided. Participating groups include Oklahoma Upward Bound Science/Math Program, Ardmore High School AP and Science Club, and Southern Oklahoma Technology Center Biotechnology Program. These annual enrichment opportunities will stimulate student interests in science, plant biology, and natural product biochemistry. An international symposium will be hosted in year 3 which will provide a forum for the latest advances in saponin research and serve to highlight the outcomes of this project. Postdocs funded by this proposal would serve key leadership roles in organizing and executing the workshops.

NSF MC #1038679 A Joint NSF and JST Workshop: Identifying Potential Collaborative Research Opportunities in Metabolomics.

Intellectual Merit: The specific aims of this proposal are 1) to acquire funds to enable a workshop that will lead to a consensus report that identifies and prioritizes key strategic areas where metabolomics offers the greatest opportunity to advance novel biological knowledge in the areas of energy and environment, and 2) to foster greater collaborative interactions between Japan and US scientists in these priority research areas. The Japanese have invested heavily in metabolomics and are ideal partners for collaborative research. To achieve the above goal, a team composed of approximate 10-15 scientists from Japan and from the USA will meet for two days, May 6-7, 2010, at The University of California, Davis. The workshop will focus upon current technical challenges and optimum collaborator opportunities related to plant, algal, and microbial metabolomics. Specific technical challenges to be

discussed include defining the Metabolome, metabolite annotation, spatially and temporally resolved sampling, flux'omics', dynamic range and depth-of-coverage, instrumentation and infrastructure, informatics and databases, standardization, putative national plant, algal, microbial metabolomics facility(s). Collaborative application opportunities will be discussed with regards to bioenergy, environment, functional genomics & gene discovery, secondary metabolism, metabolomics & genome-wide association mapping (plant, algae, microbe), systems biology and metabolic modeling in plant, algal, and microbial metabolomics. A report of the meeting outcomes will be drafted on-site, refined through peer review, and a final report delivered to NSF and JST. This report will be considered by NSF and JST in developing a future and joint Research Funding Announcement.

Broader Impacts: This meeting will bring together an international team of leading scientists in the field of plant, algal, and microbial metabolomics, and provide a forum for the critical discussion of current challenges. These discussions are expected to identify and prioritize the current and most critically limiting challenges. More importantly, the discussions are also expected to lead to a consensus opinion for the best scientific approaches to address these challenges. The consensus opinions are also expected to unify the community towards a systematic attack on the challenges which will ultimately provide the most efficient approach to solving the challenges. The meeting will also foster and encourage collaborative interactions between US and Japanese scientists that will provide combined resources in applying advanced metabolomics technology to the solution of major questions related to plant, microbial, and algal biology.

NSF MCB #820823, Arabidopsis 2010 Renewal: Metabolomics: A functional genomics tool for deciphering functions of Arabidopsis genes in the context of metabolic and regulatory networks

Summary of the proposed project: Global profiling technologies enable comprehensive overview of the consequences of genetic alterations and can be used to annotate gene functions. However, the functions of over 1/3 of the annotated protein-coding genes of the Arabidopsis genome are still unknown, and the annotation of an even larger portion of the genome is not sufficiently accurate for unambiguous assignment function at the biochemical and physiological levels. This proposal builds on a prior pilot project that enabled a consortium of multidisciplinary collaborators to establish pipelines for generating metabolomics data streams and to integrate the outcomes with bioinformatics, computational, and database capabilities. Our goal is to develop novel capabilities that will enhance the research community's ability to formulate testable hypotheses concerning Arabidopsis gene function. The consortium has developed metabolomic platforms that together detect approximately 1,800 metabolites, of which 900 are chemically defined. The aims of the current proposal is to apply these established platforms to reveal changes in the metabolome associated with knockout mutations in 450 genes of unknown function and compare these to similar mutants in 50 genes of known function. To enhance the power of the metabolomics platforms the consortium will begin analytical efforts to expand the chemical identity of the Arabidopsis metabolome. Finally, the consortium will disseminate these data via the multifunctional metabolomics database developed in the pilot project. Enhancement of this database and associated statistical and visualization toolsets will enable researchers to formulate testable computational models of the metabolic network of Arabidopsis. The successful completion of these goals and integration with other NSF-sponsored functional genomics and cyber infrastructure developments will generate transformational resources for ultimately modeling the complex metabolism of Arabidopsis.

