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Filling the Knowledge Gap: Integrating Quantitative Genetics and Genomics in Graduate Education and Outreach

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ABSTRACT: The genomics revolution provides vital tools to address global food security. Yet to be incorporated into livestock breeding, molecular techniques need to be integrated into a quantitative genetics framework. Within the U.S., with shrinking faculty numbers with the requisite skills, the capacity to train professionals with such expertise is at risk. Those same proficiencies are also necessary to guide adoption of genomic-enhanced tools within animal agriculture. A solution is to share resources across academic and research institutions, and industry, to deliver high-quality instruction to a broad audience. Here we describe two such collaborative efforts – an across-institutional graduate curriculum and a joint university, USDA and beef cattle industry training project – that use innovations in educational and outreach programing to prepare professionals in genetics and genomics. Only through such partnerships, will genomic technologies be fully integrated into livestock production.

Keywords: graduate training; outreach; quantitative genetics; genomics; distance-delivery; partnership

Introduction

The genomic revolution offers tremendous opportunity to address global food security and health. The increasing availability and use of high density genomic-arrays is generating tremendous amounts of data on individual animals, allowing clearer delineation of heritable differences in production efficiencies and product quality. Yet, such volumes of data also pose technical challenges and only through placing them in a quantitative framework can they usefully and seamlessly be incorporated into farming and food systems.

Over the past 25 years in land-grant institutions in the U.S., focus on quantitative areas of genetics, particularly animal breeding, has reduced sharply as programs have focused on new hires in molecular genetics. Arguably, this degradation in quantitative genetics within life sciences programs was not inadvertent, but in part reflected its cost and perceived benefits within academic units. As an outcome, many faculty members with expertise in this discipline are in the later stages of their careers. Thus, at a time when integrating genomic information with quantitative genetics is imperative, our capacity to train professionals with such expertise is at risk.

This concern was highlighted in the “Blueprint for the USDA efforts in Agricultural Animal Genomics 2008-2017.” In that document, the need to develop a “solid infrastructure … to facilitate advances in discovery science in animal genomics in a timely and cost effective manner” is highlighted. Noting that there is a “dearth of qualified candidates for scientific and technical support positions in the animal industry” and fears that “the critical mass of expertise in animal genomics at colleges and universities across the globe that train these scientists is diminishing at a rapid pace,” a key recommendation of the “Blueprint” is educating students in “genome-enabled animal science” to help prepare our next generation of scientists. Such training must also prepare students to work in interdisciplinary teams, and facilitate them developing strong communication skills.

Clearly, there is a global need for advanced training integrating quantitative genetics and genomics. Yet, with shrinking numbers of faculty with the requisite expertise, providing such instruction is challenging. A solution is to share resources and capacities across-institutions to develop and deliver high-quality instruction to a broad and more diverse audience. The success of such an initiative depends on at least three key elements: (i) a sustainable academic partnership that safeguards the long-term continuity of the curriculum; (ii) a course delivery mechanism that is sufficiently flexible to reach traditional and non-traditional students across wide geographies; and, (iii) an infrastructure that fosters high academic standards and cost effectiveness for participants.

A metric for the impact of such a training program is its capacity to fulfill not only academic but industry needs for individuals with professional skills. The need to seamlessly integrate traditional quantitative genetics and genomics in livestock breeding systems is a current reality. Although clear benefits of this augmentation of data (phenotypic and molecular) have been shown, the application of this in practice has elucidated complexities that require advanced skill sets at the interface of molecular and quantitative genetics. Moreover, the clear communication of science to industry clientele such that the technology is adopted is increasingly needed given the increase in the use of genomic data in selection programs. This need for education and clear communication is most evident in industries where genetic selection decisions are made by numerous individuals. A prime example of such need is found in the current context of the U.S. beef cattle industry.

In the U.S., beef cattle production has a pivotal role in animal agriculture. Moreover, the beef industry differs as compared to other livestock industries in that selection decisions are made at the producer level, and not by breeding companies. As a consequence, there has been large investment in outreach directed toward that industry. We therefore will illustrate the integration of genetics and genomics in training using beef cattle as our example.

From a historical point of view, there have been considerable changes in the arena of beef cattle genomics.

