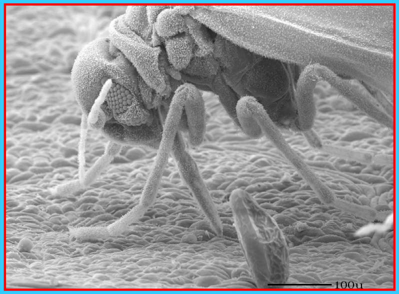
The *Bemisia tabaci* complex



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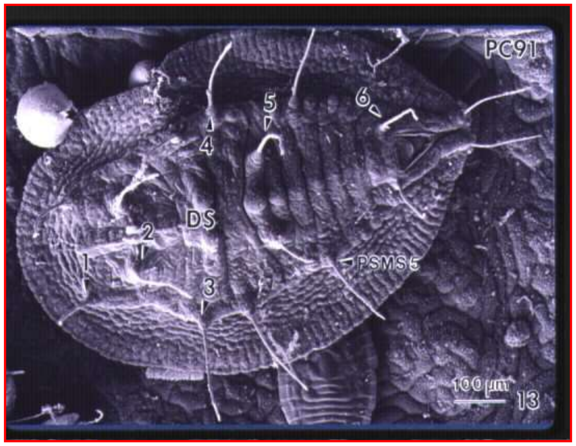
V. The Whitefly Vector

Adult

Pupal stage /4th Instar

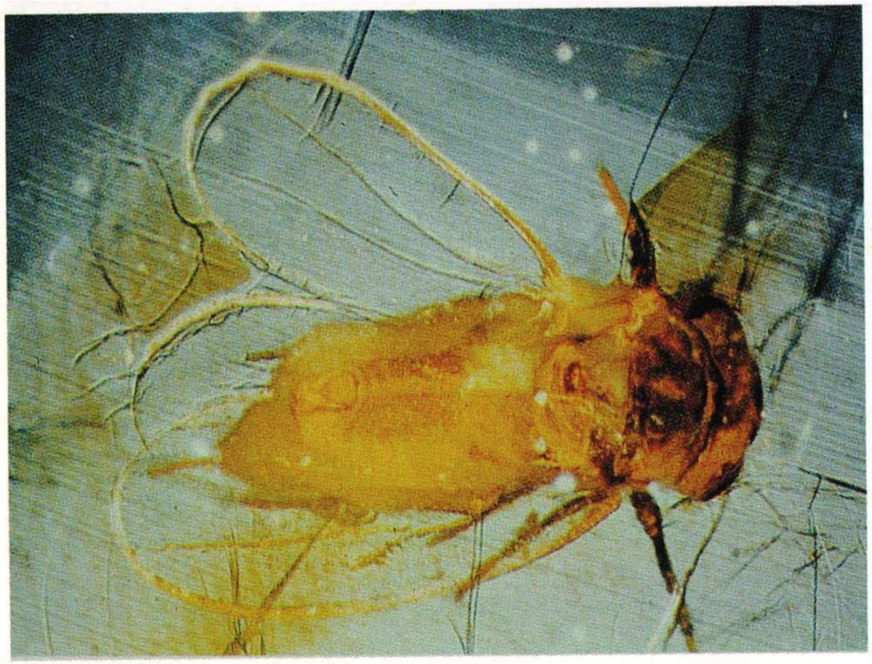


Bemisia tabaci (Genn.)

