

USE OF SNP CHIP TECHNOLOGY FOR IMPROVED UTILISATION OF LIVESTOCK GENETIC RESOURCES IN DEVELOPING COUNTRIES

K. Marshall

The International Livestock Research Institute (ILRI), P.O. Box 30709, Nairobi 00100, Kenya.

SUMMARY

Livestock play a critical role in the livelihoods of the one billion people who comprise the world's rural poor. Given the recent advances in genomic technologies, and the availability of SNP chips for a number of predominant livestock species in developing countries, an emerging question is if, and how, livestock SNP chip technology may benefit the world's rural poor. This paper discusses this issue in relation to a number of applications including within-breed improvement, matching breeds to livestock production systems, and genetic characterization and conservation. It is suggested that the use of SNP chips in determining the underlying breed composition of animals from admixed populations for studies aimed at identifying the best breed or breed composite for a particular production system could have high impact to a number of livestock sectors both in the short and longer-term future.

INTRODUCTION

Genomic technologies for livestock are rapidly advancing, with dense single nucleotide polymorphism (SNP) chips now available for a number of important livestock species, allowing for the genotyping of tens or hundreds of thousands of SNPs at an ever decreasing cost. Many livestock industries in developed countries are well-placed to capitalize on this technology, with genomic selection for within-breed improvement an increasingly popular application (Hayes and Goddard 2010).

Livestock play a critical role to the livelihoods the approximately one billion people who live in extreme poverty in rural areas – the world's rural poor (IFAD 2011). The functions of livestock to the rural poor are varied, and include financial and food security, as well as risk diversification and insurance, amongst others. Within developing countries, however, many livestock breeds and breed-crosses remain poorly characterized, and there are few examples of successful (in terms of impact and sustainability) within-breed genetic improvement programs. It follows that one emerging issue is if, and how, livestock SNP-chip technology may benefit the world's rural poor. This paper discusses this issue in further depth.

APPLICATIONS OF LIVESTOCK SNP CHIPS AND IMPLICATIONS TO THE LIVELIHOODS OF THE WORLD'S RURAL POOR

Within-breed improvement. Genomic selection uses dense markers across a genome, such as those arrayed on a SNP chip, so that quantitative trait loci are in linkage disequilibrium with one or more SNPs. The effects linked to the SNPs across the genome are summed to give genomic estimated breeding values (Hayes and Goddard 2010). Advantages of this approach include breeding values which can be predicted early in life, a reduced (though not eliminated) need for phenotypic records on animals in subsequent generations to the reference population, and the possibility of training the predictive algorithm based on data from one environment (for example, field data) and then select in another environment (for example, a breeding station).

The general lack of success of within-breed genetic improvement programs in developing countries is due to a number of complex and inter-related reasons. These include (though are not limited to) lack of incentive for livestock keepers to participate due to both slow-rates of genetic

change as well as other constraints to livestock productivity being of higher priority; breeding programs being designed as a 'stand-alone' technology, without adequate attention being paid to other system requirements (such as access to inputs including feed and health-care, access to markets, and natural resource management issues); lack of mechanisms for the breeding program to be sustainable in the long-term (many are discontinued after external funding has ceased); lack of scale resulting in few improved animals and thus limited impact; and lack of supporting institutions and policies. Other often-cited reasons, though in many cases likely of less significance because they are more readily dealt with, include inappropriate breeding objectives and, for community-based breeding programs, lack of recording systems.

Whilst the use of genomic selection within developing country livestock systems decreases the need for community-level recording, genomic selection would not address the other key constraints mentioned above (Marshall *et al.* 2010). Indeed there is little to suggest that genomic selection would succeed in developing countries under the same circumstances where traditional breeding programs have failed. Further, it can be argued that recording systems at the community level should be encouraged, as they provide valuable data for other purposes such as animal management and marketing. Overall it would appear that many livestock systems in developing countries, and in particular those that are less market oriented, are unlikely to significantly benefit from this technology in the short to medium term (e.g. next 5 to 20 years).

