

Animal Breeding Genomic Selection for Improved Animal health: A review of challenges and opportunities in Zimbabwe

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January 4, 2021

Introduction

Demand for animal protein is set to increase dramatically over the next few decades (FAO, 2002; Alexandratos and Bruinsma, 2012). This represents a significant challenge in terms of increasing productivity against a backdrop of reducing resources including land and water. It will require the application of many different technologies including genetic improvement (Ludu and Plastow, 2013). Whilst the largest cost of production is associated with feed, another significant element is the impact of disease. The cost of disease may be underestimated due to its multifactorial nature and the relative success, at least in the developed world. Bush et al., 2011 state that the role of genetics in improving animal health will become increasingly important as focus increases on tackling antimicrobial drug resistance.

Technological innovations have been drivers of social and economic change. They have played a pivotal role in enhancing the quality of life and the safety of animals and humans. In the last four decades there has been an unprecedented surge in the development of biotechnology in animal production and health, with gene-based biotechnologies becoming most prominent in the last decade. While the vast majority of these technologies has been developed and utilized in developed countries, they have the potential to alleviate poverty and hunger, reduce the threats of diseases and ensure environmental sustainability in developing countries. Some of the technologies have a long history of successful use, others have been used with varied success, and many more are at different stages of development and commercialization.

In selective breeding, the potential of individuals to transmit good genes to the next generation is estimated (i.e. their breeding value is calculated). With genomic selection it is possible to estimate an animal's breeding value quite accurately without the need for own performance or performance of large number of offspring. Modern breeds of livestock differ markedly from their ancestors as a result of breeding strategies. For example, milk production per cow has increased among Holstein dairy cattle. Similarly, breeding programs have resulted in lean, fast-growing pigs (Notter., 1999). Chickens from modern breeds each produce more than 250 eggs per year, approximately double that produced in 1950, again mainly due to genetic selection. Currently countries that are following genomic selection are United States of America, Canada, New Zealand, Netherlands, Australia, Denmark, Sweden and Brazil. Benefits of genomic selections have well been demonstrated in developed countries that include reduced generation interval accuracies of above 70% have been reported for young genomic proven bulls, higher rates of genetic gains. Genomic systems in developed countries are characterized with large reference populations, collaboration among countries, well defined phenotypes but mostly within pure breeds

Overview of Genomic Selection in Zimbabwe

Animal production is likely to grow in both the developed and developing countries. To meet future needs, genetic and genomic improvement of animals must increase. Agriculture currently contributes about 6

% to the gross domestic product (GPD) and ranks third after mining and tourism in the economy of Zimbabwe. Livestock are estimated to contribute about 19% to the agricultural GDP. This is in contrast to 45% contribution in highly developed economies, clearly indicating a production gap. About 66% of the population derives its livelihood from agriculture, with 40% doing so from the livestock sector. Rural farmers have an average of 1-4 beehives for subsistence, with a few commercial producers with up to 300 beehives. Production by most smallholders is largely for home consumption. Production is estimated at 150 tonnes annually, leaving a 60% unmet demand, especially by pharmaceuticals firms and supermarkets. As a result, this gap is met by imports from Zambia, Malawi and South Africa.

Variation among individual animals is caused by genetic and environmental differences. If one considers all the different breeds of sheep and goats and various strains within breeds one can conclude that there is a wide variation in performance traits for o small ruminants. All traits provide a high selection potential. There is much greater potential for increasing both biological and economic efficiency of lamb and kid production through genetic improvement. Such potential depends on the magnitude of genetic parameters for the traits of economic importance. Selection for traits of economic importance has not been exploited fully in small ruminants. This is well illustrated with Matabele goat. In Matabeleland South and North provinces there are differences in the Matabele goat in terms of horns and ears. This is so conspicuous that one can categorize them into local area strains. There are Matabele goat strains of Gwanda (Tuli), Kezi, Plumtree Ntabazinduna, Beitbridge and Mbembesi districts. Similarly this can also be said of the Mashona East African type of goat and the Save sheep of Zimbabwe.

The Zimbabwe Herd Book was established by an Act of Parliament in 1980 to oversee the registration of pedigree livestock. Stud breeding involves the controlled mating of livestock and detailed birth notifications of progeny with parents are recorded with the Herd Book. In addition, stud breeders record the fertility, survival and growth performance.

