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Differentiation of *Bemisia tabaci* (Genn.) (Hom., Aleyrodidae) populations in Colombia

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Abstract

We obtained evidence for genetic differentiation (detected by electrophoresis) of geographical populations of the whitefly, *Bemisia tabaci* (Genn.), in Colombia. The differences are undetectable by conventional taxonomic characters but are expressed at an esterase marker locus. There was no indication of host-race formation.

The present data on geographic differentiation of *B. tabaci* in Colombia, provide support to earlier reports that *B. tabaci* population in different parts of the world – in particular in South America – are biologically heterogeneous. The recent outbreaks of *B. tabaci* in Florida and the Caribbean, and the colonization of previously uninfested host plants, may be due to the spread of rare or new genetic variants.

We have shown in the first part of this study (WOOL et al. 1993) that frequencies of electrophoretic variants at an Esterase locus in Israel are not the same in commercial, insecticide-treated fields as in samples from unsprayed sites. That result, coupled with the present data, indicates that subtle genetic variation exists in *B. tabaci* also in traits which are important for agriculture.

1 Introduction

This is the second report of 3 years of cooperative research (1987–1990) on genetic differentiation of whitefly populations (*Bemisia tabaci* Genn.) in Israel and Colombia. The first report, on the results from Israel, was WOOL et al. (1993).

B. tabaci became a primary pest of cotton relatively recently. An outbreak was first reported in the Sudan in the sixties, and efforts at control of the pest failed completely in 1980–1981 (DITTRICH et al. 1985, 1986). Control problems were reported in California (PRABHAKER et al. 1985), in Israel (GERLING et al. 1980; GERLING 1984), and in India (JAYARAJ et al. 1986). The use of pesticides is often blamed for the outbreaks (AHMED et al. 1987; DITTRICH 1987; DITTRICH et al. 1990; PRABHAKER et al. 1985; JAYARAJ et al. 1986). *B. tabaci* is a major threat to crops in all these areas, despite heavy use of pesticides and attempts at biological control (GERLING 1984, 1985; BYRNE et al. 1990; ONILLON 1990; DITTRICH et al. 1990).

Whitefly damage is caused by direct feeding of very large populations of immatures and adults on the plants and by contamination of the crop with sticky honeydew, a favorable substrate for molds. The transmission of viral diseases by whiteflies (e.g., MOUND 1983; DUFFUS 1987) is sometimes even more costly and devastating (e.g., ROBERTSON 1987). Other than commercial crops, *B. tabaci* infests a wide range of ornamental plants and weeds (COCK 1986). The taxonomy and identification of whiteflies is based on the morphology of the pupal case (MARTIN 1987; GILL 1990), although some studies have shown that pupal characters may vary among host plants within species and is affected by environmental factors (e.g., MOUND 1963; MOHANTY and BASU 1986). Taxonomically, the world populations of *B. tabaci* from India, Africa, Europe and the Americas, are considered one and the same species. However, the insects in different countries appear to differ in biological characteristics including fecundity, developmental rates and host range

(COSTA and RUSSELL 1975; GERLING 1986). BIRD (1982, and actually as early as 1958), described differences in virus transmission properties among *B. tabaci* populations in Latin America, and suggested that these populations may represent distinct "biotypes". There are differences among populations of *B. tabaci* in their ability to colonize different host plants. ROBERTSON (1987) reported severe yield losses in cassava (*Manihot esculenta*) varieties, imported from Brazil, that were heavily infected with *B. tabaci* borne viruses in Kenya. However, in Colombia and most of the tropical Americas, *B. tabaci* does not colonize cassava. Strong host preferences of *B. tabaci* were reported by COSTA and RUSSELL (1975) in Brazil. These biological differences suggest that *B. tabaci* may be a complex of distinct populations or biotypes. In the present study we used electrophoresis in search for genetic markers which would enable the identification of genetic variants within Israeli and Colombian populations of *B. tabaci*. The project was designed so that work could be carried out in parallel in Israel and at CIAT, Colombia, using similar equipment and identical methods.

A recent compilation of review articles on electrophoretic variation in agricultural pests was edited by LOXDALE and DEN HOLLANDER (1989). "Cryptic" strains and species of insects were detected by electrophoresis, where morphology failed to detect them (some examples: in *Simulium* (SNYDER 1982), in butterflies (BRITTNACHER et al. 1978; GEIGER and SCHOLL 1985), in weevils (HSIAO and STUTZ 1985), in aphids (STEINER et al. 1985; LOXDALE CASTANERA and BROOKS 1983; TOMIUK et al. 1979).

