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variations of C-type MPSP gene were observed among the isolates. In some isolates, C types consisted of one major and several minor populations.

To analyse parasite population dynamics during serial passages between calves, and during persistent infection in a single host, parasite DNAs obtained from six calves infected with the same stock of C type *T. sergenti* were systemically analysed. Comparison among parasites that appeared at the first parasitemia peak in each animal by DGGE revealed that the parasite population was different in each animal. This result indicated that a certain population of *T. sergenti* selectively grew in a particular host. Between the

first and second parasitemia peaks in individual calves, changes in populations were not detected.

In the experimental infection of cattle with a C-type parasite clone, mutations on MPSP gene were detected. However, this appearance of MPSP variants seemed to be due to random mutations in MPSP gene and these variants did not seem to undergo positive selection in infected calves during the persistent infection.

The method of mutation or population analysis based on DGGE developed in this study may be a good tool to analyse molecular epidemiology and to develop effective control methods against *T. sergenti* infection.

#### Expression of tumor necrosis factor- $\alpha$ receptors mRNA in sheep infected with bovine leukemia virus

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Bovine leukemia virus (BLV) is associated with enzootic bovine leukosis (EBL), which is the most common neoplastic disease of cattle. The BLV infection can remain clinically silent with cattle in an aleukemic state, or it can emerge as a persistent lymphocytosis (PL), characterized by an increased number of B lymphocytes, and more rarely, as B-cell lymphomas in various lymph nodes after a long latent period.

Many studies have reported factors involved in the disease progression of BLV infection, including major histocompatibility complex (MHC) haplotypes, the mutation in the *p53* gene and the changes in cytokine profiles. The importance of proinflammatory cy-

tokines, such as tumor necrosis factor (TNF) - $\alpha$  has been documented for the antiviral and antiparasitic immune responses. In addition, the expression of TNF $\alpha$  receptors (TNF $\alpha$  R 1 and 2) on B cells in patients of chronic B-lymphatic leukemia were analyzed providing evidence that the importance of R 2 for B cell activation. It has also been reported that TNF $\alpha$  R 1 leads to programmed cell death through their respective death domains while TNF $\alpha$  R 2 mediates the inhibition of apoptosis. The aim of this study was to investigate the relationship between the expressions of TNF $\alpha$  and TNF $\alpha$  receptor mRNA from peripheral blood mononuclear cells (PBMCs) and disease progression of BLV

infection.

The levels of TNF $\alpha$  and TNF $\alpha$  R mRNA were measured in sheep infected with BLV by using the reverse-transcriptase polymerase chain-reaction system. The levels of TNF $\alpha$  mRNA in sheep resistant to BLV expansion was higher than in susceptible sheep. On the other hand, the expressions of both TNF $\alpha$  R 1 and R 2 mRNA were detected in BLV-resistant sheep whereas only R 2 was expressed in susceptible sheep as well as KU-1,

a BLV tumor cell line. Furthermore, to investigate the effect of TNF $\alpha$  on the proliferative responses of lymphocytes, the proliferation assay was performed with PBMCs from BLV-resistant and susceptible sheep. Significantly higher lymphocyte proliferative responses were observed in BLV-susceptible than resistant sheep. These results suggest that clearance of BLV infection by BLV-resistant sheep was TNF $\alpha$  R 1 expression and not R2.

The differences in the kinetic changes of lymphocyte populations and cytokine profiles between chickens genetically susceptible and resistant to Marek's disease

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Genetic resistance or susceptibility to T cell lymphoma formation induced by Marek's disease virus (MDV) is associated with the major histocompatibility complex (MHC) haplotypes of chickens. It was hypothesized that in susceptible chickens the generation of activated CD 4<sup>+</sup> T cells through intensive immune responses during the early phase of MDV infection provides a large pool of target cells for transformation. However, it remains unclear whether difference in the amounts of activated CD 4<sup>+</sup> T cells can indeed determine the degree of resistance to MD *in vivo*. In addition, currently, only a few information is available for relationship between disease progression of Marek's disease (MD) and cytokine profiles in host chickens, though cytokine profiles have been reported to play an important role in the outcome of several infectious diseases. Thus, in this study, the differences in the kinetic changes of lymphocyte

populations and cytokine profiles were studied between genetically susceptible and resistant chickens during MDV infection.

The results obtained from the kinetic analysis of lymphocyte populations by flow cytometer were not in good agreement with the previous hypothesis. A transient increase in the number of CD 4<sup>+</sup> cells was observed in both susceptible and resistant lines of chickens at 7 days post infection (pi), but no significant difference was shown in the degree of the increase between the two lines of chickens. Instead, more MDV was re-isolated from genetically susceptible chickens than resistant chickens. These results suggest that the differences in the numbers of infected cells and/or virus loads per cell, due to the differences in the numbers and/or affinities of virus receptors on the cell surface, can decide the degrees of susceptibility to MD during the early phase of infection. Since the numbers of