



Diversity of begomoviruses causing disease in chilli peppers in Asia

Lawrence Kenyon, Sanjeet Kumar, Su-Ling Shih, Li-Mei Lee and Yuan-Li Chan
World Vegetable Center, Shanhua, Tainan 74199, Taiwan



Lawrence.Kenyon@worldveg.org

INTRODUCTION

Chilli or pepper leaf curl diseases have emerged over the last 10-15 years to be some of the most damaging constraints to *Capsicum* pepper production across much of Asia. The diseases are caused by begomovirus(es) (Whitefly-transmitted Geminiviruses) either as single infections or sometimes as mixed infections. Often in the field the diseases are combined with or confused with leaf curl or bunchy top caused by mites and/or thrips resulting in “Chilli leaf curl complex”. So far, attempts to breed for resistance to Chilli leaf curl for this region have been largely unsuccessful because identified resistance has not been transferable to other locations or has broken down relatively quickly. Our aim in this study was to assess the diversity of begomoviruses able to infect chilli or sweet peppers across the region in order to identify a better strategy for identifying more durable leaf curl resistance and deploying it more sustainably.

METHOD

All the full-length Begomovirus DNA-A component sequences marked as being from chilli or pepper plants (and some very similar sequences from tomato plants) from different countries in Asia (as of January 2018) were downloaded from NCBI database and with some unpublished sequences from our lab formed a set of 102 sequences for analysis. The number of Begomovirus species present was assessed based on pairwise sequence identity threshold of 91% using the Sequence Demarcation Tool (SDT) as described by Brown et al, (2015). Phylogenetic analysis of the set of sequences was also performed using MEGA 7.

