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Characterization of the Saxitoxin Biosynthetic Starting Gene, *sxta* in the Toxic Dinoflagellate *Alexandrium tamiyavanichii*

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ABSTRACT

Recently, molecular genetics of the Saxitoxin (STX) biosynthesis pathway has become one of the major focuses in paralytic shellfish poisoning (PSP) toxin-related studies after the recent discovery of STX biosynthetic genes in toxic cyanobacteria and later in the toxic dinoflagellates. Here we described the two domains of *sxtA*, SAM-dependent methyltransferase coding gene, *sxtA1* and the class II aminotransferase coding gene, *sxtA4* from a toxic strain of *Alexandrium tamiyavanichii* isolated from Samariang, Sarawak. The partial coding sequences of *sxtA1* and *sxtA4* were 432 bp and 639 bp respectively, with the deduced amino acid sequences revealed polypeptides of 144 and 213 amino acid residues, respectively. The present results showed high sequence similarity and identity (~91% and ~98%, respectively) compared to other PSP toxins-producing dinoflagellates. Indeed, our protein phylogenetic analyses revealed close relationship of both *A. tamiyavanichii sxtA1* and *sxtA4* to others PSP toxins-producing dinoflagellates, with *sxtA* from PSP toxins-producing cyanobacteria and putative toxin-related genes forming the sister clades.

Keywords: saxitoxin, paralytic shellfish poisoning, SAM-dependent methyltransferase (*sxt*A1), class II aminotransferase (*sxt*A4), *Alexandium tamiyavanichii.*

INTRODUCTION

Saxitoxin (STX) is a highly potent neurotoxin that caused paralytic shellfish poisoning (PSP), which is an affliction to human health and coastal shellfish industries. In the marine environment, the eukaryotic dinoflagelates in the genera of *Alexandrium*, *Pyrodinium* and *Gymnodinium* are the major species that capable of producing STXs. While in the freshwater ecosystem, some prokaryotic cyanobacteria such as *Anabaena circinalis*, *Aphanizomenon* sp. *Cylidrospermopsis raciborskii* and *Lyngbya wollei* are the major STXs producers.

Production of STX and its derivatives, involves a very complicated biosynthesis pathway. The first saxitoxin biosynthesis pathway was elucidated base on precursor-feeding experiments (Shimizu *et al*., 1984). And two decades later, the saxitoxin biosynthesis genes (sxt) were discovered from cyanobacteria by *in-silico* functional homology analysis and LC-MS analysis of the biosynthesis intermediates (Kellmann *et al.,* 2008a; Kellmann *et al.,*