Changes include introduction of new genotyping platforms and the incorporation of genomic information into genetic selection decisions. Considerable focus has been devoted to defining the usefulness of genomic information, and how best to integrate it, in predicting genetic merit. When genomic information was first integrated into National Cattle Evaluation (NCE) by the American Angus Association in 2009, the paradigm was completely different than it is today. At that time the identification of animals included in training was largely unknown, and thus the relationship between them and the target population was also unknown. Furthermore, only molecular scores were returned for use in NCE, with the actual genotypes held by the commercial genotyping company.

In short time, the global understanding of key issues began to penetrate the industry. Retraining, or recalibration, became a necessity, and the beef industry understood that the efficacy of genomic predictors was not robust over several generations. The issue of robustness was also very clear across breeds. For instance, genomic predictors developed in Angus were not useful for prediction in a closely related breed like Red Angus (Kachman et al. (2013)). Consequently, for breeds to capitalize on the benefits of augmenting traditional EBV with genomic information, they must first invest in developing a training population. The choice of animals in the initial training population has been mostly ad-hoc.

Genomic assays, or SNP panels, also changed. The initial "backbone" of genomic prediction was the Ilumina SNP50K assay. The Ilumina High-Density (HD) assay that included approximately 770,000 SNP was later released but did not penetrate the commercial market, likely due to the increased cost and early research results that showed little predictive advantage of the HD assay over the 50K. More recently, an 80K product (GGP-HD; GeneSeek) and a reduced assay (GGP-LD; GeneSeek) have been released. Along with changes in panel density, there has been a considerable evolution in the entity that performs training. Initially, two primary companies performed this service and marketed the resulting genomic predictions: Pfizer Animal Genetics (now Zoetis) and Merial Igenity. Other breed associations desired to own the intellectual property behind the genomic predictions they used and turned to the National Beef Cattle Evaluation Consortium (NBCEC) to perform the exercise of developing prediction equations.

These evolutions, although progressive, have been relatively rapid paced and thus continuing education efforts of both end users (producers) and service providers (e.g., breed associations) relative to methodology and efficacy has been critical. Although traditional outreach mediums have been reasonably useful to increase knowledge and awareness of issues, a more 'hands-on' approach is warranted to increase familiarity of changes in the technology overtime, facilitating wide-spread acceptance and use.

The first objective of this paper is to describe our experiences in developing and implementing a multi-state, Master's-degree level curriculum in quantitative genetics and genomics. This program began in 2007, and is offered primarily by distance-delivery. Our second objective is to describe how such training integrates into outreach efforts designed to increase knowledge and aid in the rate of technology adoption (i.e., use of genomic predictors). We will primarily use the Weight Trait Project, a collaboration between the U.S. beef cattle industry, several universities and U.S. Meat Animal Research Center (USMARC), to illustrate that integration. Lastly, we will describe the challenges and opportunities we foresee to extend these efforts in order to establish a network of educators and outreach specialists that can facilitate the integration of quantitative genetics and genomics into livestock production systems globally.

Graduate training

A sense of crisis. The biological revolution over the past few decades has redefined modern genetics. Society benefits from an ever-increasing understanding of the behavior of genes and their networks. However, the use of such vast information depends on its integration into a quantitative genetics framework, particularly for its routine incorporation in animal selection programs. Yet, within the U.S. land-grant system, this focus on molecular genetics has led to substantial reduction in graduate training in quantitative genetics (Misztal (2007); Lewis et al. (2008); Misztal and Bertrand (2008)).

Sensing a crisis in the making, early in 2005 the NBCEC, along with Virginia Tech and Montana State University, developed a broad strategy to redress this problem. One of its components was to leverage expertise across-universities to develop and implement a Master's-degree level, distance-delivered curriculum on a national (U.S.) scale.

Before undertaking such a large effort, it was considered imperative to ascertain the extent and demand for such a program. Therefore, in 2006, a national survey was conducted to seek input on need and acceptability of an online curriculum for graduate training in genetics. In total, 125 faculty members from 73 universities were contacted, with 47% responding. Most of the institutions (78%) trained graduate students in genetics. However, graduate student numbers were small; the norm for most institutions was 3 to 5 Master's-level (43%) and 1 or 2 doctoral-level (38%) students enrolled concurrently. With stratified start dates for students entering graduate programs, class sizes were even smaller making regular face-to-face offering of courses unsustainable. At least partly as a consequence, 90% of respondents endorsed asynchronous distance-delivery as a method to redress shortfalls in their curriculums (Lewis et al. (2008); Bullock et al. (2010)).