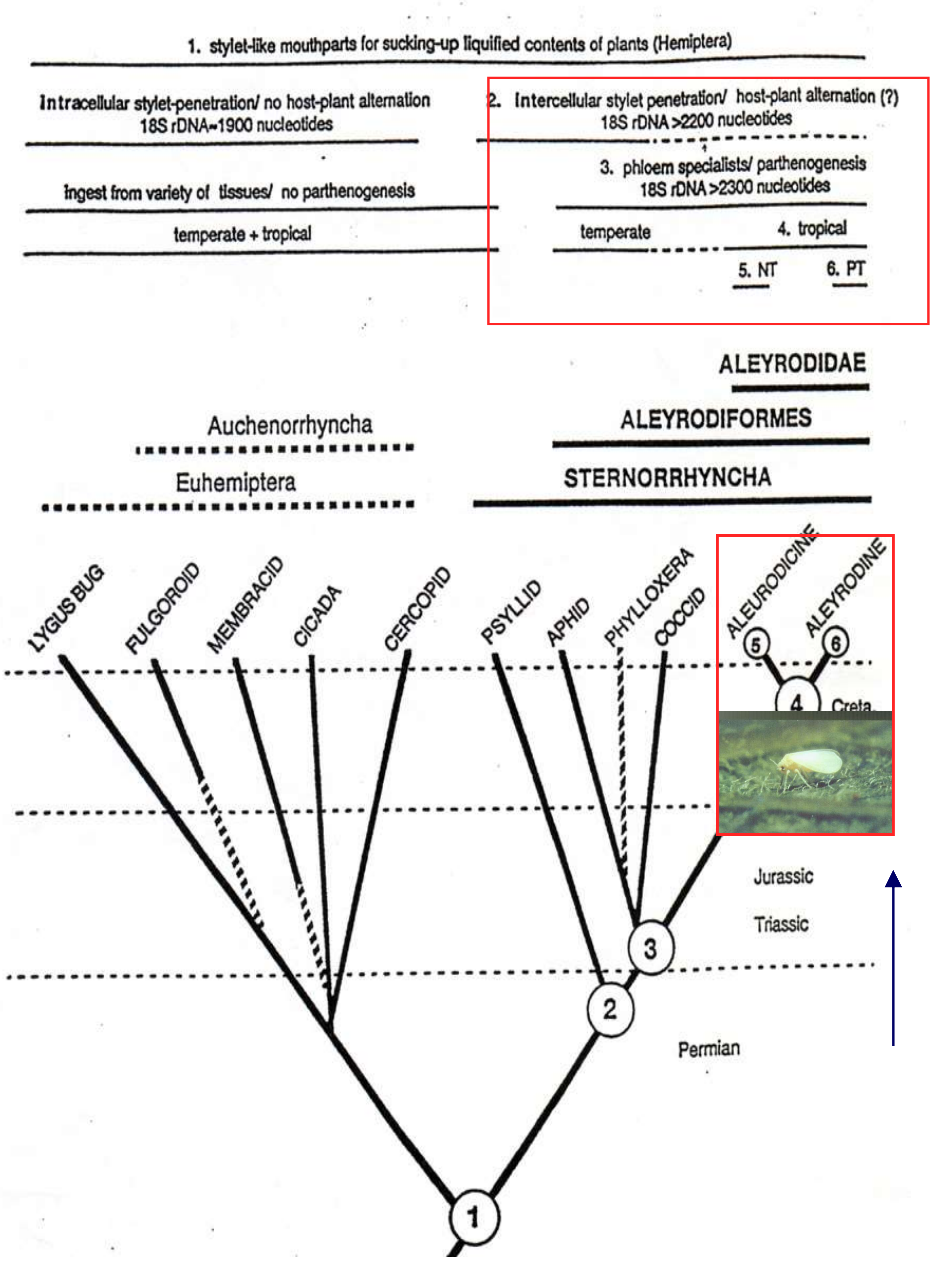
- Worldwide, most important whitefly vector of plant viruses: irrigated cropping systems subtropics/tropics
- Only whitefly vector for Begomoviruses
- Species rich in biological variants-lacks distinguishing morphological (4th instar) characteristics
- Synonymized from numerous species and variants by Russell, 1957 (historical evidence: cryptic species)
- Recent evidence for phenotypic & genotypic variants

Bemisia tabaci has been here for a long time…

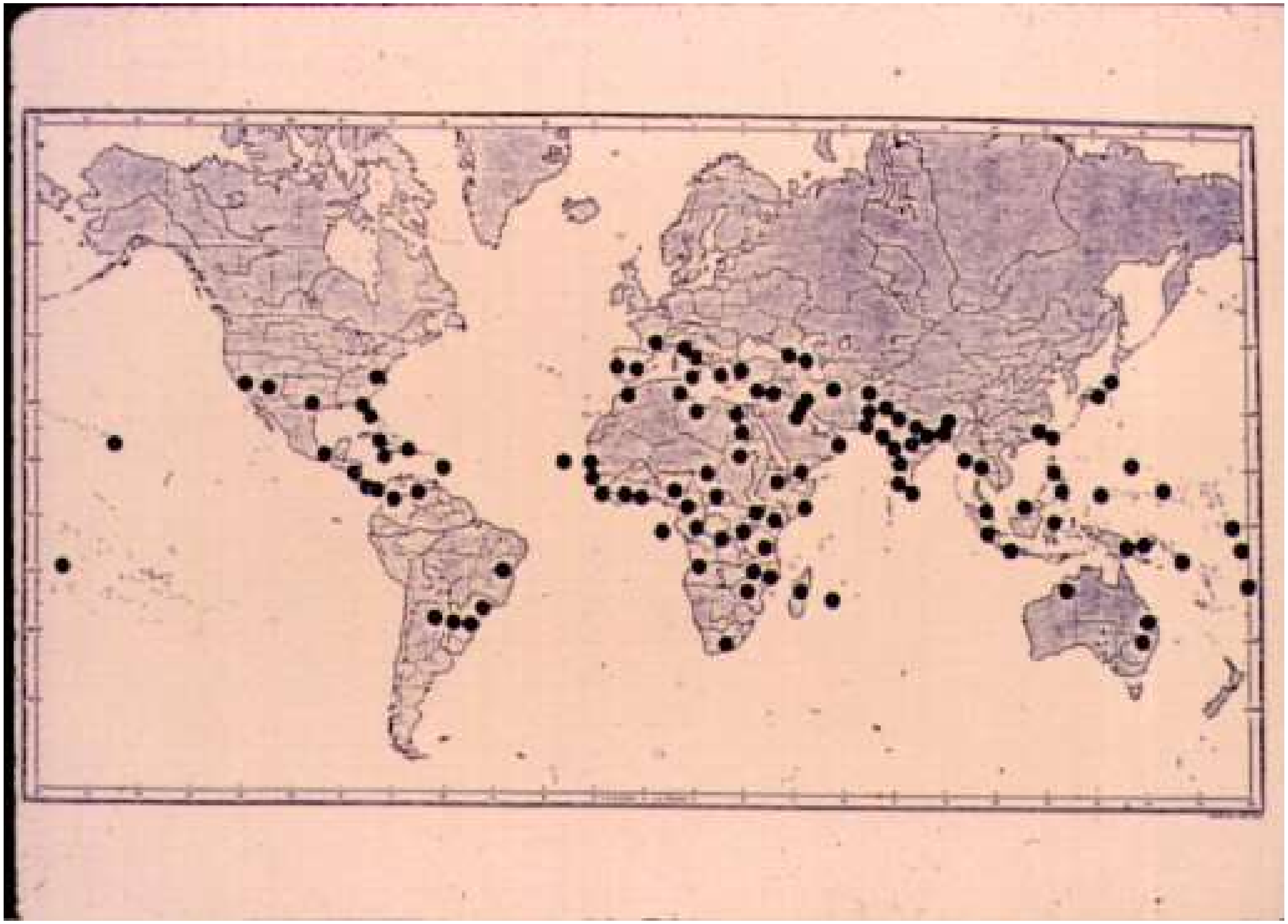
- Tropical origin
- Phloem specialists - intercellular stylet penetration
- Parthenogenesis



