



Coordination of the Agricultural Research
In the Mediterranean Area

Report for Research Project No. 131169712

Predicting whitefly population outbreaks in changing environments

Research period reported: 1/7/2012 – 1/7/2015

Year of the project: 3rd and final

Submitted to: The Chief Scientist in Agriculture, ARIMNet initiative by:

Einat Zchori-Fein, Department of Entomology, ARO, Newe Ya'ar Research Center,
P.O.B. 1021, Ramat Yishay 30095. Email: einat@agri.gov.il

Shai Morin, Department of Entomology, Hebrew University of Jerusalem, Rehovot
76100. Email: shai.morin@mail.huji.ac.il

Efrat Morin, Department of Geography, Hebrew University of Jerusalem, Israel.
msmorin@mscc.huji.ac.il

תקציר

כנימת עש הטבק (כע"ט) גורמת בגידולים חקלאיים הן לנזק ישיר הנגרם כתוצאה מפעולת המציצה, והן לנזק עקיף הנגרם מווירוסים אותם היא מעבירה. לאורך חופי הים התיכון, מהווה כע"ט מזיק מפתח בשורה ארוכה גידולים בעלי חשיבות כלכלית וחברתית ראשונה במעלה, ובשנים האחרונות תועדו התפרצויות ופלישות לאיזורים חדשים, כנראה בשל שינויי אקלים המונעים קרה ומאפשרים לכנימה להעלות את מספר הדורות בשנה. ענינה של הצעת מחקר זו הוא קידום יישומן של שיטות הדברה ידידותיות לסביבה של כע"ט וכן פיתוח מודל ראשוני לחיזוי התפרצויות של המזיק. כמו חרקים מוצצים אחרים, גם כע"ט תלויה בחיידקים סמביונטיים להשלמת תזונתה. הנחת העבודה הנמצאת בבסיס המחקר המוצע היא שחיידקים סימביונטיים מעורבים באופן ישיר בהיבטים שונים של הביולוגיה של הפונדקאי, ומשפיעים גם על יכולתו להתמודד עם תנאי סביבה משתנים. בפרויקט שותפים חוקרים המתמחים בדינמיקה של אוכלוסיות (Fabrice Vavre, Lyon University, צרפת), ביואינפורמטיקה של סמביונטיים (Andres Moya, Valencia University, ספרד), מינים פולשים (Alex Aebi, Agroscope שוויץ), סמביונטיים של כע"ט (ישראל, ארה"ב (Martha Hunter, University of Arizona), יוון (Anastasia Tsagkarakou, National Agricultural Research Foundation)) וכן אקולוגיה וגנטיקה של כע"ט בתנאי עקה (יוון, תורכיה (Oktay Gurkan, Ankara University), ישראל) ובמרכז עומד הרעיון כי שיתוף פעולה של חוקרים בעלי התמחויות שונות, הנמצאים בארצות המייצגות תנאי אקלים שונים, יביא ליצירת מאגר נתונים שיוכל לשמש את כולם ולאפשר התקדמות מהירה. למען השגת יעדי הפרויקט, מטרת המחקר המיידיות שהוגדרו לו הן: (1) איפיון הסמביונטיים הנמצאים ביחסי גומלין עם כע"ט והביטיפיים בכל מדינה; (2) בחינת מתאם בין ביטיפיים, סמביונטיים וצמחים פונדקאים; (3) אנליזה של רצפי החיידקים הסמביונטיים השונים לנוכחות גנים העשויים להקנות עמידות לתנאי סביבה קיצוניים; (4) קביעת דפוסי המעבר של כע"ט בין מדינות; (5) בניית מודל המאפשר חיזוי של תגובת אוכלוסיות הכנימה לתנאים האקלימיים השונים הצפויים בעשורים הקרובים באגן הים התיכון; (6) ייסוד שיתוף פעולה הדוק שיאפשר מעבר מידע בין החוקרים. בשלושת שנות המחקר של הפרויקט נעשה שימוש בשיטות מולקולריות, ביולוגיה קלאסית, מודלים חישוביים וביואינפורמטיקה, ואלו הביאו לעמידה ברב המוחלט של היעדים. בחלק הארי של העבודה שנעשתה בישראל הונח בסיס ביולוגי וחישובי למודל המסוגל לחזות התפרצויות של המזיק. המודל הנוכחי מבוסס על התפתחות כע"ט על ענבי שועל, ועל מנת שניתן יהיה ליישם אותו כמערכת תומכת החלטה בחקלאות יש לכייל אותו לכל גידול בנפרד.

הצהרת החוקרת הראשית:

הממצאים בדו"ח זה הינם תוצאות ניסויים.

הניסויים מהווים המלצות לחקלאים: לא

חתימת החוקרת:  : לי-מייסין

תאריך: 30.12.2015



Coordination of the Agricultural Research
In the Mediterranean Area

SWIPE – Final report (M36)

Report for Research Project No. 131169712

Predicting whitefly population outbreaks in changing environments

Research period reported: 1/7/2012 – 1/7/2015

Year of the project: 3rd and final

Submitted to: The Chief Scientist in Agriculture, ARIMNet initiative by:

Einat Zchori-Fein, Department of Entomology, ARO, Newe Ya'ar Research Center,
P.O.B. 1021, Ramat Yishay 30095. Email: einat@agri.gov.il

Shai Morin, Department of Entomology, Hebrew University of Jerusalem, Rehovot
76100. Email: shai.morin@mail.huji.ac.il

Efrat Morin, Department of Geography, Hebrew University of Jerusalem, Israel.
msmorin@mscc.huji.ac.il


