

6 SUMMARY

Examination of the time course of rumen epithelium adaptation

Structure and function of the ruminal epithelium vary according to the diet. Increased amounts of concentrate fodder result in considerable changes of the rumen fluid (increased concentration of short-chain fatty acids (SCFA), decrease in pH, increased osmotic pressure), increase in the number and size of ruminal papillae, hornification becomes more pronounced and the transport rate for different ions is increased. The chronological sequence and regulation of these complex adaptation processes are not yet fully understood and were investigated in the thesis presented here.

Functional adaptation was investigated on the basis of sodium flux rates in ussing chamber experiments. It was established that sodium flux rates increase markedly shortly after diet change and remain relatively constant in the following weeks. The results thus obtained prompted the examination of the adaptation process on a cellular level. To that end, it became necessary to select various transport proteins potentially involved in the adaptation process. Subsequently, gene expression profiles of the selected transport proteins were determined using real time PCR experiments in tissue samples (ruminal epithelium tissue) and in permanently cultivated ruminal epithelium cells (REC).

Tissue samples exhibited an upregulation in the transcription of the sodium-hydrogen-exchanger 3. However, this occurred distinctly later than the functional changes observed in the ussing chamber experiments using tissue samples from the same animals.

On the basis of gene expression profiles determined in REC, effects reported in previous studies could be confirmed and information concerning the role of gene regulation in the adaptation of the ruminal epithelium was obtained. The upregulation of the apical anion exchanger 2 (AE2) which was measured may possibly serve to increase the intake capacity of short-chain fatty acids in their dissociated form. In addition, the expression induction of the vacuolar HATPase by lactate and by butyrate as well as by the growth factors IGF1 and EGF demonstrated in these experiments suggests that the vHATPase is involved both in the process of the pH homeostasis and in maintaining an electrical gradient essential for numerous passive transport processes. Similarly, the upregulation of vHATPase and NHE1 may be interpreted as mechanisms to ensure pH-homeostasis during inflammatory processes mediated by PGE₂.