Broader Impacts of the proposed research project: The proposed consortium will develop new resources for the research community that will enhance the capability to globally profile genome expression at the metabolite level. These resources are critical to reveal the function of genes of currently unknown function. These resources will be developed in collaboration with other NSF-funded resource development projects, and will enable researchers in the community to formulate credible, testable hypotheses concerning gene function. The consortium will foster the development of the science of metabolomics as a functional genomics tool through workshops, internships and organization of national and international meetings. The consortium will also develop new activities to enhance the impact of science education and training in the community. Specifically, workshops for researchers will be provided at consortium labs and at international biological meetings. In addition, research internships will be offered to undergraduate students, eight of whom will have the opportunity to experience international science training in a European genomics laboratory. These research-based training internships will illustrate to the students the synergy that is accompanied with the integrated applications of chemistry, biochemistry, genetics, bioinformatics and computational sciences to solving complex biological problems.

Oklahoma Center for the Advancement of Science and Technology (OCAST) #PSB10-027: Elucidation of *Medicago* triterpene saponin biosynthesis (graduate student support)

The fundamental goal of this project is to discover and characterize novel genes responsible for triterpene saponin biosynthesis in the model legume *Medicago truncatula*. Triterpene saponins are structurally diverse plant natural products with a wide range of demonstrated bioactivities including allelopathic, antifungal, antibacterial, antiinsect, antinutrient, and anti-cancer activities. Saponins in legume forages, such as alfalfa, are of particular and substantial economic importance because they result in impaired digestion in ruminant animals, and reduced weight gain. This project will use cutting-edge genomic, metabolomics, transcriptomics, and genetic approaches for gene discovery and the fundamental elucidation of the triterpene saponin biosynthetic pathway in the model legume *Medicago truncatula*. This will be achieved via the following specific aims.

- SPECIFIC AIM 1: *Medicago truncatula* genome analysis will be used to identify gene clusters and specific genes co-localized with β -amryin synthase which are highly likely co-regulated gene candidates associated with triterpene saponin biosynthesis.
- SPECIFIC AIM 2: Cutting-edge, high resolution biochemical profiling will be utilized to identify hyper and hypo accumulation of triterpene saponin content in a *Medicago truncatula* core germplasm collection.
- SPECIFIC AIM 3: Comparative gene expression analyses of hyper and hypo saponin accumulating lines will be performed using Affymetrix *Medicago* Gene Chips™ to identify putative biosynthetic enzymes involved in triterpene saponin biosynthesis and regulation.
- SPECIFIC AIM 4: Molecular and genetic confirmation of the two highest priority candidate genes related to triterpene saponin biosynthesis will be performed using molecular cloning and recombinant DNA-based *in vitro* functional characterization. The functional confirmation of the two candidates will also be sought outside of this project using reverse-genetic screens of a *Medicago truncatula* retrotransposon mutant population to identify specific saponin biosynthetic mutants useful in future genetic validation of function in these knock-out lines.

NSF Plant Genome Research (0605033): Comparative genomics of secretory trichomes – biofactories for production of plant secondary metabolites

Collectively, plants are a rich source of natural products, chemicals that often function to protect the plant from infection or insect pests. Natural products also form the basis of many currently used drugs, such as aspirin, morphine, taxol or the antimalarial compound artemisinin. Plant natural products are often synthesized and accumulated in secretory trichomes, which are appendages found on the aerial organs of plants. Trichomes have a unique capacity for chemical synthesis and secretion, and have been described as biofactories for the production of natural products. However, with few exceptions, little is known about the molecular aspects of trichome metabolism and secretion. The production of many natural products in specialized trichome cells facilitates genomics-based approaches to characterize biosynthetic and secretory processes. In this project, a large number of expressed sequence tags (ESTs) will be generated corresponding to genes expressed in trichomes of five species representing different plant families and both model and crop plants; *Medicago truncatula* and *M. sativa* (alfalfa), Leguminosae; *Nicotiana benthamiana* and *Lycopersicon esculentum* (cultivated tomato), Solanaceae; and hops (*Humulus lupulus*), Cannabaceae. Potato leafhopper resistant and susceptible alfalfa lines will be compared. At the same time, the full spectrum of natural products produced in the trichomes of these five species will be determined. The EST collection will be mined for genes involved in the regulation, biosynthesis and transport of natural products, and the functions of a selection of those genes that are common to multiple species will be determined by over- or under-expressing them in *Arabidopsis thaliana*.

