Summary

In the present study, 100 lungs were collected from clinically diseased calves and they were subjected to bacterial isolation and histopathological examination. Microscopical examination of our material evidenced that most of the cases showing chronic suppurative bronchopneumonia with lymphoplasmacytic peribronchial cuffing and multifocal caseous necrosis which have central accumulation of necrotic cells with peripheral wall of fibrinous tissue and infiltration of many mononuclear cells.

The effect of tracheal antimicrobial peptide against different bacterial pathogens that cause respiratory diseases in cattle has been evaluated by using radial diffusion assay and dilution methods and it was found that TAP has bactericidal rather than bacteriostatic effect. Moreover we compared the bactericidal effect of two different peptides, one with serine and the other with asparagine at position 20. We found, for all 3 isolates of *M. haemolytica* tested, that the number of surviving bacteria were higher with the peptide containing serine compared to the peptide containing asparagines. From what we have discussed before we can safely come to a conclusion that the bovine TAP gene contains a non-synonymous SNP in the coding region, which affects the bactericidal activity of the resulting peptide against *M. haemolytica.*

In this study, we found that stimulation of BTEC with 0.1ug/ml LPS for 16 hours induced significant up regulation of TAP expression however, treatment of BTEC with different doses of levamisole for 16 hours resulted in low level of expression of TAP mRNA.

Real time PCR and promoter activity assay have been used to investigate the effect of single nucleotide polymorphism (SNPs) in the promoter region on TAP gene expression. The PCR results showed 10- to 60-fold up regulation of TAP

mRNA expression upon Stimulation of BTEC of 23 calves by LPS. We observed that although the expression of TAP mRNA was significantly different ($p<0.001$) between LPS-treated and non-LPS-treated BTEC, the level of this expression didn't correlate with the genotype of the animals. The promoter activity assay was done by cloning the promoter region of TAP of 5 calves into PGL4.17 plasmid upstream to the luciferase gene and then transfected into BTEC. LPS stimulation of the transfected BTEC resulted in variable increase in luciferase expression (gene expression) in all 5 calves, while low level of gene expression was found with non-LPS stimulated cells; we noticed that these differences did not correlate with the genotype of the animals.