

## INTISARI

*Rehmannia mosaic virus* (ReMV) merupakan salah satu virus anggota genus Tobamovirus yang telah teridentifikasi menginfeksi tanaman tembakau (*Nicotiana tabacum* L.) di Indonesia, khususnya di wilayah sentra produksi tembakau di Jawa Tengah dan D.I. Yogyakarta. Penelitian ini bertujuan untuk melakukan analisis molekuler dan uji kisaran inang terhadap isolat ReMV dari kedua daerah tersebut. Penelitian ini dilakukan melalui beberapa tahapan yaitu pengambilan sampel tanaman tembakau bergejala, inokulasi mekanik pada tanaman indikator *Chenopodium amaranticolor*, ekstraksi RNA, RT-PCR, elektroforesis, sekuensing, analisis filogenetik, serta uji kisaran inang pada beberapa spesies tanaman dari tujuh famili berbeda. Hasil analisis molekuler menunjukkan bahwa isolat ReMV asal Magelang 1, Magelang 2, Temanggung, dan Yogyakarta memiliki kekerabatan dekat dengan isolat ReMV dari Jepang dengan persentase homologi berkisar 90,48% hingga 96,49%. Sedangkan isolat Demak memiliki kekerabatan tertinggi dengan isolat ReMV asal Amerika Serikat dengan persentase homologi sebesar 97,98%. Uji kisaran inang menunjukkan bahwa ReMV mampu menginfeksi sembilan spesies tanaman dari tujuh famili berbeda yaitu *Gomphrena globosa*, *Zinnia elegans*, *Chenopodium amaranticolor*, *Cucumis melo* L, *Phaseolus vulgaris*, *Nicotiana tabacum* L, *Solanum melongena* L, *Capsicum annum* L, *Bougainvillea* Comm. ex Juss. Hasil penelitian ini diharapkan dapat menjadi acuan dalam pengelolaan ReMV di lahan pertanaman tembakau, khususnya dalam strategi rotasi tanaman dan pengendalian penyebaran virus.

**Kata kunci: ReMV, kisaran inang, tembakau, PCR, filogenetik**

## ABSTRACT

*Rehmannia mosaic virus* (ReMV) is one of the viruses belonging to the Tobamovirus genus that has been identified to infect tobacco plants (*Nicotiana tabacum* L.) in Indonesia, particularly in the tobacco production centers in Central Java and Yogyakarta Special Province. This research aims to conduct molecular analysis and host range testing on ReMV isolates from both regions. This research was conducted through several stages, namely sampling symptomatic tobacco plants, mechanical inoculation on the indicator plant *Chenopodium amaranticolor*, RNA extraction, RT-PCR, electrophoresis, sequencing, phylogenetic analysis, and host range testing on several plant species from seven different families. The results of the molecular analysis show that the ReMV isolates from Magelang 1, Magelang 2, Temanggung, and Yogyakarta are closely related to the ReMV isolates from Japan, with a homology percentage ranging from 90,48% to 96,49%. Meanwhile, the Demak isolate has the highest genetic similarity with the ReMV isolate from the United States, with a homology percentage of 97,98%. Host range tests showed that ReMV is capable of infecting nine plant species from seven different families, namely *Gomphrena globosa*, *Zinnia elegans*, *Chenopodium amaranticolor*, *Cucumis melo* L, *Phaseolus vulgaris*, *Nicotiana tabacum* L, *Solanum melongena* L, *Capsicum annum* L, *Bougainvillea* Comm. ex Juss. The results of this research are expected to serve as a reference in managing ReMV in tobacco cultivation areas, particularly in crop rotation strategies and controlling virus spread.

**Keywords: ReMV, host range, tobacco, PCR, phylogenetic**