

# Minding Our A's, B's and Q's: Tracking Whitefly Biotypes

*Emergent Q type already in Arizona*

by Susan McGinley



The whitefly *Bemisia tabaci*

Judith K. Brown

Arizona's cotton crop succumbed in 1990-91 to the B biotype of *Bemisia tabaci*, an ancient whitefly species with nearly worldwide distribution. Numerous biotypes or variants have evolved that are all part of the same species. Tracking its origins, along with the symbiotic bacteria it carries, the viruses it transmits and its host ranges across continents offers an intriguing picture of a highly adaptable insect pest. A new arrival to the United States, dubbed whitefly biotype Q, was first identified by University of Arizona scientists on poinsettias in 2005. It awaits the right conditions to explode in population size and advance into urban landscapes, vegetables or cotton crops.

*B. tabaci* attacks arid irrigated, subtropical and tropical cropping systems, often sweeping in giant waves across fields to lay eggs on vegetables, cotton, and even native landscape plants. Blanketing the leaves and fruit, the tiny larvae, less than a millimeter long, use their piercing-sucking mouthparts to extract vital fluids from the host plants, causing them to wilt or die. The sticky honeydew the whitefly exudes while feeding results in a black sooty mold that blocks light to the leaves, spoils cotton fiber's marketability and renders food crops inedible.

This whitefly species also carries and readily transmits two unique groups of pathogens, the most damaging and widespread being in the genus Begomovirus (family: Geminivirus). Begomoviruses include *Squash leaf curl*, *Cotton leaf crumple*, *Tomato yellow leaf curl*, *Cassava mosaic virus* complex, and others that at the very least rob farmers of their profits and at worst cause widespread famine and death.

Widely distributed between the 30-degree parallels across the center of the globe, *B. tabaci* goes where humans go, catching rides on imported plants and then jumping to crops and landscape plants nearby. Some biotypes feed on more than 500 species and collectively have racked up billions of dollars in economic damage in more than 100 countries. Called the cotton or sweetpotato whitefly and numerous other common names, the *B. tabaci* species is responsible for the whitefly infestation of Arizona's cotton crop in the early 1990s. The native A biotype caused outbreaks previously in the desert Southwest in the 1950s and again in the early 1980s, and currently the "Invader" haplotype is wiping out the staple cassava crop, in sub-Saharan Africa, where millions are starving as their staple food collapses from whitefly-borne mosaic disease.

Whitefly vector biologist Judith Brown tracks different biotypes of *B. tabaci*, analyzing their DNA in her laboratory in the Department of Plant Sciences at The University of Arizona to find out more about how and where they migrate and transmit begomoviruses. After 25 years, she knows this insect intimately, from its genetics and biological traits to its host ranges and the diseases it transmits. She has developed population genetics approaches to identify and track Old and New World variants, comparing and mapping them to understand how ancient biotypes of whiteflies are migrating and adapting.

Brown uses these tools to recognize the introduction or emergence of newer biotypes that are resistant to pesticides, for example, or have adapted to new cropping practices. They may also have evolved different host ranges, confounding control measures that worked on the old biotypes. Brown's research is helping growers and scientists correctly identify and track the various races of *B. tabaci* to prevent or control potential upsurges in their populations that could reach crippling levels.

Often the appearance of a new begomovirus disease is Brown's first clue that a new biotype has invaded or evolved. This is how she noticed the B biotype that first emerged in the late 1980s. "When this population showed up on plants that were not hosts of the local *B. tabaci* in the States and in



the Caribbean, I figured, 'something is going on here.' People were noticing the new diseases, but I thought there had to be a vector component to explain this," she says. She tracked and traced the origin of the B biotype in the Sahel region of Africa, including Eritrea, southern Sudan, and northern Uganda. It eventually made a jump to the Middle East, and later spread all over the world on ornamental plants, according to Brown. When it came to the United States it spread like wildfire, in the late 80s and early 90s, nearly wiping out the vegetable and cotton industries in Arizona, California and Texas, along with Florida's vegetable and ornamental crops.

"Early on, we ran gels to visualize different protein patterns in the lab," Brown explains. "We used those specific patterns to track the movement of the B biotype. These studies revealed an incredible amount of diversity among *B. tabaci* populations." She then developed a more sensitive DNA-based test based on molecular markers to distinguish them. Early protein patterns were designated according to the alphabet and the respective letters were assigned to each variant, some of which are now recognized as troublesome biotypes. The most recently discovered Q biotype comes from the Mediterranean where it is a problem in greenhouses in Spain.

Brown credits her mentor Julio Bird, a professor at the University of Puerto Rico Experiment Station in Rio Piedras (now retired), for discovering and proposing the concept of biotypes in *B. tabaci*. He had observed identical populations that exhibited different host ranges and virus transmission capabilities in Puerto Rico. Of the numerous begomoviruses on the islands, Bird noticed that some stayed put in certain areas while others appeared to move around. Bird and Brown together later found that the

---

The most recently discovered Q biotype comes from the Mediterranean where it is a problem in greenhouses in Spain.

---

introduced B biotype was capable of mobilizing some previously known and newly emergent viruses between plants.