The project is multidisciplinary, combining genomics, informatics and molecular biology with analytical biochemistry, enzymology, and metabolic engineering, and provides excellent training for postdoctoral fellows and undergraduate students in the skills increasingly required in the post-genomics age. The Noble Foundation and University of Minnesota will link the subject area of the project to the curricula of their existing student outreach programs. A major deliverable of the project, TrichOME, a publicly available database of genes and metabolites expressed in plant trichomes, will be an important addition to plant genome sequence information, as genes only expressed in trichomes may be under-represented in non-tissue-targeted EST sequencing projects. As the project develops, gene sequences in the database will be linked to functional information describing the involvement of the genes in trichome-specific processes. The project will also improve our understanding of the synthesis, storage and secretion of a range of useful bioactive natural products, from anti-insect lipid amides in alfalfa to health-beneficial prenyl chalcones and bitter acid flavors/antimicrobials in hops.

The State of Oklahoma: The Consortium for Legume Research: An integrated approach to cotton root rot disease of alfalfa

The objectives of this research are to characterize *Phymatotrichopsis* root rot in alfalfa at the biological, chemical and genetic levels, with the long-term goal of developing resistant alfalfa varieties. We will approach the problem from the joint perspectives of the plant and the pathogen. Sequencing the genome of the pathogen (OU Advanced Genome Center) will provide access to the genetic blueprint that determines how this fungus causes disease and evades resistance mechanisms in so many plant species, as well as suggest molecular targets for disease control mechanisms. Developing a transformation system and other genetic resources for the fungus (OSU, Department of Plant Pathology) will enable us to delete specific fungal genes to test their involvement in causing disease. Breeding, selection and mutant screening strategies will identify lines of alfalfa and the closely related model legume *Medicago truncatula* with varying degrees of tolerance or susceptibility to the fungus (Noble Foundation Forage Improvement and Plant Biology Divisions). Application of genomic technology, metabolite profiling and antifungal screens (Noble Foundation Plant Biology and Forage Improvement Divisions) will determine how infected plants respond at the molecular level, and define chemical pathways and gene regulatory regions that can be used for engineering novel resistance mechanisms against the fungus.

The development of a cotton root rot resistant variety of alfalfa will greatly expand the alfalfa growing region of Oklahoma. This will allow Oklahoma farmers to produce a valuable crop which can be sold at a profit to a growing dairy industry in both western Oklahoma and Texas, as opposed to the present practice of importing alfalfa from other states.

Arabidopsis 2010 Award# 0520140: Metabolomics: A functional genomics tool for deciphering functions of Arabidopsis genes in the context of metabolic and regulatory networks

Summary of the proposed project: The aim of this proposal is to establish a multi-institutional, international consortium of labs that will develop metabolomics as a new functional genomics tool for elucidating the functions of Arabidopsis genes whose functions are currently unknown. The consortium has developed metabolomic platforms that detect approximately 2,000 metabolites, of which 900 are chemically defined. The consortium will apply these established platforms to reveal changes in the metabolome associated with knockout mutations in genes of unknown function and compare these to similar mutants in genes of known functions. In addition, the consortium will provide an initial genetic and morphological characterization of these mutants. Furthermore, the consortium will begin analytical efforts to expand the chemical identity of the Arabidopsis metabolome. Finally, the consortium will develop unique databases for the dissemination of these data. The successful completion of these goals will generate new tools and resources for ultimately determining the function of the many Arabidopsis genes, whose functions are still to be defined.

Broader Impacts of the proposed research project: The proposed consortium will develop new resources for the research community, which is required for determining the function of genes whose functions are currently unknown. These resources will be developed in collaboration with other NSF-funded resource development projects, and will enable researchers in the community to formulate credible hypothesis-driven projects that will ultimately define the functions of these genes. The consortium will foster the coordinate international development of metabolomics as a tool in functional genomics by collaborating with key European efforts, by organizing metabolomics workshops at international meetings, and in the 3rd year of the project offering a-for-fee metabolomics service to the research community. The consortium will also develop new activities that will enhance the impact of science education and training in the community. Specifically, workshops for high school science teachers will be offered during the three summers of the project. In addition, research internships will be offered to undergraduate students, and 8 of these students will be provided with an international experience to observe science in European genomics, metabolomics and bioinformatics laboratories. These research-based training internships will illustrate the synergy accompanied by the integrated application of chemistry, biochemistry, genetics and bioinformatics to solving biological problems in post-genomic sciences.

