

## INTISARI

*Bemisia tabaci* merupakan hama pertanian yang mengganggu pertumbuhan tanaman, serta menjadi serangga vektor dari berbagai jenis virus salah satunya kelompok *geminivirus*. *B. tabaci* disebut juga *CrypticSpecies Complex*, yang mana morfologi tidak berbeda namun secara genetik berbeda. Perubahan iklim dan peningkatan transportasi global produk pertanian dapat meningkatkan populasi *B. tabaci* dan dapat menjadi potensi munculnya genetika yang berbeda. Penelitian ini bertujuan untuk mendapatkan informasi terbaru mengenai homegenasi populasi pada empat kabupaten di Daerah Istimewa Yogyakarta dan mendapatkan informasi potensi perbedaan susunan nukleotida dan asam amino sebagian wilayah sitokrom c oksidase I. Identifikasi molekuler dengan teknik PCR menggunakan primer C1-J-2198/L2-N-3914 dilakukan pada *B. tabaci* yang dikoleksi. Pensejajaran dilakukan pada data sekuens dan dianalisis pohon filogenetik. Hasil penelitian menunjukkan bahwa populasi *B. tabaci* di Indonesia masih homogen dibuktikan dengan memiliki biotipe yang sama yaitu biotipe non B berdasarkan analisis filogenetik. *B. tabaci* Yogyakarta memiliki persamaan basa nukleotida sebesar 100% dengan *B. tabaci* dari negara Singapura (AY686095) dan Thailand (AY686092) dan 99.78% dengan *B. tabaci* asal Bangladesh (AJ748388). Terdapat perbedaan komposisi basa nukleotida dari empat kabupaten pengambilan *B. tabaci*, hal ini terjadi karena adanya mutasi. Namun perbedaan basa nukleotida tidak mempengaruhi komposisi asam amino, dengan demikian ada kecenderungan lingkungan mendorong terhadap mutasi tapi bersifat sinonimous.

Kata kunci: *Bemisia tabaci*, biotipe, identifikasi molekuler, sinonimous.

## ABSTRACT

*Bemisia tabaci* is an agricultural pest that interferes with plant growth, as well as being an insect vector of various types of viruses, one of which is the *Geminivirus* group. *B. tabaci* is also called *Cryptic Species Complex*, which is morphologically not different but genetically different. Climate change and increased global transportation of agricultural products could increase in the population of *B. tabaci* and could potentially lead to the emergence of genetic diversity. This study aims to obtain the latest information on population homogenization in four districts in the Special Region of Yogyakarta and their potential differences in nucleotide sequences. Molecular identification by a PCR (*Polymerase Chain Reaction*) technique using primers C1-J-2198/L2-N-3914 was performed on the collected *B. tabaci*. Sequence characterization was compared for phylogenetic analysis, similarities, and differences in nucleotide bases. The results showed that the population of *B. tabaci* in Indonesia was still homogeneous, as evidenced by having the same biotype, namely non-B biotype based on phylogenetic analysis. *B. tabaci* Yogyakarta has a nucleotide base similarity of 100% with *B. tabaci* from Singapore (AY686095) and Thailand (AY686092) and 99,69% with *B. tabaci* from Bangladesh (AJ748388). There were differences in the nucleotide base composition of the four *B. tabaci* uptake districts, this was due to mutations. However, the difference in nucleotide bases does not affect the amino acid composition, thus there is a tendency for the environment to encourage mutations that are synonymous.

**Keywords:** *Bemisia tabaci*, biotype, molecular identification, synonymous.