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Identification and Molecular Evolution of *Bacillus anthracis* Based on REP-PCR Genomic Fingerprinting and Amplified Fragment Length Polymorphism

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Bacillus anthracis, the etiological agent of anthrax has been classified into the *Bacillus* subgroup I with *B. cereus*, *B. mycoides* and *B. thuringiensis* based on morphological and DNA similarity. DNA studies have further indicated that these species have very AT-rich genomes and high homology, indeed it has been proposed that these four sub-species be recognized as members of the one species. Several methods have been developed to obtain good differentiation between these species. However, none of these methods provides the means for correct differentiation. In this study, we evaluated genomic fingerprinting procedure based on REP-PCR and AFLP to investigate genetic relatedness and evolution according to dendrogram with seventeen strains of *B. anthracis* and closely related species.

The Rep-PCR and Eric-PCR results showed that all strain of *B. anthracis* were classified into the same group at the 75% and 70% of genetic similarity level, respectively, whereas Box-PCR, *B. coagulans* KCTC 1013, *B. mycoides* KCTC 3453 and *B. cereus* KCTC 1014 were clustered into *B. anthracis* group. The best grouping result was obtained by using the analysis of Rep-PCR. By the AFLP, all tested strains of *B. anthracis* were clustered into the same group defined at genetic similarity level of 92%. On the basis of these studies, we propose that genomic fingerprinting techniques such as Rep-PCR and AFLP can be used as rapid, reliable, reproducible and highly discriminatory screening techniques to determine the taxonomic diversity and phylogenetic structure of bacterial populations.

Therefore, it was concluded that the Rep-PCR and AFLP could be used for the rapid identification and classification of *B. anthracis* and would be useful for epidemiological studies of anthrax.