

## C005255 : MAJOR MEDICAL MICROBIOLOGY

KEY WORD : NUMERICAL TAXONOMY/Pseudomonas pseudomallei

KAMPOL CHAROENSUKSOPON : NUMERICAL TAXONOMY OF Pseudomonas pseudomallei. THESIS ADVISOR : INSTRUCTOR KRIENGSAK SAKITANU,  
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The numerical study of Pseudomonas pseudomallei was carried out. P. pseudomallei, 43 strains, and other Pseudomonas spp., 57 strains, were compared in a numerical taxonomic study using 170 unit characters. Similarity between strains were computed by using the simple matching coefficient ( $S_{sm}$ ) and the jaccard coefficient ( $S_j$ ). The clustering of the strains studies were achieved using the unweighted pair group method with the arithmetic average (UPGMA) technique.

Results from the two methods,  $S_{sm}$ /UPGMA and  $S_j$ /UPGMA have similar cluster composition. At the 56% similarity level of the jaccard coefficient a total of 100 organisms studied were divided into 13 clusters. Cluster 1, 2, 3, 4, 5, 7, 8, 9, 10, 11, 12 and cluster 13 were identified as P. pseudomallei, P. cepacia, P. putida, P. fluorescens, P. aeruginosa, P. pickettii, Pseudomonas species group VE-2, P. stutzeri, P. diminuta, P. maltophilia, P. alcaligenes, and P. acidovorans, respectively. Cluster 6 was unclassified Pseudomonas.