

Predicting whitefly population outbreaks in changing environments

- ❖ The sweet potato whitefly *Bemisia tabaci* is one of the most devastating plant pests throughout tropical and subtropical regions. Its ability to transmit over 200 types of plant viruses makes it the largest threat to many crops. While in the past its distribution was limited to temperate zones, during the last two decades, it has invaded every continent except Antarctica. As global warming continues, whitefly populations are expected to increase, and with them pesticide applications and subsequent environmental contamination.
- ❖ SWIPE involved 13 institutes from 6 countries and brought together scientists from various disciplines, covering a broad range of expertise. It was initiated to identify the factors involved in *B. tabaci* population outbreaks and to use the information gathered to develop models able to predict such changes.
- ❖ The SWIPE team thrived to determine how future changes in temperatures will affect population dynamics of the insect pest, taking into account genetic variability and symbiotic associations.

Objectives

Bemisia tabaci

Pest invasion

Climate change

Precision agriculture

Symbiont

- ❑ We aimed to understand the effects of genetic variability and symbiotic associations in the context of interactions between temperature patterns and insect performance.
- ❑ To achieve this goal, the following objectives were pursued:
 - Determine the geographic distribution of *B. tabaci* genetic groups, their population genetic structure and symbiotic complement around the Mediterranean basin;
 - Determine whitefly invasion routes within the Mediterranean basin;
 - Determine the respective influence of nuclear and symbiotic variations on stress resistance;
 - Model the influence of climate change on whitefly population outbreaks;
 - Establish a network of researchers.

Scientific results & innovation potential

- ✓ The combined effort of the SWIPE team resulted in a new modelling framework for projecting pest population dynamics and supporting environmental decision-making under climate change.
- ✓ Together with the invasion risk assessment performed, the modelling framework developed will allow the necessary incorporation of pest risk assessment and simulation models into comprehensive management planning systems of both natural and agricultural ecosystems in response to global warming.

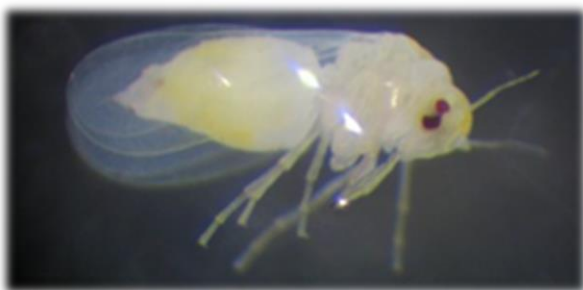


Figure 1. The sweet potato whitefly (*Bemisia tabaci*)

Coordinator

Dr Einat ZCHORI-FEIN

Newe Ya'ar Research Center, Agricultural Research Organization (ARO)

ISRAEL

einat@volcani.agri.gov.il

Partners

- LBBE, University Lyon 1, **FRANCE**
- Dept. of Evolutionary Genetics, Cavanilles Institute for Biodiversity and Evolutionary Biology, University of Valencia, **SPAIN**
- Dept. of Environmental and Natural Resources, University of Western Greece, **GREECE**
- Dept. of Entomology, The Hebrew University of Jerusalem, **ISRAEL**
- Portici Unit of IPP, CNR-Istituto per la Protezione delle Piante, **ITALY**
- Hellenic Agricultural Organisation-"DEMETER" Institute of Olive Tree, Subtropical Crops and Viticulture, Laboratory of Entomology and Agricultural Zoology, **GREECE**
- Dept. of Plant Protection, Ankara University, **TURKEY**
- Dept. of Entomology, University of Arizona, **USA**
- Laboratory Molecular Entomology, University of Crete, **GREECE**
- Instituto Valenciano de Investigaciones Agrarias, **SPAIN**
- Plant health Research Dept., Ankara Plant Protection Central Research Institute, **TURKEY**
- Dept. of Plant Protection, Cukurova University, **TURKEY**
- Dept. of Geography, Hebrew University of Jerusalem, **ISRAEL**



Why collaborating?

(i) Genetic groups and symbiotic bacteria

- To identify the genetic groups found around the Mediterranean, over 480 whiteflies were collected in 48 sampling efforts in five countries and analyzed by using molecular techniques.
- The bacterial symbionts carried by each individual whitefly were also determined.

(ii) Symbionts' influence on host stress resistance

- The influence of the symbionts associated with *B. tabaci* on parasitoids, thermal and pesticide resistance as well as on virus transmission capacities were studied by both analyzing the bacterial genomes and conducting field and laboratory experiments.