תקציר

כנימת עש הטבק (כע"ט) גורמת בגידולים חקלאיים הן לנזק ישיר הנגרם כתוצאה מפעולת המציצה, והן לנזק עקיף הנגרם מווירוסים אותם היא מעבירה. לאורך חופי הים התיכון, מהווה כע"ט מזיק מפתח בשורה ארוכה גידולים בעלי חשיבות כלכלית וחברתית ראשונה במעלה, ובשנים האחרונות תועדו התפרצויות ופלישות לאיזורים חדשים, כנראה בשל שינויי אקלים המונעים קרה ומאפשרים לכנימה להעלות את מספר הדורות בשנה. ענינה של הצעת מחקר זו הוא קידום יישומן של שיטות הדברה ידידותיות לסביבה של כע"ט וכן פיתוח מודל ראשוני לחיזוי התפרצויות של המזיק. כמו חרקים מוצצים אחרים, גם כע"ט תלויה בחיידקים סמביונטיים להשלמת תזונתה. הנחת העבודה הנמצאת בבסיס המחקר המוצע היא שחיידקים סימביונטיים מעורבים באופן ישיר בהיבטים שונים של הביולוגיה של הפונדקאי, ומשפיעים גם על יכולתו להתמודד עם תנאי סביבה משתנים. בפרויקט שותפים חוקרים המתמחים בדינמיקה של אוכלוסיות (Fabrice Vavre, Lyon University, צרפת), ביואינפורמטיקה של סמביונטיים (Andres Moya, Valencia University, ספרד), מינים פולשים (Alex Aebi, Agroscope שוויץ), סמביונטיים של כע"ט (ישראל, ארה"ב (Martha Hunter, University of Arizona), יוון (Anastasia Tsagkarakou, National Agricultural Research Foundation)) וכן אקולוגיה וגנטיקה של כע"ט בתנאי עקה (יוון, תורכיה (Oktay Gurkan, Ankara University), ישראל) ובמרכזו עומד הרעיון כי שיתוף פעולה של חוקרים בעלי התמחויות שונות, הנמצאים בארצות המייצגות תנאי אקלים שונים, יביא ליצירת מאגר נתונים שיוכל לשמש את כולם ולאפשר התקדמות מהירה. למען השגת יעדי הפרויקט, מטרת המחקר המיידיות שהוגדרו לו הן: (1) איפיון הסמביונטיים הנמצאים ביחסי גומלין עם כע"ט והביטיפיים בכל מדינה; (2) בחינת מתאם בין ביטיפיים, סמביונטיים וצמחים פונדקאים; (3) אנליזה של רצפי החיידקים הסמביונטיים השונים לנוכחות גנים העשויים להקנות עמידות לתנאי סביבה קיצוניים; (4) קביעת דפוסי המעבר של כע"ט בין מדינות; (5) בניית מודל המאפשר חיזוי של תגובת אוכלוסיות הכנימה לתנאים האקלימיים השונים הצפויים בעשורים הקרובים באגן הים התיכון; (6) ייסוד שיתוף פעולה הדוק שיאפשר מעבר מידע בין החוקרים. בשלושת שנות המחקר של הפרויקט נעשה שימוש בשיטות מולקולריות, ביולוגיה קלאסית, מודלים חישוביים וביואינפורמטיקה, ואלו הביאו לעמידה ברב המוחלט של היעדים. בחלק הארי של העבודה שנעשתה בישראל הונח בסיס ביולוגי וחישובי למודל המסוגל לחזות התפרצויות של המזיק. המודל הנוכחי מבוסס על התפתחות כע"ט על ענבי שועל, ועל מנת שניתן יהיה ליישם אותו כמערכת תומכת החלטה בחקלאות יש לכייל אותו לכל גידול בנפרד.

הצהרת החוקרת הראשית:

הממצאים בדו"ח זה הינם תוצאות ניסויים.

הניסויים מהווים המלצות לחקלאים: לא

חתימת החוקרת:  : לי-מייסין

תאריך: 30.12.2015



Coordination of the Agricultural Research
In the Mediterranean Area

1. Identification of project and participants

ERA-NET Grant Agreement No: KBBE 219262

ERA-NET acronym: ARIMNet

PROJECT FULL TITLE: Predicting whitefly population outbreaks in changing environments

Project acronym: SWIPE

Starting date of the project: 1 July 2012

Project coordinator: Einat Zchori-Fein

Name, title and organization of the representative of the project's coordinator: Prof. Yoram Kapulnik, Head, Agricultural Research Organization

Tel: +972-4-9539549

E-mail: einat@agri.gov.il



Identification of project participants

- Partner 1 Laurence Mouton - Laboratoire de Biométrie et Biologie Evolutive, UMR CNRS 5558, Université de Lyon, France. laurence.mouton@univ-lyon1.fr
- Partner 2 Anastasia Tsagkarakou - Plant Protection Institute of Heraklion, Laboratory of Entomology and Agricultural Zoology, Greece. tsagkarakou@nagref.gr
- Partner 3 Birol Akbas - General Directorate of Agricultural Research and Policy, Turkey. bakbas@tagem.gov.tr
- Partner 4 Francisco Silva - Cavanilles Institute, University of Valencia, Spain. francisco.silva@uv.es
- Partner 5 Massimo Giorgini - National Research Council of Italy (CNR), Institute for Plant Protection (IPP). Italy. giorgini@ipp.cnr.it
- Partner 6 John Vontas - University of Crete, Greece. vontas@biology.uoc.gr
- Partner 7 Cem Erdogan - Plant Protection Central Research Institute, Turkey. cmerdogan@yahoo.com
- Partner 8 Shai Morin - Department of Entomology, Hebrew University of Jerusalem, Israel. shai.morin@mail.huji.ac.il
- Partner 9 Francisco J. Beitia - Valencian Agricultural Research Institute, Spain. beitia_fra@gva.es
- Partner 10 Kemal Degirmenci - Plant Protection Central Research Institute, Turkey. k_degirmenci@hotmail.com
- Partner 11 Efrat Morin, Department of Geography, Hebrew University of Jerusalem, Israel. mamorin@mscc.huji.ac.il
- Partner 12 Hakan Fidan - Biological Control Research Station Direction, Turkey. hakanfidantr@hotmail.com
- Partner 13 Nurper Guz - Ankara University, Turkey. nurperguz@hotmail.com
- Partner 14 Einat Zchori-Fein, Department of Entomology, Agricultural Research Organization, Israel. einat@agri.gov.il