Multi-institutional collaboration. Based on the results of the survey and, as a proof of concept, a 5-week online course in matrix algebra, in 2007 funding was sought and awarded by the USDA Higher Education Challenge Grant program to develop and implement an online graduate curriculum in quantitative genetics. In 2011, additional funding was obtained to extend the content of that curriculum to include genomics.

A key feature of the program has been the establishment of a large and successful collaboration of land-grant institutions to develop and teach the distance-delivered courses. Ten institutions have contributed

(Virginia Tech, University of Nebraska-Lincoln, Colorado State University, Iowa State University, North Carolina State University, South Dakota State University, Kansas State University, University of Georgia, Cornell University and Montana State University), 7 of which are currently offering courses. This partnership has garnered a number of benefits. Individual faculty members have been able to provide instruction in their area of expertise to a wider audience while avoiding unnecessary duplication. With larger course enrollments, the sustainability of course offerings is assured.

Curriculum content. An increasing challenge in designing a graduate curriculum relevant to modern genetics is to define its content. Our philosophy was, and remains, that our online courses supplement, but do not replace, face-to-face graduate training. For instance, our expectation is that graduate course work in the life sciences, including molecular biology, biochemistry, bioinformatics and statistics, is provided at a student's home institution. We therefore focused our course offerings on foundational knowledge in quantitative genetics and associated statistical methods, and their interface with genomics.

The current online curriculum consists of 10 credits of core curriculum and 6 credits of electives. The courses are taught as 1-credit modules offered as a series over 4 academic terms (2 years). Within a term, a student would typically enroll in 1 to 3 core courses, and as many as 2 electives. A list of the course offerings, including syllabi, is provided on the curriculum website (http://enbgeo.iddl.vt.edu/). In addition, 2 non-credit short-courses are being taught every other summer.

The original aim in offering the courses as 1-credit modules was to allow students the flexibility to select among the online courses to fill gaps in offerings at their home university. However, most students complete the entirety of the core curriculum, and several electives. For some students, this curriculum provides their only exposure to formal training in quantitative genetics during their Master's-degree level studies (Lewis et al. (2013)).

Instructional design process. The courses being offered are taught by faculty members from several institutions. Therefore, to ensure continuity in the curriculum delivery, the project team adopted a common systematic process of instructional design (ID). The ADDIE model (Gustafson and Branch (2002); Larson and Lockee (2014)) was used to guide each stage of module development. Those stages are Analyze, Design, Develop, Implement, and Evaluate.

In the first phase of the ID process, Analyze, we explored and refined the educational need. As a component of the national survey, information was garnered on specific topics to include in the curriculum. Another facet of this phase was to identify the specific knowledge and skills that learners need to be successful. An entry-level quiz has been used to identify students' prior knowledge of quantitative genetics when they begin the curriculum. Defining a single starting point appropriate for all students has proven challenging, as their backgrounds have proven quite variable depending on the student's undergraduate experiences. As a consequence, an introductory course was added to the curriculum to assist students in their transition to Masters-degree level training in genetics.

The Design phase has centered on the instructional planning aspects of ID. An instructional development coordinator has worked with subject matter experts to identify specific learning outcomes for each module, and to create corresponding assessment instruments to measure those outcomes.

As part of the Development phase, subject matter experts have planned and created instructional materials using distance-delivery technologies. Adobe Presenter and Camtasia software have been used to record voice narration to accompany visual materials developed in Microsoft PowerPoint. The resulting instructional presentations have been incorporated into a course website for each module, all of which have been housed within Virginia Tech's open source course management system, Scholar. Using a common web management system has facilitated seamless student access to course materials across universities and a consistent blueprint for the modules.

During the Implementation stage, the modules have been pilot tested by graduate students from various institutions across the U.S. Each project team member responsible for developing course content has also been responsible for its implementation, for interacting with the enrolled students, and for assisting in collection of formative student evaluations.

Evaluation has been conducted throughout the earlier stages of the ID process. Formative student evaluation has occurred during the development and implementation of the modules. Instructional, technological, socio-psychological, and logistical aspects of each module have also been evaluated by an ID expert to ensure the most effective design for the final curriculum. Each module has also been reviewed by at least two content experts, one internal and one external to the project, to ensure the quality and rigor of the course materials. Based on formative feedback from students, and the expert reviews, the modules have been revised prior to their subsequent implementation, thereby completing all stages of the ADDIE model.

