Whitefly surveillance and bio-typing: implications for spread of CMV and other WF transmitted diseases

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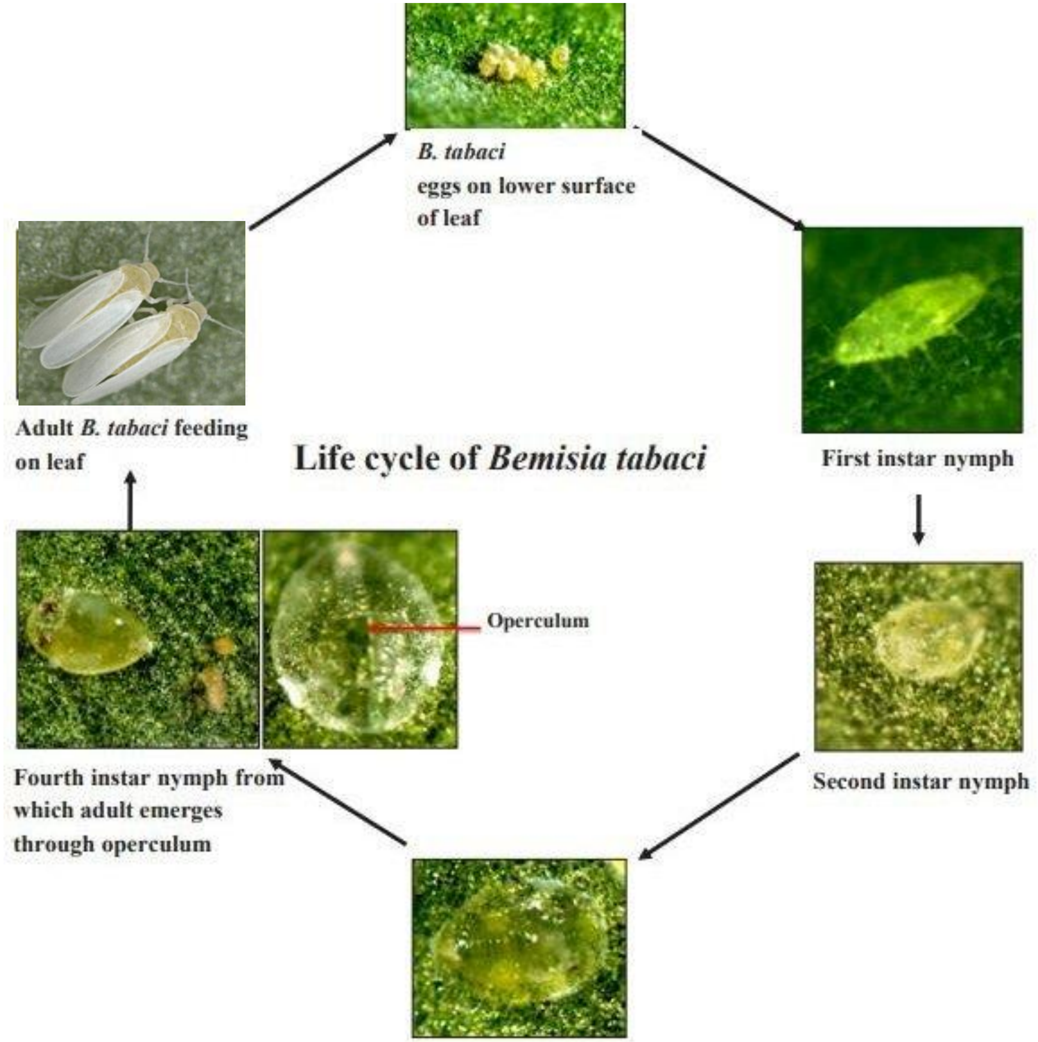
Whitefly (*Bemesia tabaci*) as a vector of Cassava Mosaic Disease (CMD)