Arabidopsis 2010 (MCB # 0520283): Functional analysis of pollen exine assembly

Summary of Proposed Project: This project will determine the function of the gene network required for exine synthesis, patterning and adhesion. This outer pollen wall is made of sporopollenin, an unusually strong, chemically inert, and distinctively patterned biopolymer. Exine protects desiccated pollen and binds to the stigma with strong and selective adhesives. Its importance in pollination, implications for polymer chemistry, and utility as a contact adhesive make an understanding of exine composition a high priority; nonetheless, its inert and irregular nature has

confounded chemical analyses. Recent Arabidopsis genetic surveys are more promising, revealing genes and pathways required for exine structure and function. This project addresses the 2010 program goal of functional analysis of every Arabidopsis gene by screening mutant lines for exine phenotypes, assessing gene roles in exine assembly, patterning and adhesion, and sorting these genes into genetic and metabolic pathways. This work will impact multiple disciplines, improving the understanding of 1) genes that mediate pollination and crop breeding, 2) evolutionary controls over exine diversity and plant speciation, 3) exine moieties that form two-component adhesives, 4) phenolic and fatty acid metabolism, 5) biopolymer self-assembly, and 6) >250 genes in exine development, ~75% of which have not been targeted in other 2010 projects.

Broader Impacts of the Proposed Project: This project will integrate research and education in several ways. First, the Preuss laboratory will host Drs. Edlund and Swanson and an undergraduate from each of their home institutions (Spelman and Valparaiso) for each summer of the proposal period. This will provide minority undergraduates with experience in planning and performing experiments and in presenting their work at undergraduate research conferences. Moreover, it will provide their mentors with information that they will incorporate into their laboratories and courses. Second, two undergraduates from the PI's laboratory will collaborate with these visitors to perform phenotypic analyses and genetic screens. Over the past 10 years, the PI has trained 32 undergraduates (14 women and 7 underrepresented minorities). Third, this project will enable a postdoctoral associate to supervise technicians and undergraduate students, providing her with invaluable mentoring experience. Fourth, researchers from the PI's laboratory will spend 6 months at the Noble Foundation, sharing their knowledge of pollination biology, and receiving training in plant biochemistry that will benefit their home institution. Lastly, the PI regularly participates in venues that introduce policy makers to plant genetic engineering, and in opportunities to teach and train business leaders in the challenges of translating research to the commercial sector.

NSF Plant Genome Research Award #0109732: An Integrated Approach to Functional Genomics and Bioinformatics in a Model Legume

Medicago truncatula is a close relative of the world's most important forage legume, alfalfa (*Medicago sativa*). It is a rich source of natural products, such as flavonoids, isoflavonoids and triterpenes, which impact its properties as a forage legume. The main experimental approach of this project is to perturb the expression of these natural products, and other areas of metabolism, by exposing cell cultures to biotic and abiotic elicitors. Use of cell suspension cultures will allow sufficient material to be collected and analyzed in parallel. Three experimental conditions have been chosen that mimic natural environmental challenges. The ultimate goal of this project is to generate a truly functional genomics data set for control and elicited cell cultures. Such data will encompass expressed sequence information and the associated mRNA, protein and metabolite identities and concentrations. This project will produce a variety of data so it becomes imperative to establish integrative models and software to facilitate relational analysis of the data to each other and to previous knowledge on sequences and pathways. Software is a facilitator of the discovery process when it enables the user to "navigate" the biological data in a dynamic and transparent way, requiring only the most basic computational skills. The bioinformatics component of this project will: i) construct a relational database to store all data; ii) construct an expandable analysis server that will facilitate processing the data with several statistical and numerical algorithms; and iii) integrate the above components through a web interface. The data as well as the software will be made available publicly. The data generated by this project will be used to construct a quantitative predictive model of the time courses after elicitation, which is required to interpret the regulation of the underlying complex biological processes. The data will provide information about the extent and nature of gene expression reprogramming in response to biotic and abiotic signals at the transcription, translation and metabolic levels. There will also be practical applications in directed gene discovery for important agronomic traits involving plant natural products. Finally, this project will make available to the scientific community a bioinformatics system capable of supporting functional genomics ranging from the transcriptome to the metabolome.