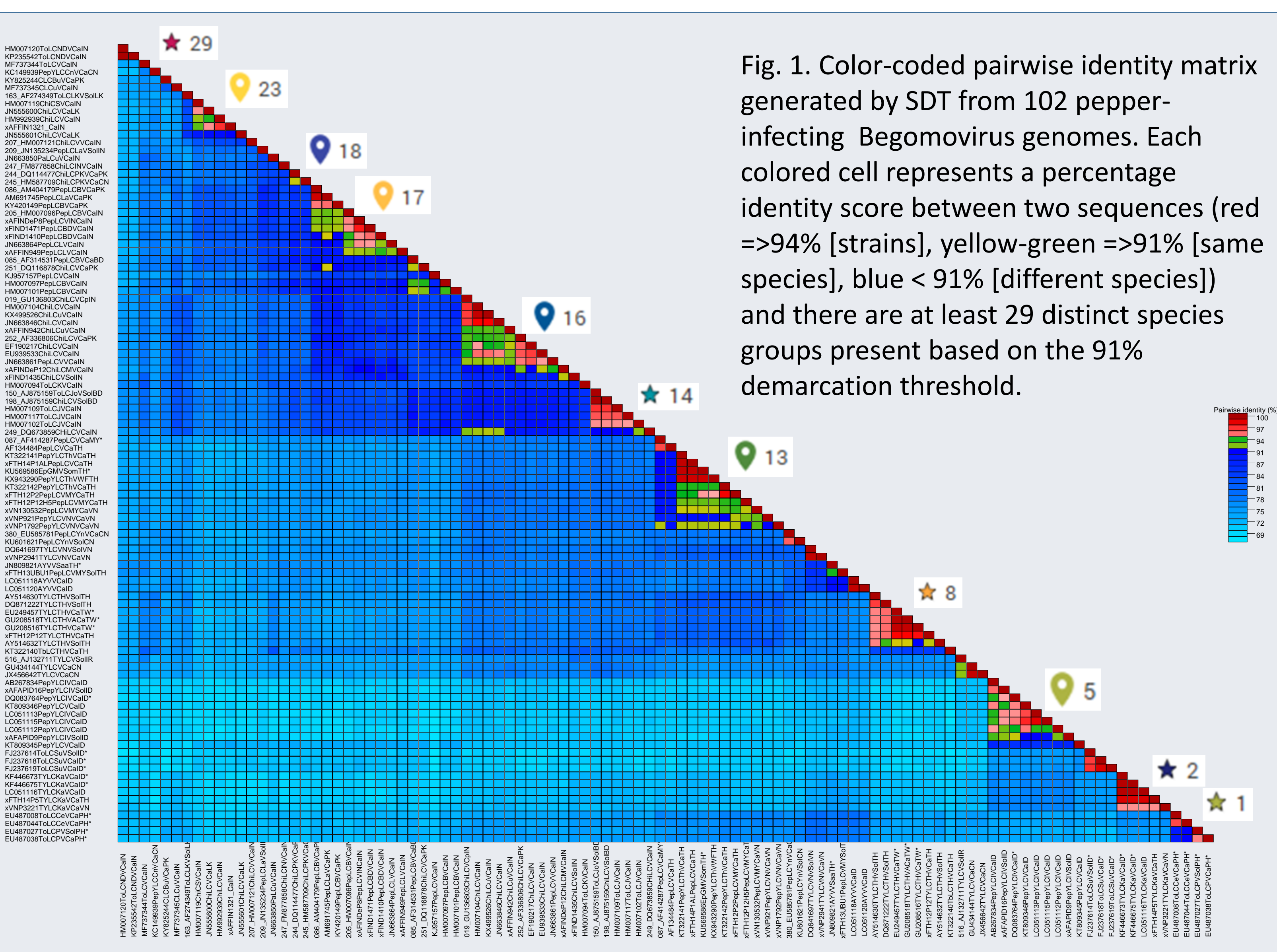


Fig. 1. Color-coded pairwise identity matrix generated by SDT from 102 pepper-infecting Begomovirus genomes. Each colored cell represents a percentage identity score between two sequences (red =>94% [strains], yellow-green =>91% [same species], blue < 91% [different species]) and there are at least 29 distinct species groups present based on the 91% demarcation threshold.