In Israel, no host plant-related differences were detected in the 700 samples, collected over the 3-year study (WOOL et al. 1993). There was considerable and significant heterogeneity in frequencies of two alleles at a major EST locus, among localities. These differences were unrelated to geography. However, we found differences in the frequency of the slow-migrating (S) allele between samples from insecticide-treated and insecticide-free sites. In samples from commercial fields, S was predominant (almost fixed in some places). In control, untreated populations the alternative (F) allele was predominant (WOOL et al. 1991; WOOL et al. 1993). We also established that carriers of S showed lower esterase activity (WOOL and GREENBERG 1990).

The present report summarizes the results of the electrophoretic analyses of Colombian samples. Colombia is about 200 times larger than Israel, and is divided geographically by three great mountain ranges of the Andes, which reach altitudes of more than 5,000 m in places, and must be formidable, geographical barriers for gene flow in whiteflies (most of their host plants, both wild and commercial, grow in lower elevations and valleys isolated by the mountain ranges). This geographical subdivision makes Colombia an ideal country for the search for geographical genetic variation in *B. tabaci*.

Our working hypothesis was that Colombian *B. tabaci* may be an aggregate of strains or races, morphologically indistinguishable but genetically different from each other. We use this as an alternative to the null hypothesis (in the statistical sense) that no substructure exists in Colombian populations of *B. tabaci*.

2 Materials and methods

2.1 Collection sites and principal host plants

Samples were collected in 13 Colombian Departamentos (states) and in two neighboring countries – Ecuador to the south and Venezuela to the north-east. (The regional governments in Colombia are called Departamentos. In Ecuador they are Provincias, and in Venezuela, Estados. For simplicity, these subunits are referred to as "states" in this paper.) Approximate locations of some collection sites are shown on the map (fig. 1).

Adult *B. tabaci* were aspirated off the host plants. Samples were deep-frozen in liquid nitrogen upon collection and later stored in liquid nitrogen until they were analyzed. Control populations (see below) were reared at CIAT on bean plants in the laboratory.

