

EVALUATION OF GENETIC VARIATION AND DIFFERENTIATION OF *SHIGELLA FLEXNERI* BY AMPLIFIED FRAGMENT LENGTH POLYMORPHISM FINGERPRINTING (POSTER)

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Background: Amplified Fragment Length Polymorphism (AFLP) has been developed to identify the taxonomic and epidemiological relationships of microbial genomes. The advantages of this technic over conventional method is that it provides more highly reproducible polymorphic banding patterns and it is able to analyze the total genome content without having knowledge of the genome sequences. Since AFLP demonstrates high discrimination power, this study aimed to evaluate the use of AFLP to determine genetic variation within and between a variety of *S. flexneri* serotypes.

Methods: Sixty three isolates of *S. flexneri* consisting of serotype 1, 1b, 2a, 3a, 4, 6, and 14 uncharacterized isolates were investigated. Genomic DNA samples were digested with *MseI* and *EcoRI* restriction enzymes and ligated with the adaptors. The ligated fragments were subjected to preselective amplification followed by selective amplification. The amplification products were analyzed by automated capillary gel electrophoresis.

Results: Three primer combinations were selected from 30 tested selective primer combinations according to the number of informative bands and polymorphism detected between isolates. Similarity analysis yielded a grouping of isolates into 5 clusters according to their serotypes. Within each serotype, AFLP demonstrated the similarity between individual profiles ranging from 80-100%. For uncharacterized samples, 11 isolates were grouped into serotypes 1 cluster and 3 samples belonged to serotype 4 cluster (more than 80% similarity).

Conclusion: This study has demonstrated that AFLP can be used for genetic fingerprinting and discrimination of *S. flexneri* strain in serotypic levels as well as applied for bacterial identification.

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