Primitive whitefly, *Bernaea neocomica* Schlee in Lebanese amber - 120 to130 MY BP -Stuttgart Natural History Museum collection



Extant *B. tabaci* - widely distributed ~b/t 30^0 parallels N& S



- -Evidence for morphological variation = taxonomic confusion (Basu & Mohanty; Mound)
- -Most - highly polyphagous, but some are ‘host-adapted’

First evidence for biologically distinct populations

Bird (1957) recognized Jatropha race was 'host-restricted'; Low fecundity

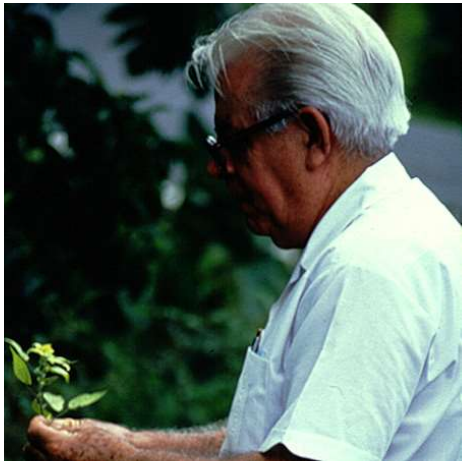
Sida race was polyphagous; moderate to high fecundity

Proposed 'concept' of races

Then Costa and Russell (1975) recognized that *B. tabaci* from Brazil did not colonize cassava (its center of origin) adding to J. Bird's' race' hypothesis; cassava associated populations discovered on cassava in Africa (Burban et al., 1991) (begomovirus vectors)

AZ-A and B biotypes recognized after the introduction of the B type in 1988-89 (Costa & Brown)

Jatropha

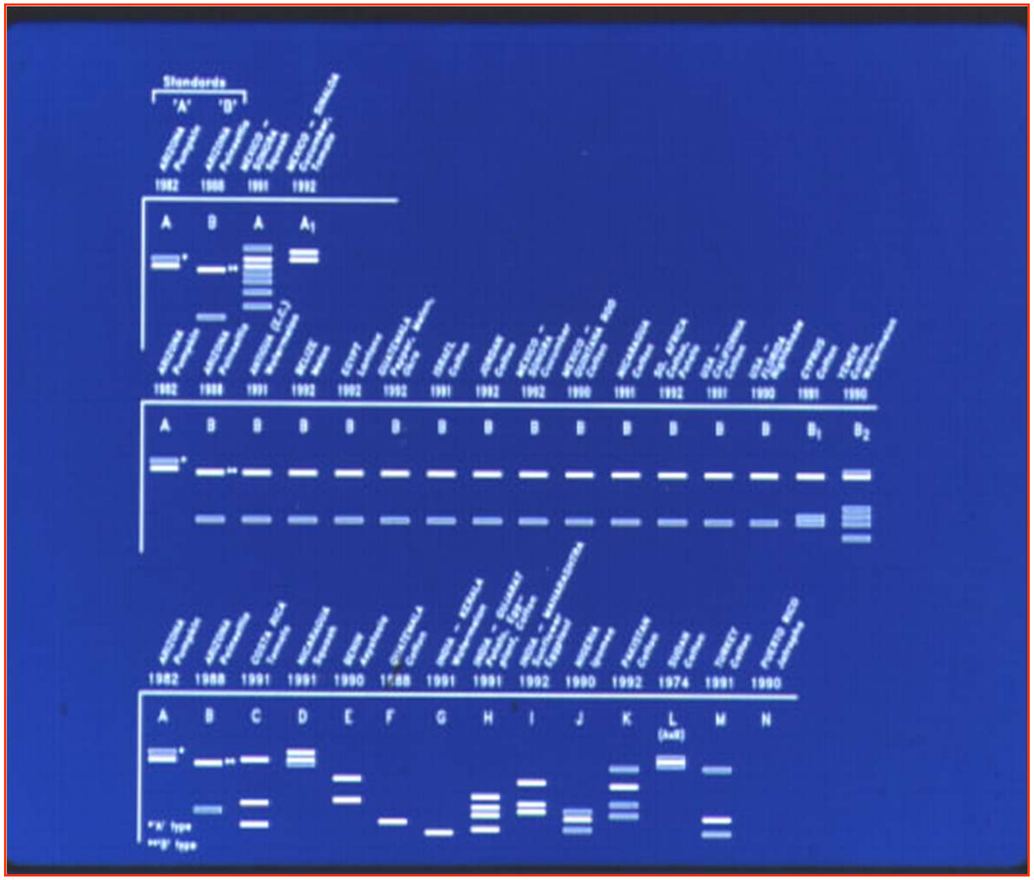


Dr. Julio Bird

Sida

1987/88 B biotype introduced to US & Caribbean, C& So America & worldwide - SSL diagnostic phenotype (Costa& Brown 1990) -Polyphagous; preferred cotton, cucurbits, poinsettia, tomato