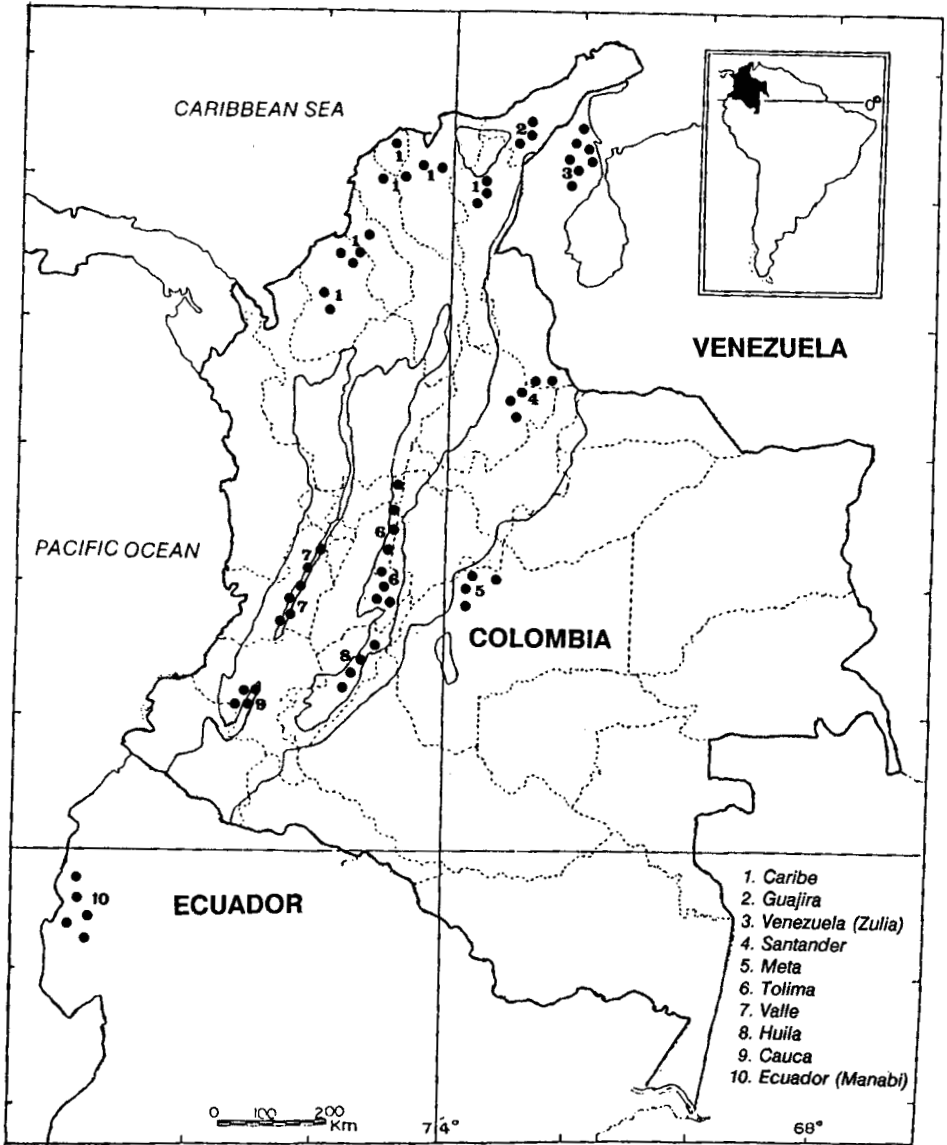


Fig. 1. Map of Colombia, showing the locations of some collection sites in different parts of the country (see legend in the figure). Departamentos (states) are identified by numbers

2.2 Electrophoresis

Each adult was homogenized separately in 10 microliters of grinding solution (containing 10% sucrose and some bromophenol blue as front-running marker dye) and then inserted in the gel pockets. Vertical Acrylamide slab-gel electrophoresis was carried out using Bio-Rad minigel sets (Mini Protean II).

Usually 8–10 individuals of a given population were run on a single gel. Two central pockets were loaded with homogenates of individuals from a standard control population (see below) for comparison of the migration distances of isozymes. The gel and running buffer was 0.155 M Borate, pH 8.2.

Usually 6 % or 7 % Acrylamide was used for the gels. Gels were generally run for 2 hours in constant current of 40 mA per gel.

Staining for Esterases (EST) was in 0.1 M phosphate buffer, pH 6.5, with α - and β -Naphthyl acetate as substrates in the ratio α : β = 9:1. Gels were fixed after staining in a 1:5:5 mixture of Acetic acid, Methanol and water. Fixed gels were sealed in plastic bags. The gels were read on an illuminated table, and the frequencies of the different isozymes recorded. The data were then stored on diskettes for analysis with an IBM-PC computer.

2.3 Data analysis

The samples were analyzed in search for genetic differences at two levels: 1. geographically related differentiation, 2. host-plant-related differentiation within localities.

Standard statistical techniques were employed (SOKAL and ROHLF 1981).

3 Results

3.1 The electrophoretic EST pattern of *B. tabaci* in Colombia

The first samples analyzed came from the agricultural area around CIAT (State of Valle). The EST pattern at this site is illustrated in fig. 2. It involved a fast (F) and a slow (S) band, behaving like two alleles at a single locus, with the appropriate double-banded (FS) heterozygote. A faster and weaker isozyme (ff) appeared on almost all gels from most of the States of Colombia and appeared to be monomorphic in almost all individuals. Therefore, it served as a useful marker in the interpretation of the various electrophoretic patterns. (A similar band was also detected in Israeli *B. tabaci*, but there it was detectable only on good gels (WOOL et al. 1991, 1993).

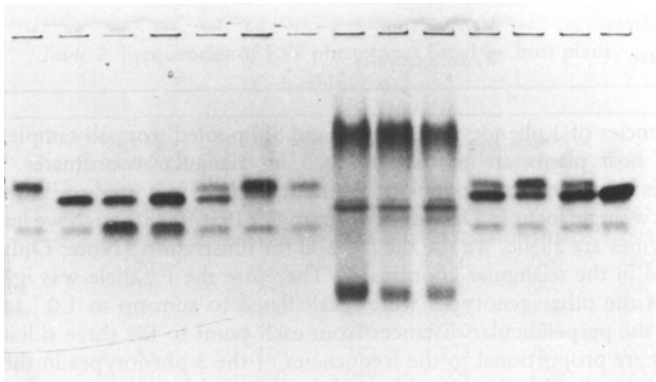


Fig. 2. The major EST pattern in samples from Valle, Colombia. Cells 8–10 from left are individuals of *Bemisia tuberculata*. The others are *B. tabaci*. From left: SS, FF, FF, FF, FS, SS, SS; *B. tuberculata*; FS, FS, FS, FF. Notice the faster isozyme ff, which is present in all *B. tabaci* individuals (see text)

A laboratory colony of *B. tabaci* which had been maintained in cages on beans (*Phaseolus*) for several years, consistently carried the EST polymorphism just described. This population was, therefore, chosen to be our control. Two or 3 individual adults from this population were run on every gel for comparison.

Additional isozyme patterns were detected when we extended our sampling to other Colombian states. At first, 8 phenotypic isozyme patterns were identified, and tentatively described as different races (WOOL et al. 1991). However, a later examination of the 8

patterns revealed many similarities among them, and the number of phenotypes can be reduced to 6. Taken as a whole, the Colombian EST pattern appears to be composed of 3 isozymes. To be consistent with the Valle pattern and with our earlier work, we label the isozymes S, F, and F* (which migrate faster than F but not as fast as ff; see fig. 6 and 7). Combinations of the 3 isozymes give 6 phenotypes: 3 appearing as a single band, SS, FF, and F*F*, and 3 two-banded phenotypes, SF, FF*, and SF*. All 6 were in fact identified (at varying frequencies) in the samples, and only 28 of nearly 3000 individuals could not be assigned unambiguously to a phenotype.