PRESENTATIONS & OUTREACH:

2011

- (Invited) March 9-10, 2011 – KSU's Functional Genomics Consortium spring symposium for 2011.
(Invited) 6April, 2011– Systems Biology Institute of Georgia Institute of Technology

2010

- (Invited) Jan 28, 2010 – Waters Corporation, Beverly, MA.
(Invited) Feb. 16, 2010 – Colorado Biological Mass Spectrometry Society Meeting, UC Denver Anschutz Medical Campus in Aurora, Colorado
(Education & Outreach) Feb 19, 2010 – Host HPLC & HILIC training workshop sponsored by Supelco
(Invited) March 11, 2010 – Washington State University, Institute for Biological Chemistry, Pullman, WA.
(Invited) March 25-26, 2010 – New Mexico Bioinformatics Symposium [NMBIS], Santa Fe, NM.
(Invited) March 3-5, 2010 – Review Panel, NIH National Center for Complementary and Alternative Medicine (NCCAM/NIH), the Office of Dietary Supplements (ODS/NIH) and NCI
(Invited) April 9, 2010 – 4th Professional Development Experience at Texas A&M University-Commerce
(Organizer & Chair) May 5-7, 2010 – NSF and JST Joint Metabolomics workshop conference. UC Davis, Davis, CA.
(Invited) Aug 15-17, 2010 – Arkansas EPSCoR meeting.
(Education & Outreach) Sept. 8, 2010 – 01March2010 Host Prof. Ken Korth for sabbatical.
(Invited) 18-21 Oct. 2010 - 1st Middle Eastern and Mediterranean Sea Region Countries Mass Spectrometry Workshop, Weizmann Institute of Science, Rehovoth, Israel.
(Invited) 15-20Dec2010 – Pacifichem 2010, Honolulu, Hawaii. Metabolomics symposium in Agrochemistry session.

2009

- (Invited) Feb. 17-19, 2009 – Visit and presentation, University of California, Davis. Host Oliver Fiehn.
(Education & Outreach) March 23-27, 2009 - NF Metabolomics Workshop and Mini-symposium.
(Education & Outreach) April 23-24, 2009 – Host Alain Goossens visit to Noble
(Education & Outreach) May 15, 2009 – Host:
 Summer intern, Chao Zhang, MU
 Summer intern, Aaron Hightower, SEOSU
 Visiting Scientist, Dr. Joel T. Smith, SEOSU
(Participant) May 31 - June 4, 2009, 57th American Society for Mass Spectrometry Conference, Philadelphia, PA.
(Invited) June 7-8, 2009 Society for In Vitro Biology, Charleston, South Carolina.
(Invited) June 21-22, 2009 – University of Wisconsin Biotechnology Center, Madison WI.
(Selected Oral) July 12-16, 2009 – *Medicago truncatula* Model Legume Congress, to be held at the Asilomar Conference Grounds in Pacific Grove, CA.
(Participant) July 18-22, 2009 – American Society for Plant Biology, Honolulu Hawaii
(Invited & Co-organizer) August 29-September 2, 2009 – 5th International Conference of The Metabolomics Society, Edmonton, Alberta, Canada
(Education & Outreach) September 14-18, 2009 – Noble Metabolomics Workshop
(Participant) October 25-30, 2009 - 9th International Congress of Plant Molecular Biology (IPMB), St. Louis, Missouri.
(Invited) October 28, 2009 – Monsanto Company, St. Louis, MO
(Education & Outreach) December 11, 2009 – hosted “Science Carnival” for Oklahoma Upward Bound Math/Science Program for approximately 30 students from East Central University, Ada, OK

(**Education & Outreach**) December 11, 2009 – hosted “Science Carnival” for approximately 30 students from the Ardmore High School AP Chemistry class and Southern Oklahoma Biotechnology Course.

