# Scientific curriculum vitae - Steven Cannon

April, 2008

## EDUCATION

1999-2003 Ph.D. Plant Biology, University of Minnesota. Focus: plant genomics and evolution, phylogenetic methods, bioinformatics, molecular evolution of gene families. Dissertation: "New tools for understanding plant gene family evolution."
1992-1994 M.P. Urban Planning, University of Minnesota. Focus: geographic information systems; methods to integrate demographic and spatial data.
1991-1992 M.A. American Culture Studies, Bowling Green State University.
1984-1990 B.S. Biology and Math Education, Utah State University.

## EMPLOYMENT

2006-present: Research Geneticist, USDA-ARS Corn Insect and Crop Genetics Research Unit, and Department of Agronomy, Iowa State University
2004-2005 Postdoctoral Associate, University of Minnesota
Project 1: Assist in project management for the international Medicago truncatula genome sequencing project. Oversee database and web site development for the project. Conduct initial whole-genome analysis.
Project 2: provide bioinformatic support and analysis for the NSF funded project "comparative analysis of legume genome evolution".
1999-2003 Fellowship/teaching assistant/research assistant, U of MN.
Ph.D. student in Plant Biology
1995-1999 Content Specialist and Software Designer, The Learning Company.
Designed software and simulation models for educational software.
1993-1995 Planner I, Washington County Planning and Public Affairs

## AWARDS AND HONORS

•Outstanding Professional and Academic Employee, Plant Pathology Dept., 2005
•Philip C. Hamm Memorial Graduate Student Scholarship for the Colleges of Biological Science, Agricultural, Food and Environmental Science, and Natural Resources, 2003
•U of Minnesota Plant Molecular Genetics Institute Doctoral Fellowship, 2003
•USDA National Needs Doctoral Fellowship, 1999 – 2002

## PAPERS

Bertioli D, Moretzsohn M, Madsen LH, Sandal N, Leal-Bertioli S, Guimares P, Hougaard BK, Fredslund J, Shauser L, Nielsen AM, Sato S, Tabata S, Cannon S, Stougaard J. (2008) An analysis of synteny of Arachis with Lotus and Medicago sheds new light on the structure, stability and evolution of legume genomes. (submitted)

Shoemaker RC, Grant DM, Olson T, Warren WC, Wing R, Yu Y, Kim H, Cregan PB, Joseph B, Futrell-Griggs M, Nelson W, Davito J, Walker J, Wallis J, Kremitski C, Scheer D, Clifton S, Graves T, Nguyen H, Wu X, Luo M, Dvorak J, Nelson R, Cannon SB, Thomkins J, Schmutz J, Stacey G, Jackson S (2008) Microsatellite Discovery from BAC End Sequences and Genetic Mapping to Anchor the Soybean Physical and Genetic Maps. Genome 51:294-302

Ameline-Torregrosa C, Wang B-B, O'Bleness M, Deshpande,S, Zhu H, Roe BA, Young ND, Cannon SB (2008) Identification and Characterization of NBS-LRR Encoded Genes in the Model Plant *Medicago truncatula* Plant Physiology, 146:5-21

Ameline-Torregrosa C, Cazaux M, Danesh D, Chardon F, Cannon SB, Esquerre-Tugaye M-T, Dumas B, Young ND, Samac DA, Huguet T, Jacquet C. (2008) Genetic dissection of resistance to anthracnose and powdery mildew in Medicago truncatula. Mol Plant Microbe Interact 21:61-69

Zhang X-C, Wu X, Findley S, Wan J, Libault M, Nguyen HT, Cannon SB, Stacey G (2007) Characterization of plant LysM domains and molecular evolution and comparative genomics of plant LysM type receptor-like kinases. Plant Physiology 144:623-636.

Febrer M, Cheung F, Town C, Cannon S, Young N, Abberton M, Jenkins G, Milbourne D (2007) Construction, characterization and preliminary BAC-end sequencing analysis of a bacterial artificial chromosome library of white clover (Trifolium repens L.) Genome 50:412-421.

Cannon SB, Sterck L, Rombauts S, Sato S, Cheung F, Gouzy JP, Wang X, Mudge J, Vasdewani J, Scheix T, Spannagl M, Nicholson C, Humphray SJ, Schoof H, Mayer KFX, Rogers J, Quetier F, Oldroyd GE, Debelle F, Cook DR, Ernest F. Retzel, Roe BA, Town CD, Tabata S, Van de Peer Y, ND Young (2006) Legume genome evolution viewed through the *Medicago truncatula* and *Lotus japonicus* genomes. PNAS 103(40):14959-64.

