

Nuntaporn Pungsungvorn 2011: Effect of Probiotic *Lactobacillus reuteri* KUB-AC5 to Microbial Community in the Broiler Chicken Intestine. Doctor of Philosophy (Biotechnology), Major Field: Biotechnology, Department of Biotechnology. Thesis Advisor: Associate Professor Sunee Nitisinprasert, D.Sc. 134 pages.

The effects of dietary supplementation with antibiotic and *Lactobacillus reuteri* KUB-AC5 with concentration of 7log CFU/g to the change of villus height and bacterial changes in jejunum of broiler comparing to the control were studied at different ages of 1, 3, 7, 21, 42 and 49 days. The results showed that the height of villus from the treatments of KUB-AC5 addition increased from d 1 to d 42 chick while the ones of control and antibiotic treatments started to increase after 21 d. However, the villus height of 49 d chick from KUB-AC5 treatment were higher than the control and antibiotic treatment for 29.97% and 29.17%, respectively. Considering to microbial community in jejunum of chick by PCR-DGGE, the supplement of KUB-AC5 affected the reduction of various specie number detected from chick 1 d and growth inhibition of *Streptococcus pasteurianus*. The existing of *Enterococcus faecium* detected would support the increment of villus high during 1-42 d.

The effects of dietary supplementation with 5log, 6log, 7log CFU/g of KUB-AC5 on villus height and bacterial changes in two model of broiler chickens contaminated with *Salmonella* Enteritidis S003 of 6log CFU per chick by the same time as experimental feeding (SIM) and after two days experimental feeding (SEP). The results showed that 5 logCFU/g of KUB-AC5 treatment affected the growth inhibition of *Salmonella*. While abundance of *Lactobacillus acidophilus*, *L. johnsonii*, *L. salivarius* and *L. reuteri* belonging to the similar strains of PIL73, LP970 including KUB-AC5 had occurred. In addition, *L. reuteri* was also detected even the strain KUB-AC5 did not supplemented during 21-28 d. This would support the highest of villus height obtained.

By phylogenetic tree analysis of these treatments, 4 different bacterial groups of Low GC Gram positive, β -Proteobacteria, γ -Proteobacteria and Actinobacteria were detected. Different genus or specie of each bacterial group found depended on their treatment condition.

Student's signature

Thesis Advisor's signature