Molecular characterisation of rice tungro bacilliform virus isolated from Bario, Sarawak

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ABSTRACT

Aims: Rice tungro disease is one of the most damaging and destructive diseases of rice in South and Southeast Asia. The disease is caused by the co-infection of two viruses, the Rice tungro bacilliform virus (RTBV) and Rice tungro spherical virus (RTSV). The symptoms and severity of the disease depend on these two viral agents, if rice is co-infected by both viruses, it will show the typical severe symptoms of yellow-orange leaf discoloration, plant stunting and reduced in yield. On the other hand, if rice is infected only with RTBV, it shows milder symptoms and in contrast, rice plants will show no symptoms if they are infected only with RTSV. The disease had been detected in Malaysia since the 1930s. However, the first incursion of the disease was only reported in Sarawak in 2012. Since the disease was not seen in the Sarawak until recently, very little information on local virus isolate is available. This study was conducted to obtain and record the nucleotide sequence of partial coat protein gene of two primary isolates of RTBV collected from Bario, Sarawak in 2012 and 2013.
Methodology and results: Based on the phylogenetic analysis, the isolates cluster with the Southeast Asia group with sequence identity at nucleotide and amino acid level of 91.1 to 95.1% and 98.6 to 99.5% respectively.
Conclusion, significance and impact of study: This study provide the first genetic information on RTBV isolates from Sarawak. This data is important for future reference of the virus variants and diversity for epidemiological and diagnosis purposes.

Keywords: Tungro, RTBV, isolate, Sarawak

INTRODUCTION

Rice tungro bacilliform virus (RTBV) is a plant *paraterovirus* in the genus *Tungrovirus* of the family *Caulimoviridae* (Bousalem *et al.*, 2008). RTBV together with Rice tungro spherical virus (RTSV) caused rice tungro disease (RTD) (Hibino *et al.*, 1978) in rice plants grown in South and Southeast Asia (Ling, 1972; Azzam and Chancellor, 2002). Symptoms of RTD are caused by RTBV (Hibino *et al.*, 1978) but RTBV can only be transmitted into host plant by green leafhopper (*Nephotettix* spp.) in the presence of RTSV (Hibino, 1983).

RTBV has a circular double-stranded deoxyribonucleic acid (dsDNA) of about 8 kb and one site-specific discontinuity in each strand (Bao and Hull, 1993). The genome has four open reading frames (ORFs) namely ORF1, ORF2, ORF3 and ORF4 (Hay *et al.*, 1991). Only ORF2 and ORF3 have known functions. ORF2 encodes a protein that is involved in capsid protein assembly (Herzog *et al.*, 2000) while ORF3 encodes movement protein (MP), coat protein (CP), aspartate transferase

(AT) and reverse transcriptase/ ribonuclease H (RT/ RNase H) which are involved in virus replication and assembling (Hay *et al.*, 1991; Qu *et al.*, 1991; Laco *et al.*, 1995; Marmey *et al.*, 1999).

Rice tungro disease (RTD) was first reported in Sarawak in 2012 (Yee and Eng, 2013) but no nucleotide sequence of RTBV circulating in this region is available. Although RTD had been detected in other parts of Malaysia as early as 1930s, not much genetic information of the viruses is available. The sole RTBV complete genome from Malaysia deposited in NCBI GenBank is of the isolate from Serdang which was reported in the 90s (Marmey *et al.*, 1999). Therefore, this study was conducted to obtain and record the partial CP gene sequence of RTBV from Sarawak to study the virus diversity in East Malaysia.

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