

**Ryan J. Percifield**  
**Research Associate II**  
**Department of Biochemistry**  
West Virginia University  
Morgantown, WV 26506  
rpercifield@hsc.wvu.edu  
304-293-6391 (work)  
515-450-9695 (cell)

### **Education**

<b><u>School</u></b>	<b><u>Years</u></b>	<b><u>Degree</u></b>	<b><u>Major</u></b>
Boise State University	1994-1998	B.S.	Biology
Iowa State University	1998-2000	M.S.	Plant Pathology

### **Relevant Work Experience**

**Title:** Research Associate II, Department of Biochemistry

**Dates:** August 2010 to present

**Location:** West Virginia University

**Principal Investigator:** Dr. Peter Stoilov

**Description:** As the initial hire in a newly formed lab, I have been instrumental in establishing basic lab protocol, as well as research protocols relating to the high-throughput sequencing and fragment analysis as they relate to alternative pre-mRNA splicing in multiple mammalian cell lines. I have also significantly contributed to the development of a new high-throughput RNA isolation procedure that will be presented in a soon to be published manuscript. During my time in the Stoilov Lab, I have helped train one new PhD student, three PhD rotation students, and one REU student.

**Title:** Research Professional III, Department of Genetics

**Dates:** August 2007 to August 2010

**Location:** University of Georgia

**Principal Investigator:** Dr. Jeffrey Bennetzen

**Description:** In addition to managing the daily activities of a large academic research lab, I was involved in several projects related to bioenergy and grass genomics. Specifically, I was responsible for providing The Joint Genome Institute (JGI) with *Setaria italica* (foxtail millet) genomic DNA, in addition to RNA from multiple tissue types and treatments. These materials were instrumental in the soon to be released foxtail millet genome sequence. I also played a crucial role in the isolation of a *Panicum virgatum* (switchgrass) specific Ubiquitin promoter that is currently being used in the Bio-Energy Science Center (BESC) to drive over-expression constructs in switchgrass. While in the Bennetzen lab I was helped train three PhD students, two Post Doctoral Researchers, and three undergraduate interns.

**Title:** Assistant Scientist, Department of Ecology, Evolution, and Organismal Biology

**Dates:** February 2002 to July 2007

**Location:** Iowa State University, Ames, IA

**Principal Investigator:** Dr. Jonathan Wendel

**Description:** I was responsible for the day-to-day maintenance of a large academic research lab. This included carrying out complex scientific procedures, writing coherent synopsis of research results for publication, as well as, supervising and training all new lab personnel in the field of molecular evolution. Using cotton as a model organism, the majority of the research that I conducted in the Wendel lab dealt with gene expression and how it is effected by polyploidy. I also designed and conducted a study examining worldwide diversity within the genus *Hypericum* with an emphasis on *Hypericum perforatum* (St. John's Wort). In addition to the bench research, I was responsible for maintaining the most diverse greenhouse collection of cotton plants in North America. During my time in the Wendel lab I trained many personnel in advanced lab techniques. These personnel include: one Post Doctoral Researcher, three visiting scientists, and multiple graduate and undergraduate students.

**Title:** Graduate Research Assistant, Department of Plant Pathology

**Dates:** May 1998 to December 2000

**Location:** Iowa State University, Ames, IA

**Principal Investigator:** Dr. Forrest Nutter Jr.

**Description:** My MS thesis research focused on quantifying the effects of prescribed burning on disease progress and overall health and productivity of Iowa's tallgrass prairies using remote sensing technologies, geographical information systems, and visual disease assessments.

**Title:** Undergraduate Research Assistant, Department of Biology

**Dates:** November 1997 to May 1998

**Location:** Boise State University, Boise, ID

**Principal Investigator:** Dr. Robert Rychert

**Description:** I developed a bioassay to determine the toxicity of *cry* proteins associated with different strains of *Bacillus thuringiensis* using fluorescent imaging detector and *Photobacterium phosphoreum* as the reporter organism.

### **Skills and Techniques**

**Bench:** DNA/RNA purification and manipulation, PCR amplification, various cloning technologies, high-throughput cloning and Sanger (ABI) sequencing and genotyping technologies, large insert library-construction and screening for genes of interest, BAC/fosmid sub-cloning, sequencing, assembly, and feature annotation, Amplified Fragment Length Polymorphism (AFLP), Single Strand Conformation Polymorphism (SSCP), Simple Sequence Repeat (SSR), and microarray analysis.