3.2 EST phenotype frequencies on different host-plants in Colombia

Table 1 lists the host plants from which *B. tabaci* was collected in Colombia. In contrast with Israel (WOOL et al. 1993), where most samples were collected from agricultural crops, most Colombian samples came from wild plant species (especially species of *Euphorbia*).

Table 1. List of host plants from which *B. tabaci* was collected in Colombia

Wild plants are listed by their scientific names; commercial crops by their common names

Family	
Euphorbiaceae	<i>Euphorbia hypericifolia</i> ; <i>E. hirta</i> ; <i>E. heterophylla</i> ; <i>E. prunifolia</i> ; <i>Croton</i> sp.
Leguminosae	Beans; cowpeas; <i>Cajanus cajan</i> ; <i>Rhynchosia minima</i>
Solanaceae	Tomato
Malvaceae	Cotton; <i>Sida acuta</i>
Cucurbitaceae	Squash
Convulvulaceae	<i>Merremia</i> sp.
Compositae	<i>Wedelia latifolia</i>

The frequencies of 3 phenotypes (FF, FS, and SS) pooled from all samples collected on the principal host plants are plotted in fig. 3 in triangular coordinates. This type of presentation is borrowed from population genetics, where it is used to illustrate genotype frequencies at a single locus [a De Finetti diagram (LI 1956)]. Although we have not shown that our isozymes are allelic, we use the method for illustration. [Note: Only 3 genotypes can be plotted in the triangular coordinates. Therefore the F* allele was ignored and the frequencies of the other genotypes were recalculated to sum up to 1.0.] In this graphic presentation, the perpendicular distances from each point to the three sides (labeled fast, slow, and FS) are proportional to the frequencies of the 3 phenotypes in the sample. The parabola plotted in fig. 3 is the assemblage of the expected frequencies at Hardy-Weinberg equilibrium in the one-locus, two-allele case. The frequency of the F isozyme increases from left (0.0) to right (1.0) along the base of the triangle.

Many Colombian samples contained high frequencies of FS, and were much closer to Hardy-Weinberg equilibrium frequencies than any of the samples from Israel (WOOL et al. 1991) (but were still significantly different from expectation: e.g., for beans, $\chi^2 = 16.6$, 2 df, $P < 0.01$; for *Euphorbia*, $\chi^2 = 56.4$, 2 df, $P \leq 0.001$). All samples except beans (control) show predominance of the S isozyme and low frequencies of F: the points tend towards the left-hand corner of the triangle (fig. 3).

A list of EST phenotype frequencies in Colombia arranged by host-plants is given in table 2. Pooling data from different localities by host plant species turned out not to be very informative, due to the sharp geographical differentiation of Colombian *B. tabaci* (see below).

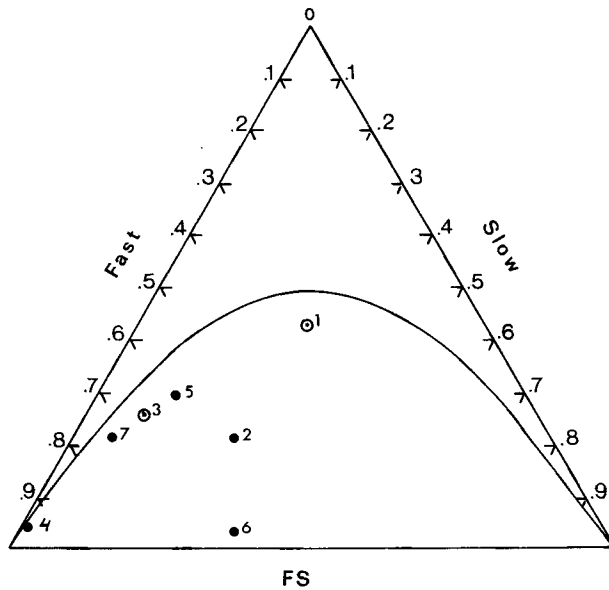


Fig. 3. Frequencies of EST genotypes FF, SS, and FS at the major locus, in samples from different host plants, in Colombia. The data are plotted in triangular coordinates. The perpendicular distances of each point from the three sides of the triangle are proportional to the frequencies of the three genotypes in the sample. (See text for further explanation). 1. beans (control); 2. cotton; 3. *Euphorbia*; 4. *Merremia*; 5. *Rhyncosia*, 6. *Sida*; 7. *Wedelia*