2008

- (Invited) Feb. 23, 2008 – Cameron University Distinguished Alumni Award Luncheon
- (Invited) March 26-28, 2008 –University of North Carolina Research Campus
- (Invited) April 25, 2008 –Cornell University, Ithaca, New York
- (Outreach) April 28-May 1, 2008–Noble Analytical Chemistry Core Facility Training Course on Metabolite Profiling
- (Outreach) May 14, 2008 –Dr. Fabiola Janiak-Spens, Oklahoma City Community College tour and demos
- (Outreach) May 14, 2008 –Ardmore High School Chemistry Class & Science Club tour and demos
- (Outreach) May 16, 2008 –Oklahoma School of Science and Math, presentation, tour, & demo
- (Invited) May 20-21, 2008 –University of Minnesota Symposium, Secondary Metabolism: Good Things Made in Plants.
- (Invited) May 22-23, 2008 – University of Wisconsin Madison (Host Jan-Michel Ane, Medicago group, and Botany Dept)
- (Selected Oral) June 1-5, 2008 – 57th American Society for Mass Spectrometry Conference, Denver, CO.
- (Outreach) Sept. 22-27, 2008–Noble Analytical Chemistry Core Facility Training Course on Protein Profiling
- (Outreach) Oct 1-2, 2008 –Host Dr. Peter Davies from Cornell University. Presentation - Plant Hormone Review.
- (Invited) 17-19 November, 2008 - “Plant Metabolomics As A Tool For Functional Genomics”. Busan, Korea. A Korea Conference on Innovative Science and Technology (KCIST)

2007

- (Invited) Jan 21-26th, 2007 - Gordon Research Conference on Temperature Stress in Plants, Ventura, CA.
- (Invited) February 23, 2007 (Invited) Graduate Recruitment and Career Awareness, Cameron University, Lawton, OK. Host Elizabeth A. Nalley
- (Invited) March 1, 2006 –Colorado State University, Cell and Molecular Biology Graduate Program, Fort Collins, CO.
- (Invited) 24-25 March, 2007 –2nd Louisville Metabolomics Symposium, Louisville, KY
- April 9-13, 2007 Noble Foundation Metabolite Analysis Workshop and Tutorial, “Weighing Molecules and The Large-scale Biochemical Analysis of Plant Proteomes and Metabolomes”
- (Invited) April 15-17, 2007 – The Role of Metabolomics & Nutrigenomics in Creating Healthful Foods and Healthy Lives, Charlotte, North Carolina
- (Outreach) May 11, 2007 – Ardmore High School Chemistry visit and tours
- (Invited) May 23-25th, 2007 –First annual Plant Proteomics Symposium at the University of Missouri-Columbia, Host Jay Thelen, organizer.
- (Organizing committee & participant) June 11-15, 2007 - 3rd Annual Metabolomics Society Meeting, Manchester International Convention Centre Manchester, UK
- (Participant) July 7-11, 2007 American Society for Plant Biologist Annual Meeting, Chicago, IL.
- (Outreach) August 7, 2007 – 2007 Noble Scholars & Teachers Workshop on “*Weighing Molecules and The Large-scale Biochemical Analysis of Plants*”
- (Outreach) September 10-14, 2007 Noble Protein Analysis Workshop and Tutorial
- (Invited) September 16-20, 2007 – 121st AOAC Annual Meeting & Exposition, Anaheim, California USA
- (Outreach) October 8, 2007 –Host Oklahoma Sectional ACS Meeting, Speaker Eugene Stevens, SUNY@Binghamton, Chemistry Dept, “Green Plastics”.
- (Invited) October 25-26, 2007 – Mass Spectrometry in the Heartland, a conference on biological mass spectrometry in the Midwest, Inn at Grand Glaize in the Ozarks, Osage Beach MO.
- (Invited) Nov. 4-7, 2007 - 63rd Southwest Regional Meeting of The American Chemical Society, Lubbock, TX. 2006
- (Outreach) Nov. 17-18, 2007 – Host project meeting for NSF 2010 Metabolomics: A functional genomics tool for deciphering functions of Arabidopsis genes in the context of metabolic and regulatory networks .

