

Statement of Research

Nicholas Santantonio

Winter wheat comprises a substantial portion of Colorado's agriculture output, which relies on the public wheat breeding program at Colorado State University to provide improved varieties. I intend to develop the foundational capacity to implement 21st century breeding technology in this program, providing ample opportunities for extramural funding. This will include the collection, storage and accessibility of genome-wide information, pedigrees, high-throughput phenotypes collected through proximal sensing, and traditional phenotypes from field trials. Integration of these technologies with advanced statistical and machine learning methodology should maximize product development for Colorado growers and provide long-term sustainability of the breeding program. Demonstration of these new techniques and resources should help pique public interest in crop improvement at CSU.

Short-term gains

The most easily exploited terms in the breeders equation are cycle time and selection intensity. The number of lines evaluated can be drastically increased by reducing or eliminating replication in early-stage trials, thus increasing selection intensity. Genotyping some lines within each family will increase reliability and allow for estimation of genetic correlations of locations and prediction of genetic merit within locations. All materials that are advanced to the second year yield trials will be genotyped. Aerial phenotypes will be used in multi-trait models to substantially increase trial sizes and reduce the number of plots that need to be harvested.

Initially, the breeding cycle will be shortened by recycling materials after the second year of yield trials, using genotypic information to drive crossing decisions. A Smith-Hazel economic selection index including yield and test weight will be constructed through consultation with local grain elevator operators. This index will be used as the genetic merit criterion to transition to a genomic selection program. Optimal contributions will then be used to maximize genetic gain while minimizing the reduction in genetic variance through time.

I also aim to target specialty flour markets, providing farmers with unique products that demand a premium price from millers. Selection indices can be modified to include milling and baking quality traits in the decision making process. These indices would be built in coordination with millers, to optimize selection for the specific flour qualities necessary for specialty products.

Long-term sustainability

The infrastructure to support regular genotyping and proximal sensing must be developed before the program is overwhelmed by incoming data. While I intend to host a local breeding program database, I would like to work with the T3 database to host proximal sensing images along with phenotypic trial data, pedigrees and genotypes. Quality control of genetic markers, pedigrees and phenotypes must be implemented and standard operating procedures must be developed.

Genotyping will allow for construction of a multi-trait, multi-environment genomic prediction model that will be updated yearly. Field experimental design will then be optimized to leverage all phenotypic information available, using genotypic information to link otherwise unrelated trials and traits. High-throughput phenotypes may also be used to account for spatial variation within the field, observe growth through time and monitor response to biotic and abiotic stress. These phenotypes may also be used in longitudinal random regression models to build genotype specific growth curves. Plasticity in growth curves may shed light on how response to stress allows for stability or sensitivity to varying environments.

Once genotyping and rapid recycling has been hammered out and sufficient genotypic and phenotypic information is generated (≤ 5 years), a recurrent population will be constructed using current breeding materials. This population will be subjected to rapid cycling twice a year to increase the genetic merit of the population, generate unique meiotic recombinations and minimize inbreeding using optimal contribution. Materials will be pulled out of the recurrent population on a yearly basis for two generations of high intensity genomic selection and two generations of inbreeding in the greenhouse. Family sizes will vary based on predicted family means and variances. Materials will also be pulled directly out of the recurrent population and phenotyped for generating information highly connected to the recurrent population to increase accuracy of selection.

Breeding for synergistic organism interactions

A legume rotational crop with wheat could drastically improve soil health, nitrogen and long-term sustainability. The wheat-soybean double cropping system has allowed many farmers in the Midwest to profit from growing winter wheat by production of a late season soybean crop, but breeding efforts have largely focused on improving each crop independently. I intend to investigate the implementation of a legume double cropping system for Colorado using field peas. By breeding both organisms for synergistic combinations well suited for the tight double cropping system, I hope to produce variety pairs that mature early, yield well and sustain adequate soil moisture for the more valuable wheat crop.

While the number of potential wheat-pea genotype pairs is very large and generally intractable, clever testing of select pairs will allow for genomic prediction of unobserved combinations. This is similar to the $G \times E$ problem, where one crop (e.g. pea) can be thought of as an environment to which the genotype (e.g. wheat) is subjected to. In this case, the genetic correlation of genotypes *and* environments would be estimated with genome-wide markers. All pairwise combinations would then be predicted using multivariate linear mixed models. Promising predicted pairs would then be evaluated the following season, and crosses made to further beneficial $G \times G$ interactions.