Table 2. Frequencies of EST phenotypes listed by host plant
Colombian data

Plant	No. of indiv.	Frequency of phenotype					
		SS	FF	SF	F*F*	SF*	FF*
1. Beans	428	.280	.187	.362	.000	.007	.164
2. Cotton	158	.177	.114	.127	.101	.095	.392
3. Cowpea	53	.226	.038	.000	.000	.000	.736
4. Cucurbits	111	.243	.018	.000	.000	.027	.712
5. <i>Euphorbia</i>	1135	.440	.073	.078	.036	.047	.326
6. <i>Merremia</i>	107	1.000	.000	.000	.000	.000	.000
7. <i>Rhyncosia</i>	55	.109	.382	.273	.000	.000	.236
8. <i>Sida</i>	111	.892	.099	.009	.000	.000	.000
9. Solanaceae	110	.255	.209	.146	.018	.000	.373
10. <i>Wedelia</i>	30	.300	.133	.500	.000	.067	.000
11. <i>Jatropha</i>	32	1.000	.000	.000	.000	.000	.000
12. <i>Croton</i>	40	1.000	.000	.000	.000	.000	.000
13. <i>Vigna</i>	32	.000	.000	.000	.000	.000	1.000
14. <i>Macroptilium</i>	38	.342	.000	.000	.000	.658	.000
15. <i>Desmodium</i>	30	.000	.000	.000	.000	.000	1.000

3.3 Geographical differentiation of *B. tabaci* in Colombia

Samples from different Colombian states, and from the two neighboring countries, Venezuela and Ecuador, differed in frequencies of the 6 phenotypes (table 3).

Examination of table 3 shows that the sampled localities can be arranged in 3 groups,

Table 3. Frequencies of EST phenotypes in samples from Colombian states

State	Total	SS	FF	SF	F*F*	SF*	FF*
CIAT	543	.361	.267	.372	.000	.000	.000
Valle (not incl. CIAT)	212	.231	.274	.368	.123	.009	.009
Cauca	259	1.000	.000	.000	.000	.000	.000
Meta	188	.984	.011	.005	.062	.000	.000
Santander	48	.167	.771	.062	.000	.000	.000
Tolima	305	.624	.007	.010	.109	.207	.053
Huila	200	.820	.035	.015	.000	.125	.005
Ecuador	104	.683	.380	.010	.106	.163	.000
Guajira	83	.000	.072	.000	.096	.000	.831
Venezuela	519	.000	.002	.000	.002	.000	.998
Caribe	140	.007	.093	.000	.021	.000	.879

based on the similarity of electrophoretic patterns (but *not* always of geographical proximity): 1. The "Valle" group (with the 3 phenotypes FF, SS and FS). This group includes CIAT, Santander, Meta and Cauca. Santander and Meta are geographically separated from Cauca and Valle. A pooled sample from several sites in Valle other than CIAT was also included in the "Valle" group. This pooled sample was different from the others in the group in that 26 F*F* individuals and 2 each of SF* and FF* were found in the total sample of 212. 2. The "Tolima" group, with phenotypes SS, F*F* and SF* – including Tolima and Huila. The samples from Ecuador also have these phenotypes. 3. The "Guajira" group, including Guajira, Caribe and Venezuela. (Caribe designates samples that were collected from the northern coastal plain of Colombia [States: Cesar, Bolivar, Atlantico, Sucre and Cordoba]. This is a homogeneous ecological region which also has a common cropping system.) This group contains the phenotypes FF, F*F* and FF*. We shall discuss the 3 groups separately.

3.3.1 The Valle group

Electrophoretically mostly FF, SS, and FS were found in the 4 states in this group. But there was a sharp genetic differentiation within the group, with Meta and Cauca fixed or almost fixed for the SS phenotype (see an example in fig. 4), and Santander with a very high frequency of FF. Only Valle segregated for the two isozymes (fig. 5). (It is not clear if the

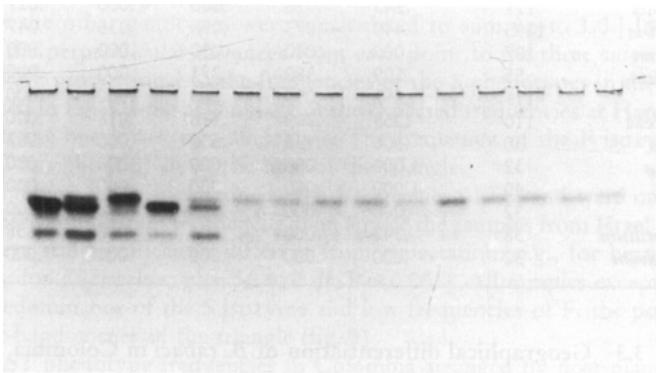


Fig. 4. EST pattern in *B. tabaci* samples from Quilcace, Cauca, Colombia, (cells 6–15, showing only the SS genotype). Cells 1–5 contain control individuals from CIAT (on beans). From left: FF, FS, SS, FF, FS