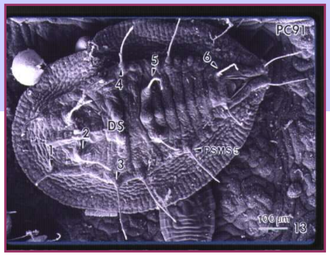
‘Discovery’
of
the B
biotype



Using general esterases first demonstrated widespread genetic polymorphisms genus-wide throughout the subtropics

Brown et al., UAZ - 1989-1993)

A number of biotypes are now known, but cannot be distinguished using morphological characters



Biological Characters That Can Differ

-Geographic range: limited vs. widespread/

-Fecundity: ~50 to 300+ offspring

-Begomovirus transmission competency - co-evolution

-Host range: monophagous to polyphagous

-Dispersal behavior: short or long distance

-Mating behavior /some are isolated by geography/host?

-Hybrids for certain haplotype crosses, others incompatible (produce only males = no fertilization)

-Insecticide resistance - highly variable and plastic

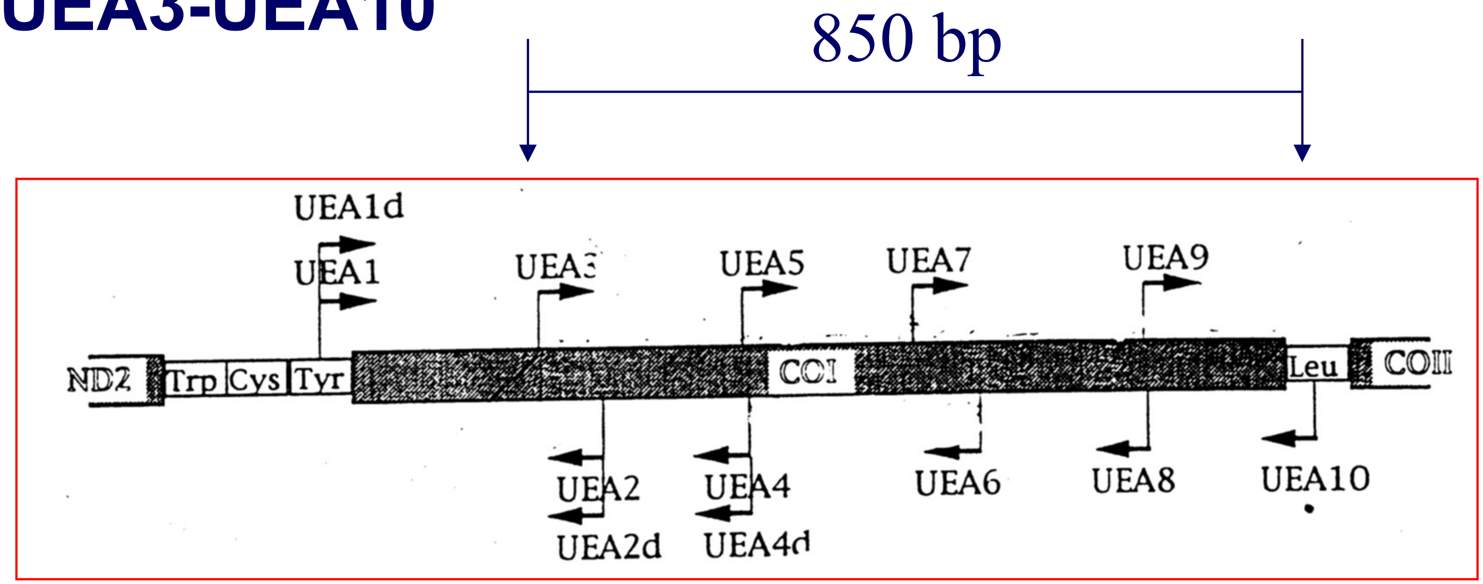
Molecular marker-DNA sequence used for identification

- **Mitochondria**

  -Cytochrome oxidase I gene

  -Primer locations

  UEA3-UEA10



PCR Primers

Forward C1-J-2195

5’ ttg att ttt tgg tca tcc aga agt 3’