These synergistic genomic selection models could also be adapted to other goals, allowing for much wider collaborations between animal breeders, microbiologists and soil scientists. Examples include root/soil microbiome using wheat as a model, forage/animal and forage/rumen-microbiome using alfalfa as a model, and even barley/yeast interactions using malting barley as a model. Products specifically improved for one another could be marketed as a package (e.g. maltsters could offer specific yeasts with certain barley malts), or a service (e.g. genotyping a farmers field to determine optimal varieties for their soil microbiome).

Research Philosophy

In the era of big data, a shift away from small designed experiments to large observational studies at the breeding program scale is inevitable. When genotyped and made publicly available with FAIR data principals, the vast amount of data generated in a breeding program becomes a treasure trove for asking questions and informing breeding decisions. Clever experimental design will offset genotyping costs by trading replication at an individual level for replication at the genetic level.

I believe in a collaborative model, where breeding programs do not operate in isolation. They share germplasm, resources, expertise, and most importantly, ideas. I intend to contribute to the collaborative effort at CSU and across the globe to build the foundational capabilities needed to deploy the latest technology for variety development. As climate change progresses, heat, drought, intense storms and hard frosts will be the new norm, and we must work together to help defend our food security through accelerated genetic improvement.

Statement of Teaching

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Plant breeders have traditionally been generalists, combining genetics with a range of plant sciences to identify farmers' needs and turn out products to meet those needs. However, the range of skills required in the field is rapidly increasing. Proficiency in statistics, programming, bioinformatics and machine learning are now expected in addition to the traditional skills in physiology, pathology, agronomy and genetics. As educators, we must update our curriculum to best prepare students for careers in the new era of genomics and digital agriculture.

The widening breadth of the plant breeding discipline may demand multiple paths of instruction. This should integrate a solid plant breeding background with a more structured series of quantitative courses to benefit students seeking specialization. Students who chose this path will finish graduate school with the comprehension and ability to effectively adapt the latest computational techniques to meet future breeding goals. I plan to work closely with the new quantitative genomics professor to develop plant breeding courses that complement the quantitative genomics course material.

Teaching experience

During graduate school, I led several activity-based learning sections as a Teaching Assistant (TA) for an introductory biology course at Cornell, [BIOMG1350](#). As a TA for an introductory plant breeding course, [PLBRG2010](#), I built a pdf based online homework medium, managed the course website, coordinated labs, aided in exam development, and constructed and delivered several lectures. In my third year of graduate school, I was asked by several members of the second year cohort to lead a weekly discussion of a quantitative genetics textbook ([Bernardo, 2010](#)). As a postdoc, I continued to hone my teaching experience and philosophy by co-instructing an advanced graduate-level course on the evolution of genetic modeling in plant breeding, [PLBRG7420](#).

Teaching philosophy

Inclusive teaching tactics are key to ensuring equal access to knowledge in the classroom. Expectations must be made clear, and reinforced throughout the semester so that students do not get behind and fail to meet milestones. It is important for students to be exposed to plant breeding and quantitative genetics ideas from multiple perspectives, and they must be given the opportunity to demonstrate critical thinking on different levels. While some students may show analytical thinking and synthesis on exams, others may shine in more hands-on projects. Most mathematical and computational learning occurs through doing, not watching. The lecture is important to present material in a concise, structured manner, but concepts are cemented when the student reconstructs the ideas on their own time.

Longer term projects provide students the opportunity to practice and apply concepts in a more autonomous environment, and are invaluable for assessing comprehension and critical thinking. Regularly assigned homework and hands-on labs are crucial for evaluating the pace and overall understanding of the material presented. Greenhouse and field facilities on campus provide opportunities to get students out of the classroom to see plant breeding in practice. Public databases provide resources where students can get experience working with real datasets. Computer simulations are useful tools to evaluate comprehension, where in order to simulate a system correctly, the student must understand that system well.

All courses I instruct would contain a term project of relevant complexity to augment exams, in-class labs and homework assignments. For quantitatively oriented courses, these projects would

be computational in nature, where students would use real or simulated data to explore the ideas covered in the course. They would then be asked to present their results in written and oral formats that mirror typical scientific communication. Projects may be team oriented to promote collaborative skills and project management.

Courses

I intend to develop a yearly, introductory undergraduate course in plant breeding to augment an undergraduate quantitative genetics course. This course would target 21st century plant breeding concepts with a focus on the use of genome-wide information to drive decision making. In addition, I intend to develop an advanced graduate course that would be held every other year, focusing on the complexities of crop improvement. Both courses would include a hands-on computational component to reflect the skills currently desired in the field.