Livestock production depends on three pillars: genetics, health and husbandry. Stud Breeding - genetics - is the cornerstone of commercial livestock production. A strong commercial industry is dependent on a healthy and vibrant stud industry to offer stud/breeding stock that meet requirements in a range of production environments and market scenarios. At its annual National Sales, all animals on offer have undergone veterinary examination and inspection so that the livestock industry is offered a wide range of top-quality genetics. Stud breeding is a long-term passion where breeders strive to breed the 'best' animal. Breeders apply modern breeding technologies to carefully select animals to be parents of the next generation and in so doing, improve the genetic merit of future generations.

Breeders also select parent material from outside the country in the form of live imports, semen and embryos. Stud breeding also requires the meticulous recording of parentage (pedigree) as well as specific performance data that measures reproduction, survival and growth. These performance figures, together with the parentage information, are used to select the best animals to be parents of the next generation. Genetic improvement is therefore passed on from generation to generation and from the stud herd to the commercial herd.

ZHB has recently implemented Breed Plan, the leading performance evaluation software from Australia. The industry can now avail itself of the latest technologies that provide both breeders and commercial producers with accurate genetic assessment of animals that are selected for breeding purposes. A wide range of genetic material is also available for commercial producers who want to select the best breeds and breed combinations to meet their particular production environments. It is more economical to select the right breed for a particular production environment than adapt the environment to meet the requirements of the breed.

In Zimbabwe, Pure breeds of Tuli, Nguni, and Mashona cattle are available but there a very few breeders registered with the Zimbabwe Herd Book. No performance recording scheme has been developed for small ruminants (sheep and goats) in Zimbabwe. The Zimbabwe Herd Book (ZHB) records ancestry of all recognized livestock breed societies. Almost all major small ruminant (sheep and goat) breeds have registered breed

societies. Breed societies were founded for the purpose of establishing breed purity by recording ancestry and defining the standards towards which selection should be made. Identification of sheep and goats is done by individual farmers. They also record ancestry. There is a need for a national performance recording scheme in small ruminants. This should involve data collection by participating farmers or a responsible agent and submission to a data processing centre. The data should be analyzed at the centre to obtain estimates of breeding values of tested animals. These estimates are returned to the farmer and form the basis of selection within, and between herds. Farmers can have selection programmes on their farms and also make informed decisions when buying breeding stock; focus on traits of economic importance taking into account the age. To have a huge impact, selection needs to be done at a large scale hence clustering, forming cooperatives and swapping animals can be helpful. This approach also decreases inbreeding that characterises the small -scale sector. Records and information are critical in breeding and selection together with some infrastructure.

Application of modern genomic breeding technologies in African livestock

Rapid improvement of African livestock productivity can benefit from current modern breeding technologies but many limitations abound (Eveline et al., 2019). Some breeding programs that have been implemented for genetic improvement of livestock in Africa and the challenges faced shall be highlighted below.

Livestock in the African continent are highly adapted to the prevailing environmental conditions characterized by heavy disease burden and marginal feed resources, but with marginal productivity because they are still largely unselected. African countries can benefit from genomic selection because it could be done even without pedigree information which is essential to traditional best linear unbiased prediction (BLUP)-EBV and the selection of candidates does not necessarily have to be based on trait records (Eveline et al., 2019). The potential to generate GEBV using molecular information makes genomic selection a very attractive alternative to improving livestock in developing countries where adequate phenotypes and pedigree records are lacking. Genomic breeding has been reported to be more accurate than traditional BLUP because genomic relationships are more accurate than pedigree relationships (Meuwissen et al., 2016). Moreover, understanding of the fundamental genetic mechanisms influencing traits can be useful for setting up priors for (genetic) variances to increase the accuracy of genomic selection. Several successful approaches have been introduced such as BLUP| GA (BLUP-given genetic architecture; Zhang et al., 2014) or BayesRC (which adapted BayesR methods) incorporating prior biological information in the analysis by defining classes of variants likely to be enriched for causal mutations (MacLeod et al., 2016) or single step GBLUP with prior information (Fragomeni et al., 2017). These methods can be particularly useful for genomic selection in Africa with some prior biological knowledge of traits obtained from studies in the populations and other populations. Using genomic selection, Pitchford et al. (2017) concluded that heterozygosity effects were substantial for reproduction and growth in a tropically adapted composite beef program.

