#### **OVERVIEW**

JOB: Maize Breeding and Quantitative Genetics

UNIVERSITY: Texas A&M University DEPARTMENT: Soil and Crop Sciences APPLICATION DATE: 02/15/2008 JOB START DATE: 09/01/2008

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## POSITION DESCRIPTION

Job Open Date 12-07-2007 Position Title Assistant Professor Hiring Unit Soil & Crop Sciences Department NOV Number 03055 Job Type Full-Time Salary

Starting salaries for positions may be negotiable based upon qualifications and experience Commensurate Pay Basis Monthly Budgeted? Budgeted - with benefits Position open to internal candidates only?

(TCE County Programs positions only) No Location College Station District (required for TCE County Programs positions only) County (required for TCE County Programs positions only) Major/Essential Duties of Job The position is located in the Department of Soil and Crop Sciences, Texas A&M University in College Station, Texas. This position reports to the Head of the Department of Soil and Crop Sciences. The individual filling this position will oversee its entire operation, manage intramural and extramural research funds, and supervise undergraduate students, technicians, graduate students and postdoctoral research scientists.

Develop a highly respected research and teaching program. The research must enhance Texas agriculture through the application of quantitative genetics to crop improvement, including but not limited to corn. Assume leadership over ongoing research on and breeding for (i) tolerance and/or resistance to mycotoxin contamination, and (ii) introgression of traits from tropical germplasm into temperately adapted corn germplasm. Interact with other crop improvement programs through coadvising graduate students and, where appropriate, research collaboration. Must (i) procure extramural funding to support research efforts, and (ii) participate and work effectively in collaborative research teams.

Participation in departmental, college, university and professional society activities.

Supervision of associated support staff and undergraduate, graduate students and student workers.

This position is a combination of research and teaching appointment. Teaching responsibilities include the development of a nationally recognized graduate program along with classroom teaching responsibilities. Formal responsibilities include teaching one graduate course in quantitative plant genetics and the training of graduate students in plant breeding and related degree programs.

Seth C. Murray; <a href="mailto:sethmurray@tamu.edu">sethmurray@tamu.edu</a>; <a href="mailto:http://soilcrop.tamu.edu/people/murray-seth-c/">http://soilcrop.tamu.edu/people/murray-seth-c/</a>

Other duties as required. Occasional Duties Required Education and Experience Preferred Education and Experience Required Education: Ph.D. in Plant Breeding, Genetics or related area. Preferred Education: Required Experience: Published refereed journal articles. Teaching experience as an instructor and/or teaching assistant. Preferred Experience: - post-doctoral research experience

- experience in plant breedingexperience in the statistical analysis of molecular data sets
- experience in the use of molecular methods for analysis of quantitative traits Required special knowledge, abilities, and skills: Must compete successfully in one or more arenes for external sur
- knowledge, abilities, and skills: Must compete successfully in one or more arenas for external support or research, and conduct an internationally recognized research program.

Ability to establish effective working relationships. Ability to multi-task and work cooperatively with others. Preferred special knowledge, abilities, and skills: Comments to Applicants Review of applications will begin February 15, 2008 and will continue until a suitable candidate is identified. Applicants should submit via this online employment system (i) a faculty form, (ii) a cover letter, (iii) a 2-page statement that highlights key applicant qualifications and defines applicant research and teaching interests, (iv) their curriculum vitae, and (v) the names and contact information of three references via this online employment system. Direct inquiries should be made to Dr. David Baltensperger, Head, Department of Soil & Crop Science, Texas A&M University, College Station, Texas 77843-2474, dbaltensperger@tamu.edu.

Employment is contingent upon the agency's verification of credentials and/or other information required by agency procedures, including the completion of a criminal history check.

Texas law requires all males 18-25 show proof of compliance with federal Selective Service law to be eligible for employment.



# Institute for Genomic Diversity

157 Biotechnology Building Ithaca, NY 14853

Seth C. Murray 10/24/2018

Dr. D. Baltensperger Department of Soil and Crop Sciences Texas A&M University College Station, TX 77843-2474

Dear Dr. Baltensperger;

I am writing to apply for the position of Assistant Professor: Quantitative Geneticist which was advertised at the 2007 CSSA meeting. I am presently pursuing a *Ph.D* at Cornell University in the Department of Plant Breeding and Genetics under the supervision of Dr. Stephen Kresovich. The central focus of my dissertation research, partially funded by a USDA/DOE grant I helped to author, is understanding yield and composition tradeoffs between grain, stem sugar, and lignocellulosic biomass for improving sorghum as a biofuel feedstock. I have submitted two manuscripts and I am writing a third on this project, I am also writing a manuscript on a statistical technique for plant breeders to identify loci they have selected for local adaptation and agronomic improvement. I will finish all work for the *Ph.D* before April 2008. I believe my experience and continuing interest in quantitative genetics for crop improvement makes me a strong candidate for this position.