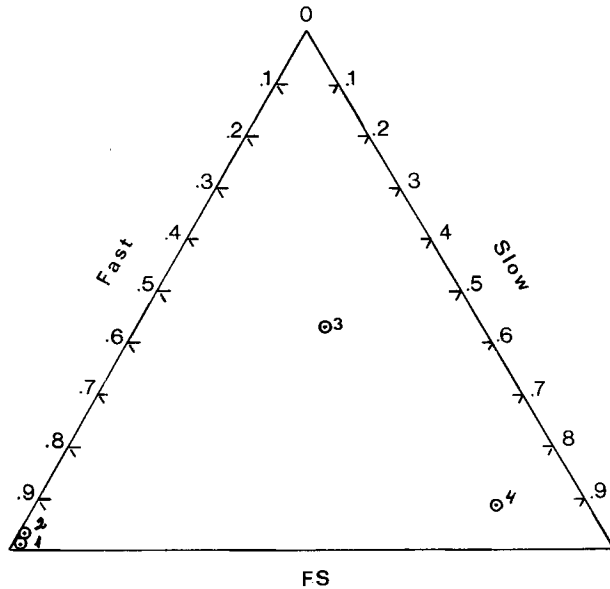


Fig. 5. Frequencies of EST genotypes at the major EST locus in samples from Colombian states Cauca (1), Meta (2), Valle (3), and Santander (4) (the "Valle group"). Data plotted in triangular coordinates as in fig. 3

28 individuals carrying F^* were collected at one or more sites in Valle. To plot Valle in fig. 5, we ignored these individuals and recalculated the frequencies to sum to 1.0.) The CIAT control population, shown in fig. 3, was originally established from a field sample from this area, which may not have contained the F^* isozyme and remained free of it in subsequent laboratory culture.

This group of states is quite heterogeneous in terrain; Valle is a mountain valley between the central and western mountain ranges, and the samples from Cauca were collected in an isolated mountain valley that is on the eastern slope of the western range near the Patia river which flows into the Pacific Ocean. The samples from Meta were collected near the llanos east of the eastern mountain range. The samples from Santander were collected from a mountain valley on the western slope of the eastern range. While Valle and Cauca are in close geographic proximity, and Meta and Santander are in close proximity, these two pairs of states are distinctly isolated from each other. The genetic similarity between Cauca and Meta cannot be explained by geographical proximity but the same genotype may have been independently fixed in the isolated populations.

3.3.2 The Tolima group

The F isozyme was rare in samples from the Tolima group area; likewise was the SF phenotype. They were replaced by F^* and SF^* (fig. 6). Samples from Ecuador, Huila, and Tolima all contain a large majority of SS , a relatively small proportion of F^*F^* and 12–20% double-banded SF^* individuals (table 3). Tolima and Huila are parts of the same mountain valley system, but the samples from Ecuador were collected along the Pacific coast of Ecuador, and this is a distinct ecological and geographical region that is distant from the Tolima valley. The genetic similarity between these samples deserves notice.

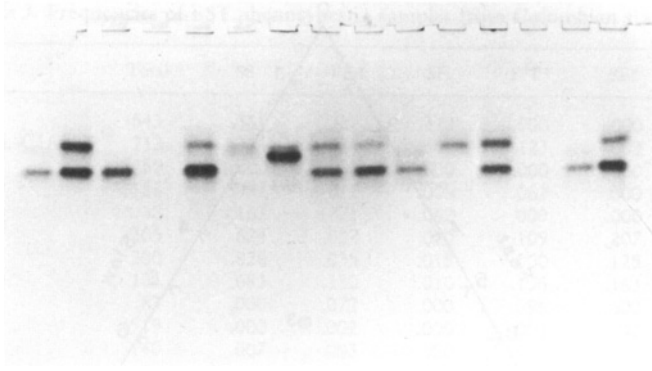


Fig. 6. EST pattern of *B. tabaci* individuals from Nataima, Tolima. Cells 6, 7 are control individuals from CIAT (both FS). Notice the pattern prevalent at Tolima (SS, SF*, F*F*)

3.3.3 The Guajira group

Samples from Cesar, Bolivar, Sucre, Cordoba and Atlantico were originally considered separately, then assembled into one group (Caribe) due to geographical and ecological similarity, and were finally included in the Guajira group due to the similarity of the isozyme pattern. These states are all located near the Caribbean Sea and are in close geographic proximity. This group is distinct from the other two by the near absence of the slow phenotype (a single SS individual was found in the sample of 140). The samples contained FF, F*F* and FF*. In fact, most individuals collected were double-banded FF* and the samples from Venezuela (collected at Zulia, near Lake Maracaibo) were fixed for this phenotype (fig. 7). Guajira, Bolivar and Cesar are quite similar in proportions of the three phenotypes (table 3).