The high enthusiasm about the potential application of genomic selection in African countries is immediately dampened with the reality that animals are held in small populations and in many small holder units. Furthermore, male animals that drive the genetic gain are often sold to generate income for farm families. These caveats can be overcome by the formation and practice of communal management and breeding systems.

Lack of phenotypes recorded in accurately defined contemporary groups is one of the constraints to the implementation of genomic selection in Africa and many developing countries (Burrow et al., 2017). Acquiring the genomic information for genomic selection is limited because genotyping is still expensive in many developing countries because incomes are very low compared to developed countries. The few studies on genomic selection in developing countries are characterized by small population sizes and validations were undertaken with test day data sets (Neves et al., 2014; Brown et al., 2016; Kariuki et al., 2017; Ducrocq et al., 2018; Mrode et al., 2019).

Traditional animal breeding requires the use of pedigree records to support selection decisions but most small holder farms in Africa do not have these types of records and the measure of relationships between animals are merely speculative. Furthermore, the application of genomic selection will require the use of

reference populations which are generally lacking in Africa and many developing countries (Burrow et al., 2017). Mrode et al. (2019) reported the presence of small reference populations of between 500 and 3,000 animals (composed of mostly cows) in dairy and beef cattle in developing countries. The use of small reference populations that combined both bull and cow data, as in the case in Africa, has implications for the accuracy of genomic prediction, which is lower when compared to those obtained in Western countries given the limited information of the response variables when using cow records. It is important to state here that the inclusion of cows in the reference population has resulted to up to fivefold increase in the size of the reference population in some cases and increases of up to 12% in accuracy of selection compared to using bulls alone (Boison et al., 2017; Mrode et al., 2019). Mrode et al. (2018) reported some success by modeling and pooling data on the accuracy of genomic prediction in limited dairy data in East Africa. Brown et al. (2016) specifically reported the practice of genomic selection in a crossbred cattle population using data from the dairy genetic project of East Africa.

The cost of genotyping is a major issue limiting the adoption of genomic selection in Africa and to overcome this problem, the use of low density SNP panels have been suggested and this can be followed with imputation to improve the accuracy of genomic predictions (Meuwissen et al., 2016; Boison et al., 2017). Furthermore, low cost genome wide genotyping solution like genotyping-by-sequencing can generate high numbers of population specific SNPs (De Donato et al., 2013; Ibeagha- Awemu et al., 2016; Gurgul et al., 2018) that can support genomic selection in African livestock populations. Illumina7 and Affymetrix8 commercial SNP panels used for genotyping contains SNPs discovered in breeds and population of animals of Western origin and only very few breeds of African origin were included in the discovery of SNPs. This is the reason for ascertainment bias, which may affect accuracies of genomic selection from the use of commercially available SNP panels to genotype African indigenous livestock. Thus, the development of genotyping solutions specific for African breeds is necessary and the genotyping-by-sequencing approach can play a major role.

Some notable developments in the use of genomic tools include the sequencing of some indigenous cattle in Africa (Kim et al., 2017), developments on the genomic selection for disease resistance (Hanotte et al., 2010; Mwai et al., 2015) and for adaptation to hot arid condition (Kim et al., 2016). Other important efforts that may increase the quality of data includes the project of epidemiology of the Infectious Diseases of East African Livestock and a longitudinal calf cohort study in western Kenya (de Clare Bronsvort et al., 2013) and strategies for bridging the gap between the developed and developing livestock sector (Van Marle-Koster and Visser, 2018). Recently, Canovas et al. (2017) discussed the application of new genomic technologies including transcriptomics, metagenomics, metabolomics, and epigenomics that are pertinent to speed-up genetic improvement of cattle. As a matter of priority, Burrow et al. (2017) suggested that research to improve grazing livestock should include cross-country genetic/genomic evaluations, use of sequence data in genetic evaluations, multi-breed genomic evaluations, selection index and genotype -environment interactions. Furthermore, numerous studies in Nellore, an indicine beef cattle breed suggests that genomic selection is a realistic alternative to traditional selection strategies (Neves et al., 2014). In small ruminants like sheep and goats, Mrode et al. (2018) observed that innovative genetic selection strategies will be needed to ensure adaptive balance between production and adaptation.