The undergraduate course would emphasize how the latest technologies can be incorporated into a modern breeding program. Hands-on labs would be used to augment student understanding of course material through greenhouse mating experiments and computer simulation of breeding programs. Students would use available computational tools to determine optimal breeding strategies based on genetic architecture, logistical constraints and reproductive systems. For the term-project, students will be split into groups, and given a breeding scenario and a dataset. They will determine the genetic architecture of their trait and propose a breeding strategy based on their scenario and what they can learn from the data. By the end of the semester, students will be able to demonstrate critical thinking of plant breeding methods and ideas, with the ability to synthesize when given new plant systems or breeding goals.

The advanced graduate plant breeding course would be based on primary literature review, focusing on complex breeding systems that incorporate genome-wide information, multiple traits with differing genetics architectures and economic values. Students would be evaluated using a gain in understanding approach. This approach would require students to submit responses to questions developed to guide understanding of the reading materials prior to class, with the ability to resubmit revised answers after attending. Concepts and questions would be sufficiently complex that prior effort and in class learning can be assessed.

Curriculum

Currently, most life science students do not acquire in-depth statistics and programming skills until graduate school, impeding their progress while they learn to grapple with these new languages. Moving forward, I would like to work with faculty in SCS, statistics and computer science to build a quantitative/computational genetics undergraduate curriculum. Genetics is a vast field; it is imperative that students get exposure to and training in the rapidly changing environment in which they will soon be seeking jobs. Students in essentially all sub-fields of genetics will need to be able to deal with large datasets, using tailored algorithms to make inferences, predict the unobserved, and guide decision making. Big data management requires skills in programming, linear algebra, statistics and machine learning that must be incorporated into the curriculum at earlier stages.

Genomics and digital agriculture are only just starting to change the landscape of food production. Quantitative skills are one of the specializations imperative in plant breeding, and CSU must be at the forefront of best preparing the individuals who will usher in this new era.

Statement of Diversity, Equity and Inclusion

Nicholas Santantonio

***Note to CSU:** I have spent much time considering these issues. You can find a detailed version of my thoughts and the initiatives I intend to pursue here: github.com/nsantantonio/ColoradoStateQG/blob/master/SantantonioDEIContributionLong.pdf*

Everyone deserves an equal chance to show their potential. Often, it takes the right time, place, person or simply an opportunity to inspire someone. As a high school dropout, it took several tries for me. I struggled through the first two years of my undergrad at New Mexico State (NMSU), failing to meet a 2.0 GPA by the end of my fourth semester. With the help of several professors at NMSU and continued support from my family, I found a passion for genetics during my third year and everything changed.

How can I provide adequate support and opportunity to help create that spark in those far less privileged than I? As an educator, I can work to create opportunities for students from underrepresented groups to pursue further education and expose students to different cultural perspectives in and outside of the classroom. I can take active measures to include students as part of a healthy lab culture, where expectations are clear and everyone is given equal opportunity to succeed in their own pursuits. Importantly, I can continue my own education into diversity, equity and inclusion (DEI) so that I can adapt my own efforts to better serve the community.

I have worked toward learning about, and engaging in DEI concepts and initiatives to further my understanding and to help me become a better ally. To actively engage in increasing the diversity of graduate students in the plant sciences, I joined the Diversity Preview Weekend at Cornell as a co-leader, currently serving as fundraising chair. I have attended several workshops on the hidden curriculum to learn how I can identify and help shed light on the unspoken expectations in academia that may be foreign to those unfamiliar with the academic environment in the US.

It is important that we recognize the need for education in DEI concepts and ideas. To enact societal change, individuals need to be willing to be taught and engage in the conversation. During this learning process many will make mistakes, including me. Mistakes are okay! As long as we learn from them and strive to better ourselves and our understanding of and compassion for others. It is paramount that we cultivate an environment where people can learn, practice and ask questions about DEI concepts without fear of retribution if they misstep.

As faculty, we must educate ourselves on how to provide an inclusive environment and work to make resources equally available and expectations clear. We must reevaluate our own practices and implicit biases to ensure we have not unintentionally created an inequitable or exclusive situation. The curriculum needs to be built to reflect of the breadth of diversity, such that students recognize a bit of themselves, their culture or contributions that were made by people they can relate to. To address these needs, I want to work to develop a series of DEI related requirements for faculty, staff and graduate students, and engage with the community both on and off campus. Details of initiatives I aim to pursue can be found [here](#).

The most effective teams with the best ideas come from diverse backgrounds and experiences. Women, minorities, LGBTQIA and members of other underrepresented groups continue to face less opportunity and numerous obstacles, especially in STEM. Unfortunately, this has lead to a lack of perceived academic “merit” by some, when these differences are purely environmental in nature and driven by legacy and current social biases. I am committed to helping reverse these trends by building a diverse team and an environment in which everyone is valued and given the resources and opportunities they need to succeed.