Thesis Title	Cloning and DNA Sequencing of Flagellin Genes of *Pseudomonas* Species
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ABSTRACT

Flagellar filaments in prokaryotes are composed of protein subunits, flagellin. Protein sequence analysis of flagellins from different genera of bacteria such as *Escherichia*, *Salmonella*, and *Serratia* demonstrated that the termini of flagellin protein are conserved. Primers designed from the 5' and 3' regions of published flagellin genes of *Pseudomonas aeruginosa* PAK and *P. putida* PaW8 were used to amplify flagellin genes of four species of *Pseudomonas* as follows : one strain of *P. aeruginosa*, *P. fluorescens*, and *P. stutzeri* and four isolates of *P. putida*. PCR amplification of flagellin genes of these 7 bacteria showed different patterns, only PCR products that hybridized with the *P. aeruginosa* flagellin gene probe were cloned and sequenced. The gene fragment sizes have been found to vary among species. *P. aeruginosa* and *P. fluorescens* flagellin genes are 1.2 kb whereas flagellin gene size of *P. stutzeri* is 1.4 kb. For *P. putida*, the flagellin genes are divided into three types; type A, B, and C whose flagellin sizes are 2.0, 1.4, and 0.8 kb, respectively. Comparison of the deduced amino acid sequences of these seven flagellin genes of *Pseudomonas* species with other flagellins supported the established concept of highly conserved terminal regions flanking a variable central region. Dendrogram derived from the sequence comparison of flagellins data can be used for grouping some bacterial genera such as *Borrelia*, *Salmonella* and *Pseudomonas*.