Leebens-Mack J, Vision T, Brenner E, Bowers JE, Cannon S, Clement MJ, Cunningham CW, dePamphilis C, deSalle R, Doyle JJ, Eisen JA, Gu X, Harshman J, Kellogg EA, Koonin EV, Philippe H, Pires CJ, Qiu YL, Rhee SY, Sjolander K, Soltis DE, Soltis PS, Stevens P, Stevenson DW, Warnow T, Zmasek C (2006) Taking the first steps towards a standard for reporting on phylogenies: Minimal Information About a Phylogenetic Analysis (MIAPA). OMICS 10(2): 231-237.

Johnson JR, Owens KL, Clabots CR, Weissman SJ, Cannon SB (2006) Phylogenetic Relationships among Clonal Groups of Extraintestinal Pathogenic Escherichia coli as Assessed by Multi-Locus Sequence Typing. Microbes and Infection 8(7):1702-13.

Cannon SB, Crow JA, Heuer ML, Wang X, Cannon EKS, Dwan C, Lamblin A, Vasdewani J, Mudge J, Cook A, Cheung F, Kenton S, Kunau TM, Brown D, Kim D, Cook DR, Roe BA, Town CD, Young ND, Retzel EF. (2005) Databases and Information Integration for the Medicago truncatula Genome and Transcriptome. Plant Physiology, Plant Physiology, 2005.

Mudge J, Cannon SB, Kalo P, Oldroyd GED, Roe BA, Town CD, Young ND (2005) Hypersyntenic Regions in the Genomes of Soybean, Medicago truncatula, and Arabidopsis thaliana. BMC Plant Biology, 2005.

Young ND, Cannon SB, Sato S, Tabata S. (2005) Sequencing the Genes Spaces of *Medicago truncatula* and *Lotus japonicus*. Plant Physiology, 2005.

Cannon SB, Mitra A, Baumgarten AM, Young ND, May G (2004) The roles of segmental and tandem gene duplication in evolution of large gene families in Arabidopsis thaliana. BMC Plant Biology 4:10.

Anderson JP, Mueller JL, Rosengren S, Boyle DL, Schaner P, Cannon SB, Goodyear CS, Hoffman HM (2004) Structural, expression, and evolutionary analysis of mouse CIAS1. Gene 338:25-34.

Graham MA, Silverstein KAT, Cannon SB, VandenBosch KA (2004) Computational identification and characterization of novel genes from legumes. Plant Physiol. 135: 1179-1197.

Cannon SB, Kozik A, Chan B, Michelmore R, Young ND (2003) DiagHunter and GenoPix2D: programs for genomic comparisons, large-scale synteny-discovery, and visualization. Genome Biology 4:R68.

Cannon SB, Young ND (2003) OrthoParaMap: distinguishing orthologs from paralogs by integrating comparative genome data and gene phylogenies. BMC Bioinformatics 4:35.

Cannon SB, McCombie WR, Sato S, Tabata S, Denny RL, Palmer L, Katari M, Young ND, Stacey G (2003) Evolution and microsynteny of the apyrase gene family in three legume genomes. Mol Genet Genomics 270:347-361.

Bertioli DJ, Leal-Bertioli SCM, Lion MB, Santos VL, Pappas Jr G, Cannon SB, Guimares PM (2003) A large scale analysis of resistance gene homologues in Arachis. Mol Genet Genomics 270:34-45.

Baumgarten AM, Cannon SB, Spangler R, May G (2003) Genome-level evolution of NBS-LRR resistance genes in Arabidopsis thaliana. Genetics 165:309-19.

Cannon SB, Zhu H, Baumgarten AM, Spangler R, May G, Cook DR, Young ND (2002) Diversity, distribution, and ancient taxonomic relationships within the TIR and non-TIR NBS-LRR resistance gene subfamilies. J Mol Evol 54:548-62.

Zhu H, Cannon SB, Young ND, Cook DR (2002) Phylogeny and genomic organization of the TIR and non-TIR NBS-LRR resistance gene family in Medicago truncatula. Mol Plant Microbe Interact 15:529-39.

BOOKS, CHAPTERS, PROCEEDINGS

Cannon SB (in press)
Legume Comparative Genomics. In Soybean Genomics, ed. Gary Stacey.

Cannon SB (in press)
Comparative Genomics in Legumes. In Proceedings of Molecular Breeding of Forage and Turf, ed. Toshikiko Yamada.

MA Graham, KAT Silverstein, SB Cannon, KA VandenBosch (2005) Computational identification of legume-specific genes. In Genome Exploitation: Data Mining the Genome. Stdler Symposia Vol 23, ed Gustafson PJ, Shoemaker R, Snape JW.

Cannon SB, Young ND (2002) The Evolution and Genomic Architecture of NBS-LRRs. In: Stacey G, Keen NT (eds) Plant-Microbe Interactions. American Phytopathological Society, St. Paul, Minnesota, p 81-95.

Cannon SB (2003) New tools for understanding plant gene family evolution. Ph.D. Dissertation, University of Minnesota. December.