**Computational:** All Microsoft Office applications, Mac OS, Bioedit, Muscle sequence alignment, Clustal alignment, Apollo, Perl (usage), some familiarity with Unix environment, PAUP\*, MacClade, and many publicly available primer design software packages.

### **Refereed Journal Publications**

Bennetzen, J.L., Schmutz, J., Wang, H., **Percifield, R.J.**, Hawkins, J.S., et al. Full genome sequence analysis of the model plant *Setaria*. *Nature Biotechnology*. *accepted*

\* Genomic DNA and multiple RNA preparations for next-generation sequencing and assembly of the foxtail millet genome.

Mann, D.G., King, Z.R., Liu, W., Joyce, B.L., **Percifield, R.J.**, Hawkins, J.S., LaFayette, P.R., Artelt, B.J., Burris, J.N., Mazarei, M., Bennetzen, J.L., Parrott, W.A., and Stewart, C.N., 2011. Switchgrass (*Panicum virgatum* L.) ubiquitin gene (*PvUbi1* and *PvUbi2*) promoters for use in plant transformation. BMC Biotechnology. 11:74.

\* Large-insert library construction, screening, shot-gun and/or next-generation sequencing, assembly, and annotation for the discovery of ubiquitin promoters for use in switchgrass gene over-expression.

Smagghe, B.J., Hoy, J.A., **Percifield, R.**, Kunda, S., Hargrove, M.S., Sarath, G., Hilbert, J., Watts, R.A., Dennis, E.S., Peacock, W.J., Dewilde, S., Moens, L., Blouin, G.C., Olson, J.S., and Appleby, C. 2009. Correlations between oxygen affinity and sequence classifications of plant hemoglobins. Biopolymers. Biopolymers 91: 1083-1096.

\* Genomic DNA preparation and Hemoglobin gene isolations from plant genomic DNA followed by cloning and Sanger sequencing to ensure proper genes were isolated for binding study.

**Percifield, R.**, Hawkins, J., McCoy, J., and Wendel, J.F. 2007. Genetic diversity in *Hypericum* and AFLP markers for species-specific identification of *H. perforatum* L. Planta Medica 73: 1614-1621.

\* Genomic DNA preparation for AFLP genotyping and fragment analysis on many accessions of *Hypericum spp.* to isolate species specific markers, all aspects of experimental design and writing of manuscript.

Udall, J.A., Swanson, J.M., **Percifield, R.J.**, and Wendel, J.F. 2006. A novel approach for characterizing expression levels of genes duplicated by polyploidy. Genetics 173: 1823-1827.

\* Multiple DNA and RNA isolations for SSCP analysis followed by fragment cloning and Sanger sequencing confirmation.

Keyte, A. L., **Percifield, R.**, Liu, B., and Wendel, J.F. 2006. Intraspecific DNA methylation polymorphism in cotton (*Gossypium hirsutum* L.). Heredity 97: 444-450.

\* Genomic DNA isolation and fragment analysis for AFLP genotyping.

Adams, K.L., **Percifield, R.**, and Wendel, J.F. 2004. Organ-specific silencing of duplicated genes in a newly synthesized cotton allotetraploid. Genetics 168: 2217-2226.

\* Multiple RNA isolations for AFLP genotyping and fragment analysis on cDNA.

Adams, K.L., Cronn, R.C., **Percifield, R.**, and Wendel, J.F. 2003. Genes duplicated by polyploidy show unequal contributions to the transcriptome and organ-specific reciprocal silencing. Proceedings of the National Academy of Sciences USA 100: 4649-4654.

\* Many DNA and RNA isolations for SSCP analysis followed by fragment cloning and Sanger sequencing confirmation.

### **Manuscripts in Preparation**

**Percifield, R.J.**, and Stoilov, P.G. Development of a PCR array to elucidate splicing changes occurring during the epithelial to mesenchymal transition. *in preparation*.

Hawkins, J.S., **Percifield, R.J.**, Jogi, A., Estep, M., and Bennetzen, J.L. Cloning and characterization of gene families associated with switchgrass cell wall development. *in preparation*.

Chaluvadi, S., **Percifield, R.J.**, and Bennetzen, J.L. Characterization of the metagenome associated with two different cultivars of *Panicum virgatum*. *in preparation*.

Baucom, R.S., **Percifield, R.J.**, and Bennetzen, J.L. Characterization of the metagenome associated with Bt and non-Bt lines of maize. *in preparation*.