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How to account for adaptation in breeding schemes for ruminant production under tropics: focus on resistance to strongyles in small ruminants?

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This paper summarises host genetic variation in resistance to gastrointestinal nematode parasites in sheep and goats, as observed under humid tropical conditions, and considers incorporation of this genetic variation into breeding programmes. Genetic variation in parasite resistance is invariably seen in both sheep and goats, for various measures of resistance and tolerance. Large breed differences have often been documented both formally and anecdotally, as have significant heritabilities, however the heritabilities tend to be higher in sheep than goats. Several studies have found QTL for resistance and tolerance, but these tend to be scattered throughout the genome. The critical step in ensuring adaptation of animals to challenging environments is choice of breed. Once the correct choice of breed is made, breeding programmes under humid tropical conditions should focus on simple traits that are easy to measure such as FEC, PCV or the FAMACHA indicator of anaemia. Success in breeding schemes is dependent upon meeting the needs of the producer, and thus the breeding goal should include performance as well as resistance and tolerance traits. Currently there are few genetic markers that are generally suitable to use when selecting for resistance. This conclusion may alter once full evaluations of SNP chips for genome-wide selection have been made for sheep and goats. Several relevant studies are currently underway in both sheep and goats, and the results of these studies will determine the applicability of this technology to extensive low-cost breeding systems.

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QTL affecting resistance to gastro intestinal parasite infection in sheep: which applications in selection programs?

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Resistance to anthelmintic drugs amongst the major nematode parasites of sheep has now reached alarming proportions throughout the world and threatens the future viability of continued small ruminant production in many countries. Because of the excellent climatic conditions for the parasite, tropical countries are the most affected. Consequently, gene selection could be an attractive further strategy to help to control the parasite infections. The present paper presents a QTL detection study based on 2 experimental challenges with *Haemonchus contortus* in backcross Black Belly * INRA401 lambs, sired by 5 F1 rams. This design was previously used to detect QTL using microsatellite markers (Moreno *et al.*, 2006); this paper reports the first results of a QTL detection study for resistance to *H contortus* using the ovineSNP50 beadchip.

Sixteen SNP were found to be associated with one of the resistance traits (Faecal egg count, packed cell volume, parasite population examination after necropsy). Four regions, previously mapped with microsatellites on OAR3, 5, 7 and 12 have been confirmed. However the fitted thresholds based on a Bonferroni correction were extremely restrictive since every SNP are not independent of each other. We hope to confirm these QTL and to detect other QTL in further analyses using multi-marker approaches.

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