2. Final publishable summary report Final publishable summary report of the key findings and impacts written for a non-technical audience, which ARIMNet may use to communicate results to users. (max 2 pages)

Both climate change and global trade are important factors influencing the abundance and distribution of insects of agriculture and medical importance. Whiteflies (Hemiptera: Aleyrodidae) are key plant pests and virus vectors in many agricultural systems worldwide. Among them, the sweet potato whitefly *Bemisia tabaci* is considered the most devastating pest of vegetables, ornamentals, and agronomic crops throughout the tropical and subtropical regions of the world. Previous distributions of the whitefly were limited to temperate climate zones but in the past two decades, it has invaded every continent in the world except Antarctica. The main scientific question addressed by the SWIPE team was how the future changes in temperatures will affect the population dynamics of the insect pest, taking into account genetic variability and symbiotic associations. We aimed to understand the various effects in the context of interactions between temperature patterns and the insect performance measures. To achieve this goal, the following objectives have been set: 1) Determine the geographic distribution of *B. tabaci* genetic groups, their population genetic structure and symbiotic complement around the Mediterranean basin in light of climatic changes; 2) Determine whitefly invasion routes within the Mediterranean basin; 3) Determine the respective influence of nuclear and symbiotic variations on stress resistance in the whitefly; 4) Model the influence of climate change on whitefly population outbreaks; 5) Establish a network of researchers.

To identify the genetic groups (referred to as “species”) found around the Mediterranean, over 480 *B. tabaci* individuals were collected during the course of the study in 48 sampling efforts in five countries, mainly from three host plants. Analyses of the genetic backgrounds of these samples revealed that in Western Mediterranean mainly MED species occurred with the Q1 and Q2 genetic variants: in Greece only MED Q1; in Spain, MED Q1 populations were prevalent and mixed with SSA2; and in Italy, both Q1 and Q2 genotypes. In contrast, *B. tabaci* populations in Eastern Mediterranean were almost exclusively the MEAM1 species, with the exception of very few individuals of MED Q2 in Israel.

Many arthropods host one or more inherited bacterial symbionts, the effects of which have important implications for ecologically-based pest management strategies. The symbionts carried by each individual whitefly were determined, and the results show differences in their composition among populations of the same genetic variant in different geographic areas; while infection rate of *Hamiltonella* was over 90% everywhere, the infection of other symbionts varied. For example, Greece Q1 populations were characterized by the absence of *Cardinium* and 27% individuals infected by *Wolbachia*, while in Italy the same species harboured both *Cardinium* (30%) and *Wolbachia* (15%). One route by which the possible influence of symbiotic partners may be evaluated is looking at their genomes. During the project, the genome of the obligate symbiont *Portiera* was analyzed, and although it is highly reduced, it was found to supplement the insect diet with carotenoids and amino acids. This result conforms to the role of most other known obligate symbionts of sap-feeding insects which supplement the diet of their hosts. It was additionally discovered that the genome of the facultative symbiont *Hamiltonella* is able to complement some metabolic pathways and might be essential for some whiteflies, while the genome of *Cardinium* exhibits characters that suggest its role in defending the host against parasitoid wasps.



The influence of the symbionts associated with *B. tabaci* on parasitoids, thermal and pesticide resistance as well as on virus transmission capacities were studied. It was discovered that individuals infected with *Rickettsia* were more susceptible to pesticides than others, while no influence (or a marginal one) of the bacteria could be detected on either heat and parasitoid resistance, or virus transmission capabilities of the host.

Four main sources of data were used to determine potential whitefly invasion routes within the Mediterranean basin: (i) the worldwide geographic distribution; (ii) the amount of potential host plants transported to the EU; (iii) the presence or the cultivated area of host plants in EU; (iv) the number of *B. tabaci* interceptions. From these data, the following risks have been calculated: a pathway risk, arrival to a given country risk and an entry risk (ER). Results indicate that all countries around the Mediterranean are highly susceptible to pest invasions. Importantly, the varying number of interceptions among countries is reflected in the ER, with Italy, Greece and Turkey and, to a lesser extent, Spain, probable routes for *B. tabaci* introduction. The analysis identified Brazil and the USA, and within Europe France and Spain as countries at risk for *B. tabaci* exportation. 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.

Various computational approaches were applied to model changes in *B. tabaci* population dynamics under anticipated climate changes for the next decades. In order to insert to the model data on the performance of the insects under real conditions, field-experiments were performed in four countries to determine life history traits of the whitefly under varying temperatures. The climatic model developed predicts that temperatures around the Mediterranean basin will increase about 1.5-2.5°C on average until 2050. *B. tabaci* populations are in turn expected to be 5-10 times larger, with 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.

The SWIPE project included 13 institutes in six countries, and united expertise of scientists from various disciplines. The combined effort resulted in a new modelling framework for projecting insect-pest population dynamics and supporting environmental decision-making under climate changes. The weather generator developed allows exploring the population 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, such as distinct intra-annual temperature patterns that lead to especially large or small population sizes. The ample additional data collected (species distribution patterns, symbiotic associations, resistance to environmental factors and more), could be incorporated into the model in the future. Together with the invasion risk assessment performed we believe that the modelling framework developed here 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.