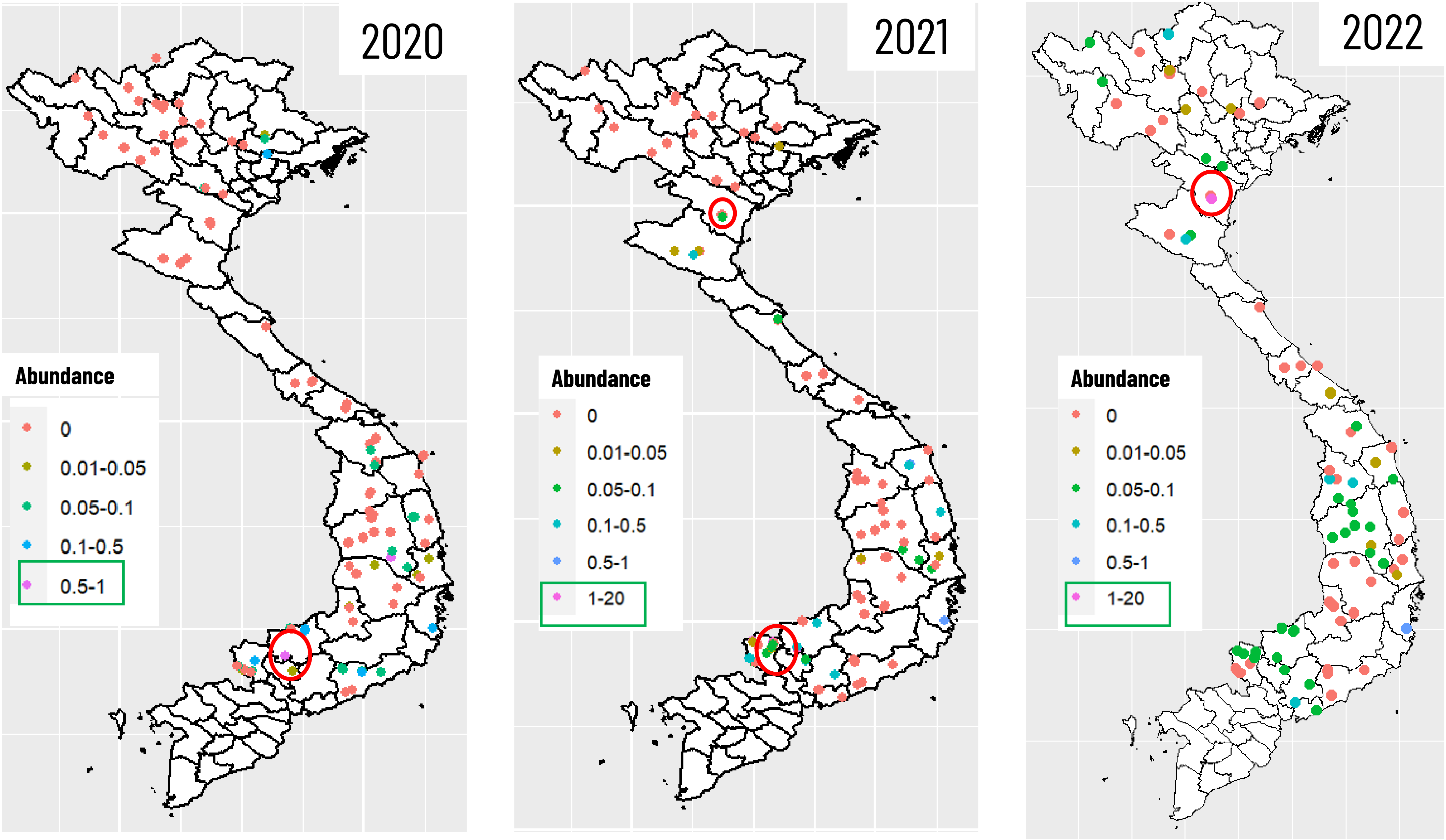
Whitefly distribution in Laos, Vietnam, and Cambodia: https://pdptest.ciat.cgiar.org/projects/PDP_00088/map#4.63/15.94/103.6

