Matthew McGowan

Molecular Plant Science
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Education

Ph.D.	Molecular Plant Science	Washington State University	2020 (expected)
M.S.	Biomedical Science	Kansas State University	2014
B.S.	Microbiology, Anthropology	Kansas State University	2011

Academic Experience

Graduate Research Assistant. Department of Crop and Soils, Washington State University. Current.
- Incorporates conditional co-expression network data into GWAS for ensemble analysis
- Develops, maintains, and troubleshoots computational tools for high-throughput genotyping and RNA-seq network analysis using R, Python, and Slurm Workload Manager
- Leverages high-performance computing clusters to analyze complex gene co-expression networks
- Performs QC analysis on publicly available transcriptomic data for RNA-seq network research
- Maintains internal Github project repositories for research reproducibility
- Completed coursework in bioinformatics, statistical genomics, and data science
- Presented biological research at international scientific conferences

Graduate Research Assistant. Department of Pathobiology, Kansas State University. Mar 2010 – Dec 2013.
- Deployed epidemiologically sound strategies to isolate representative commensal bacterial populations and extract nucleic acids from animal blood, feces, and tissue for further phenotypic and genotypic analysis
- Contributed scientific research that resulted in co-authorship on a peer-reviewed published paper
- Utilized PCR and real-time PCR approaches to measure the burden of antibiotic resistance present in cattle herds
- Introduced high-throughput automated equipment into laboratory processes to decrease data turnaround time, improve consistency, and minimize labor requirements
- Provided USDA and Canadian resistance surveillance programs with Sensititre MIC and growth curve assay data for foodborne pathogen strains
- Collaborated on a large multi-institutional grant project aimed at developing antibiotic resistance intervention strategies by presenting research, editing papers, and acting as conference rapporteur to assemble annual reports on project milestones
- Completed coursework required to complete a M.S. in Biomedical Science

Non-Academic Experience

Research Associate. Heartland Plant Innovations. Manhattan, KS. Jan 2014 – Dec 2015.
- Coordinated daily and long-term operations of a molecular biology services laboratory
- Managed corporate genotype-by-sequencing projects for diverse plant species: wheat, barley, corn, soybean, and strawberry
- Streamlined automated molecular methodologies to reduce turnaround time and material costs
- Maintained laboratory equipment, wrote standard operating protocols, and trained laboratory technicians in proper equipment usage
- Curated project databases and handled quarterly data backups
- Assisted in seasonal wheat doubled haploid production processes including mother plant emasculation, pollination, embryo rescue, tissue culture, colchicine treatment, and greenhouse management
- Communicated with customers to assess project goals, deadlines, and progress updates

Academic Advisors
Dr. Stephen Ficklin (2017 – present)
Dr. Zhiwu Zhang (2016 – present)
Dr. H. Morgan Scott (2012-2014)

Publications and Scholarly Work

Publications
- M. Mcgowan, "Calling SNPs Out of DNA Array for Diverse Hexaploid Wheat Population by Using Gaussian Mixture Models", Proceedings of the World Congress on Genetics Applied to Livestock Production, vol. Technologies - Genotyping, p. 946, 2018.

- Kanwar et al, "Effects of Ceftiofur and Chlortetracycline Treatment Strategies on Antimicrobial Susceptibility and on tet(A), tet(B), and blaCMY-2 Resistance Genes among E. coli Isolated from the Feces of Feedlot Cattle," PLoS ONE 8(11)" e80575, doi: 10.1371/journal.pone.0080575

Theses
- McGowan, M., *The Epidemiology of Tetracycline and Ceftiofur Resistance in Commensal Escherichia coli,* M.S. Thesis, Kansas State University, Department of Pathobiology, 2014.

Presentations at Conferences, Symposia, and Workshops
- *Conditional Gene Co-Expression Networks for Aphanomyces Root Rot Response (ARR) in Lentil,* Plant and Animal Genome Conference, San Diego, CA (January 2019)

- *Improved SNP Calling for Diverse Hexaploid Wheat Using GGcall,* World Congress on Genetics Applied to Livestock Production, Auckland, NZ, (February 2018)

- *Calling SNPs Out of DNA Array for Diverse Hexaploid Wheat Population by Using Gaussian Mixture Models*, Plant and Animal Genome conference, San Diego, CA (January 2018)

- *SNPs from Sequence: Genotyping in Wheat*, Western Wheat Workers Meeting, Pullman, WA (July 2016)

- *Relationships between antibiotic use and resistance genetics in commensal E. coli using pairwise bacterial growth parameters*, Federation of European Microbiological Society (FEMS) general conference, Leipzig, Germany, (July 2013)

- *Genotypic surveillance of tetracycline resistance in Canadian beef cattle 2002-2011*, Antimicrobial Resistance in Animals and the Environment (ARAE) Symposium, Ghent, Belgium, (July 2013)

- *Antibiotic use versus antibiotic resistance profiles of commensal E. coli in beef cattle: explaining their association via bacterial growth parameters*, Conference of Research Workers in Animal Diseases (CRWAD), Chicago, IL, (December 2012)

Academic Awards
- Howard Hughes Undergraduate Research Scholar, 2006-2008
- WSU Hardware Engineering Hackathon 2nd Place, *Cyberthumb plant sensor*, 2017

Institutional, Professional, and Outreach Activities
- Board Member of the College of Veterinary Medicine Graduate Research Association, 2012-2013
- Molecular Plant Science Seminar Organizing Committee Member, 2016-2018
- Franklin Elementary School Science Fair Judge, 2017-2019
- Pullman USDA ARS Peoples' Garden Volunteer, 2017-2018