



# Piper yellow mottle virus: A deep dive into the genome

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## ARTICLE INFO

Edited by Jormay Lim

### Keywords:

Piper yellow mottle virus  
Genome comparison  
Country-specific SNPs  
Haplotype  
Reverse transcriptase

## ABSTRACT

The piper yellow mottle virus (PYMoV) is a member under the genus *Badnavirus* and family *Caulimoviridae*. This virus has been causing nuisance and massive yield loss to the black pepper farming industry globally as it causes the stunt disease. In this study, we venture into the unattempted genome comparison across different isolates from different countries to look into the country-specific divergence. As a result, the genome comparison unraveled that the GC contents of the genomes isolated from host species *Piper nigrum* are comparatively lower in contrast to that isolated from other species. The genome fragment lengths of ORF2 and ORF4 tend to show country-specific patterns. The haplotype analysis further disclosed on the country-specific SNPs necessary for marker development. The whole genome phylogenetic tree constructed provides higher resolution in distinguishing country-specific clusters, in contrast to reverse transcriptase gene tree alone. The reverse transcriptase protein modelling further reinforced our apprehension on the regulators of these country-specific divergences. It is suggested that more PYMoV genomes to be sequenced from other countries to deepen our understanding on the virulence and variations of this virus in order to prevent massive harvest loss in the future.

## 1. Introduction

The piper yellow mottle virus (PYMoV) is grouped under the genus *Badnavirus* and family *Caulimoviridae*. It is a non-enveloped 30 × 125 nm sized (on average) bacilliform encompassing a circular double stranded DNA (Bhat et al., 2016). This virus is selective on its host range and known to only infect plants categorized under the genus *Piper* (Bhat et al., 2016).

The black pepper plant (*Piper nigrum*) is one of the most popular hosts for the PYMoV, besides *P. longum* and *P. betel* (Siju et al., 2008). This plant is famous for its fruit (peppercorn) which is known as the king of spices. Upon the infection by PYMoV, the host plant shows the symptoms of stunt disease, such as mottling of leaves, imperfect formation of fruits, shoot stunting, fruits reduction and shrinkage, internodes shortening and chlorosis (Kueh and Ahmed, 1986; Miftakhurohmah et al., 2019). To the best of our knowledge, there is no statistics reported to date on the global loss caused by PYMoV. However, in Indonesia, one of the largest black pepper exporters of the world (around 6 % of the global needs) (Miftakhurohmah et al., 2019), the disease incidence rate is as high as 86 to 93.75 % in Yogyakarta (Alif et al., 2018), 66.67 % in Sukamulya (Mariana and Miftakhurohmah, 2016) as well as 95 % in

Lampung and Bangka in 2005 (Lakani, 2006). This has severely impacted the yield of the pepper planting industry worldwide, particularly across Thailand, China, Indonesia, Malaysia and Sri Lanka (Lockhart et al., 1997; Sarma et al., 2001; De Silva et al., 2002; Miftakhurohmah et al., 2019; Che et al., 2020). The mastermind orchestrating the viral infection is none other than the genome of the PYMoV.

The major orchestrator of the PYMoV virulence is the reverse transcriptase protein. The process of reverse transcription happens within the virus capsid with the aid of the reverse transcriptase protein in synthesising plus- and minus-strand circular DNA double strands prior to the resultant DNA being transported to the nucleus (Hohn and Rothnie, 2013). In the nucleus, these DNAs were checked for defects and are repaired rapidly. Then, these supercoiled DNAs are unified with the histone proteins via covalent bonding eventually forming the mini-chromosomes (Hull, 2014). These mini-chromosomes is transcribed with the assistance from the host-encoded DNA-dependent RNA polymerase II, resulting in the synthesis of a terminally redundant RNA which functions both as polycistronic and pregenome messenger RNA (Hull, 2014). The last replication procedure involves the conversion of pregenomic RNA back to the double stranded DNA via the actions of the

Abbreviations: ORF, open reading frame; PYMoV, piper yellow mottle virus.

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<https://doi.org/10.1016/j.genrep.2022.101680>

Received 10 May 2022; Received in revised form 19 August 2022; Accepted 7 September 2022

Available online 13 September 2022

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