By using this formal instructional design process, we have tried to ensure that the content and structure of this online curriculum provides high-quality and dynamic graduate level training.

Organizational infrastructure. Currently, the online curriculum is supported by a USDA-NIFA grant. However, once that funding ends, an organizational infrastructure will be necessary to continue the program. That infrastructure is currently being established through collaboration with AG*IDEA, an affiliate of the Great Plains IDEA. The Great Plains IDEA is a collaborative project supporting internet-based programs.

Academic programs are the core of the AG*IDEA Alliance. Each member institution awards academic credit and degrees for programs in which they participate. Curricula are developed by inter-institutional faculty teams and institutions choose the programs with which to affiliate. All courses and curricula receive full institutional review prior to implementation and meet institutional academic standards. Students seek admission to the Alliance member institution of their choice and institutional admissions standards and processes prevail. Assessment of instructional program quality and student learning outcomes are coordinated centrally by the Alliance.

Using this structure, our aim is to offer a separate program in quantitative genetics and genomics within the AG*IDEA portfolio. The successful integration of this curriculum into AG*IDEA will be key to its long-term continuity.

Impact. The success of providing graduate-level training in genetics and genomics on a national scale through distance-delivery can only be measured by its impact. The evidence thus far is encouraging. During the most recent academic year (fall 2012 and spring 2013) enrollment in the curriculum has grown nationally, and even internationally. Sixty-four individuals from 22 U.S. and 5 international academic institutions completed as many as 8 of the modules offered; 12 of these students completed the entirety of the curriculum. Three of the students were enrolled in a historically black university. Four of the participants were in industry or professional positions. In total, 199 credit hours of instruction were completed, which was twice that of the previous year. Between 6 and 24 students completed the individual courses offered. Those counts are between 2- and 6-fold that of graduate student numbers in this discipline at a majority of individual universities.

As a broader summary of the overall impact of this initiative, from fall 2007, when the curriculum was started, through spring 2013, 179 students from 31 universities across the U.S. (Figure 1) have completed 636 course credits. Course enrollments have varied from 6 to 31, with as few as 1 and as many as 6 students from an institution completing a given course. Furthermore, many participants have mentioned such coursework would otherwise be unavailable to them without this curriculum

Anonymous student feedback on the content and structure of the courses has been overwhelmingly positive. As an illustration, students who had completed the curriculum have stated: "As a distance learner, I got practice on not only lecture contents, but also communication skills"; "My overall experience was very positive. The curriculum helped me quickly learn concepts and skills that would have been difficult to learn on my own"; "I think the instructors did a good job and the courses were a success ... An expansion of offerings and spreading more course material and assignments out over a longer period of time would be beneficial, in my opinion."

As a key outcome, this curriculum has provided a high quality, customized program to fulfill academic and industry needs for individuals with professional skills in quantitative genetics and genomics. Importantly, that knowledge base is central to the application, and outreach, of genomic technologies in commercial animal agriculture.

Outreach

Educational delivery overhaul. The traditional vehicle for outreach has been face-to-face delivery of educational and written material. These delivery approaches are generally targeted towards increasing knowledge and awareness. Unfortunately, despite decades of effort using these two traditional approaches to outreach, little has been accomplished relative to attitude and behavior changes. Survey results suggest that upwards of 70% of U.S. beef cattle producers in the commercial sector do not utilize EBV as their primary selection criterion (e.g., Weaber et al. (2014)).

Using the thesis that current adoption of fundamental genetic selection tools by bull buyers is archaic, and that traditional means of outreach has not been able to penetrate the beef industry such that behavior changes have occurred, a new approach was needed in order to ensure technology adoption of emerging tools like genomics. A hands-on approach where beef cattle producers could 'learn by doing' was clearly needed to augment traditional outreach vehicles. Moreover, this approach lends itself to training beef cattle producers and breed association personnel to be effective educators themselves. The latter point is critical given the general lack of outreach personnel that are trained in quantitative genetics/genomics.