3. Detailed description of activities and final results

List major results of the project. Describe briefly whether the objectives of the research have been achieved and outline the principal outcomes of the work and their significance to the field. (max. 10 pages).

Work package 1: *Determine the geographic distribution of *B. tabaci* biotypes, their population genetic structure and symbiotic complement around the Mediterranean basin in light of climatic changes*

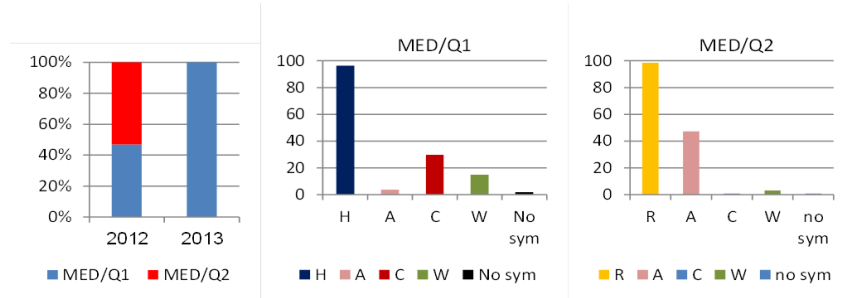
Task 1.1 Insect collections. Insect collection has been completed. In total 48 *B. tabaci* samples have been collected in five countries (SP, IT, GR, TU and IS) on 2012 and 2013 mainly on *Solanum nigrum*, *Malva silvestris* and *Ipomoea indica*. The samples were preserved and shipped for analysis to IS (31 samples) and FR (17) to determine the distribution of a) biotypes and symbiont complexes (Task 1.2) and b) genetic variability among and between samples (Task 1.3). Laboratory colonies have been established from samples collected from *S. nigrum* in three partner's laboratories (IS, SP and GR) and maintained on *S. nigrum*. These colonies have been used to establish preliminary field-experiments in order to determine life history traits of *B. tabaci* under varying temperatures.

Task 1.2 Identification of biotypes and symbionts. Species identity and composition of known symbionts have been determined for all samples. Genetic variants of *B. tabaci* were identified analysing individuals by PCR-RFLP and/or sequencing the *mtCOI* gene. Symbionts screening has been performed through Denaturing Gradient Gel Electrophoresis and diagnostic PCR. The genetic composition of *B. tabaci* was geographically structured. In **Western Mediterranean** only MED species occurred with the Q1 and Q2 genetic variants: in GR only MED Q1; in SP, MED Q1 populations were prevalent and mixed with SSA2 (biotype S); and in IT, both Q1 and Q2 genotypes. In **Eastern Mediterranean**, populations of *B. tabaci* were almost exclusively the MEAM1 species, with the exception of very few individuals of MED Q2 in IS.

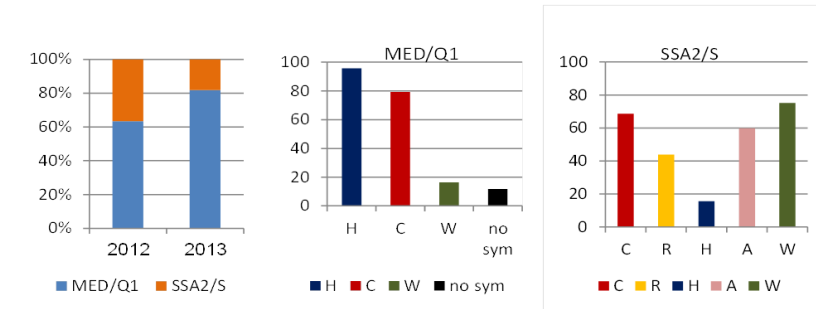
Differences were observed in the symbiont composition among populations of the same genetic variant in different geographic areas; while infection rate of *Hamiltonella* was over 90% everywhere, the infection of other symbionts varied. GR MED Q1 populations were characterized by the absence of *Cardinium* and 27% *Wolbachia* infection. IT MED Q1 individuals harboured both *Cardinium* (30%) and *Wolbachia* (15%). In SP the infection frequency of *Cardinium* was higher (80%) than IT and GR, while infection of *Wolbachia* (16%) was similar to IT. SP SSA2 populations showed the highest symbiont diversity. Only minor differences of symbiont composition were observed between IS and TU MEAM1 populations (summarized in Fig. 1).

To assess the full diversity of *B. tabaci* symbionts, 11 pools of MEAM1 and MED representatives of the complex were analysed by deep sequencing. Within samples, bacterial communities are highly enriched, while the diversity among the examined samples is rather low. Statistically significant differences were detected between the two whitefly species. Gammaproteobacteria was the most dominant group in all tested samples and *Portiera* (the obligate symbionts) and *Hamiltonella* the most dominant genera (Fig. 2). Taken together, the pattern of association between the mitotypes of *B. tabaci* and the profile of the symbiotic communities is very clear.

