Interleukin-3 (IL-3) is one of the cytokines that act during the early and late stages of blood cell formation. To enable the study of the role of IL-3 in bovine haemopoietic stem cell differentiation, the polymerase chain reaction (PCR) was used to amplify an IL-3 cDNA from first strand cDNAs's prepared peripheral blood mononuclear cells (PBMNC) from N'Dama and Boran cattle. An analysis of the cDNA sequence reveals that it contains a 432-nucleotide (nt) open reading frame which codes for 144 amino acids (aa). Cleavage of the putative signal peptide consisting of the first 17 aa yields the mature form of the protein (14.5 kDa). Comparisons of the bovine IL-3 sequence shares 90.7, 55.8, and 51.9 percent nt identity, respectively, in the coding region, and 85.4, 35 and 27.7 percent aa identity, respectively.

The availability in recombinant form of large quantities of the mature protein encoded by this cDNA has enabled studies on the role of the cytokine in bovine haemopoiesis. These studies have shown that bovine IL-3 is a multipotential colony stimulating factor (CSF) whose activities include stimulation of the in vitro formation from bone marrow cells of eosinophil, neutrophil and macrophage colonies and in the presence of erythropoietin, of burst forming unit-erythroid (BFU-E) and mixed colonies.

The expression of IL-3 mRNA was evaluated by reverse transcriptase (RT PCR) in cells from several organs from healthy Boran and N'Dama cattle to determine the sites of IL-3 gene expression and to gain an understanding of how the expression of the gene is controlled in cattle. IL-3 mRNA could not be detected in unstimulated PBMNC, unsorted bone marrow mononuclear cells (BMMNC), BMMNC enriched for T lymphocytes, lymph node mononuclear cells (LNMCN) and pleen mononuclear cells (SPMNC). However, following stimulation with ConA, large amounts of the transcript were detected in all the cells with the exception of unsorted BMMNC. Studies of the kinetic patterns of IL-3 mRNA accumulation in LNMCN and SPMNC revealed that the mRNA accumulates rapidly following ConA stimulation, peaks after 3-6 h of stimulation and thereafter declines.

To determine if there are any shared regulatory elements between the bovine and human IL-3 genes that might explain the similar patterns of gene expression observed in this study, a DNA containing a portion of the 5' flanking region of the bovine IL-3 gene was amplified by PCR from a bovine genomic DNA library. A search for homology with known IL-3 sequences in the GenBank database reveals that the first 487 nt of this DNA share 93.3, 66.5, 65.6 and 57.4 percent identity, respectively, with the sequences of the 5' flanking regions of the ovine, human, Rhesus monkey and murine IL-3 genes. A computer-assisted analysis of the sequence reveals several potential regulatory motifs, which closely match regulatory elements of the promoter of the human IL-3 gene both in their nt composition and spatial distribution. The further characterization of these DNA motifs will contribute to the understanding of how the expression of the IL-3 gene is regulated cattle.

The expression of IL-3 mRNA in LNMCN, PBMNC and SPMNC from Trypanosoma congolense-infected cattle was also investigated to determine if depressed IL-3 gene expression plays a role in the ineffective haemopoiesis observed during infections of cattle with the African trypanosomes. In both Boran and N'Dama cattle infected with Trypanosoma congolense, IL-3 mRNA expression was never detected in unstimulated cells at all times of assay. Following stimulation of the cells with ConA, the amounts of IL-3 mRNA induced in LNMCN and
PBMNC from the infected cattle were equal to those induced in cells from the non-infected controls. However, the amounts induced in SPMNC from infected cattle were significantly lower than those induced in cells from control animals.

In summary, results of these studies demonstrate that bovine IL-3 has similar biological activities as IL-3 from other species, and suggest that bovine IL-3 is an important growth factor in induced haemopoiesis in cattle. They also show that, although the capacity of bovine T lymphocytes to express the IL-3 gene might not be impaired at the cellular level during infections of cattle with *T. congolense*, overall the production of IL-3 might be affected due to reductions in IL-3 gene expression in the spleen initially, and possible in other lymphoid organs in long-term trypanosome infections.