



## Detection, genetic diversity and antibiotic resistance profiles of *Bacillus cereus* isolated from sago processing plants in Malaysia

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### ABSTRACT

**Aims:** *Bacillus cereus* is a Gram-positive, rod-shaped and spore-forming bacterium. It is a ubiquitous bacterium which is widely distributed in several environments such as soil and plants and is commonly isolated from food and its processing environment. This study was aimed to determine the genetic diversity and antibiotic resistance of *B. cereus* isolated from sago processing in Sarawak.

**Methodology and results:** Out of 120 samples, 42 *B. cereus* isolates were detected with the presence of *hly* gene of *B. cereus* by using specific polymerase chain reaction (PCR). Twenty *B. cereus* isolates were randomly selected and further characterized by pulsed-field gel electrophoresis (PFGE) of chromosomal DNA digested with *NotI* to examine the genetic diversity. The result of the PFGE analysis confirmed that the *B. cereus* strains in sago processing were genetically diverse. Based on the dendrogram generated, *B. cereus* strains were grouped into two major clusters and these clusters were grouped together based on sources of isolation. The investigation on the antibiotic resistance of *B. cereus* strains revealed that the *B. cereus* strains were uniformly highly resistant to penicillin and ampicillin and highly susceptible to imipenem and norfloxacin.

**Conclusion, significance and impact of study:** The results of this study suggest that the *B. cereus* isolated from sago processing derived from a mixture of sensitive and resistant strains with diverse genetic contents.

**Keywords:** *B. cereus*, sago processing, genetic diversity, PFGE, antibiotic resistance

### INTRODUCTION

Sago processing industry is a high potential industry in Sarawak and are grown commercially in Malaysia, Indonesia, Philippines and New Guinea (Bujang, 2008). Sago is an important food for millions of people (Adeni *et al.*, 2010). In Malaysia, approximately 90% of sago planting area can be found in Sarawak and 75% are in Mukah, Sarawak (Bujang, 2010). Sago industries in Sarawak have great contribution to Sarawak economy whereby the export of sago product from Sarawak procuring income approximately RM 81 million per year (Department of Agriculture Sarawak, 2013). However, in food processing industries, some of the preparation, processing and storage procedures were exposed to the risk of contamination of bacterial contaminants. *B. cereus* is one of the known causes of foodborne illness. *B. cereus* is a Gram-positive, spore-forming and motile rod-shaped bacterium that can cause gastrointestinal diseases such as food poisoning (Kotiranta *et al.*, 2000; Sandra *et al.*, 2012). Hence, it is important to monitor their presence in foodstuffs by using rapid and reliable molecular method (Merzougui *et al.*, 2013). To the best of our knowledge, this is the first study on the genetic

diversity of *B. cereus* isolated from the processing steps of sago in Sarawak by PFGE method. However, the study of genetic diversity of *B. cereus* by PFGE had been reported in other food products/processing plants such as in milk, spices, rice salad, yogurt and cheese (Merzougui *et al.*, 2014), rice and ready-to-eat cereal (Park *et al.*, 2009) and chilled zucchini puree processing plant (Guinebretiere *et al.*, 2003) whereby all these studies revealed the genetic differences among the *B. cereus* from the samples isolated. Hence, present study was aimed to investigate the diversities of *B. cereus* in sago processing by PFGE method. In addition, the antibiotic resistance of *B. cereus* strain was also examined.

### MATERIALS AND METHODS

#### Sample collection and preparation

A total of 120 samples comprise of bark swab (n=20), sago pith (n=20), sago effluent (n=20), starch slurry (n=20), sago milk (n=20) sago flour (n=20) were collected from sago processing mill in Sarawak. Approximately 50

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