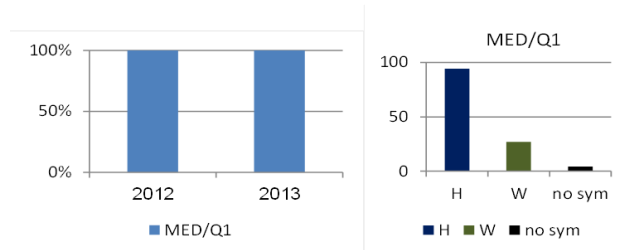
ITALY



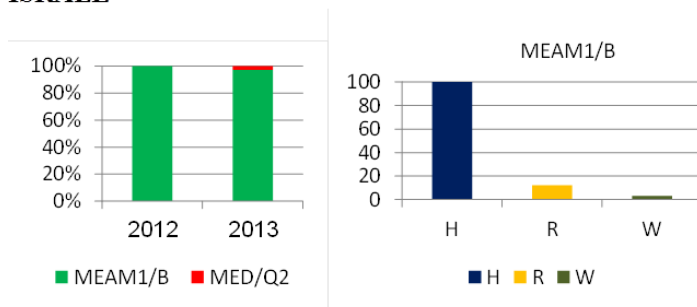
SPAIN



GREECE



ISRAEL



TURKEY

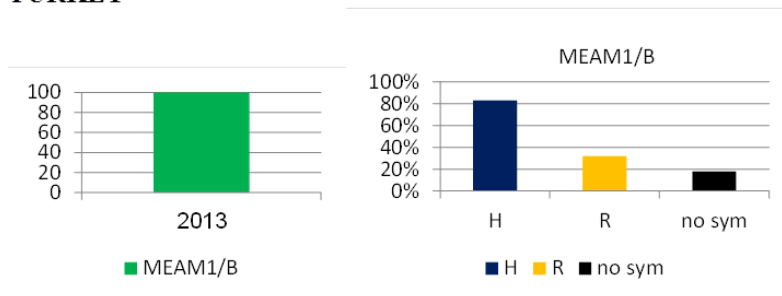


Figure 1. Frequency (% of sampled individuals) of *B. tabaci* genotypes (MED/Q1, MED/Q2, MEAM1=biotype B and SSA2=biotype S) over two-years sampling and average infection frequency by facultative bacterial endosymbionts (A=*Arsenophonus*; C=*Cardinium*; H=*Hamiltonella*; R=*Rickettsia*; W=*Wolbachia*; no sym=absence of symbionts) of each *B. tabaci* genotype in five Mediterranean countries.

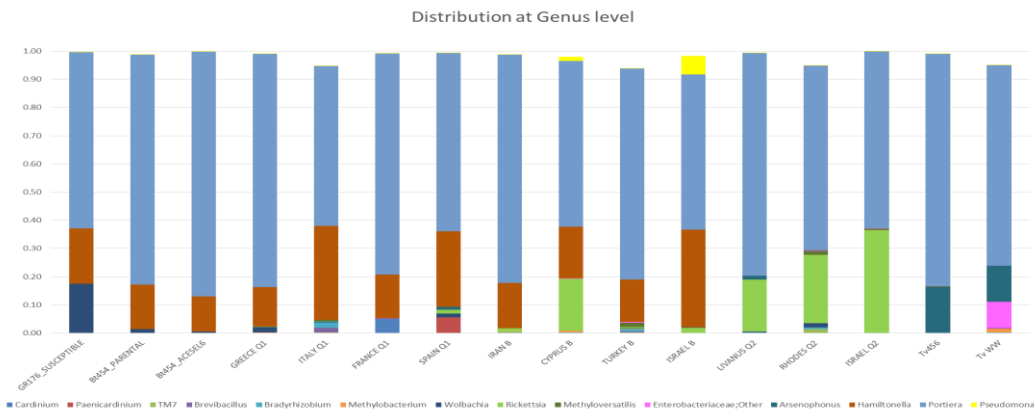


Figure 2. Bacterial distribution at genus level, after the exclusion of the most dominant genera, *Portiera* and *Hamiltonella*. X axis - different populations; Y axis - percentage of 16S rRNA gene sequences obtained for each genus.

Task 1.3. Population genetic structure. A new tool which allows genome-wide population genetic studies has been developed based on next-generation sequencing techniques: RADSeq markers. Although preliminary experiments showed that this tool is usable for *B. tabaci*, due to the very small size of these insects, the amount of DNA obtained was low and, during the last year, we worked in the optimization of the protocol. At the end of the project, sequences have been obtained and data analyses are in progress.

Work package 2: Determine *B. tabaci* invasion routes within the Mediterranean basin.

Although this part has been minimized due to the withdrawal of the Swiss partner, some analyses have been performed and provide useful information. For a complete description of the method, see Bacon et al. (2012, 2013). Four main sources of data were used: (i) the geographic distribution of *B. tabaci* worldwide, (ii) the amount of potential *B. tabaci* host plants transported to the EU, (iii) the presence or the cultivated area of host plants in EU, and (iv) the number of *B. tabaci* interceptions. From these data, the following risks have been calculated: a pathway risk (PR), arrival to a given country risk, and an entry risk (ER), where PR is corrected by the number of interceptions. Results indicate that all countries around the Mediterranean basin have a high PR, implicating that they are highly susceptible to *B. tabaci* invasion (Fig. 3). Importantly, the varying number of interceptions among countries, is reflected in the ER, with Italy, Greece and Turkey and, to a lesser extent Spain, probable routes for *B. tabaci* introduction (Fig. 3). This analysis also allowed identifying countries at risk for *B. tabaci* exportation. These included Brazil and the USA and, within Europe, France and Spain. Interestingly, this is not correlated with the number of interceptions (highest in India, Thailand and Israel), which suggests that interception efforts may not be targeted at the riskiest countries.



Figure 3. A heat map showing the likelihood of *B. tabaci* invasions. The index takes into account the probability that *B. tabaci* arrives the country and not been intercepted. Risk is higher with reddish colours. Some countries are not shown because of insufficient data.

Work package 3: Determine the respective influence of nuclear and symbiotic variations on stress resistance in *B. tabaci*.

Task 3.1 Resistance to thermal stress. Influence of the symbiotic combination on *B. tabaci* resistance to thermal stress was studied on laboratory lines MED (Q1 biotype) harbouring either *Hamiltonella*, *Hamiltonella* and *Cardinium* or *Hamiltonella* and *Rickettsia*. To avoid bias due to variation in the host genetic background experiments were performed on F1 females. Females were subjected to three temperatures, 40, 42 and 45°C, with a control condition at 25°C (10 replicates per modality) for 3h. Survival was checked after 3, 24 and 48h. At 45°C all individuals were dead 3h after exposure. At 40 and 42°C mortality was higher than at 25°C with a significant difference between 40 and 42°C. However, there was no effect of the symbiotic composition on the resistance to heat stress (Fig. 4). On the other hand, females infected with *Hamiltonella* and *Rickettsia* produced more eggs than females infected with *Hamiltonella* and *Cardinium*.