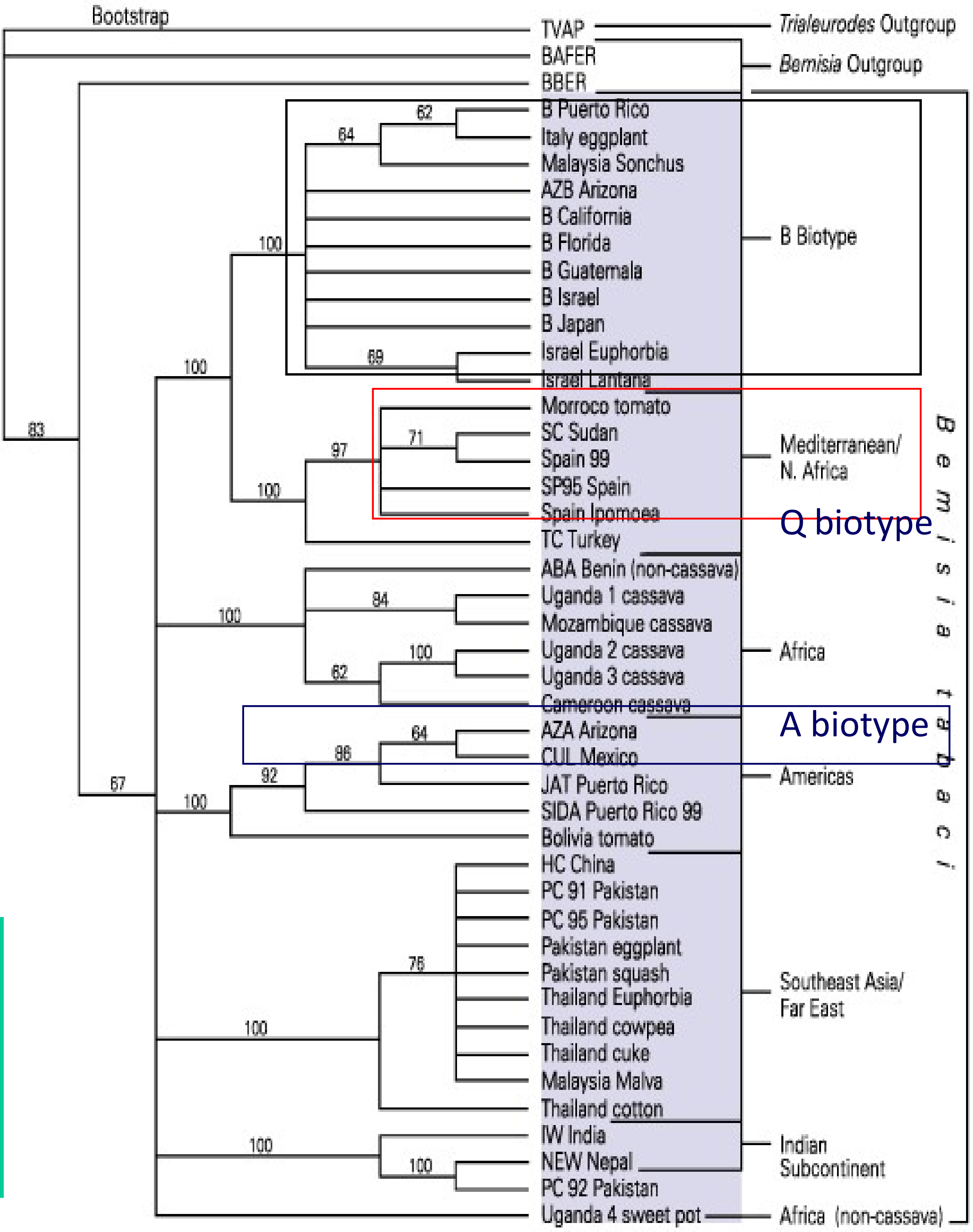
Reverse L2-N-3014

5’ tcc aat gca cta atc tgc cat att a 3’

(UBC Insect Mitochondrial DNA Primer Oligonucleotide Set, compiled by B. J. Crespi and C. Simon, with most sequences taken from Simon et al., 1994)