Emerging gene editing technologies like transcription activator-like effector nucleases (TALEN), zinc finger nucleases (ZFN), and clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9 which can achieve any change in the genome, including introduction of alleles of interest into a recipient genome and switching on/off genes of interest can also play vital roles in rapid genomic improvement of African livestock traits. These tools offer an opportunity to intensify the frequency of desired alleles in a population through gene edited individuals more rapidly than conventional breeding (Bhat et al., 2017). Genome editing in livestock has been reported for the double muscling gene in cattle, sheep, and pigs (Proudfoot et al., 2015; Qian et al., 2015), the polled allele introduction in dairy cattle (Tan et al., 2013; Carlson et al., 2016); gene edits that confer resistance to African Swine fever virus in pigs (Lillico et al., 2013; Whitworth et al., 2016) and the low-density lipoprotein receptor gene in a pig model of atherosclerosis (Carlson et al., 2012). These examples indicate that attempts at gene editing in livestock have targeted traits controlled by few variants with major effects. However, most livestock traits of economic importance are quantitatively

controlled by many genes each contributing small effects, suggesting potential pitfalls in the implementation of these technologies for such traits. However, a recent simulation study indicated that editing for fewer casual variants of polygenic traits can double the rate of both short term and long-term genetic gains when compared to conventional genomic selection (Jenko et al., 2015).

Challenges for improved animal health in Zimbabwe

1. Quantitative genetic studies to identify markers of health traits

- The rate limiting step in studies aiming to detect genetic markers for health is invariably the collection of phenotypes, rather than genotypes. This is a general problem in many genomic studies, including studies on non-disease traits, and it is known generically as the 'phenotype gap.'
- The situation is exacerbated for disease traits as phenotypes of disease susceptibility/resistance to infectious diseases are often more difficult and/or expensive to measure than those for performance traits
- Some diseases are multifactorial. For example, mastitis may be caused by many *pathogens* (e.g. *Escherichia coli*, *Staphylococcus aureus*, *Mycoplasma bovis*, *Streptococcus uberis*, *Streptococcus agalactiae* etc), and the pathogenesis resulting from these specific infections may differ dramatically. Therefore, an important issue is whether with these different forms of the disease it is possible to have generic solutions to the disease or, conversely, pathogen-specific solutions are required invoking considerable complexity in data recording.
- In many cases, disease outcomes may be the result of infection coinciding with stress induced immune suppression in livestock. An example is the respiratory diseases of livestock and poultry in intensive animal production systems caused by several different pathogens (viral and/or bacterial) in association with transport, co-mingling of pooled animals, dietary changes and administration of various veterinary treatments. Mastitis is another example of a disease where clinical cases often have an underlying issue of immune suppression in early lactation. In such cases, addressing animals' ability to cope with stress may be as effective as concentrating on animals' resistance to infection.
- Quantitative genetic studies require knowledge of animal pedigrees relating to animals upon which selection is performed.
- To establish reference populations for all commercial and indigenous breeds of economic interest in the region for the future implementation of Genetic Selection (Pollak et al., 2012).
- So far, there are no reported experiences in the application of full-scale GS in the SADC region, only arbitrary plans.

For new technologies to be successful and effective in small-holder systems, it needs to fit into the existing system and be seen as a priority intervention (Marshall et al., 2011).

Dense SNP chips (tens or hundreds of thousands of SNPs) are the key to effective and portable genetic marker studies. Currently these are costly and only truly available in species with a genome sequence (e.g., man, mouse, chicken). Another significant issue with animal genome sequences is the lack of annotation, which is mostly based on homology to genes in other animal species and not actual experimental testing in the species of interest.

The step from discovery of significant marker associations to utilizable markers for animal health is long, difficult and expensive.

2. Functional genomics to understand host-pathogen interactions

- There is a critical need to develop animal disease models that mimic field infections using statistically significant numbers of animals per group and standardized challenge inocula. Also critical is the need to share challenge inoculums from a single source to reduce experimental variations.
- There is a lack of livestock and poultry breeds with well characterized genotypes and disease phenotypes whose variations can be correlated with innate and acquired immune status of the host.
- Animal health research laboratories lack bioinformatics infrastructure computer hardware, software,

and trained scientists in computational biology. There is also a lack of animal and pathogen species-specific genomics and proteomic tools with well-annotated genome databases to predict key immunogenic epitopes in the context of different target species to understand the triggering mechanisms of the protective immune response and to evaluate vaccine-induced immunity for the animal health research community.