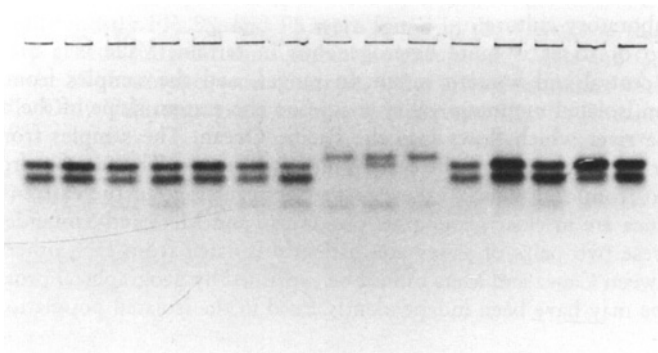


Fig. 7. EST pattern of *B. tabaci* in samples from Colombian state Cordoba illustrating a fixed pattern of FF* isozymes (cells 8-10 are control individuals from CIAT: from left: SS, FS, SS)

4 Discussion

This paper presents the first clear evidence that *Bemisia tabaci*, although morphologically similar across its range in 4 continents, is genetically not a single entity.

The simplest genetic interpretation of the electrophoretic patterns assumes that S, F, and F* are allelic at a single locus. In this case, 6 genotypes should be expected which should correspond to the 6 observed phenotypes. In the absence of controlled genetic crosses between individuals with different genotypes, this explanation must remain tentative.

Whether these isozymes are allelic or not, *B. tabaci* whiteflies in Colombia are differentiated geographically, as demonstrated by our EST marker system, and where certain isozymes are fixed, or nearly so, in samples from large areas (such as Cauca, Caribe or Maracaibo, Venezuela) they may be considered "geographical races". The geographical barriers created by the mountain ranges must have facilitated this differentiation, because the different "races" seem to be separated by these ranges (fig. 1).

Moreover, samples from an ecologically homogeneous region like the Caribbean coast, are very similar electrophoretically, while samples from a heterogeneous region like Valle show electrophoretic differentiation from its adjacent state (Cauca) in isozyme patterns.

The study of Colombian populations of *B. tabaci* began simultaneously with the work in Israel (WOOL et al. 1993). We made every effort to standardize the methods so that the data from the two countries will be comparable. However, we strictly avoided sending live whiteflies between countries. Several attempts were made to send preserved samples over by air from Colombia to Israel (using various methods) but attempts were unsuccessful and all the samples had lost their EST pattern on arrival. Therefore, we could not run Israeli and Colombian whiteflies side by side on the same gel and had to judge the similarity of isozymes from their relative migration distance, when measured against a control.

The Colombian F and S isozymes migrated further apart from each other and double-banded individuals were easily detectable, unlike the situation in Israel. Moreover, although the staining substrate was routinely a 9:1 mixture of α - and β -Naphthylacetate, no preferential staining of F with β -substrate was detected in Colombia, while this was characteristic of the Israeli F isozyme. It is, therefore, possible that even the 3 genotypes FF, SS, and FS identified in Valle are not identical to the F, S, and FS from Israel. The high proportion of FS in Valle and the CIAT control samples is unparalleled in Israel (WOOL et al. 1993), suggesting again that the isozymes – and therefore genes coding for them – are not identical in the two countries.

The simple assumption that the major EST system in Colombian *B. tabaci* is controlled by a single locus with 3 alleles, should be put to test in the future with controlled crosses. However, if this assumption is wrong and F, F*, and S represent different loci, then our claim for genetic differentiation of Colombian *B. tabaci* becomes even stronger. Allelism is not only the simplest, but also the most conservative hypothesis for this case. A peculiar genetic problem is the apparent fixation of FF* in Caribe and Venezuela. If F and F* are allelic, then in a sexually breeding population this situation is highly unlikely (and the samples were far too large to assume sampling error). Nor is it likely that only haploid males were found in the Venezuelan sample of more than 500 individuals (if this were the case, then either F or F* would be carried by each male but not both, since males cannot be heterozygous). The fixation of double banded heterozygotes may be explained if reproduction at these sites is parthenogenetic. In whiteflies, generally males develop from unfertilized eggs (arrhenotokous parthenogenesis). For the present case, we have to postulate thelytokous parthenogenesis – like in aphids – females should give rise to females without fertilization (some whiteflies do reproduce parthenogenetically: for a recent report see UYGUN et al. (1990). If such evidence can be found it will provide strong support for the argument of genetic race formation in Colombian *B. tabaci*. However, we have no data on this point.