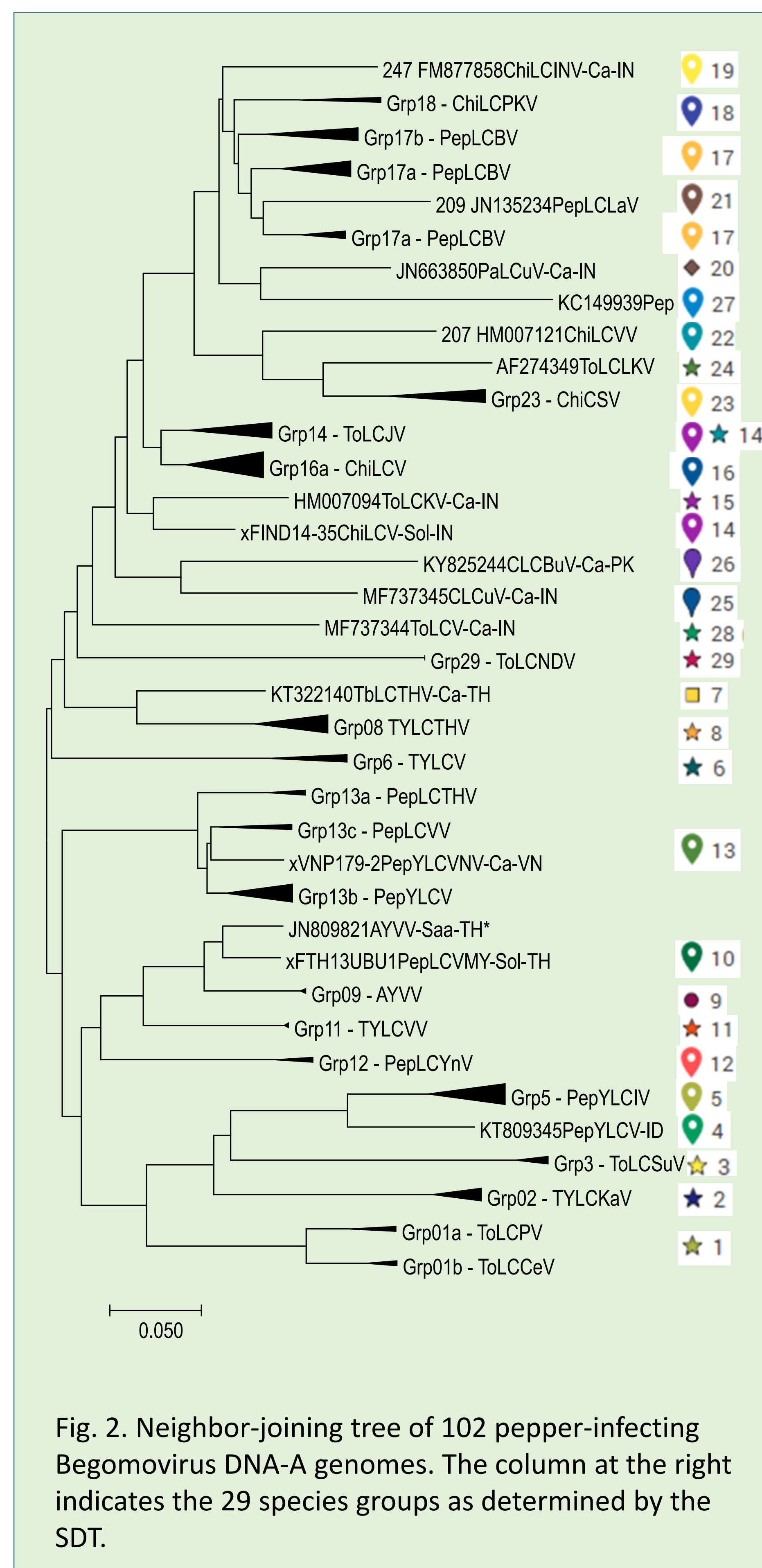


Fig. 2. Neighbor-joining tree of 102 pepper-infecting Begomovirus DNA-A genomes. The column at the right indicates the 29 species groups as determined by the SDT.



Diverse range of symptoms: 1 = late infection after fruit set, 2 = mild infection by a “Tomato” virus, 3 = chilli leaf curl without much yellowing, 4 = severe pepper yellow leaf curl, 5 = severe stunting & leaf curl by very early infection, 6 = “chilli leaf curl complex” caused by Begomovirus and mite infestation.



Fig. 3. Locations where the 29 different pepper-infecting Begomovirus species were collected. The symbols are the same as those in the right hand column in Fig. 2. (Stars [] are begomoviruses with “Tomato” in the name, pins [] are begomoviruses that have (or should have) “Pepper” or “Chilli” in their name.

RESULTS AND CONCLUSIONS

- The STD delimited at least 29 species within the set of 102 Begomovirus sequences from Asia (Fig.1.), some represented by a single sequence (e.g. Grp 7), others represented by several sequences and where different strains (<94% identity) were delimited (e.g. Grp 13) and outliers could be distinct species.
- The phylogenetic analysis (Fig. 2.) delimited roughly similar species clusters, though sometimes split larger SDT delimited species into distinct sub-clusters (e.g. Grp 17) making complex overlapping species groups.
- GenBank sequence records do not indicate the severity of symptoms (if any) in the pepper plants the sequences were obtained from, so the identified species may not necessarily have caused major disease.
- No distinction was made between mono-partite and bipartite begomoviruses, nor the presence of alpha- or betasatellites which can greatly affect transmission rates and severity of symptoms induced.
- Major geographic gaps in the data include Myanmar, northern Laos & southern China, Brunei, Malaysia (Sarawak & Sabah) and Indonesia (Kalimantan & Islands east of Sulawesi).
- Greatest Begomovirus diversity is in Indian subcontinent, followed by Thailand (+Cambodia, Lao, Vietnam).
- Further east, e.g. in Philippines and Taiwan, the species were originally identified from tomato and may represent more recent adaptations to infecting pepper.
- The existence of so many species, some with overlapping geographical distributions means that screening for sources of resistance is difficult since mixed infections may mask species/strain specific resistance.
- Ideally, screening should be done separately (under controlled conditions) with different virus species so that species/strain specific resistances can be identified; it may then be possible to identify combinations of resistances that are more likely to be durable in certain locations.