FACT1:The population of whiteflies on cassava in SEA different from Africa

Uganda >200+

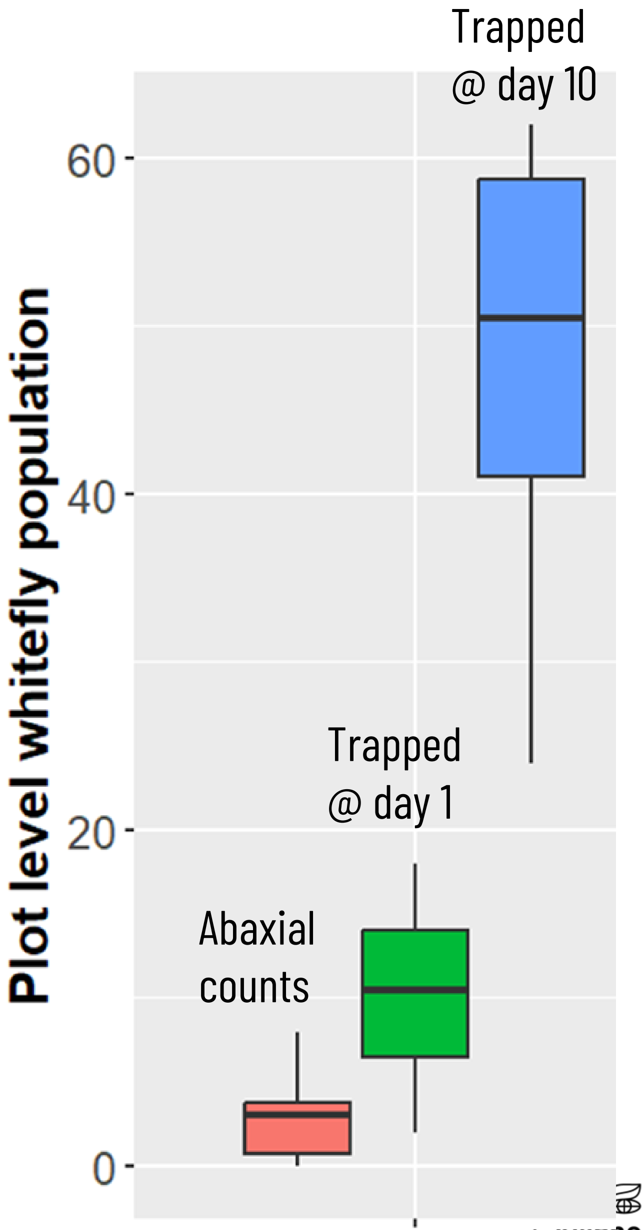
e.g., Vietnam (0-20)

Fact 2: Whitefly population building up in some countries e.g. Vietnam



Fact 3: The whitefly numbers in cassava fields could be more!

Evidence-based on plot level traps



Fact 4: Though infection appears to be primarily through infected stems, whitefly transmission observed in the field

Possibly stem infection

Possibly whitefly (only newly emerging leaves showing symptoms

Fact 5: The most abundant species is Asia II 1 & 6

insects

MDPI

Article

Mitochondrial Genetic Diversity of *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) Associated with Cassava in Lao PDR

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Simple Summary: The whitefly species *Bemisia tabaci* is a known pest of cassava and a vector of cassava geminiviruses in Africa and India, but its role in the recent spread of Cassava Mosaic Disease (CMD) in Southeast Asia is not well known. This is in part due to a lack of data on the occurrence and distribution of *B. tabaci* in this region. We show here the first results of any country-wide survey and identification of *B. tabaci* colonizing cassava in Lao PDR.

Abstract: Cassava Mosaic Disease (CMD) caused by Sri Lankan cassava mosaic virus (SLCMV), has rapidly spread in Southeast Asia (SEA) since 2016. Recently it has been documented in Lao PDR. Previous reports have identified whitefly species of *B. tabaci* as potential vectors of CMD in SEA, but their occurrence and distribution in cassava fields is not well known. We conducted a countrywide survey in Lao PDR for adult whiteflies in cassava fields, and determined the abundance and genetic diversity of the *B. tabaci* species complex using mitochondrial cytochrome oxidase I (mtCOI) sequencing. In order to expedite the process, PCR amplifications were performed directly on whitefly adults without DNA extraction, and mtCOI sequences obtained using nanopore portable-sequencing technology. Low whitefly abundances and two cryptic species of the *B. tabaci* complex, Asia II 1 and Asia II 6, were identified. This is the first work on abundance and genetic identification of whiteflies associated with cassava in Lao PDR. This study indicates currently only a secondary role for Asia II in spreading CMD or as a pest. Routine monitoring and transmission studies on Asia II 6 should be carried out to establish its potential role as a vector of SLCMV in this region.

