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*BURKHOLDERIA MALLEI* (A NON-MOTILE SPECIES). THESIS ADVISORS :  
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*Burkholderia mallei* is a gram negative rod-shape bacteria and it is a sole species in genus *Burkholderia* which is non-motile. *B. mallei* is considered to be the parasite on equines, in which it causes glanders and the infection can be transmissible to a large variety of animals. *B. mallei* is genetically related with *B. pseudomallei*, a causative agent of melioidosis, due to 16S rRNA sequence showing 100% homology. Although the motility property can be used to distinguish the two species, the genetic markers might be a rapid and simple method for accurate identification of the species. We therefore attempted to search for a genetic difference between the two species. Based on motility property, specific primers for amplification of flagellin gene from *B. pseudomallei* were used. A 1.1 kb of PCR product was obtained. Surprisingly, sequencing analysis of the 1.1 kb product showed a 99% nucleotide sequence homology or 100% amino acid sequence identity to *B. pseudomallei*. Thus, we tried to investigate the regulation of the gene expression in transcription and translation level in *B. mallei* compared with *B. pseudomallei*. The results suggested that mRNA was not transcribed and we were not able to detect flagellin protein from *B. mallei* by Western blot analysis. The 5'upstream sequence of *B. mallei* flagellin gene, which is nearly the same as the regulatory region of *B. pseudomallei* strains reported by Neubauer et al. Southern blot hybridization was performed to determine GATC methylation of 5' untranslated sequence. The methylated upstream region of flagellin gene in both *B. mallei* and *B. pseudomallei* sequence show the same pattern. In addition, chemotaxis protein CheW gene and Chemotaxis response regulator CheY gene were able to be isolated from chromosomal DNA of *B. mallei* by PCR. The sequence analysis of both genes is also identical to CheW and CheY of *B. pseudomallei* respectively. Existence of the same methylation pattern on upstream region of flagellin gene and the appearance of both chemotaxis involving genes lead one to believe that expression of *B. mallei* flagellin gene is under control of upper operon in flagellar hierarchy. In addition, *Sau3AI* and *MboI* restriction patterns of *B. mallei* and *B. pseudomallei* are different, especially DNA fragment of above 1.2 kb. As no sequence data have been available, these patterns are worthy to elucidate the genetic dissimilarities among this two *Burkholderia* species.