EDITORIAL

Resemblance between two relatives – animal and plant breeding

Animal and plant breeding trace back to common roots and are built on the same theoretical principles. Mendel's laws of inheritance and the concepts of evolutionary biology postulated by Charles Darwin are the main scientific basis on which both disciplines operate. The statistical concepts of biometry and quantitative genetics introduced by Francis Galton, Karl Pearson and Ronald A. Fisher paved the way for addressing the selection of plants and animals in a formal way. Since that time, the theoretical basis of breeding has constantly evolved. This has by no means been a continuous development, but has happened in discrete developmental waves often triggered by the introduction of a novel technology such as the adoption of hybrid breeding in maize in the 1930s, artificial insemination in cattle in the 1960s, the implementation of best linear unbiased prediction of breeding values in cattle in the 1980s or at the same time the production of fully homozygous doubled haploid lines in cereals. Thus, while the conceptual fundament of breeding has remained largely the same across species, theoretical concepts and breeding schemes have diverged heavily depending on the availability, practicability and usefulness of different breeding technologies and methods.

So how related are animal and plant breeding today? Both disciplines are engaged in the genetic improvement of complex, highly polygenic traits. The common goal is to maximize selection gain per unit time and budget spent for numerous target traits on condition that sufficient genetic variance is maintained. Exploitation of heterosis and rigorous improvement of base populations through recurrent selection is shared by some breeding programmes but not by all. However, the demarcation line does not run between animal and plant species but rather is determined by specific features of the respective livestock or crop such as the number of progeny that can be produced per female per year (e.g. varying from one in cattle and horse to few hundred in chicken) and the mode of reproduction (e.g. autogamy or allogamy and seed or vegetative propagation in plants). Thus, in some cases, theoretical concepts underlying individual breeding programmes might be more similar across than within the animal and plant kingdom.

But still, animal and plant breeding do exhibit clear differences. In many plant species, genetically identical individuals can be produced in large numbers as inbred lines, hybrids or clones. As a consequence, phenotypic data collection is generally conducted in well-designed experiments repeated over locations and years. In most animal breeding programmes, phenotypic data come from the production farms, so the possibilities to impose structured designs are limited. Thus, in animals, the development of methods and tools to analyse large scale, highly unbalanced data has been emphasized, leading to the BLUP paradigm with most efficient numeric implementations. In addition, much effort has been spent on developing appropriate models for different kinds of complex phenotypes, such as discrete, highly multivariate, longitudinal or survival time data. In some plant breeding programmes, mixed-model-based theory has been adopted and proved highly useful in the analysis of genotype-environment interaction and the prediction of hybrid performance, but until recently it has not attained the recognition it deserves. The inherent conceptual differences in animal and plant breeding programmes have even led to a different interpretation of basic quantitative genetic parameters. While in animal breeding, the focus is clearly on additive genetic variance, non-additive components such as dominance and epistatic variance often are of negligible magnitude and thus are generally treated as nuisance parameters if modelled at all. Trait heritabilities are generally reported as narrow sense heritabilities and are strictly defined at the level of individuals derived from a random mating population in a given environment. Plant breeders generally report broad sense heritability estimates based on progeny means. Thus, heritability in plant breeding is a function of the type of population and the experimental dimension in which it has been estimated.

The advancement of new breeding techniques has also contributed to the divergence of animal and plant breeding, which both have highly effective biotechnological toolboxes. Cell and tissue culture as well as *in vivo* haploid induction techniques are nowadays fundamental components of many plant breeding programmes. They allow the targeted production of completely homozygous individuals and

in combination with contra season nurseries a significant shortening of generation interval. In animal breeding, artificial insemination, embryo transfer and recently sperm sexing have become technologies of practical importance in some of the major farm animal species. Transgenic technology is available and fully implemented in a number of crops, while there is not a single example of the successful implementation of a transgenic animal in a food production context. In plant breeding, molecular markers became important during the 1990s for diagnostics, analysis of germplasm diversity and early selection of individual genes or quantitative trait loci (QTL), but have gained practical importance in animal breeding only for the selection of a handful of qualitative genes. The growing importance of biotechnology has had not only a strong impact on the direction of breeding research and development but has also led to a reform of university curricula in both fields. Increased emphasis has been put on molecular and biotechnological methods at the expense of quantitative genetics and selection theory. Consequently, the common grounds of the two disciplines in research and training have dwindled slowly.

So what is it that makes animal and plant breeding converge again? Large-scale genome discovery has become possible for many animal and plant species. Even though the genomes of animals and plants are very different in terms of genome size, stability and diversity, similar challenges have arisen from the wealth of data that has become available through next-generation genotyping and sequencing techniques. Both disciplines face the need to resort to big data science. Within the context of genome-based prediction, the new technologies have brought about the 'large p small n' problem. It can be addressed within the mixed-model framework that has a long, successful tradition in animal breeding. The same is true for Bayesian methods and semi- and nonparametric methods that build upon the substantial body of theory and practical experience generated in the animal breeding community over the last decades. Plant breeding has profited immensely from these developments. However, many research questions are still to be answered in the context of genome-based prediction and are similar for many animal and plant breeding programmes, such as prediction in structured populations and prediction of hybrid performance. Thus, the strength of both disciplines should be united to jointly tackle these research questions and develop and apply most efficient genomic selection concepts and tools.

Beyond the prediction of phenotypes, genome discovery opens many avenues to address questions that quantitative geneticists have always shared, whether they are working on animal or plant species. What is the true architecture of genomes and traits? How important are gene–gene, gene–environment and gene–trait interactions? What are the actual mechanisms underlying genetic progress, inbreeding depression and heterosis? During the last decades, we have learnt about trait architecture, selection and genetic phenomena from model species such as yeast, *Drosophila* and *Arabidopsis*. Along the same lines, an exchange of knowledge and expertise between animal and plant breeding has the potential to generate deeper and more general insights than can be achieved within either of the two disciplines alone. While within a discipline, certain concepts are widely accepted as dogmas and hardly reflected anymore, such concepts are challenged in cross-disciplinary collaborations and need to be reconsidered and justified. A still small, but growing number of scientific publications applying the same innovative methods to animal and plant breeding data demonstrate that the border between the two disciplines is starting to get porous.

The genomics era has only just begun and has already started to pose substantial challenges to animal and plant breeding research and practice. To meet these challenges, interdisciplinary networks and collaborations have the potential to build more critical mass, to foster intellectual cross-fertilization and to train a next generation of breeders with a broader scope and deeper knowledge. Animal and plant breeding, being identical by descent and in many aspects alike in state, will mutually benefit from such collaborations.

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