Keywords: *Bemisia tabaci*; whitefly; nanopore; mtCOI; Southeast Asia; haplotype; Cassava Mosaic Disease

check for updates

Citation: Leiva, A.M.; Chittarath, K.; Lopez-Alvarez, D.; Vongphachanh, P.; Gomez, M.I.; Sengsay, S.; Wang, X.-W.; Rodriguez, R.; Newby, J.; Cuellar, W.J. Mitochondrial Genetic Diversity of *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) Associated with Cassava in Lao PDR. *Insects* **2022**, *13*, 861. https://doi.org/10.3390/insects13100861

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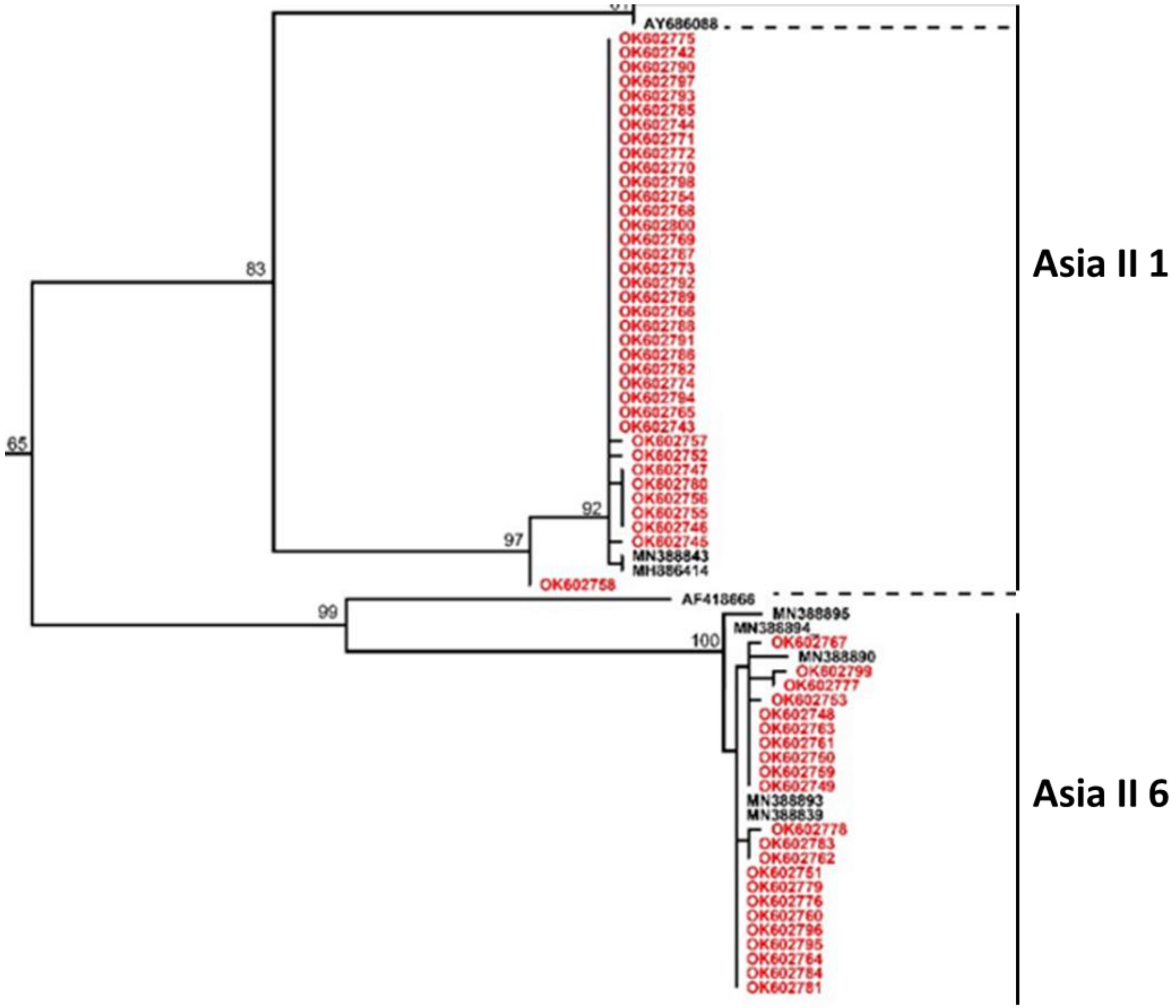
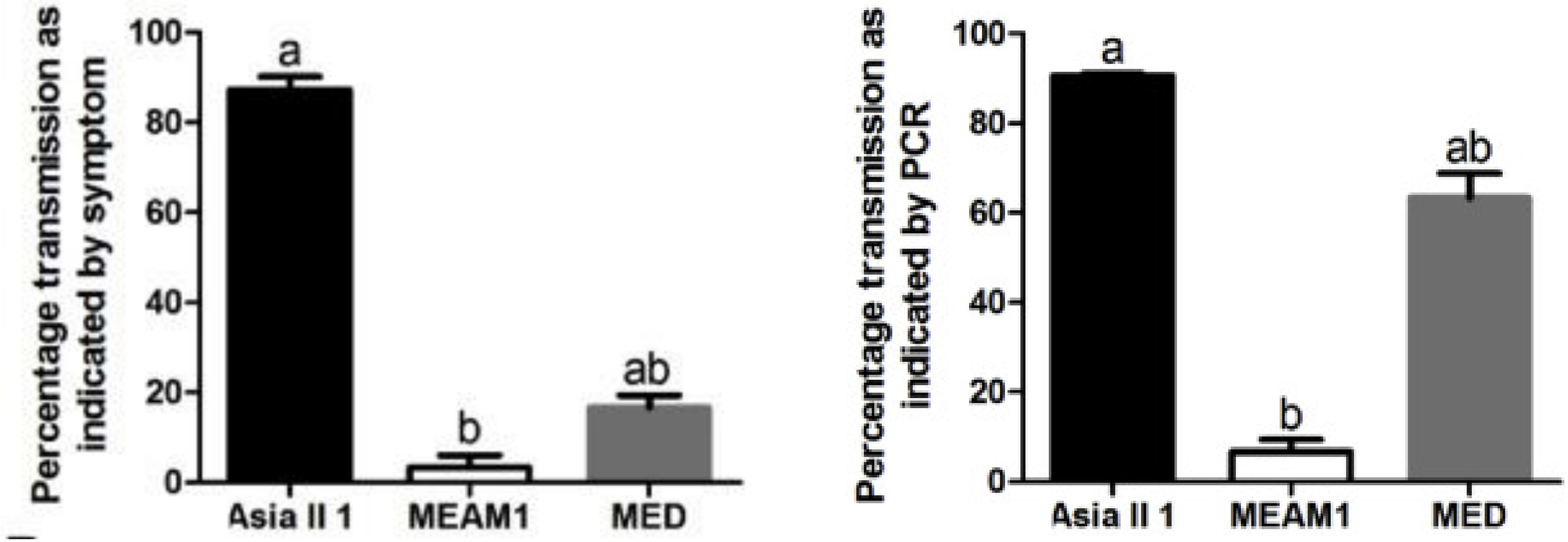


Is Asia II 1 an efficient vector of SLCMV?



Chi et al., 2020

Questions to ponder

A. In the current project area (Laos, Vietnam, Cambodia, and Thailand)

- Is Asia II 1 likely to adapt to cassava with cassava production expansion?
- cassava and become aggressive on cassava?
- Is a new biotype likely to emerge?

See discussions, stats, and author profiles for this publication at: https://www.researchgate.net/publication/354271675

First report of the invasive MEAM1 whitefly [Bemisia tabaci (Gennadius)], vector of tomato leaf curl viruses in a major tomato-growing region of Maharashtra, India

Article *in* Acta Horticulturae · August 2021

B. New landscape (Indonesia and the Philippines) and new strains

- Are current CMD-free high cassava production countries prepared for possible outbreaks?
- How are countries prepared for emergence of new strains?

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