2006

- (Invited) January 14-18, 2006: International Plant and Animal Genome XIV Conference, workshop 'Forage and Turf Plants', San Diego, CA from 14-18 January 2006.
- (Invited) February 18-20th, 2006: AAAS Elected Fellows Forum Award Ceremony, St. Louis, MO.
- (Invited) March 20-21, 2006: Emerging Scientific Technologies: Impact on Dietary Supplement and Functional Foods Research, Kauai, Hawaii.
- (Invited) April 7th - 10th, 2006: 4th International Conference of Plant Metabolomics to be held at Wokefield Park, Reading, UK.
- (Invited) April 25-26, 2006: Review Panel, Canada Foundation for Innovation, Vancouver, BC, Canada.
- (Invited) May 15-18, 2006: Workshop Systems Biology - From Genome to Phenome; Plant Biotechnology Centre, Victoria Department of Primary Industries, Melbourne, Australia.
- (Invited) May 19, 2006 Australian National University, Canberra, Australia.
- (Invited) May 27, 2006 - Waters Users' Workshop, Seattle, WA
- (Participant) May 28-June 01, 2006 54th ASMS Conference, Seattle, WA.
- (Organizer) June 24-28th, 2006: 2nd Meeting of The Metabolomics Society, Harvard Medical School, Boston, MA.
- (Invited) 1-2 August, 2006 Advisory panel for W.R. Wiley Environmental Molecular Sciences Laboratory (EMSL) National User Facility equipment/capital refreshment plan workshop for the suite of User Facility capabilities provided by the Department of Energy (but with the particular focus on environmental molecular science).
- (Invited) 23-24 August, 2006 University of Arkansas Medical School, INBRE invitation
- (Invited) October 16-18 2006: French society for electrophoresis and proteomic analysis. St Malo, France. LWS Presentation Title: "*Discoveries through Integrated Functional Genomics Studies of the Model Legume Medicago truncatula*"

2005

- (Invited) January 16, 2005 "Proteomics and Integrated Functional Genomics of Medicago", Proteomics Workshop, Plant and Animal Genome XIII Conference, San Diego, CA.
- (Invited) January 19, 2005 "Metabolomics and Integrated Functional Genomics of Medicago", Functional Genomics Workshop, Plant and Animal Genome XIII Conference, San Diego, CA.
- (Invited) February 18, 2005: University of Kentucky, Plant and Soil Science Departmental Seminar, Lexington, KY.
- (Invited) April 20-22, 2005 – NSF Plant Genome Grant sponsored Proteomics Workshop and Symposium at the Donald Danforth Plant Science Center (<http://www.danforthcenter.org/symposia/proteomics/>).
- (Invited) May 2-4, 2005. Metabolomics Workshop: Techniques - data processing – applications. Wageningen, The Netherlands. Host: Raoul Bino.
- (Invited) May 10,, 2005 - Institute of Food Research, Norwich Research Park, Norwich UK.
- (Oral) June 5-9, 2005, Metabolomics Session, 53rd ASMS Conference on Mass Spectrometry San Antonio, Texas.
- (Invited) June 8-12, 2005 - 5th Symposium on Post-Transcriptional Regulation of Plant Gene Expression, University of Texas at Austin.
- (Invited) June 20-23, 2005 1st International Conference of The Metabolomics Society, Tsuruoka City, Yamagata Prefecture, Japan.
- (Invited) July 10-15, 2005: Gordon Research Conference on "Plant Metabolic Engineering," Tilton, NH.
- (Invited) July 17-22, 2005 – XII International Congress on Molecular Plant-Microbe Interactions, Cancun, Mexico. "Innovative approaches to study plant-microbe interactions" session.
- (Invited) August 1-2, 2005 - NIH-sponsored Standards Workshop for Metabolomics, Bethesda, MD
- (Oral) August 3-4, 2005 – Joint Salk Institute and Noble Meeting, LaHolla, CA.

- (Invited) August 28 – Sept. 1, 2005, ACS National meeting in Washington D.C., Chemical Biology Division of the ACS “Studying the Metabolome.”
- (Invited) 21-24 Sep. 2005, Umea Plant Science Center, Dept. Forest Genetics and Plant Physiology, Swedish University of Agricultural Sciences, SE-901 87 Umeå, Sweden.
- (Invited) Oct. 13, 2005, 9:30am-5pm Symposium on Frontiers in Plant Science and Agriculture, Hosted by the Samuel Roberts Noble Foundation, Goddard Center, Ardmore
- (Oral) October 17-18, 2005 – Noble-York Retreat, Ardmore, OK
- (Invited) October 25-27, 2005 Noble FID Conference “Medicago Genomic Function and Response to Biotic Stress” (<http://www.noble.org/events/medicago2005/index.html>).
- (Organizer & Oral) October 31 – November 2, 2005 NSF-VBI-Noble Summer Workshop, Integrated Systems Biology, Ardmore, OK
- (Invited) November 6-9, 2005 - Emerging Scientific Technologies: Impact on Dietary Supplement and Functional Foods Research, Kauai, Hawaii.