MT COI sequence reveals phylogeo-graphic clusters

Hypothesis: species complex



The Big Picture

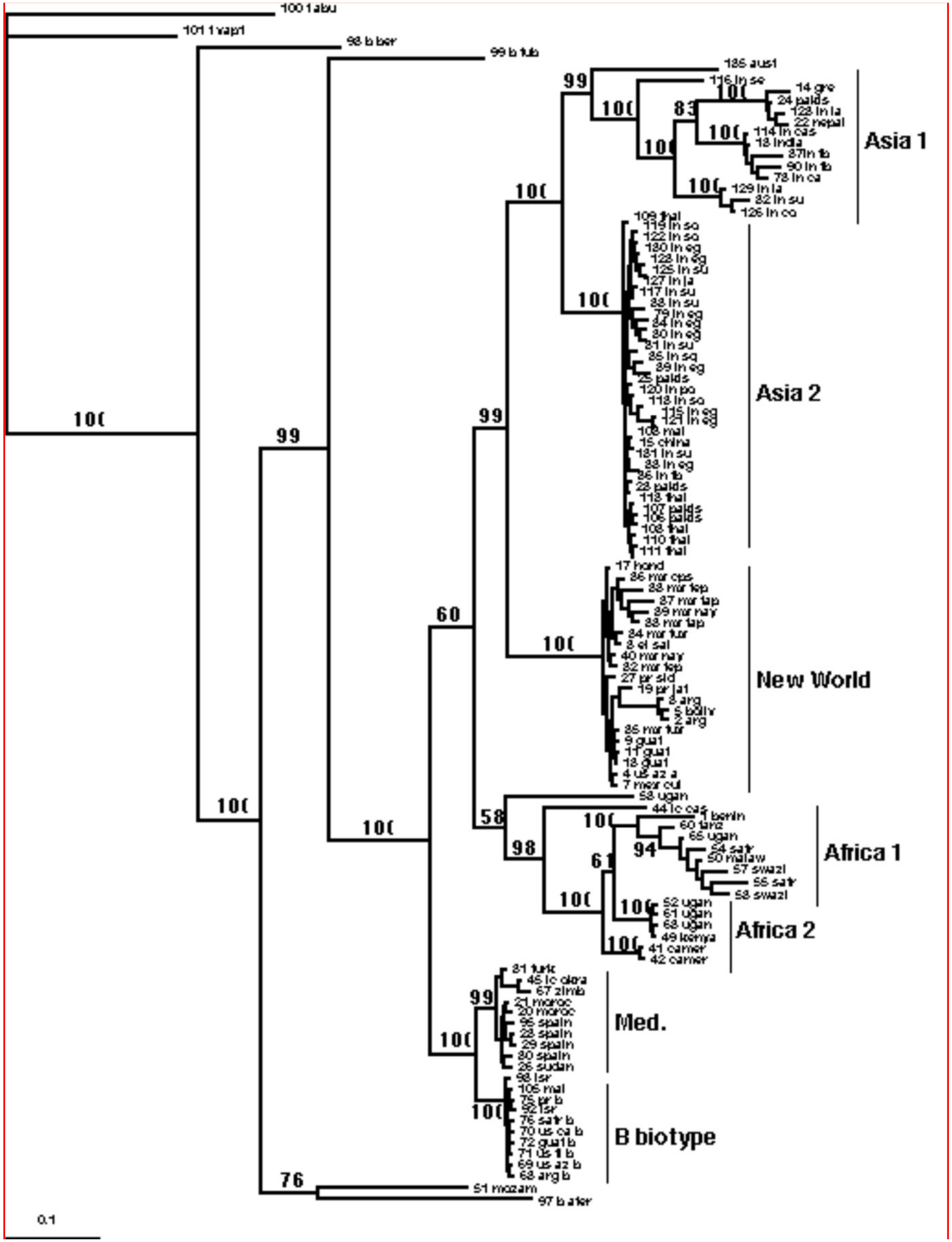
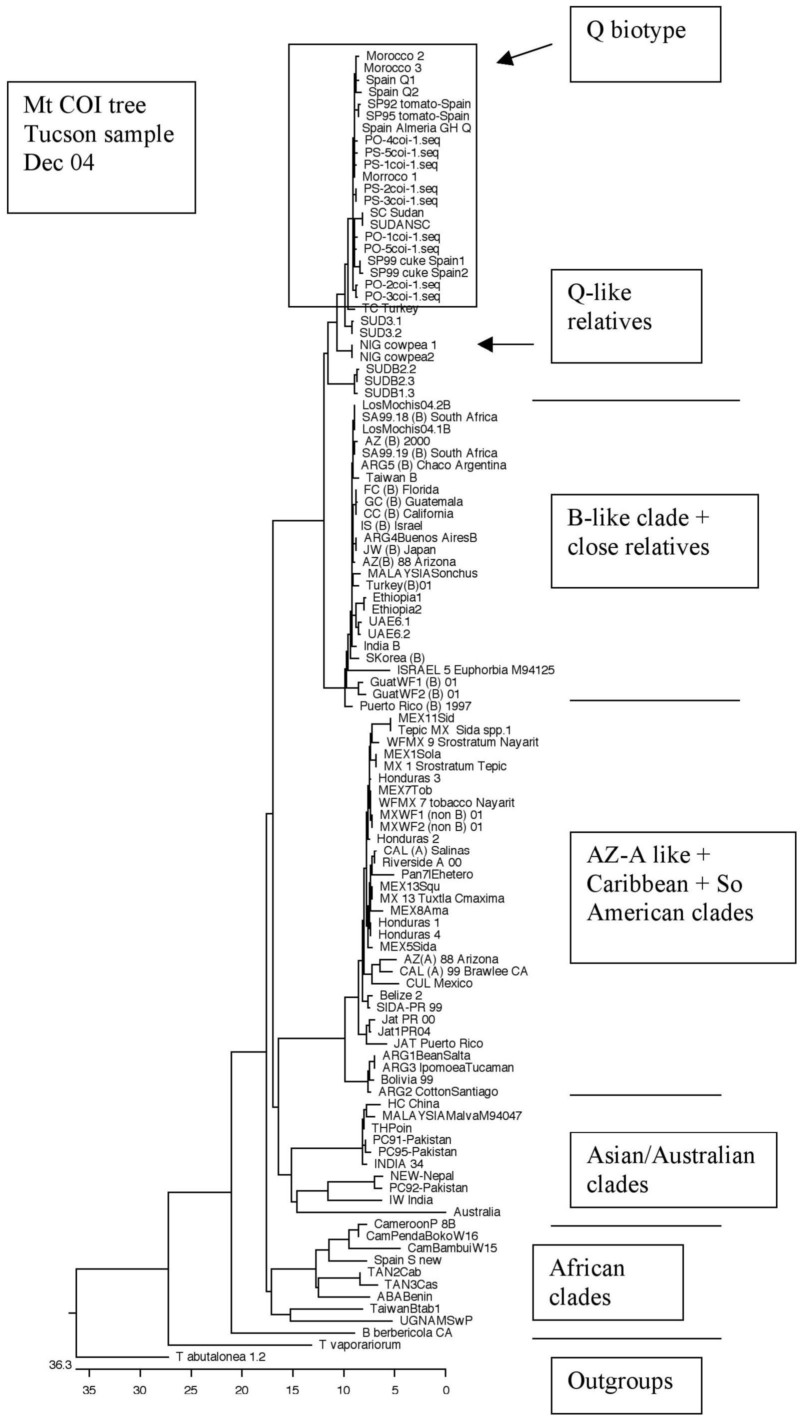


