EDITORIAL

Shortage of quantitative geneticists in animal breeding

More and more I receive phone calls from various breeding companies looking to hire a PhD in quantitative genetics. They inquire if I know of a graduate versed in quantitative genetics and mixed models, with some programming skills, who can speak and write passable English, has a general understanding of markers and molecular genetics, can run and troubleshoot a genetic evaluation, and in general be a problem solver. I do not know of anyone available, I reply. There were many of them 10–15 years ago, but now they are rare. If they show up, they usually have very good offers well before graduation. My colleagues outside the USA are telling me of similar problems, although the severity of the PhD shortage is country dependent.

Why are PhDs in animal breeding with quantitative skills rare in the USA as well as in many other countries? Some 15 years ago there was a shift in governmental funding away from animal breeding and quantitative genetics to almost exclusively molecular genetics. Universities liked grants in molecular genetics because they were large (including equipment and lab supplies) and carried a large overhead. By contrast, grants in animal breeding areas were usually much smaller and often carried no overhead. Subsequently, enrollment in graduate programs for animal breeding/quantitative genetics shrunk, faculty who retired were not replaced, and many programs that survived lost the critical mass necessary to provide adequate graduate student training. Another factor was the greater allure for graduate students of finding major genes than of assuming 'black box' genetics, especially as the latter requires extensive training in quantitative genetics, statistics, and programming.

In the early 1990s, the major traits selected were production traits. Now, big challenges lie in developing selection tools for secondary traits, such as fertility, longevity, mortality, susceptibility to diseases, etc. Other challenges are selection for different environments, cross-bred performance, and in general, for more robust animals. Recently, the topic of heat tolerance became fashionable as global warming became accepted as a fact. An animal that is very profitable most of the time but dies under short-term stress may not be profitable after all.

Great hopes were put into finding markers for major genes (QTL) that could help solve the new challenges. Based on many association studies, there is growing consensus that few markers/QTLs can be detected, those that were detected had their estimated effects inflated, and that the benefits of using markers are limited. Of all markers found, very few were for low-heritability traits.

The new trend in animal breeding is genomic selection using SNP chips. In this methodology, one estimates effects of individual haplotypes, and genomic EBV (GEBV) is estimated as a sum of those effects. No effort is made to identify QTLs. The genomic selection is based on an assumption opposite from the previous effort in markers but the same as in 'black box' genetics: that a large number of genes are responsible for a trait.

When only a small fraction of the population is genotyped, the estimates of haplotype effects will be derived via EBV obtained through classical methods (CEBV). Poor CEBV would mean poor GEBV. Moreover, there may be more than one GEBV desired for one trait, e.g. if G × E is present or crossbreeding is involved. Subsequently, data collection and good 'classical' evaluation are as important as ever.

At first glance, it may appear that nearly all research associated with the genetic evaluation has already been carried out. For those who conduct research with real datasets, this notion is far from true, especially for secondary traits. Look for examples in the complexity of analysis of fertility in dairy cattle with all the issues of censoring (truncation and random), different types of services (heat detection or some form of synchronization), seasonal effects including delays of breeding, etc. Or analyzing calving ease, gestation length, and stillbirth, where the relationships are nonlinear. Or look at dynamics of a national evaluation where, because of ongoing changes in management, the evaluation systems no longer fulfill consistency checks (e.g. inter-bull compliance rules). Similar examples can be found in beef and pig traits. In general, obtaining accurate breeding values, especially for secondary traits, requires good understanding of the traits involved and sometimes the use of complex models. Many of such models cannot be implemented with

the available software, and many of them still require theoretical developments at the quantitative level.

The future is bright for well-trained quantitative geneticists who can adapt to new challenges; however, in many countries they are disappearing. There is still time for funding bodies to recognize an impending shortage, tap into the slowly disappearing infrastructure for training, and take action. Countries without an adequate supply of quantitative geneticists will be forced to outsource their genetic evaluation and perhaps even their breeding programs. They also may be denied some of the potential payoffs of genomic selection.

Perhaps, the final product of genomics will be a model of an animal involving at least a few hundred genes that describe dynamics and complex relationships among traits within the animal. Perhaps computer simulations will be able to look at changes in the phenotype under pressure from a variety of environments and challenges, and find genotypes useful for each environment. Perhaps, we will find a machine that creates an embryo given the genotype. Such a scenario is possible, though not anytime soon, and I bet that such a model will involve quantitatively-trained geneticists.

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