Matching breeds to livestock production systems. Developing countries have a wealth of livestock genetic diversity, though many breeds and breed-crosses remain poorly characterised (FAO 2007a). In addition, changes are occurring in some livestock systems, due to factors such as climate change and intensification (Rege *et al.* 2010), meaning that some livestock keepers are experimenting with non-traditional breeds and breed-crosses. In systems where cross-breeding does occur it can often be unstructured, resulting in an assortment of animals of unknown breed compositions (i.e. an admixed population). It follows that a critical question is which breed, or breed composite, is best suited to a particular livestock production system / environment, from the perspective of the livelihoods of the livestock keepers and other stake-holders. Answering this question is complex as it involves evaluating each breed / breed composite for a variety of parameters, including net productivity (outputs-inputs) from a socio-economic viewpoint, as well as other considerations, such as the effect of the breed / cross-breed on household vulnerability (Marshall *et al.* 2009). In addition, in order for these comparisons to be made, the underlying breed compositions of the animals comprising the population under investigation must be known. Whilst this has previously been challenging due to the lack of pedigree information, this is now feasible using SNP chip technology. Here the breed composition of the 'unknown' animals is determined using their SNP genotypes and that of reference (pure-bred) populations, and one of several analytical approaches such as that based on allele frequency (Falush *et al.* 2003). For the many developing country livestock systems where significant admixing occurs, this application could have high impact in both the immediate and longer-term future.

Characterisation of genetic diversity and conservation of animal genetic resources. In recent years there has been much interest in conserving the world's farm animal genetic resources, with guidelines to appropriate strategies suggested in the 'Global Plan of Action for Animal Genetic Resources' (FAO 2007b). For developing countries both in-situ and ex-situ (cryo) conservation strategies will be important, with in-situ conservation strategies appropriate for breeds / breed-crosses that are supported by the market (i.e. in the livelihoods interest of the livestock keeper to keep). It is recognized that some loss of breeds will be inevitable, given limitations in resources coupled with the ongoing changes in livestock production systems (FAO 2007a, 2007b).

On this background, a number of studies have focused on characterizing genetic diversity / relationships between livestock populations to help prioritise those for conservation (for example, Dorji *et al.* 2003). The more recent of these have tended to use SNP chip technology to provide the genotypes. In the developing country context, whilst such studies have resulted in valuable information, they have not always translated into conservation action and / or livelihood impact. As stressed in the Global Plan of Action (FAO 2007b) it is important that conservation action is taken, even with imperfect information. Thus whilst SNP chip technology is, and will continue to be, important in characterizing developing country livestock genetic diversity, the utilization of this information requires more attention.

SNP chip technology could play a role in other conservation related issues, such as estimating effective population size and inbreeding levels (Allendorf *et al.* 2010), which may be relevant to specific developing country livestock sectors. However, the cost to benefit ratio of using SNP technology to answer such questions would need to be carefully considered, particularly in cases where suitable but approximate information could be gained by other cheaper means such as survey-based approaches.

Development of new breeds. Marker assisted introgression involves the movement of genes from donor to recipient breeds, and SNP chips can be used to facilitate this process. However marker assisted introgression for more than a few genes poses logistical difficulties, due to the large scale of the crossing program required. As many traits of interest to developing country livestock systems (such as disease resistance) are polygenic, this application may not be widely applied.

Product traceability and market access. Market access is recognized as a key constraint to many developing country livestock sectors, and in particular for small-hold producers. Increased traceability of livestock products through the agri-food chain may help access to some markets, in particular international markets with high food-safety standards. DNA based traceability, for which SNP chips could be utilized, may provide part of the solution here. The practicalities and potential impacts of this require further investigation.