In addition to the sorghum work that I explain in my research statement, I have been involved with two maize genetics projects relevant to this position. First, selection mapping in a maize population recurrently selected for northern corn leaf blight and common rust (also described in my research statement). Second, I have assisted members of the NSF maize diversity project to phenotype the 5000 Nested Association Mapping (NAM) lines for a variety of traits. This material, soon to be publically available, has already been extensively genotyped and phenotyped and would be a valuable first resource to investigate the genetics of resistance to aflatoxin and other traits of interest in maize.

I am impressed with the progress in applied pathology, grain quality and the genetic enhancement of maize Dr. Bertran had, both in Texas and globally. Continuing this work in maize is important and I am especially interested in the integration of tropical germplasm. One of the most attractive aspects of this position to me, however, is the ability to interact and complement a wide variety of other research, both within Soil and Crop Sciences and across other departments.

I have included my *Curriculum vitae*, my research and teaching statement and the names of three references. I would be happy to supply you with additional materials such as, manuscripts, university transcripts or presentations. I will be available to talk with you at your



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convenience and can be reached on my cellular phone at (607) 262-6232. I appreciate your time and consideration, and I look forward to hearing from you soon.

Sincerely,

Seth C. Murray

e-mail: <a href="mailto:scm33@cornell.edu">scm33@cornell.edu</a> mobile: (607) 262-6232

Sett C. Many

## Seth C. Murray

157 Biotechnology Building; Cornell University; Ithaca, NY; 14853 p: (607)-262-6232, scm33@cornell.edu

#### Research Interests:

Sweet and biomass sorghum, plant breeding, quantitative and population genetics (theoretical and applied), genetics of perennialism, statistical methods for detecting selection, crop domestication, preservation and use of exotic germplasm, sustainable agriculture, agricultural paradigm change.

#### **Education:**

- Cornell University, Ithaca, NY (August 2002- present) Ph.D candidate in Plant Breeding and Genetics under Dr. Stephen Kresovich, minors in Genetics and Development (Dr. E. Buckler) and Biological Statistics and Computational Biology (Dr. C. Bustamante) GPA: 3.67
- Michigan State University, East Lansing, MI (August 1998-Dec 2001) B.S. December 2001. Major: Crop and Soil Sciences. Minors: Honors College, Bailey Scholars Program, Biotechnology: GPA: 3.93
- Wageningen Agricultural University, Wageningen, Netherlands (Spring 2000) Crop science exchange

#### Extra Curricular:

-President of Synapsis, plant breeding graduate student group at Cornell, 2004-2005

## **Honors and awards:**

- The Barbara McClintock Graduate Student Award, one of four students in the College of Agriculture and Life Sciences, 2007
- Cornell Graduate School Travel Grant to present at the National Sorghum Producers Conference, 2007
- Plant Breeding and Genetics Munger / Murphy Award for outstanding graduate work, 2006
- Cornell Graduate School Travel Grant to present at Plant and Animal Genome Conference, 2006
- ISPMB student travel grant to present at Plant and Animal Genome Conference, 2006
- NC State Summer Institute in Statistical Genetics Scholarship, 2004
- NSF Graduate Research Fellowship, honorable mention, 2004
- Cornell Department of Plant Breeding Graduate School Fellowship, 2002-2003
- Highest GPA in graduating class, College of Agriculture and Natural Resources, Fall 2001
- Eagle Scout, Boy Scouts of America, 1998

#### Recent Employment:

- Graduate research assistant, Fall 2002 Summer 2003, Spring 2004 present
- Teaching assistant, graduate level class: Crop Evolution, Domestication and Diversity, Fall 2003
- Growing In Place, organic community supported agriculture farm, Summer 2001

### **Publications**

- **Murray SC**, Rooney WL, Mitchell SE, Kresovich S. (In preparation) Sweet sorghum diversity and association mapping for plant carbohydrate yield partitioning.
- **Murray SC**, Wisser RJ, Kresovich S, Nelson RJ (In preparation) Selection mapping: comparisons of methods for the identification of temporally selected loci associated with functional trait variation.

