

The genetics of parasite resistance in tropical animal production: Some insights

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Summary

The control of parasites is mainly based on the use of acaricides. Resistance to acaricides is a major problem associated with parasite control. Host genetic resistance to parasites has been increasingly used as a complementary control strategy and it has been documented in the tropics for both small and large ruminants. Results from several quantitative trait loci studies on parasite resistance have not always been consistent, mainly due to the different factors such as parasites studied, parasite loads, breeds, ages, climates, natural infections versus artificial challenges and infection level at sampling periods, among others. The use of genetic markers in genome-wide studies offers the potential to identify loci or regions associated with nematode resistance, as well as understand the mechanisms underlying resistance. This can be incorporated in breeding schemes and has the potential of reducing levels of infection and improving livestock productivity.

Keywords: parasite resistance, genetic markers, goats, sheep, cattle

Introduction

Parasite infections are a constant drain on the financial resources of livestock keepers and on livestock productivity. Due to economic losses and reduced wellbeing of infected animals, the control of external parasites such as ticks and internal parasites such as Barber's pole worm remains a challenge for the livestock industry in tropical and subtropical regions. Control strategies are based almost entirely on the frequent use of anthelmintics and acaricides, which are increasingly regarded as unsustainable, given the emergence of multiple drug-resistant parasites. In addition, consumer demands for organically produced commodities and reduction in drug residues in the environment has led to increased restrictions on the use of chemicals.

In most tropical developing countries, production takes place under very challenging conditions including heavy parasite loads. In addition to that, farmers are resource-constrained, and do not have access to either anthelmintic or land management practices to mitigate the influence of parasites. This has led to the need for new sustainable control measures based on exploiting the genetic variation for host parasite resistance. Before control measures based on host resistance are put in place, it is vital that the nature and pattern of inheritance of this trait be fully understood particularly since it is a polygenic complex trait.

Trait definition

Host parasite resistance refers to an animal's ability to prevent the infestation of parasites as well as developing immunity to parasitic diseases. External parasite resistance can be measured using counts e.g. tick counts in cattle (Marufu *et al.*, 2011, Mota *et al.*, 2017, Mapholi *et al.*, 2017, Marima, 2017), sheep (Thutwa, 2016), and immune responses in cattle (Marufu *et al.*, 2013). The main difficulty with selecting for host resistance in cattle to ticks is that identifying highly resistant individuals using the standard tick count method is not a feasible option in a commercial setting (Piper *et al.*, 2017). It is therefore difficult to mass phenotype animals in the form of a recording scheme. In addition to that, tick resistance could be attributed to different factors such as skin colour, thickness, humoral and cellular responses to tick attachment (Marufu *et al.*, 2013). In this study tick count had positive correlations with eosinophil counts, significant negative relationships with basophil and mast cell counts. The genetic correlations of these traits are unknown.

Some of the common indicators of resistance for internal parasites include faecal egg counts (FEC; Zvinorova *et al.*, 2016), worm loads in the gut (Mohammed *et al.*, 2016), packed cell volumes, immune response factors, and antibody response (Wilkie *et al.*, 2016). The use of FEC is an indirect measure of parasite resistance and it is one of the most common methods used, mainly because it is relatively easy to measure in animals. Faecal egg count is a poor predictor of actual worm burden primarily because it is highly variable and season-dependent.

As with external parasites, there are problems which may be associated with phenotyping this trait, especially in resource-constrained farming systems, due to lack of infrastructure and proper record-keeping. Routine recording outside research setups remains a challenge even in commercial flocks. The use of worm loads as a method of phenotyping is expensive, as it involves slaughtering of animals to access the parasites. Proper phenotyping is essential as this facilitates the identification of individuals which are resistant to parasites.

For both internal and external parasites the season effect needs to be treated with caution. Different QTL may be expressed, depending on the environment. e.g. QTL on BTA 2 and 10 were associated with tick resistance during the dry season. QTL on BTA 5 and 11 were associated with the same trait during the wet season (Machado *et al.*, 2010; Mapholi *et al.*, 2016). Ngere *et al.* (2017) concluded that the use of low worm populations may not be beneficial for estimation of genetic parameters. For effective selection of animals for resistance and resilience traits, warm season data only should be used, as it is a good indication of animal responses to parasite challenge.

For accurate trait definition it is important to clearly define the parasite(s) being studied and the breed of host it parasitizes. This is because the parasite species being studied could elicit different forms of host resistance, i.e. resistance to *Trichostrongylus* spp. and that of *Haemonchus* spp. differs within the same animal species. Similarly, the resistance to *Rhipicephalus* tick species by Brahman cattle may differ from Nguni cattle. Marima (2017) has postulated that resistance to external parasites like ticks in cattle may be influenced by the co-evolution of the host and the parasite. In the same line of thought, the relationship between artificial and natural infestation needs to be closely examined. Artificial challenge is expensive and is undesirable on welfare grounds, while natural infection suffers the drawback of varying from year to year with the weather. In addition artificial infestation studies are almost always single species infestation studies whereas natural infestation studies involves multiple species. To further confuse this picture is the preference by difference species of different body parts or organs of the animals (Mapholi *et al.*, 2017).

Nature of trait

Parasite resistance is a complex polygenic trait. Studies of complex diseases, mostly in humans, have generally failed to explain most of the known genetic variation influencing the trait resulting in the so-called ‘missing heritability’. A study by Kemper *et al.* (2011) concluded that there are several polymorphisms of small effect underlying variation in FEC. In the same study about 0.08 - 0.48% phenotypic variance was found explaining the additive genetic components.

Traditionally the genetic control of complex traits in livestock has been studied without identifying the genes/gene variants underlying observed variation, with selection being conducted on the basis of estimated breeding values. Some studies though have been done in tropical livestock parasite resistance. Using GWA analyses in Zimbabwean indigenous goat ecotypes, chromosomes 4 and 29 were found to be associated with gastrointestinal parasite resistance in goats. Specifically *DGKB* and *HRASLS5* genes were found to be associated with *Strongyle* and *Eimeria* resistance (Zvinorova, 2017). In South African Nguni cattle chromosomes 7, 10, and 19 with genes *FER*, *LRBA* were found to be associated with tick resistance (Mapholi *et al.*, 2016), with several regions being significant at suggestive thresholds.

In New Zealand, several QTL on different regions and chromosomes (OARs) have been reported in the literature for internal parasite resistance in sheep (OAR 1, 3, 4, 5, 8, 12, 13, 22 and 23; Crawford *et al.*, 2006), tick resistance in cattle (chromosomes 1, 2, 5, 6, 7, 9, 11, 13, 14, 15, 16, 18, 21, 23, 24, 26 and 28; Mota *et al.*, 2017). Marima (2017) and Marufu *et al.* (2017) indicated that genes *LUM* and *B2M* had expression levels significantly higher in South African Brahman and Nguni cattle as opposed to Angus cattle, thus presenting them as potential biomarkers for tick resistance. According to Motta *et al.* (2017) the presence of SNP by environment interaction for tick resistance indicates that genetic expression of resistance depends upon tick burden.

Integrating marker effects into traditional breeding value-based selection schemes can improve accuracy of selection. This will require setting up of reference populations and more widespread phenotyping. In South Africa and Brazil, efforts to move in this direction are underway.

Conclusion

Before the use of genomics can be integrated into selection of resistant animals it is imperative that a number of issues be studied and clarified. It is important that the traits being measured be properly identified and defined. Ways of mass phenotyping of animals need to be found and implemented. Without proper phenotypes the selection accuracy is likely to be low leading to poor genetic gains.

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