Characterisation of genetic architecture and functional genomics. Endemic livestock breeds in developing countries are highly adapted to the environment in which they reside, able to survive in harsh conditions (such as high disease prevalence, lack of feed or water) where many exotic breeds would succumb. In this regard they represent unique resources for characterization of genetic architecture and other genomic studies, such as functional genomics. In the long-term, it is expected that such studies will lead to various applications other than genetic improvement (see, for example, Liu 2009). In particular those related to animal health (disease diagnosis, prevention and treatment) could have large impacts in developing country livestock systems.

OTHER ISSUES OF CONCERN

Representation of developing-country livestock species and breeds on SNP chips. Livestock of major importance to the world's rural poor include poultry, goat, sheep, pig and cattle, as well as others such as buffalo and camel. For the poorest or the poor, as well as women, poultry and goat are of particular importance. For developing countries to capitalize on SNP-chip technology, it will be imperative that SNP chips are available for these important species with the relevant breeds represented, which would include breeds endemic to developing countries as well as the exotic breeds that are, or could be, imported. Representation of these breeds is likely best ensured by including developing country partners in SNP chip consortia as has been done, for example, for cattle and sheep.

Capacity of developing countries to utilize SNP chip technology. The in-house capacity of national research organizations within many developing countries to utilise SNP chip technology is varied but often low. This is due to the lack of human resources (in particular there are few trained animal breeders / quantitative genetics), as well as financial and physical resources (such as research stations, laboratories, and computing facilities). However much could be achieved through strategic international collaborations, which could simultaneously be used to build national-level capacity.

Phenotypic characterization is still very important to developing country livestock systems. Developing countries have a high number of local breeds many (and in some regions most) of which are not well characterized even at a basic phenotypic level. In these cases a significant amount of fundamental research remains, including ‘old-fashioned’ phenotype-based breed comparison studies. This work, however, is not seen as being cutting edge, and attracts only a limited amount of interest from the international scientific community or donor organizations. This is unfortunate as such studies (coupled with other livestock system data) are important in informing livestock-related development interventions with potential impacts on large numbers of the world’s poorest people.

CONCLUSION

Whilst much progress could be made in improving the livelihoods of the world’s rural poor without the use of SNP-chip technology, strategic use of this technology could lead to significant impacts in specific developing country livestock sectors. In particular, the use of SNP chips to help match breeds / breed composites to livestock production systems holds much promise. However, it is important that investments in SNP chip applications are weighed up against other potential investments, and that a real path exists (or can be created) to move research results into livelihood impact.

REFERENCES

- Allendorf F.W., Hohenlohe P.A. and Luikart G. (2010) *Nat. Rev. Gen.* **11**: 697.
- Dorji T., Hanotte O., Arbenz M., Rege J.E.O and Roder W. (2003) *Asian –Aust J. Anim. Sci.***16**: 964.
- Falush D., Stephens M. and Pritchard J.K. (2003) *Genetics* **164**:1567.
- FAO (2007a) ‘The State of the World’s Animal Genetic Resources for Food and Agriculture’ Food And Agricultural Organisation, Rome.
- FAO (2007b) ‘Global Plan of Action for Animal Genetic Resources and the Interlaken Declaration’ Food And Agricultural Organisation, Rome.
- Hayes B. and Goddard M.E. (2010) *Genome* **53**: 876.
- IFAD (2011) ‘Rural Poverty Report 2011’ International Fund for Agricultural Development, Rome.
- Liu G.E. (2009) *Recent Pat on Food Nutr Agric.* **1**: 75
- Marshall K., Quiros-Campos C., van der Werf J.H.J. and Kinghorn B. (2010) *Liv. Sci.* doi:10.1016/j.livsci.2010.09.006.
- Marshall K., Okeyo A.M. and Johnson N. (2009) In ‘Use of the FecB (Booroola) gene in sheep-breeding programs’, pp. 190-198, ACIAR Proceedings No. 133. Australian Centre for International Agricultural Research, Canberra.
- Rege J.E.O., Marshall K., Notenbaert A., Ojango J.M.K. and Okeyo A.M. (2010) *Liv. Sci.* doi:10.1016/j.livsci.2010.09.003.