Integrated effort. In 2009, an integrated effort between the NBCEC, the University of Nebraska, and the 7 largest beef breeds in the U.S. (Angus, Hereford, Red Angus, Charolais, Gelbvieh, Limousin, and Simmental) was initiated in an effort to develop an educational program centered on genomics and to build a resource population for the development and evaluation of genomic predictors and related methodology. These 7 breed associations 'nominated' seedstock producers (n=24) in the Northern Plains region of the U.S. to participate in the project. Initially, producers agreed to provide hair samples on all 2009 born bull calves. These animals were genotyped with a reduced assay for

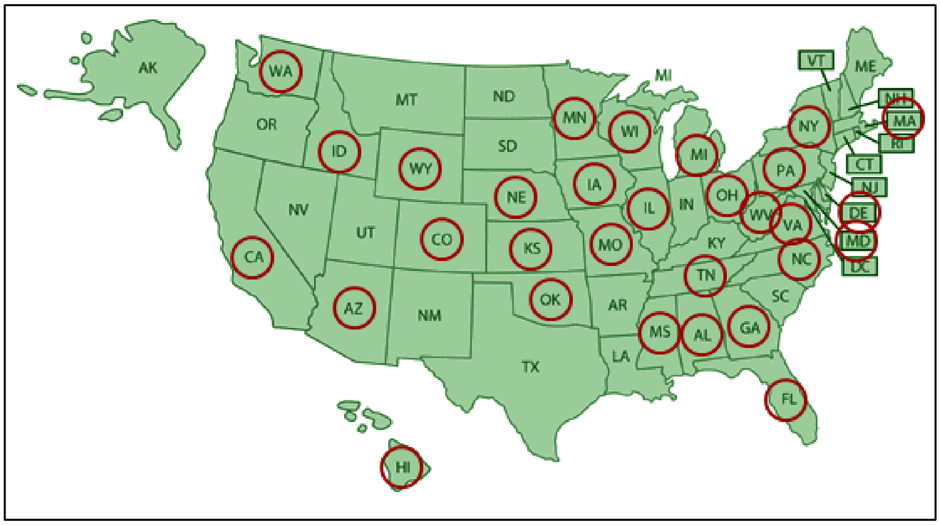

Figure 1: States with universities and colleges with students enrolled in the graduate curriculum.

weaning weight and post-weaning gain. The SNP discovery for this reduced assay occurred in the Cycle VII population at USMARC. Given the early focus on weight traits as proof of concept, the project was named the Weight Trait Project (WTP).

In subsequent years, producer-owned herd bulls were genotyped with the SNP50K, and molecular breeding values (MBV) and marker-assisted EPD were provided back to producers for growth and carcass traits. The MBV were trained using currently available genotypes in the NBCEC database using both within-breed training sets and across-breed training sets. All genotypes generated were provided to the respective breed associations to aid in the development of training sets that would eventually be used to generate MBV that were included into NCE.

Currently, this collective resource (producers and data) serves as the field demonstration project for the integrated USDA-NIFA project entitled "National Program for the Genetic Improvement of Feed Efficiency in Beef Cattle". In this capacity, the seedstock producers have provided semen from herd bulls that was used to inseminate commercial crossbred cows at a large commercial ranch or crossbred cows at USMARC. The resulting progeny were individually fed to garner feed intake data and genotyped with the BovineSNP50K assay. This resource will ultimately serve as a mechanism for industry-based evaluation of research outcomes.

Educational products and evaluation. As part of the WTP, a two-day meeting has been held annually at the USMARC, with the first day focused on short (approx. 20 minute) presentations accompanied by brief (2-page) handouts. Talks on the first day of the meeting have focused on the current status of genomic selection in beef cattle, novel trait discovery and, in more recent years, considerations related to selection for improved feed utilization. All talks have been recorded and posted at www.beefefficiency.org. All attendees of the first day meeting were asked to complete an anonymous survey indicating levels of knowledge gained and any likely behavior changes as a result of the presentations. They were also asked to provide an indication of numbers of beef cattle they owned or for which they directly influenced management decisions. On the second day, activities centered on project aims and results, and upcoming project activities. This forum allows for direct industry feedback from progressive seedstock producers and breed association personnel related to the direction of genomics research and issues of technology adoption.

Impact. The impact of an outreach program is best evaluated by changes in behaviors and practices of targeted producers and the industry at large. Of the 7 beef breeds represented in the integrated project, all but one have implemented genomically-enhanced EBV. The WTP arguably aided in developing the framework for these breeds to develop a training population and empowered group of seedstock producers to educate their peers relative to the advantages of genomic selection.