The difference in electrophoretic pattern between Colombian samples and the Venezuelan samples from Maracaibo may be explained by a geographical barrier to gene flow. On the borderline between the two countries there is a high mountain range, the Serrania

de Perija (L. M. CONSTANTINO, pers. comm.) which may prevent intermixing of the two "races". On the other hand, in recent samples taken in Florida, where an outbreak of *B. tabaci* is reported, the isozyme pattern is similar to the Maracaibo, Venezuela, pattern (L. CALVERT, pers. comm.).

It seems that, if we were to try and trace the reasons for the similarity of isozyme marker patterns in Tolima and Ecuador, or Florida and Venezuela (and perhaps other *B. tabaci* populations around the world), we should be looking for the spread of agricultural commodities by human agency, since the natural situation seems to be distinct, isolated populations.

With the exception of cotton, most of the host plants from which we collected *B. tabaci* in Colombia were different from the Israeli host plants. In Israel, the majority of the whiteflies were collected from commercial crops (cotton and cucurbits in particular). In Colombia, commercial crops provided only a minority of the samples (excluding the control population on beans). Cotton was not one of the preferred hosts of the whitefly in Colombia, and when we tried to collect them from cotton fields we often found the adults concentrated on weeds inside or in the periphery of the field and not on the cotton plants themselves. Many of these host plants were species of *Euphorbia*. Only one ornamental plant belonging to this family, poinsettia (*Euphorbia pulcherrima*), was a host of *B. tabaci* in our study in Israel. Samples from this host were fixed, or nearly so, for the F allele. BURBAN et al. (1989) reported that *B. tabaci* from cassava (*Manihot esculenta*), also belonging to the Euphorbiaceae, were electrophoretically distinct from populations on other hosts. Recently COSTA and BROWN (1991) reported that a greenhouse population collected from poinsettia in Arizona, was electrophoretically distinct and biologically different from two other *B. tabaci* populations reared on other hosts. Our present data also show that samples from Euphorbiaceae (3 in fig. 3) are different from beans (1) and cotton (2). We may assume, therefore, that the host plant does have some effect on the electrophoretic pattern at the EST marker locus – either directly on enzyme expression or indirectly as a selective agent.

Data on *B. tabaci* EST patterns in different countries are rare. The publications known to us besides our own (WOOL et al. 1984, 1989; WOOL and GREENBERG 1990; WOOL et al. 1991) are PRABHAKER et al. (1987), BURBAN et al. (1989) and COSTA and BROWN (1991). During this study we obtained small samples from Europe (Denmark, France), Africa (Kenya) and the U.S. (California, Arizona). The samples were too small to permit quantitative analysis, but the impressions were that EST patterns in these samples – especially the one from Kenya – were quite different from the Israeli or Colombian whiteflies.

All these data point to the conclusion that the worldwide *B. tabaci* is not a single genetic entity, but rather a complex of local, regional or geographical races. This conclusion is independent of whether the EST isozymes used as markers are allelic or not. This has important implications for whitefly control and quarantine.

Acknowledgements

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Zusammenfassung

Differenzierung von *Bemisia tabaci* (Genn.) – Populationen (Hom., Aleyrodidae) in Kolumbien

Es wurde mittels elektrophoretischer Untersuchungen die Existenz von genetisch differenzierten geographischen Rassen der Weißen Fliege, *Bemisia tabaci*, in Kolumbien nachgewiesen. Die Unterschiede sind bei Anwendung herkömmlicher taxonomischer Methoden nicht erkennbar.

Die vorliegenden Daten der geographischen Differenzierung von *B. tabaci* in Kolumbien werden gestützt von den Ergebnissen früherer Untersuchungen, wonach *B. tabaci*-Populationen in verschiedenen Teilen der Welt, besonders in Südamerika, sich biologisch heterogen verhielten. Die derzeitigen Massenvermehrungen von *B. tabaci* in Florida und den Karibischen Inseln sowie der Befall von früher verschonten Pflanzen könnten auf einer Ausbreitung seltener oder neuer genetischer Varianten des Schädlings beruhen.

Im 1. Teil der vorliegenden Studien (WOOL et al. 1993) wurde u. a. nachgewiesen, daß die Frequenzen der elektrophoretischen Varianten von *B. tabaci* in Israel zwischen insektizidbehandelten und unbehandelten Feldern verschieden waren. Dies weist in Verbindung mit den vorliegenden Ergebnissen auf eine Existenz subtiler genetischer Variationen von *B. tabaci* hin, die für den Pflanzenschutz von Bedeutung sein können.

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