ON THE SEARCH FOR MARKERS OF TICK RESISTANCE IN BOVINES

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Genetic differences in susceptibility to tick (*Riphicephalus* (*Boophilus*) *microplus*) are considerable in bovine. In general, *Bos taurus* is more susceptible to ticks than *Bos indicus*. On the search for the molecular basis of tick resistance we used mapping, association and gene expression approaches. A *B. taurus* × *B. indicus* F_2 population was developed by Embrapa and 300 individuals were measured for parasite load and genotyped for microsatellite markers covering chromosomes 5, 7 and 14. A suggestive chromosome-wide QTL for tick load ($P < 0.05$) was mapped on chromosome 5 and two suggestive ($P < 0.10$) QTL on chromosome 7 and 14. In the candidate gene approach, females from the genetic groups Nelore (NE - 184), Canchim × Nelore (CN - 153), Aberdeen Angus × Nelore (AN – 123) and Simmental × Nelore (SN - 120) were evaluated under natural infestation in seven to ten tick counts. Microsatellite markers close to the genes for interleukin 2 (IL2), interleukin 4 (IL4) and interferon gamma (IFNG) were analysed. Tick counts were associated to the marker for interleukin 4 ($P < 0.05$) in NE, CN and AN genetic groups. We also investigated if there were differences in cytokine mRNA of naïve versus infested Nelore as well as of resistant versus susceptible cows from NE, CN and AN genetic groups. Relative quantification of cytokines from infested compared to naïves showed down regulation of IL2. When resistant cows from the three genetic groups were compared to susceptible animals, IL8 was down regulated but no differences were found for IL4 expression.

GENETICS OF RESPONSE TO VACCINATION

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The genomics revolution has been heralded as having the potential to reduce the impact pathogens have on the health and welfare of farm animals, for example through breeding disease resistant animals and identifying more effective vaccine candidates. However genomics may also provide solutions to improving the efficacy of vaccination by identifying key host responses, particularly those of the innate immune system. It is clear that host genetic factors play a significant role in determining the magnitude of immune responses in all species studied, including livestock. However host variability in response to vaccination has been little explored even in humans. As more sophisticated vaccines are developed it is likely that genetically determined variation in responses to these vaccines will hamper their effectiveness in the field. The regulatory genes that underlie such variability in response, may play key roles in determining the outcome of the host response: protection versus no protection, or indeed adverse reaction. Research at Roslin Institute has shown that antibody response to vaccination and cell mediated immunity in a crossbred cattle population are under genetic control and a number of significant quantitative trait loci (QTL) control these responses. Identifying the genes underlying these QTLs is ongoing and understanding how polymorphisms in these genes affect vaccine response could lead to new targets for improving the host response to vaccines. In addition it is likely that at least some of these genes may also be candidates for selection of animals that are more resistant to disease.