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Molecular typing of *Bacillus cereus* isolated from sago processing mills in Sarawak.

Jaraee J.[1], *Bilung M. L.[1], Nolasco C. H.[2] & Vincent M.[1]

Corresponding author: Dr. Lesley Maurice Bilung (mblesley@unimas.my)

[1]Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak

[2]Department of Chemical Engineering and Energy Sustainability, Faculty of Engineering, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak

Abstract

Bacillus cereus is an ubiquitous bacteria which is commonly found in soil and plant-based food. In this study, thirty-nine *Bacillus cereus* isolates were detected with the presence of *hly* gene by using specific PCR. These isolates were further characterized and differentiated by using the Enterobacterial Repetitive Intergenic Consensus PCR (ERIC-PCR) to determine their genomic fingerprints. The ERIC-PCR generated several genetic profiles consisting of 1 to 7 bands with sizes in the range of 120 bp to 990 bp. Based on the dendrogram generated from the DNA fingerprinting profiles (ERIC-PCR), all of the isolates can be divided into 2 main clusters that is further divided into few sub-clusters. The heterogeneity of the isolates indicated the cross-contamination of *Bacillus cereus* occurred in sago processing mills in Sarawak.

Keywords : *Bacillus cereus*, sago processing, ERIC-PCR, genetic diversity, cross-contamination

Introduction

Sago processing industry is a highly potential industry in Sarawak whereby the export of sago product from Sarawak procuring income approximately RM 81 million per year (Department of Agriculture, 2013). However in food processing industries, some of the preparation, processing and storage procedures were exposed to the risk of contamination of bacterial contaminants. *Bacillus cereus* is one of the known causes of foodborne illness. *Bacillus cereus* is a Gram-positive and rod-shaped foodborne pathogen that can cause gastrointestinal diseases such as food poisoning (Sandra *et al.,* 2012; Kotiranta *et al.,* 2000). *Bacillus cereus* is an ubiquitous bacterium commonly found in soil and is able to live in it because it does not have complex nutrient requirements (Kotiranta *et al.,* 2000). Pasteurized food such as dairy foods of cooked chill foods, starchy food such as rice and starch, and dry foods such as spices, ready-to-eat cereals are among of food products under risk of *Bacillus cereus* contamination (Lesley *et al.,* 2013; Sandra *et al.,* 2012; Greenhill, 2010; Kontiranta, 2000). To the best of our knowledge, this is the first study providing genotypic epidemiologic data regarding the *Bacillus cereus* isolated from the processing steps of sago especially in Sarawak. However, the study on genetic diversity of *Bacillus cereus* had been reported in other food processing plant such as fresh-cut vegetable salad processing in Korea (Kim *et al.,* 2016), red pepper powder processing plant (Oh *et al.,* 2012), dairy plant (Svensson *et al.,* 2006) and chilled zucchini puree processing plant (Guinebrietre *et al.,* 2003). In the present study, the presence of *Bacillus cereus* was monitored in sago flour and sago samples from each stage of sago processing which consist of debarking, pulping, starch extraction, drying, packaging and discharging point. Molecular typing of *Bacillus cereus* was also investigated using ERIC-PCR method to identify genetic diversity of *Bacillus cereus* in sago processing in Sarawak.