A survey was conducted by Spangler et al. (2011) to gauge changes in knowledge, practices, and behavior; the survey was sent to participants in the WTP. The 17 respondents indicated that collectively they own 20,125 beef cows. Increases in knowledge were rated from 0 (none) to 4 (significant). Mean survey results were 1.5, 2.8, 2.0, 3.4, 2.4, 2.7, 2.8, and 2.9 for EBV, genomics terminology, parentage verification, marker assisted selection, across breed genomic predictions, whole genome selection and panel development, test validation, and accuracy improvement of EBV, respectively. Producers indicated adoption of methods to improve the following production practices: making mating decisions (40%), efficient use of DNA technology (75%) and selection (bull buying) decisions (47%). Mean responses for changes in behavior (1 = none; 5 = very likely) were 3.9, 3.8, 4.3, and 4.6 for making more informed selection decisions, better educating their clientele, feeling comfortable with terminology, and desiring to stay abreast of DNA technology, respectively.

A critical outcome of this integrated project is the development of a forum for researchers, breed association personnel, and seedstock producers to continue a dialogue regarding genomic technology, implementation methods for genomic selection, and discovery for novel traits.

Challenges and Opportunities

A common concern within academic institutions is the robustness of distance-delivered courses and curricula. There is a perception that student learning and engagement is dampened (Allen and Seaman (2011)), which can impact the ambience of the critique of online courses during the governance process. When faculty members from outside institutions are the named instructors for distance course offerings, anxieties heighten. There is no easy solution to address these concerns. Our approach has been to engage faculty members with solid reputations in their specialty areas as instructors. Our courses are developed using established guidelines for ID, and undergo independent ID and expert content review. Student feedback is collected routinely and helps inform course revision. Through these processes, we believe we have established a high quality curriculum that fills an important and otherwise unmet need for graduate-level training in quantitative genetics and genomics in the U.S.

A particular challenge for an across-institutional curriculum is establishing a robust infrastructure to support faculty member and student participation (Hanna (2013)). Beyond the governance process, other administrative (e.g., course enrollment, grade transfer) and financial (e.g., differential tuition rates among institutions) complexities inherent to a multi-state alliance introduce obstacles to such initiatives. Overcoming such obstacles depends on a willingness among faculty members and administrators alike to 'buy-in' to the opportunities such innovations can offer as part of a diverse portfolio of educational programs that an institution can offer.

Furthermore, we simply cannot afford to allow a hiatus in training in quantitative genetics to occur. As noted by Bullock et al. (2010), in the land grant system in the U.S., each state has an agriculture college with the mission of research, instruction and outreach. Most students with an agricultural interest within that state will matriculate at that institution. If there are no quantitative geneticists on the faculty, there is a void in the students' education in this discipline. As a consequence, there is risk that students with enthusiasm for quantitative genetics will lack encouragement or opportunity to pursue that interest. Even at institutions with small quantitative genetics faculties, challenges remain with regards to graduate training. It is difficult for 1 or 2 faculty members to provide graduate students with a balanced, diverse quantitative genetics education. Recruitment is thwarted, affecting the dynamics of every aspect of a faculty member's program.

Successful technology adoption in a diverse, segmented industry such as beef cattle requires well educated outreach personnel and novel approaches to effectively create behavior changes in learners. Those students who aspire to work closely with a livestock industry towards education in the arena of quantitative genetics and genomics, either employed by a university or in the private sector (e.g., breed association), need to be trained in the same fashion as those students who desire to teach in the classroom or conduct basic research. A fundamental core knowledge base is critical in order to inform an industry of how to best utilize emerging genetic selection tools. Without a global infrastructure for graduate education in quantitative genetics and genomics, there will be a correlated failure in the rate of technology adoption by livestock enterprises due to a lack of expertise in implementing research results.

The opportunity to redress this dilemma is through collaboration. By sharing knowledge and best practices through a national, even global, educational network in quantitative genetics, geographical distances become much less relevant. The premise of a critical mass, just like our notion of modern genetics, can be redefined. It simply requires the collective will to embrace new educational and outreach approaches in the same way as we have embraced genomic technologies.

Conclusion

Innovations in educational programming have afforded unique strategies for institutions of higher education to address the national knowledge gap in quantitative genetics. Land grant institutions, such as those described herein, have demonstrated the benefit of sharing information, expertise and resources in creative and collaborative ways. The formation of partnerships among institutions, and between industry and academia, are key factors in preparing the next generation of professionals in animal genetics and genomics. Only through partnerships among academic and research institutions, breed associations and commercial industries will the evolution in genetic technologies be fully integrated into animal agriculture systems. Our collective responsibility to meet global needs for food security and health necessitate such collaboration.

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