- There is a need to identify molecular pathways of host and pathogens that are involved in transmission, survival, virulence, innate and adaptive immune responses, and protective immune response to natural infection and vaccination. The ultimate goal is the need to identify the 'operational limits' in the genomic 'imbalance' associated with current genetic selection.
- There is a need to develop a full set of specific research reagents for the key gene products involved in immune functions.
- It is paramount that the animal health research community has access to measurable biomarkers linked to disease susceptibility, disease resistance, and mechanisms of protective immunity.

3. Translating genomic information to tools for controlling diseases

- There is a critical need to preserve animal genetic diversity and to understand the role of genetic variations on host responses to diseases, drug treatments, and vaccination.
- There is a lack of rapid, robust, accurate and cost effective genetic tests to use in analyzing disease outbreaks for both the disease agent and the host.
- There is a need to integrate studies on disease resistance with selection programmes. This will require strategic collaborations with commercial breeding companies.
- The application of animal genome-enabled tools will demand fundamental changes in the approaches used to discover and develop animal drugs and vaccines, including their delivery and application in disease control programmes. One of the main challenges is the total absence of regulatory guidelines for the applications of these new technologies, including transgenic animals.
- The ability to design drugs and vaccines for genetically defined animal populations will require additional planning. For instance, in the area of vaccines, there is a lack of established 'vaccine profiles' to identify specifically what a vaccine is expected to achieve (e.g. efficacy with one dose, mass vaccination capability, prevent disease transmission, etc.) for specific diseases in individual animals and targeted commercial populations. Vaccines must not only be designed to achieve the desired vaccine profile but must also anticipate the genetic variations of the host and pathogens to enable predicted outcomes in vaccination campaigns and the selection of good responders to vaccination.

4. Integrating stakeholder support to advance animal genomics in animal health

- There is a lack of understanding of the opportunities for new approaches and in particular what is required for progress. There is a critical dearth of funding for animal health research and bias against non-hypothesis led approaches.
- Too many groups are involved in 'protecting' Intellectual property before any is developed, inhibiting cooperation or blocking progress. Adversarial approaches to protection predominate. Possible competition between genetic and 'pharma' approaches may reduce investment. (Cloete et al., 2014).
- There is little dialogue between veterinarians and animal scientists particularly in relation to the genetics of animal health. The focus tends to be on disease challenge or in vitro approaches with limited numbers of animals or genetic variation
- There is a lack of a unified vision on the opportunity of genomics for animal health, a lack of understanding of actions required to investigate the genetics of animal health, and poor definition of new tools required to undertake the required research.
- The lack of active community involvement has often led to the failure of livestock breeding projects in developing countries like those in the SADC region (Kosgey et al., 2006). In contrast, successful projects were generally characterized by stakeholder involvement (Kahi et al., 2010).
- The regulatory environment for 'gene-based' technologies, e.g. genetic modification, cloning, RNA interference, and transgenics, is unclear and inhibits research (as well as commercialization).

Opportunities for improved animal health in Zimbabwe

1. Quantitative genetic studies to identify markers of health traits

- The rapid and sustained development of genome-enabled technologies of the last few years provides extraordinary opportunities for advancing this field of research. One of the first and most exciting options to explore is the possibility of using dense single nucleotide polymorphism (SNP) maps coupled with haplotype information.
- It is critical that dialogue is established or strengthened between contributors with complementary expertise in animal health, animal genetics/genomics and other relevant disciplines.
- Animal health experts should also be aware that opportunities to record phenotypes may occur in populations that are not standard commercial populations or well-characterized experimental lines. For example, livestock exposed to extremes of environment or disease may be a rich reservoir of traits and genes related to health issues
- Research into the identification of animals with superior ability to withstand the immunosuppressive effects of stress may open new opportunities.

2. Functional genomics to understand host-pathogen interactions

- New research strategies employing high-throughput gene expression analysis are providing novel platforms for more comprehensive understanding of host—pathogen interactions. In particular, functional genomics is rapidly revolutionizing the analysis of whole genome responses of the host to environmental, nutritional, or disease factors that affect the health of animals.
- Identify research centres that maintain genetically well-defined animal breeds with different disease phenotypes as a resource for developing animal disease models.
- Identify breeds that vary in phenotypic expression of health traits and open these resources to all scientists conducting research in animal genomics.
- Build specific databases for each target animal species and pathogen type and establish a systematic programme for training and sharing predictive tools.
- Establish bioinformatics infrastructure with state-of-the-art genomic tools and resources that can integrate genotype, phenotype and functional genomics data for each animal species and priority diseases.
- Funding agencies should consider funding longer-term projects to support the infrastructure needed to develop animal populations with desirable health traits, the extensive phenotyping of these populations, and genome-wide genotyping of these populations.