*B. tabaci* whiteflies and begomoviruses have coevolved for millions of years, according to Brown, with the viral coat protein on each virus species best matching a specific vector population. This influences transmission or vector competency, which is greatest for virus-vector pairs that have coevolved. Thus some whitefly biotype infestations

result in widespread diseases and others show more limited spread. Certain crops are susceptible to the begomoviruses the whiteflies transmit and others are not.

By knowing what kind of whitefly is present, the type of begomovirus it carries, and the susceptibility of the local plants to infection, Brown suggests it's easier to predict the effect of that whitefly in the environment and to decide on control measures. Beyond that, knowing more about the reproductive habits of the whitefly and whether biotypes can hybridize readily are also important. All known *B. tabaci* are parthenogenetic, producing populations of egg-laying females when eggs are fertilized, and males when they are not. The more females there are, the more offspring will be produced and the faster the virus will spread.

"The whiteflies are adept at upsurging when you take them out of their native home and introduce them into a new niche," Brown says. They either displace local populations the way they did in Arizona, or hybridize [cross-mate], as they have in Uganda, sweeping west to Kenya and southward to Tanzania and Burundi. "It's a clearcut pandemic of severe mosaic disease in the cassava crop," Brown says. "We had guessed there was a new vector, and indeed we discovered what we named the "Invader" population that has its closest relatives in West Africa."

More recently Brown and her colleagues found that it mated with the native vector populations and that these hybrids are responsible for at least some of the mosaic virus spread along the disease front. Now she is tracking the advancing whitefly front southward and westward in Africa using a nuclear marker to identify the hybrid. James Legg, a vector biologist at the International Institute of Tropical Agriculture in Kampala, Uganda is collaborating with Brown in this research.

Brown's extensive genetic and mating studies show there are crosses or hybrids between whitefly races. She has found that an Old World B biotype can mate with the native Arizona A population and produce offspring. In fact, there is eight percent divergence in hybrids in Uganda, showing there is potential gene flow when different biotypes end up in the same field. One of her astounding findings is that *B.*



Judith K. Brown

The whitefly-transmitted begomovirus known as *Squash leaf curl* attacks zucchini and other vegetables.





Judith K. Brown

*Cotton leaf crumple*, a virus transmitted by *Bemisia tabaci* whiteflies, causes disease in Arizona cotton, affecting both the leaves and the flowers (inset).



*tabaci* is morphologically [structurally] identical worldwide but exhibits different habits and genetic differences.

“Considering the variable niches it lives in, you would expect to see morphological differences, but there are none,” Brown says. It’s what is known as a cryptic species, in which populations don’t appear to be different from one another, but they exhibit very clearcut biological, genetic and behavioral differences. Scientists have to examine their behavior linked to their genes to classify them.

“They don’t need a new snout or another vein on their wings to adapt” Brown says. “This species is so perfectly adapted that it doesn’t need to make morphological adjustments. It corrects genetically and behaviorally instead. These whiteflies are extremely adapted to coexisting with humans.”

The Q biotype upsurged in greenhouses in Spain when the pesticide immunocloprid wiped out the B biotype and left the Q with resistance to the compound, with no brakes to hold it back. Biotype Q has since spread through the ornamental industry in Europe, China and portions of Central America and the United States. Brown presumes Q entered the United States on ornamental plants in 2004. UA entomologist Tim Dennehy and his graduate students collected poinsettias over the holidays and tested them in the lab for insecticide resistance.

“One population was incredibly resistant to several pesticides normally used on whiteflies,” Brown says. “We identified the whitefly as the Q biotype using our molecular marker, the cytochrome oxidase 1 gene. This confirmed the first introduction of the Q biotype into the United States, and indicated that the population was not the B biotype that had evolved resistance.”

The researchers traced the plants to nurseries that had imported them. Brown doesn’t expect the Q biotype to flare up right away, but she admits it certainly could. The B biotype was introduced at least as early as 1985 into the United States but didn’t cause widespread damage in the desert Southwest until 1990-91.

“The take-home message here is that the way we transport ornamentals and vegetable seedlings has facilitated the whitefly’s dispersal into vegetable and cotton crops where it can build up and become a full-scale problem,” Brown says. “We don’t know yet if the Q will out-compete the B biotype, but the first step is to know where it is, and then to manage it differently. Compounds are available to specifically control different biotypes but we need to know if we are dealing with mixed or single populations.”

The transport of whitefly-infested ornamentals is not expected to be regulated by the federal government. Brown would like to see a cooperative effort among the ornamental, vegetable and cotton industries to manage potential *B. tabaci* outbreaks for the long term. She notes that Q biotype is the most recent—but certainly not the last—to arrive. “Because *B. tabaci* is so plastic and highly adaptable, it’s a given that this ancient species is here to stay.” ✂

#### CONTACT

**Judith K. Brown**  
520-621-1402  
jbrown@ag.arizona.edu

**Whitefly Identification Websites:**  
[cals.arizona.edu/gemini](http://cals.arizona.edu/gemini)  
[cals.arizona.edu/whiteflytax](http://cals.arizona.edu/whiteflytax)