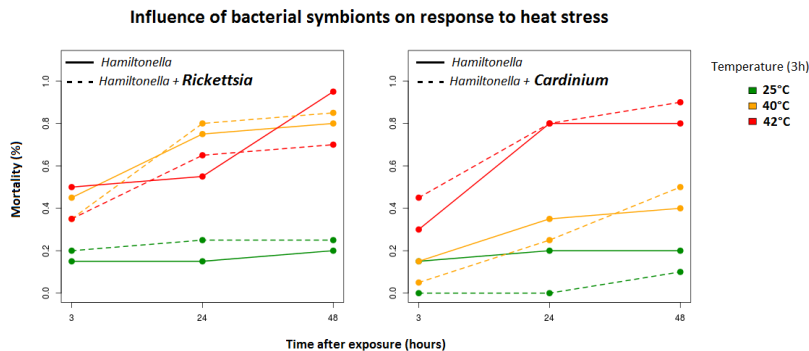


Figure 4. Percentage of females' mortality 3, 24 and 48h after exposure to heat stress (40 or 42°C, 25°C is the control temperature) according to the presence of *Cardinium* (right panel, dashed lines) or *Rickettsia* (left panel, dashed lines).

Task 3.2 Parasitoids and symbionts (all experiments preformed at IVIA, SP).

Field observations. To test for field parasitism rate, *S. nigrum* plants infested with whitefly nymphs were placed in the field. Observations were done on spring and fall of 2013 and June-July 2014. Four plants/period with a total of 12 leaves/period were observed. The plants were placed in different areas close to wild *S. nigrum* plants. In both years no parasitism on the exposed whitefly nymphs on *S. nigrum* was observed.

Laboratory experiments. The genome analysis (Task 3.4) suggests that *Cardinium* might function as a defensive symbiont against parasitoids. To test this prediction, two whitefly strains of MED Q1 (reared on cotton) have been used: Q1_{HC} (infected with *Hamiltonella* and *Cardinium* was selected in Spain), and Q1_{HR} (infected with *Hamiltonella* and *Rickettsia* and selected in France). The hymenopterous whitefly parasitoids *Eretmocerus mundus* and *Encarsia formosa* that were tested originated from Koppert Spain, and the optimal number of *B. tabaci* nymphs/leaf disc was determined in a set of preliminary experiments. No-choice tests conducted with *E. mundus* adult females coming from Koppert (reared on a whitefly population with *Cardinium*) and exposed to Q1_{HC} or Q1_{HR} whitefly nymphs showed no evidence for differences in parasitization rates (=PR). However, there were differences in PR by using wasps from a lab culture reared on the Q1_{HR} *B. tabaci* population (without *Cardinium*). The PR rate between the two populations was not statistically different with parasitoids from the 1st lab

culture generation, but there were statistical differences when using parasitoids from the 4th and the 7th generations (ANOVA's test): the PR on Q1_{HC} was almost the half than that on Q1_{HR} (Fig. 5). An experiment conducted with *E. formosa* revealed no difference of PR between wasps ovipositing on nymphs with and without *Cardinium*. The hypothesis that *Cardinium* provides *B. tabaci* defense appears to be supported only for *E. mundus*.

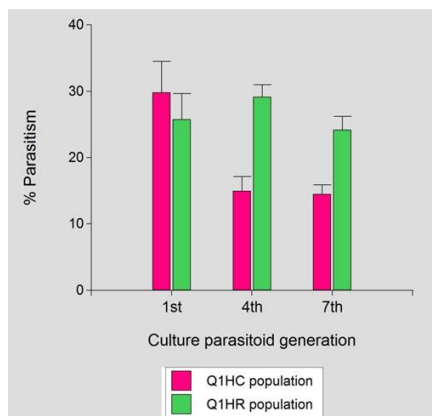


Figure 5. Percentage of *B. tabaci* Q1HC and Q1HR nymphs parasitized by *E. mundus* in no-choice tests replicated by using wasps from different generations reared on Q1HR.

Task 3.3 Resistance to pesticides.

Full dose bioassays with imidacloprid, deltamethrin and pymetrozin, as well as molecular diagnostics and biochemical assays were performed on 20 field and laboratory populations from MED Q1 (GR, SP), and MEAM (TU, IS) to determine the LC50s, the frequency of two resistance genes (*kdr* and *ace*) and the activity of detoxifying enzymes. No association was found between the presence and prevalence (%) of specific symbionts (*Wolbachia*, *Cardinium*) with resistant phenotype and resistance genes (Fig. 6). Furthermore the comparison of the relative abundance of symbionts between Q1 host strains with the same genetic background but under different level of selection pressure (parental vs. selected, survivals vs. control) did not reveal any relationship between resistance and symbionts loads (*Portiera*, *Hamiltonella*, *Wolbachia*).