### Publications continued

- Murray SC, Sharma A, Rooney WL, Klein PE, Mullet JE, Mitchell SE, Kresovich S. (submitted) Genetic improvement of sorghum as a biofuel feedstock I: quantitative loci for stem sugar and grain nonstructural carbohydrates. Crop Science
- Murray SC, Sharma A, Rooney WL, Klein PE, Mullet JE, Mitchell SE, Kresovich S. (submitted) Genetic improvement of sorghum as a biofuel feedstock II: quantitative loci for stem and leaf structural carbohydrates. Crop Science
- Wisser RJ, Murray SC, Kresovich S, Nelson RJ (submitted) Recurrent selection mapping of quantitative trait loci for northern leaf blight resistance in maize. Genetics.
- McGrath JM, Trebbi1 D, Shaw RS, Fenwick A, Panella L, Schultz B, Laurent V, Barnes S, **Murray SC** (2007) An open-source first-generation molecular genetic map from a sugar X table beet cross and its extension to physical mapping. The Plant Genome, a Suppl. to Crop Sci. 47: S27-S44.
- Hamblin MT, Casa AM, Sun H, **Murray SC**, Paterson AH, Aquadro CF, Kresovich S. (2006) Challenges of detecting directional selection after a domestication bottleneck: lessons from Sorghum bicolor. Genetics 173(2):953-64

#### **Presentations**

- **Murray SC**, Rooney WL, Klein PE, Sharma A, Mullet JE, Mitchell SE, Kresovich S. (2007) On the quantitative genetics and tradeoffs in improving sorghum as a biofuel feedstock. Oral presentation - ASA-CSSA-SSSA International Annual Meeting.
- -Murray SC, Wisser RJ, Nelson R, Kresovich S. (2007) Selection mapping A statistical methodology for plant breeders to identify loci for population improvement and local adaptation. Oral presentation ASA-CSSA-SSSA International Annual Meeting.
- Murray SC, Rooney WL, Klein PE, Sharma A, Mullet JE, Mitchell SE, Kresovich S. (2007) Identification of quantitative trait loci for stem sugar, grain yield, and biomass to improve sorghum as a biofuel feedstock. Invited speaker National Sorghum Producers Association Annual Conference.
- **Murray SC**, Rooney WL, Klein PE, Klein RR, Mullet JE, Mitchell SE, Kresovich S. (2006) Quantitative inheritance of carbohydrate partitioning and accumulation: sorghum as a biomass feedstock. Poster - Plant and Animal Genome Conference.
- Wisser RJ, **Murray SC**, Kresovich S, Nelson RJ. (2006) Recurrent selection mapping of quantitative trait loci for northern leaf blight resistance in maize. Poster Plant and Animal Genome Conference.
- **Murray SC**, Casa AM, Hamblin MT, Mitchell SE, Kresovich S. (2005) Diversity and genetics of domesticated sorghum. Poster N. American Grain Congress.
- **Murray SC**, Casa AM, Hamblin MT, Mitchell SE, Kresovich S. (2004) XGAp256 Proof of concept; a sorghum locus under selection. Poster Eastern Great Lakes Molecular Evolution Meeting.
- **Murray SC**. (2003) XGAp256 a locus under selection? Oral presentation NSF plant genome review committee.
- **Murray SC**, Howell S. (2001) Comparison of different methods to lower acidity in Seval wine. Poster Michigan State Undergraduate Research and Creative Activity Forum.
- **Murray SC**, McGrath M. (1999) Genetics of color inheritance in *Beta Vulgaris*. Oral presentation Michigan State Undergraduate Research and Creative Activity Forum.

#### **Funded Proposals**

My dissertation research was a major focus of, and I was a co-author of: DOE - USDA GTL Feedstock Genomics award "Sorghum Biomass/ Feedstock Genomics Research for Bioenergy" (9/1/06 - 9/1/08) \$800,000.

# Seth C. Murray Statement of Research and Teaching

My career goal is to improve agricultural economic and environmental sustainability through crop genetic improvement of complex traits. My research and teaching interests are a direct result of this goal.

### **Current Research**

The central focus of my dissertation research, partially funded by a USDA/DOE grant I helped to author, is to understand yield and composition tradeoffs between grain, stem sugar, and biomass for improving sorghum as a biofuel feedstock. In a completed study, bi-parental genetic mapping was used to identify quantitative trait loci (QTL) alleles that increase grain sorghum crop residue sugar and cellulose without tradeoffs in grain yield. Also, QTL alleles controlling the increase of biomass yield were identified, valuable for developing dedicated lignocellulosic biofuel sorghum varieties. The expertise and equipment needed for the wet-lab aspects of this project were not available in our lab, so I had to function very independently to learn the methodology, find the equipment, and collect the data. These methodologies included high pressure liquid chromatography (HPLC), used to quantify sugars, and developing near infrared spectroscopy (NIRS) calibrations, to analyze the composition of grain, leaf and stem tissues. Additionally, I co-developed a genetic map with candidate genes and conducted routine and customized statistical analyses on large phenotypic and genotypic datasets. This project allowed me to gain experience in managing diverse field crews (Texas A&M University) and laboratory technicians (Cornell University) as well as mentoring Cornell undergraduate researchers. Concurrently, all of the same analytical and statistical work was carried out on a diverse panel of sweet and grain sorghums for which I am presently using association mapping to follow up candidate genes suggested by the QTL mapping results. All of this research was performed in cooperation with Drs. W. Rooney, J. Mullet and P. Klein at Texas A&M University with whom I have forged a strong collaborative relationship.