(iii) Invasion routes

- Various data sources were used to determine potential whitefly invasion routes: a) Geographic distribution; b) Amount of potential host plants transported to the EU; c) Presence or cultivated area of host plants in the EU; d) Number of *B. tabaci* interceptions.
- The risk of arrival and entry to a given country was calculated.

(iv) Population outbreaks model

- Computational approaches were applied to model changes in the population dynamics of *B. tabaci* under anticipated climate change for the next decades. To insert into the model data on the performance of the insects under real conditions, field-experiments were performed in four countries (Figures 2, 3) to determine life history traits of the whitefly under varying temperatures.

SWIPE was designed as five highly interconnected work packages. Close collaboration among the different SWIPE partners was an absolute must for carrying out the different activities and achieving our goals:

- Insect samples were collected by five partners from specific host plants in their own countries. Half of these samples were shipped to Israel and half to France for symbiont and genetic analyses.
- Insecticide resistance experiments were performed in Greece on samples collected in Spain and Turkey.
- Most importantly, partners from Turkey, Spain, Greece and Israel established field experiments using the same host plant species and following identical protocols. All researchers involved followed the developmental time of the insect pest in their own countries, and created the largest available dataset of information gathered under natural conditions.
- The data jointly produced were summarized and incorporated into the model, and facilitated the development of a tool that can predict whitefly population outbreaks.



Figure 2. Experimental field sites in Israel (A), Turkey (B) and Spain (C)

Figure 3. Specific sites for which climate change and its influence on the pest population has been predicted by the model developed



ACHIEVEMENTS

(i) Genetic groups and symbionts

- Analyses of the whitefly samples revealed that each of the countries participating in the project had a unique combination of genetic variants, and that the composition of bacterial symbionts vary among populations of the same genetic variant in different geographic areas.
- Because the pattern of association between *B. tabaci* variants and the profile of the symbiotic communities is very clear, specific control methods can be designed for each geographic area.

(ii) Symbionts' influence on host stress resistance

- One of the main observations was that the genome of the bacterium genus *Cardinium* exhibits characters that suggest its role in defending the host against parasitoid wasps.
- The genome prediction result was supported by both field and laboratory experiments.
- This information can be used by those practicing biological control, which may now be able to improve the efficiency of natural enemies, both at the insectary and greenhouse level.

(iii) Invasion routes

- The invasion analysis indicates that all countries around the Mediterranean are highly susceptible to pest invasions. Italy, Greece and Turkey and to a lesser extent Spain, were identified as the probable routes for *B. tabaci* introduction.
- The analysis additionally identified Brazil and the USA, and in Europe, France and Spain, as countries at risk for *B. tabaci* exportation (Figure 4). Interestingly, this is not correlated with the number of interceptions (highest in India, Thailand and Israel), which suggests that control efforts may not be targeted at the riskiest countries.



Figure 4. Likelihood of *B. tabaci* invasions. The index considers the probability of *B. tabaci* reaching the country without being intercepted. Reddish colours indicate a higher risk. Some countries are not shown due to insufficient data

(iv) Population outbreaks model

- The climatic model developed predicts that temperatures around the Mediterranean will increase ca. 1.5 - 2.5°C on average until 2050.
- Whitefly populations are in turn expected to be 5-10 times larger, with the pest active season starting earlier and ending later. Warm spring and autumn seasons might lead to 'all-year-round' presence of *B. tabaci*, but hot summers may decrease population sizes at some locations.
- Overall, the combined effort resulted in a new modelling framework for projecting pest population dynamics and supporting decision-making under climate change. The weather generator developed allows exploring the dynamic response of *B. tabaci* to a large variety of temperature patterns, as well as the determination of the main factors controlling population size in addition to the mean annual temperature.