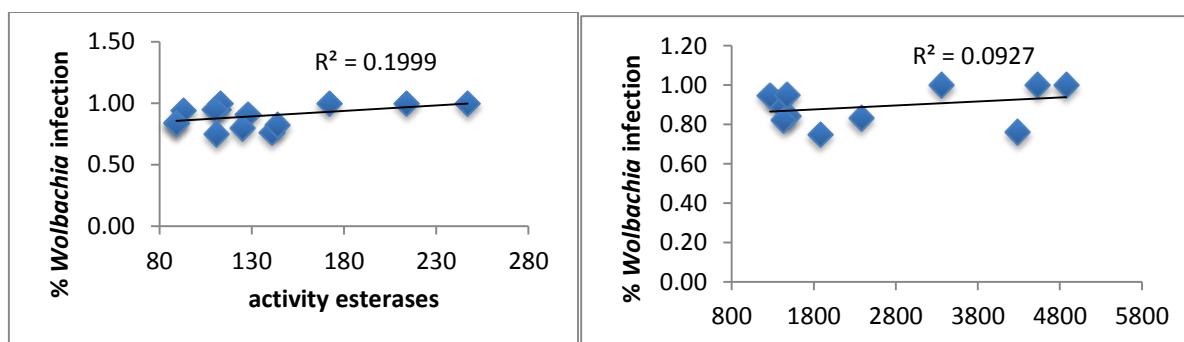


Figure 6. *Wolbachia* infection levels in populations of *B. tabaci* with different activities of detoxification enzymes

Additionally, the influence of symbiotic community on resistance to deltamethrin was tested in a controlled host genetic background. Data obtained indicated that individuals infected with *Rickettsia* were more susceptible to pesticides than others. This result is consistent with previous reports in another *B. tabaci* species, MEAM, indicating that the composition of the inherited bacterial community has an influence on resistance to pesticides.

Task 3.4 Contribution of symbionts genes to fitness traits.

Three of the genomes of *B. tabaci* bacterial associates, *i.e.* the obligate symbiont *Portiera* and the facultative symbionts *Hamiltonella* and *Cardinium* have been sequenced and analysed. The genome of *Portiera* is highly reduced (357 kb) but has kept a number of genes encoding most essential amino-acids and carotenoids. In contrast, *Portiera* lacks almost all the genes involved in the synthesis of vitamins and cofactors, and some pathways are incomplete, notably those involved in the synthesis of some essential amino-acids. Interestingly, the analyses revealed that *Hamiltonella* can not only provide vitamins and cofactors, but also complete the missing steps of some of the pathways of *Portiera*. Altogether, these results illustrate how functional redundancies can lead to gene losses in the genomes of the different symbiotic partners, reinforcing their inter-dependency (Fig. 7).

A comparison of the gene repertoires of *Hamiltonella* from *B. tabaci* and aphids revealed that they belong to two distinct clades and, while in aphids the bacterium contains highly virulent factors that allow protection and horizontal transfers, in whiteflies the genome lost these factors. However it contains genes that could be involved in the production of essential nutrients, which is consistent with a primordial role for this symbiont. In conclusion, while both *Hamiltonella* lineages have mutualistic interactions with their hosts, their genomes follow distinct evolutionary trajectories that reflect their phenotype.

Metabolic complementation between primary and secondary symbionts of *B. tabaci*

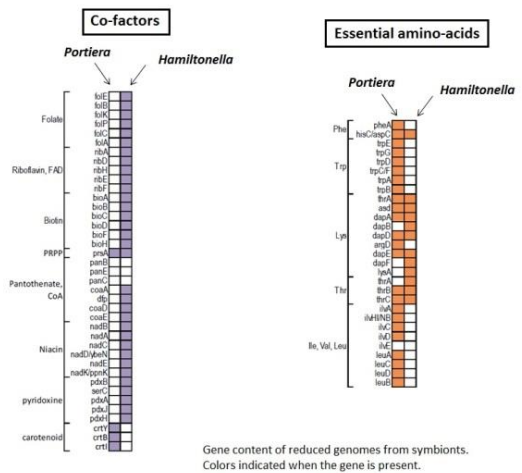


Figure 7. Metabolic complementation between obligate and facultative symbionts of *B. tabaci*.

The genome of *Cardinium* cBtQ1 displays a large proportion of transposable elements, which has recently inactivated genes and produced chromosomal rearrangements. It also contains a chromosomal duplication and a multicopy plasmid which harbors several genes putatively associated with gliding motility, as well as two other genes encoding proteins with potential insecticidal activity. As gene amplification is very rare in endosymbionts, an important function of these genes cannot be ruled out.

Task 3.5 Symbionts and virus transmission.

Six whitefly samples were collected from 8 sites (2013) and 6 sites (2014) from Muğla Fethiye. 20 individual whiteflies from 5 samples *S. nigrum*, *Ipomea*, *Malva*, Cucumber and tomato (2013) and 200 individual whiteflies (2014) from 5 different hosts in 2 sites in Hatay-Samandağ. Samples collected from *Solanum* and *Malva* were sent to Israel and France, while

samples collected from tomatoes were sent to Italy and Greece (2013). All samples were tested for *Hamiltonella*, *Rickettsia*, *Cardinium*, *Arsenophonus*, *Wolbachia*, TYLCV strains and biotype. All whiteflies sampled from tomato, *Solanum* and *Malva* in Muğla and Hatay provinces were found to be MEAM1. *Hamiltonella* and *Rickettsia* were detected in samples collected in Hatay and Muğla locations, but no other facultative symbiont was detected, as expected from the MEAM1. Different rates of TYLCV-Israel and TYLCV-Mild were recorded, but no TYLCV-Esp could be detected. The results show no significant correlation between the presence of specific bacteria (*Hamiltonella* and *Rickettsia*) and viruses.