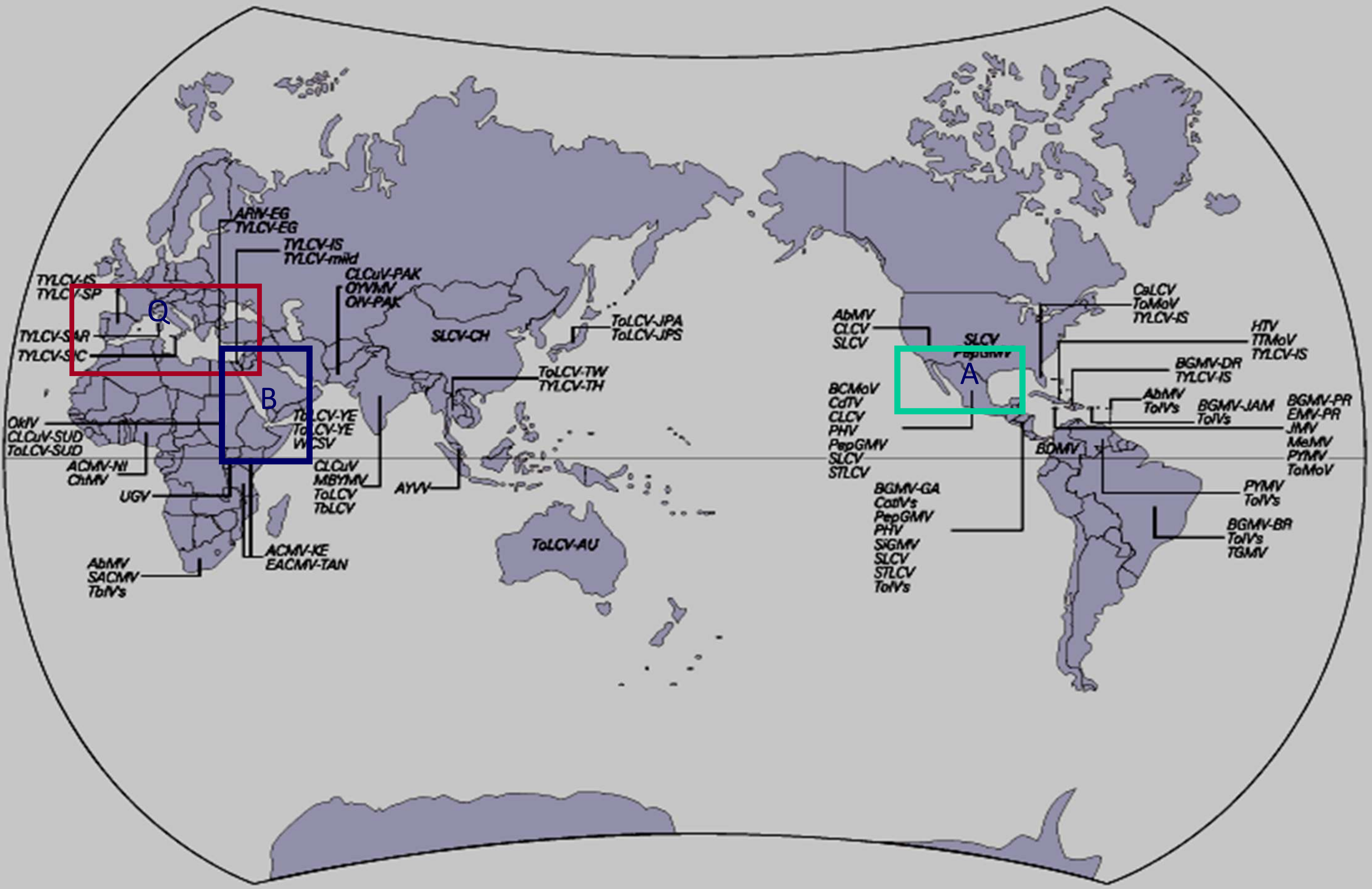
Table 3. Percent shared nucleotide identity and nucleotide divergence for within-clade comparisons of *Bemisia tabaci*, calculated by PAUP.

Clade	% nt identity	% nt divergence
New World **n = 8**	91.4 - 99.0	1.0 - 8.6
Indian Subcontinent/ Far East **n = 7**	82.8 - 98.6	1.4 - 17.2
N. Africa- Middle East-Mediterranean Region **n = 13**	81.9 - 97.2	2.8 - 18.1
Sub-Saharan Africa (w/o ABA, IC cassava) **n = 42**	88.9 - 99.7	0.3 - 11.1
Sub-Saharan Africa **N = 44**	80.3 - 99.7	0.3 - 19.7
Outgroups		
T. vaporariorum* x All *B. tabaci	71.3 - 76.5	23.5 - 28.7
B. afer* x All *B. tabaci	71.6	28.4



