**NANCY K. AGGIE**

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EDUCATION

**Texas A&M University**, College Station, TX December 20XX

*Ph.D. in Genetics*, Dissertation: The Genetic Component in Resistance to Aflatoxin Accumulation in Maize.

GPR 3.94

**University of Pittsburgh**, **Graduate School of Public Health, Pittsburgh,** PA

*Master of Science in Hygiene*, with a major in **Human Genetics**, and minor concentration in biostatistics August 20XX

GPR 3.93

**Concordia College**, Bronxville, NY May 20XX

*Bachelor of Arts in Biology*

GPR 3.97

EXPERIENCE/SKILLS IN CROP SCIENCE

**Molecular Biology**

* DNA/RNA extraction, PCR, cloning, editing with CRISPR-Cas9, carbon nanotube applications, plant tissue culture

**Bioinformatics**

* Designed RNA-Seq experiment, modified edgeR programs, wrote scripts in Linux to run Trinity, Plink, VCFtools, bowtie2 and various nucleotide substitution simulation software

**Plant Breeding/Statistics**

* Applied JMP and SAS to conduct meta-analysis on multi-environmental trials for graduate work
* Utilized contingency tables in JMP, R and Excel pivot tables for graduate and co-op data analyses
* Composed R functions to use ggplot2, principal, glm functions, RandomForest, binary classification tables and others in the development of predictive models used in selection of cultivars

RESEARCH EXPERIENCE IN GENETICS AND CROP SCIENCE **Texas A&M AgriLife Research,** College Station, TX June 20XX – Present

*Graduate Research Assistant* **Bioinformatics**

* Test the accuracy of imputation software applied to an NGS pipeline that provides a whole genome sequencing service at low coverage
* Evaluate the desirability of including a reference panel to accurately predict missing genotypes following alignment and variant calling with GATK
* Run simulation software to generate nucleotide substitutions in sequences for testing the accuracy of imputation platform

 **Gene Editing with CRISPR\_Cas9 and sgRNA** January 20xx – May 20XX

* Utilize different gene editing software to design pairs of sgRNA that matched a target region of certain genes sequenced in specific rice, wheat and millet cultivars to perform gene knockout
* Streamline a protocol for isolating high concentrations of protoplasts from rice seedlings that is used as an assay for the effectiveness of gene editing with a given sgRNA and CRISPR-Cas9
* Currently collaborating with others in finding optimal delivery agents of editing plasmids or ribonucleoprotein complexes such as Agrobacterium, gene gun, or infiltration of carbon nanotubes, and testing in a variety of tissue cultures

 **Monsanto North America Soybean Breeding. Six-month Research Co-op. City, State** May 20xx – December 20XX

* Performed retrospective analyses of soybean pipeline multi-year, multi-regional data to analyze factors contributing to rates of advancement
* Organized traits with associated haplotypes of markers in a commercial breeding pipeline
* Evaluated soybean lines for herbicide tolerance, uniformity of pod, pubescence and flower color, and rated overall appearance of plots near harvest time
* Conducted multiple linear and logistic regression for modeling decision-making in selection of soybean lines

 **Maize Breeding Program,** Texas A&M UniversityJanuary 20xx – December 20XX*Graduate Research Assistant, GENE xxx Lab*

* Analyzed differential gene expression of maize kernels in an RNA-Seq experiment through application of the Trinity platform for assembly of transcriptome from sample libraries, and edgeR of the Bioconductor platform to compare responses to different methods of fungal inoculation and different harvest times
* Designed a study to evaluate yield and disease data of maize hybrids, gathered over ten years at multiple research stations in the southern US. Applied all random and mixed models, as well as correlation and stability analyses to agronomic and disease resistance traits in sets of maize hybrids
* Contributed to many aspects of the maize breeding program including field preparation, planting, pollination, harvesting, ear rating, seed treatments, seed packaging, recommending superior lines to advance, based upon results from meta-analysis of multi-environmental trial data

TEACHING EXPERIENCE

**Department of Genetics,** Texas A&M UniversitySeptember 20xx – April 20XX

*Teaching Assistant, GENE xxx Lab*

* Lectured and supervised undergraduate students in upper level genetics laboratory.
* Evaluated all course assignments and provided assistance at a help desk.

SELECTED PUBLICATIONS

**Published Journal Article (Peer Reviewed)**

**Aggie, N**., Muray, S.C., Keit, T., Danver, M., Windhammer, G.L., Conners, W.P., , J. Jan/Feb 20XX. *Title of the paper on Maze and resistances.* Crop Sci. 57:865-215. doi 10.2356/cropsci2016.06.0753

**Manuscript Published on bioRxiv and submitted to Science Direct May 20XX**

**Aggie, N**., Muray, S.C., Zhan, H-B, Zhan, M., Robinson, C.M., and Keit, T.S. *Title of the Paper submitted to Science Direct*

SELECTED PRESENTATIONS

**Oral Presentations**

*Title of the oral poster presentation****,*** at the Gene Editing Symposium in College Station, TX in October 20XX.

*Title of the oral poster presentation****,*** presented near the end of my co-op at Monsanto covered the importance of genetic diversity, MAS and genomic selection, high-throughput phenotyping and imaging technology, and decision-making in selection and advancement

**Poster Presentation**

*Title poster presentation****,*** at the Third Annual Texas A&M University (High Performance) Computing Research Symposium in May 20XX

VOLUNTEER SERVICE/LEADERSHIP EXPERIENCE

**Crop Science Graduate Organization**, Texas A&M University*Officer*  October 20XX – May 20XX
Conducted meetings, invited special speakers and promoted events that grew membership across crop science disciplines

**Genetics Graduate Student Association**, Texas A&M University August 20XX– June 20XX
Membership Committee member that encouraged attendance of weekly seminars
 **City of College Station,** College Station TX May 20XX – September 20XX

*Teacher and Assistant in English as a Second Language classes (ESL)*

Twice a week for 15-20 students of many different ethnic backgrounds