A separate project I have developed is a simulation based statistical methodology for testing loci under temporal selection in breeding populations, termed 'selection mapping'. This project demonstrated that there is sufficient power in selected synthetic populations to detect loci for local adaptation and agronomic improvement. For new complex traits of interest, such as improved lignocellulosic composition for digestion, this method will allow simultaneous QTL mapping and population improvement. In collaboration with Drs. R. Wisser (NCSU) and R. Nelson (Cornell) this method was applied in a maize population selected for northern corn leaf blight resistance; loci were identified that have been functionally validated in subsequent experiments.

### **Future Research**

My primary research interest is in integrating crop improvement (plant breeding) with crop genetic research (applied and basic) to improve economic and environmental agricultural sustainability. Both crop improvement and genetics research will rely on the use and development of high throughput phenotyping (e.g. NIRS) and genotyping (e.g. Illumina SNP assay) tools for complex traits. For genetic research on traits of interest, QTL, association and selection mapping approaches will be used to connect biological significance with identified genetic polymorphisms. This will allow marker assisted selection and genomic selection to be combined with conventional pedigree breeding and population improvement.

I am very interested in breeding and I have specified specific interests of research positions in my cover letters, here I present two cases of my broad genetic research interest. Although my primary focus is sorghum, the tools and approaches are easily translated and applied to other C4 crops such as maize, switchgrass or sugarcane.

### Aim1: Identifying the genetic mechanisms of regrowth and perennialism

Plant regrowth after harvest and perennialism, growth over years, are important quantitative traits in biofuel, sugar, and forage crops but remain poorly studied. Regrowth and perennialism allow multiple harvests, reduce planting costs, and increase the number of days for photosynthesis

and soil protection across species. I have previously identified a QTL for regrowth in domesticated sorghum would like to apply this in future collaborative work. Perennialism, primarily in weedy and wild C4 grasses, can result from multiple mechanisms, such as rhizomes. Identifying germplasm, loci and biochemical mechanisms for rhizome initiation will give insight into phenotypes for winter survival of forage and bioenergy crops (if weediness can be repressed), and potentially approaches to disrupt the perennial rhizomes of weedy Johnsongrass. I envision many collaborative projects using biochemical, plant physiology, weed science, and metabolic engineering approaches to this perennial work.

## **Aim2: Selection mapping**

Selection mapping, explained previously, currently tests single loci for significance but could gain power and usefulness by incorporating linkage and population structure. I will continue developing the method to incorporate multiple loci, linkage, population structure and alternate breeding schemes. This approach could be useful for complex quantitative traits important in perennialism, grain aflatoxin resistance and cellulosic biomass yield where crop improvement is more important than genetic research alone. This approach may be superior over QTL mapping for complex polyploid genomes like sugarcane or miscanthus but remains untested. I plan to collaborate with others to apply selection mapping to breeding populations across species as well as in developing my own populations.

## **Teaching**

In addition to research I am looking for an opportunity to advise and teach graduate and undergraduate students. I thoroughly enjoy teaching and view it as a valuable component to my career. Although the education of students is paramount, I also benefit in teaching by reflecting on information through the students unique perspectives. Therefore, I would hope to not only advise students within my discipline but also across disciplines to encourage cross-collaborative learning in both directions.

My current teaching interests fall in the categories of molecular crop improvement, quantitative and population genetics (with associated software R, SAS, QTL Cartographer, Structure, etc.), crop genetic diversity, and agricultural sustainability. I have had three opportunities to teach at Cornell, as a lecturer and the primary teaching assistant in Crop Evolution, Domestication and Diversity (graduate level), as a guest lecturer and group leader in Advanced Plant Genetics (graduate level), and as a lecturer and volunteer teaching assistant for Introduction to Plant Genetics (undergraduate level). I also consider my two summers as a homesteading interpreter at Philmont Scout Ranch valuable, teaching hundreds of people with diverse backgrounds about agricultural systems in the 1800's. These experiences have taught me that preparation and enthusiasm are the most important tools of teaching, but to never underestimate the difficulty of conveying complex information clearly.

My current teaching philosophy can be condensed to three main beliefs: (1) All students come from different backgrounds, have different outcome expectations, and learn differently. (2) As a teacher, it is my job to make sure everyone has an opportunity to access and understand the material, to present in various ways without compromising expectations, and to make myself accessible to students. (3) Recall of facts with modern access to information is not enough, it is also the universities role to prepare all students for higher levels of thinking that allows them to parse, understand and use information appropriately. Specific ways to implement this in the classroom is with peer reviewed group projects, open book tests, and case studies when practical.