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ATCHARA KITTITHAKORN : COMPUTERIZED SYSTEM FOR EVALUATING
EVOLUTIONARY RELATIONSHIP BETWEEN VARIOUS *MYCOBACTERIUM
TUBERCULOSIS* ISOLATES. THESIS ADVISOR : SUPACHAI TANGWONGSAN, Ph.D.,
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At present, tuberculosis is an important infectious disease worldwide with more than 60,000 new patients in Thailand each year. The number of patients is increasing because of the spread of human immunodeficiency virus (HIV) infection, which can destroy the immune system and also increase the incidence of multidrug-resistant *Mycobacterium tuberculosis*. The development of rapid diagnosis, identification of the infectious sources and detection of individuals in contact with the infected persons are important aspects of controlling the spread of tuberculosis. The spreading of the bacteria has recently been studied by analyzing the DNA fingerprints of bacteria isolated from patients. Bacterial isolates with identical fingerprint are considered to be the same strain while isolates with very similar fingerprints are believed to descend from a common ancestor. Thus, the epidemiologists can infer the mechanisms of the disease either by recent transmission or reactivation of the disease. Presently, analysis of the fingerprint in Thailand is done manually. When the number of studied isolates increases, the analytic task becomes tedious, takes more time and has more errors. A computerized system, therefore, would be a better approach to solve this problem.

Using this prototype program, the DNA fingerprints are entered as images by a scanner and then the pattern of DNA bands will be recognized automatically. Southern estimation method is used for converting the position of DNA bands to the length or molecular weight using a standard DNA sample. Then, each converted value will be arranged in order of slots, the suitable data structure for this case, that can support the efficient searching algorithms. Consequently, the system permits rapid recognition of isolates with identical or similar pattern of DNA fingerprints, and can search by specifying some positions of DNA bands for partial match pattern. Moreover, it is also able to generate evolutionary relationships between isolates with similar fingerprints by using the unweighted pair group method with arithmetic mean algorithm (UPGMA method). The evolutionary relationship is represented by phylogenetic tree or dendrogram.

According to the above approach, the system will be able to recognize the DNA fingerprints quickly and accurately. In addition, the analysis of evolutionary relationships between isolates also provides both accurate results when approved by the specialist and better time performance compared with the time used in the present method. Hopefully, this prototype will be useful not only for the case of tuberculosis, but may also be applied in a wide range of organism studies as well.