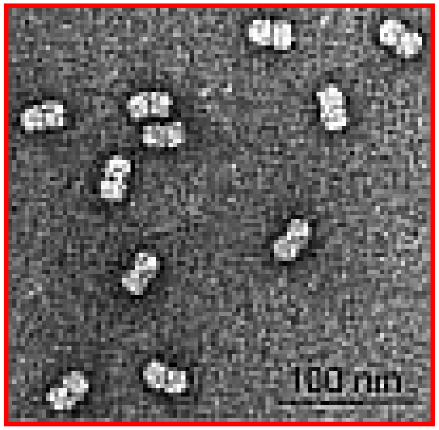
Mt COI tree
Tucson sample
Dec 04

Global origins of B. tabaci + Begomoviruses



Begomoviruses can be carried by *B. tabaci* or plants

Examples of begomovirus symptoms in AZ/CA/Sonora Mexico crops

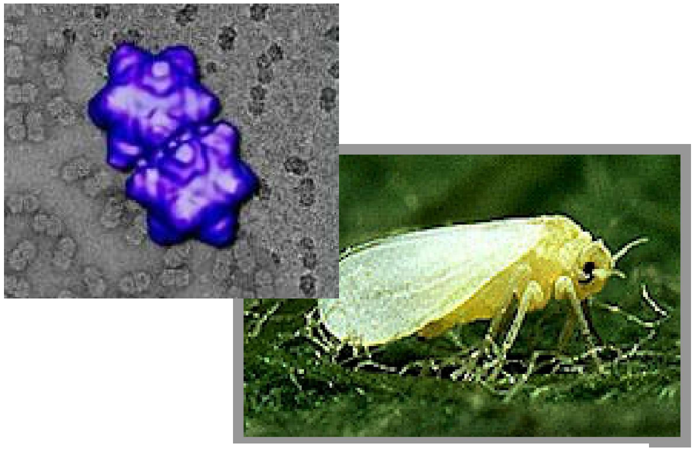


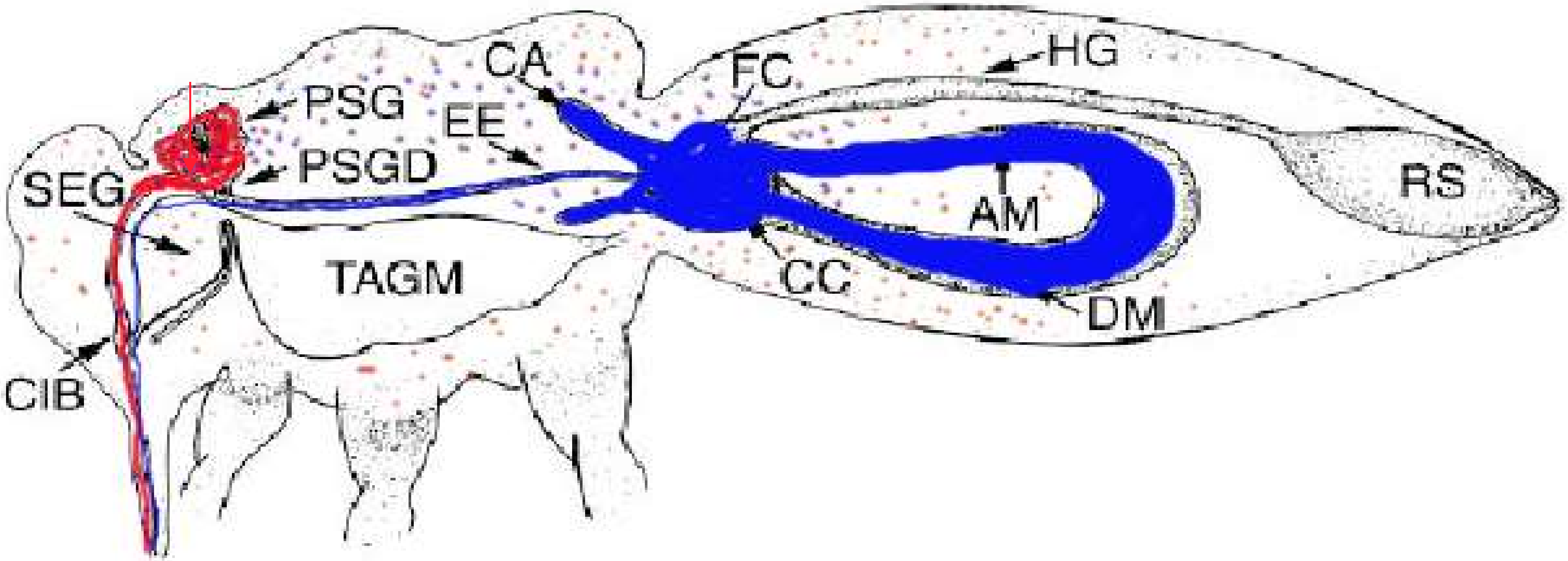
-'Paired icosahedra' (geminate) particles 20 x 30 nm

The insect vector is the *Bemisia tabaci* species complex

Transmission Pathway -

Geminiviruses are transmitted by different biotypes with similar competency if plant host is compatible





Where to go from here?
Know who and where the enemy is
Know what to do when it's found

1. Accept that the Q biotype could likely become established in the U.S. and the Americas; we will not likely be able to eradicate it.

2. The Q biotype has a very broad host range; thought to be similar to the B biotype.

3. Conduct surveys (self monitoring) to find out where it is and where it is not presently: Hot spot states: AZ, CA, TX, FL cotton, vegetables, ornamentals. Share information, not blame.

4. Diligent monitor over time to track movement and distribution to identify Hot spots for directed control to reduce potential for outbreaks.

5. Obtain additional information about host range, potential to hybridize, vector aspects, new viruses anticipated?, biology in niches in U.S., identify/optimize effective insecticides.

6. Continue to self monitor and judicious use of insecticides - effective control.

Thank you