3. Translating genomic information to tools for controlling diseases

- Genomic tools are providing new opportunities for understanding genetic diversity, the genetic variation associated with diseases processes, and host-pathogen interactions. The scientific information generated from the use of these tools in animal health research will enable the rational design of highly effective diagnostics, vaccines, drugs, biotherapeutics, and animals resistant to diseases.
- One possible solution is multi-or across-breed prediction, although its utility depends on various factors, including genetic distances among populations and the trait(s) considered (Lund et al., 2014). Such strategies have been successfully tested on relatively large dairy cattle breeds (Lund et al., 2011; Hozé et al., 2014), but are yet untested on small breeds. Given that application of GS in small breeds would require high-density genotyping, once again a specific cost-benefit analysis should be carefully considered.
- Another option, especially in populations where pedigree information is known, could be to genotype key ancestors at high-density and the rest of the population at low-medium density (Hozé et al., 2014). Imputation methods, also with a multi-breed reference population, can then be applied to obtain high genotyping accuracies for all animals (Berry et al., 2014).

4. Integrating stakeholder support to advance animal genomics in animal health

The promise of animal genomics will not be achieved without stakeholder support. The burden of communi-

cating the significant opportunities that genome-enabled technologies offer for improving animal health lies squarely on the shoulders of the animal health research community.

Recommendations for genomic selection for improved animal health

- Organized livestock production systems: cooperative farming; formation of national breed societies with regulatory agencies.
- Government should train veterinarians and provide free/subsidized veterinary services and medication. Increase/provide funding for research on livestock diseases
- Systematic characterization of animal productivity in the various production systems is necessary for implementation of improvement strategies.
- Enabling government policies must be put in place to guide/define the gainful exploitation of indigenous livestock and the roles of other stakeholders (e.g., NGOs).
- Establishment of national/regional recording and improvement scheme that will attract all stakeholders. Increase research funding and upgrade infrastructure
- Provide funding to support characterization of production systems, breeds and preservation of local breeds.
- Requires a robust national/regional cohesive strategy; more concerted effort required to educate and change the orientation of national policy makers toward funding of research in livestock sector; increased funding by government; private sectors should be encouraged to fund research; put in place infrastructure to deliver genomic services. Develop customized SNP chips based on African livestock populations. Devote financial resources to creating large reference populations with well phenotyped and genotyped animals.
- Implementation of appropriate biosafety measures and regulatory mechanisms.
- Capacity building for all stakeholders (farmers, policy makers, students, and professionals); Train Ph.D. level manpower to measure ‘not too easy to measure’ traits and statistical ability to handle big data. Collaborative research and implementation of improvement techniques with experts in Western countries.
- Building effective breed association to support producer decisions when needed.
- Government funding to support establishment of breed associations. Use of artificial insemination even in small holder systems will help to create genetic linkages across livestock populations.
- Training and adequate funding to support sustained long- term breeding programs.
- Donor organization to also support sustained long-term programs with participation of producers. Require certain roles of the breeding business section to contribute to sustainability of the development of livestock breeding.
- Appropriate selection programs adapted to each production system implemented; genomic selection suitable for all production systems; selection in nucleus herds using artificial insemination, embryo transfer or embryo sexing; development of appropriate methods/procedures of genotyping and genomic predictions for joint evaluations of small populations.

Conclusion

The availability of new animal genomics tools provides extraordinary opportunities for solving some of the most pressing and difficult problems in animal health research. Animal genomics also provides new innovative approaches for controlling diseases affecting domestic animals and wildlife. This review paper highlighted challenges and opportunities to improve animal health in line with quantitative genetics, functional genomics, translating genomics information into tools for controlling diseases, and integrating stakeholder support are priority areas for animal health research. The paper also provided recommendations in genomic selection for improved health

Conflict of Interest Declaration

The authors declare that there are no conflicts of interest.

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