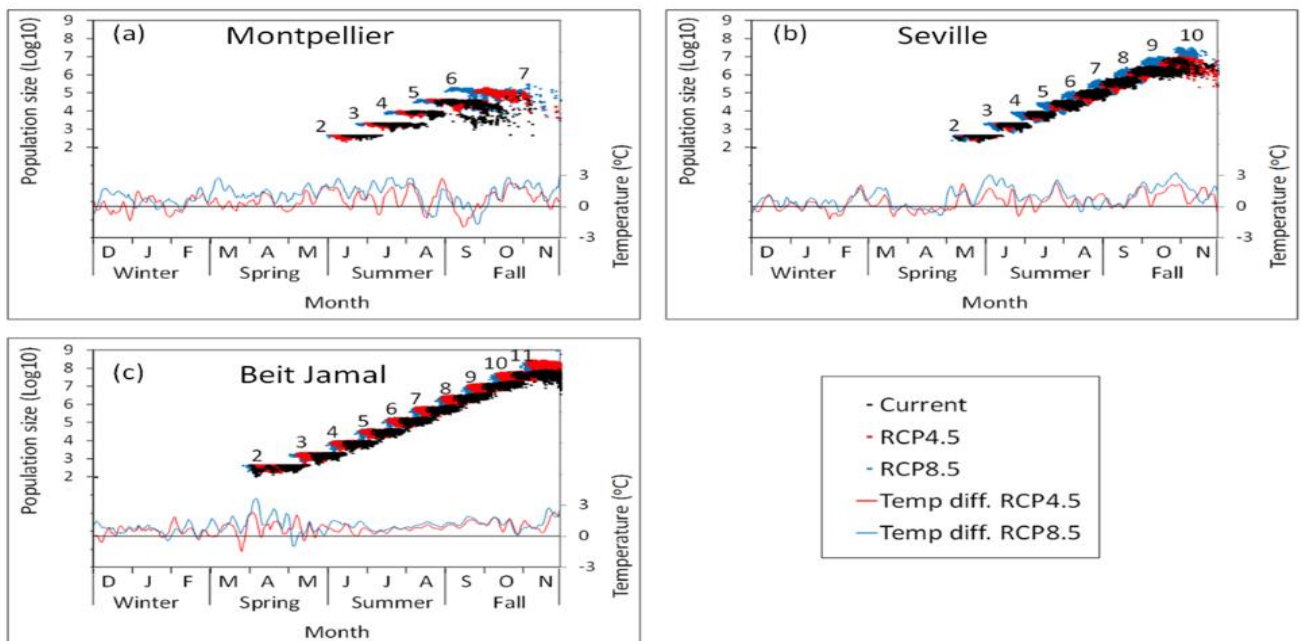


Figure 5. Model prediction of *B. tabaci* population outbreaks in three of the locations sampled (see Figure 3)



Stakeholder engagement

Three main aspects of the SWIPE results are relevant to a number of entities:

- ❑ Invasion risks should be considered by plant protection authorities.
- ❑ Industry could make use of the information on parasitoid resistance.
- ❑ Ministries responsible for agriculture, extension agencies, grower associations, etc., could apply the model for various uses.



Figure 7. The typical field experimental setting used by all partners (left) and a weather station (right)



Figure 6. The SWIPE team, Napoli, 2015

Next steps

Several actions need to be taken in order to promote the application of the results obtained as a part of the SWIPE project:

- ❑ The model, currently based on *Solanum nigrum* data, should be calibrated for specific crops of interest such as watermelons, cotton, tomatoes and beans.
- ❑ The model should be made available to relevant authorities.
- ❑ Each interested country could establish a website for farmers where model predictions will be published. This could help planning crop rotation, planting time and pest control.
- ❑ Various parts of the SWIPE team continue to collaborate under different national and international funding schemes.

Do you want to know more?

Contact: Dr Einat ZCHORI-FEIN

einat@volcani.agri.gov.il

For more information on the ARIMNet2 Network

www.arimnet2.net

Contact: arimnet@arimnet.net

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Selected publications

- Santos-Garcia, D., Rollat-Farnier P.A., Beitia F., Zchori-Fein E., Vavre F., Mouton L., Moya A., Latorre A., Silva F.J., 2014. The genome of *Cardinium* cBtQ1 provides insights into genome reduction, symbiont motility and its settlement in *Bemisia tabaci*. *Genome Biology and Evolution* 6 (4): 1013-1030
- Terraz G., Gueguen G., Arnó J., Fleury F., Mouton L., 2014. Nuclear and cytoplasmic differentiation among Mediterranean populations of *Bemisia tabaci*: testing the biological relevance of cytotypes. *Pest Management Science* 70(10): 1503-13
- Zidon R., Tsueda H., Morin E., Morinet S., 2015. Projecting pest population dynamics under global warming: the combined effect of inter- and intra-annual variations. *Ecological Applications*, <http://dx.doi.org/10.1890/15-1045.1>
- Ilias A., Lagnel J., Kapantaidaki D.E., Roditakis E., Tsigenopoulos C.S., Vontas J., Tsagkarakou A., 2015. Transcription analysis of neonicotinoid resistance in Mediterranean (MED) populations of *B. tabaci* reveal novel cytochrome P450s, but no nAChR mutations associated with the phenotype. *BMC genomics* 16: 939. doi: 10.1186/s12864-015-2161-5

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