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Random Amplified Polymorphic-Dinucleic Acids (RAPD-PCR) and 16SrDNAPhylogenetic analysis of Bacillus cereusIsolated fromfried rice samples

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Abstract: Bacillus cereus can cause two types of food poisoning as emetic or diarrheal syndrome. Fried rice is recognized as one of potential risk food especially in tropical countries. This study was conducted to detect and characterize B. cereus isolated from fried rice. A total of 70 fried rice samples were purchased from restaurants at Bangi (20), Kajang (20) and UKM's (30) cafeteria. The isolation of B. cereus was done onto Mannitol egg yolk polymyxin medium and the presence of B. cereus ranged from 1.2×10^4 to 1.6×10^6 cfu/g of fried rice samples. Of more than 110 colonies of presumptive B. cereus tested onto chromogenic B. cereus agar, 35 colonies were identified as B. cereus using biochemical test and partial sequence of 16S rDNA sequences analysis. All B. cereus isolates specifically known as BC1 to BC35, were further identified by 16S rDNA with similarity of 80% -100% when it blast in the NCBI data base shown the amplicons of B. cereus isolates using 16S rDNA universal primers which produced 711 bp in size. Genetic fingerprinting of 35 B. cereus isolates was examined by random amplified polymorphic DNA-polymerase chain reaction (RAPD-PCR) using primer (RAPD1). The results of the RAPD-PCR were analyzed using GelCompare software. RAPD-PCR with primer RAPD1 discriminated the B. cereus isolates into 5 clusters and 4 single isolates at 70% similarity level.

Keywords: Bacillius cereus, isolated, fried rice, RAPD-PCR.

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