

Margaret E. Staton

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Education

Clemson University --- Clemson, South Carolina

- PhD in Plant and Environmental Science with Minor in Genetics, GPA 4.00/4.00
Graduation May 2007: College of Agriculture, Forestry and Life Sciences
- Bachelor of Science in Computer Science, *summa cum laude*, GPA 3.98/4.00
Graduation May 2003: College of Science and Engineering

Work Experience

January 2014 - current Assistant Professor of Bioinformatics, Department of Entomology and Plant Pathology, University of Tennessee Institute of Agriculture

August 2010 – December 2013 Head of Bioinformatics at Clemson University Genomics Institute
Responsible for completion of all informatic service and research projects. Brought in \$128,242 since January 2012 to support salary and equipment. Performed a wide variety of services across many different species systems and data types including next generation sequencing and microarray platforms. Highlights:

- **Key Personnel and Bioinformaticist in support of the grant “Comparative genomics of environmental stress responses in North American hardwoods”** led by Dr. John Carlson of Pennsylvania State University and funded by NSF Plant Genome Research Program. Analyzing 454 and Illumina transcriptome sequences, evaluating assembly software methods, mining for genomic resources such as markers, primers, differentially expressed genes, and protein pathways of interest.
- **Developer of Hardwood Genomics Web (www.hardwoodgenomics.org) and Fagaceae Genomics Web (www.fagaceae.org)** websites for disseminating genomic data relating to hardwood trees. Integrating and linking genomic information through modules of code that allow browsing, searching, and downloading information in flexible interfaces. Currently developing new modules for accessing and uploading information specific to tree breeders and growers.
- **Co-PI for grant, “Genetics and Genomics of Chestnut Blight Resistance”** funded by the US Forest Service. Performing the sequence assembly and annotation for genomic QTL regions conferring disease resistance to *Cryphonectria parasitica*. Identifying candidate disease resistance genes and generating SNP and SSR markers for fine mapping. Integrating the genetic and physical maps with the sequence information and making the final products of this grant available online to the public.
- **Co-PI for grant, “Identification of the Genetic Risk Factors for Legg Calve Perthes and Patella Luxation in Miniature and Toy Poodles”** funded by the Poodle Club of American and led by Dr. Alison Starr-Moss. Analysis of SNP genotyping data and whole genome resequencing of control subjects and treatment groups exhibiting patella luxation and/or Legg-Calve Perthes.
- **Bioinformaticist in support of the Chapman lab chicken research** – Overseeing and analyzing the resequencing of six chickens in order to identify causative mutations for the tufted trait and the tail-less trait in the Araucana breed.

August 2007 – August 2010 Bioinformatics Research Scientist at Clemson University Genomics Institute

- **Fulfilling all CUGI bioinformatic service contracts** including a wide variety of sequence assembly and analysis services for model genomes and *de novo* projects, genomic database construction, and physical map construction and data analysis.

August 2003 – August 2007 Graduate Research Assistant at Main Bioinformatics Laboratory, Clemson University

- Created EST section of GDR (Genome Database for Rosaceae)
- Annotated public Rosaceae ESTs
- Updated and maintained CMD (Cotton Microsatellite Database)
- Analysis of Prunus BAC sequence
- Created conference site for the 3rd International Rosaceae Mapping Consortium

Peer Reviewed Publications in last five years:

Fang, GC, Blackmon BP, **Staton** ME*, Nelson CD, Kubisiak TL, Olukolu BA, Henry D, Zhenbentyayeva T, Saski CA, Cheng CH, Monsanto M, Ficklin S, Atkins M, Georgi LL, Barakat A, Wheeler N, Carlson JE, Sederoff R, Abbott AG. 2012. A physical map of the Chinese chestnut (*Castanea mollissima*) genome, and its integration with the genetic map. *Tree Genetics and Genomes*. Advance online publication. doi: 10.1007/s11295-012-0576-6

*corresponding author

Kubisiak TL, Nelson CD, **Staton** ME, Zhebentyayeva T, Smith C, Olukolu BA, Fang GC, Hebard FV, Anagnostakis S, Wheeler N, Sisco PH, Abbott AG, Sederoff RR. 2012. A transcriptome-based genetic map of Chinese chestnut (*Castanea mollissima*), and identification of regions of segmental homology with peach. *Tree Genetics and Genomes*. Advanced online publication. doi: 10.1007/s11295-012-0579-3

Kremer A, Abbott AG, Carlson JE, Manos PS, Plomion C, Sisco P, **Staton** ME, Ueno S, Vendramen GG. 2012. Genomics of Fagaceae. *Tree Genetics and Genomes*. 8(3):583-610.

Barakat A, **Staton** M, Cheng CH, Park J, Yassin NB, Ficklin S, Yeh CC, Hebard F, Baier K, Powell W, Schuster SC, Wheeler N, Abbott A, Carlson JE, Sederoff R. 2012. Chestnut resistance to the blight disease: insights from transcriptome analysis. *BMC Plant Biol*. 2012 Mar 19;12:38.

Wegrzyn JL, Main D, Figuero B, Choi I, Yu J, Neale, DB, Jung S, **Staton** M, Zheng P, lee T, Ficklin S, Cho I, peace C, Evans K, Volk G, Oraguzie N, Chen C, Gmitter FG, and AG Abbot. 2012. Uniform Standards for Genome Databases in Forest and Fruit Trees. *Tree Genetics and Genomes*. 8(3):549-557.

Ficklin SP, Sanderson LA, Cheng CH, **Staton** ME, Lee T, Cho IH, Jung S, Bett KE, Main D. 2011. Tripal: a construction toolkit for online genome databases. *Database (Oxford)*. 2011(0):bar044.

Saski CA, Feltus FA, **Staton** ME, Blackmon BP, Ficklin SP, Kuhn DN, Schnell RJ, Shapiro H, Motamayor JC. 2011. A genetically anchored physical framework for *Theobroma cacao* cv. Matina 1-6. *BMC Genomics*. 2011 Aug 16;12:413.

Feltus FA, Saski CA, Mockaitis K, Haiminen N, Parida L, Smith Z, Ford J, **Staton** ME, Ficklin SP, Blackmon BP, Cheng CH, Schnell RJ, Kuhn DN, Motamayor JC. 2011. Sequencing of a QTL-rich region of the *Theobroma cacao* genome using pooled BACs and the identification of trait specific candidate genes. *BMC Genomics*. 2011 Jul 27;12:379.

Fang GC, Blackmon BP, Henry DC, **Staton** ME, Saski CA, Hodges SA, Tomkins JP, Luo H. (2010) Genomic tools development for *Aquilegia*: construction of a BAC-based physical map. *BMC Genomics*. 11:621.

Sisco, P, Sederoff, R, Tomkins, J, Carlson, J, Kubisiak, T, **Staton**, M, Hebard, F, Anagnostakis, S, Powell, W and Smith, C 2009. The United States National Science Foundation project on developing tools for the study of the Fagaceae: *Castanea*, *Quercus*, and *Fagus*. *Acta Hort. (ISHS)* 844:267-274

Lewers KS, Saski CA, Cuthbertson BJ, Henry DC, **Staton** ME, Main DS, Dhanaraj AL, Rowland LJ, Tomkins JP. (2008) A blackberry (*Rubus L.*) expressed sequence tag library for the development of simple sequence repeat markers. *BMC Plant Biol*. Jun 20;8:69.