Work package 4: *Model the influence of climate change on B. tabaci biotype/population outbreaks.*

Deterministic and stochastic modelling approaches were applied to predict changes in *B. tabaci* population dynamics under anticipated climate changes for the next decades. Generating a prediction for insect population response to climate change was done by coupling general circulation models and a weather generator that produced realizations of temperature series under given climate conditions with a model representing the insect population dynamics. The research steps taken were: 1. Incubator (fixed temperature) and field (varying temperature) experiments were conducted in order to develop a performance model which describes how developmental rates of *B. tabaci* are influenced by temperature, and an exponential function to describe the influence of temperature on the number of adults produced per female (i.e. number of eggs X egg to adult survival); 2. Downscaling synoptic data using a stochastic weather generator to create realizations of local temperature time series under current climatic conditions (linked with NCEP/NCAR reanalysis data and stations temperature data); 3. Predicting local climate changes, using general circulation models data and a stochastic weather generator to generate realizations of local temperature series under future climatic conditions; 4. Predicting *B. tabaci* population response to climate change using the produced realizations in steps 1 and 2 as an input into an insect population dynamics model. The results obtained are summarized in Table 1 and Figures 8-12.

Major findings of this part of the project include:

- (I) The large variety of current and future temperature patterns produced by the stochastic framework have a strong effect on the insect's population dynamics.
- (II) In the Mediterranean climate region, a significant increase in the insect's number of annual generations, population size and season length is predicted.
- (III) Critical intra-annual periods determining large populations can be identified and show differences between the studied locations.
- (IV) The predicted earlier seasonal activity in future climate will lead to an increase in population size only if an additional generation is produced at the end of the season. Moreover, in two locations (Seville and Beit-Jamal) during most of the season, the population size at future climate is predicted to be smaller than those of current climate.
- (V) It is highly likely that the insect will become a significant pest of open-fields at Mediterranean latitudes above 40° during the next 50 years.

Table 1. A summary of results obtained from parallel experiments in member countries.

Country	Site	Species	Dates	Mean temperature \pm SD ($^{\circ}$ C)	Mean development \pm SD (Days)	n
Turkey	Adana	B	19.9-24.10.2013	21.2 \pm 5.2	24.7 \pm 2.6	269
			28.5-23.6.2014	24.9 \pm 4.0	22.7 \pm 1.0	253
Israel	Nachshon	B	26.9-28.10.2013	21.5 \pm 5.5	27.4 \pm 1.3	105
		Q2	26.9-30.10.2013	21.5 \pm 5.5	30.3 \pm 3.7	31
		B	23.3-2.5.2014	20.1 \pm 8.4*	32.2 \pm 1.8	60
		Q2	23.3-7.5.2014	20.8 \pm 8.6*	37.6 \pm 6.6	18
		B	26.9-30.11.2014	21.8 \pm 5.4*	24.9 \pm 2.7	90
		Q2	26.9-4.11.2014	21.6 \pm 5.4*	29.1 \pm 5.3	14
	Baraam	B	6.5-11.6.2014	20.1 \pm 5.9*	30.3 \pm 2.3	177
		B	5.10-22.11.2014	19.9 \pm 5.7	39.1 \pm 3.1	82
		Q2	5.10-10.12.2014	16.0 \pm 5.4	56.4 \pm 5.1	9
Spain	IVIA, Valencia	Q1	10.4-7.6.2013	19.6 \pm 2.9	49.7 \pm 4.4	11
			11.6-9.7.2013	26.5 \pm 1.7	24.4 \pm 1.5	16
			2.7-26.7.2013	27.7 \pm 1.1	18.7 \pm 1.3	45
			16.4-27.5.2014	20.3 \pm 1.5	35.4 \pm 2.5	55
			18.6-18.7.2014	25.8 \pm 1.7	24.6 \pm 2.3	96
			1.7-31.7.2014	26.4 \pm 1.4	22.6 \pm 3.2	166
			15.7-8.8.2014	27.1 \pm 1.0	19.3 \pm 2.0	140

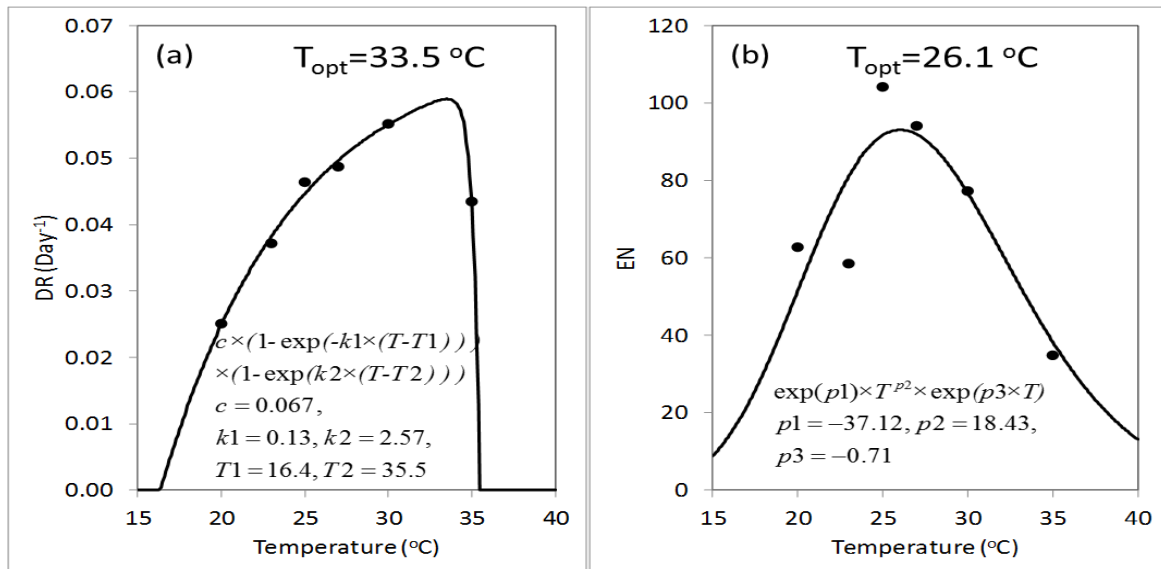


Figure 8. The developed model functions based on fixed temperature experiments For simplicity, only the MEAM functions are presented but MED Q1 and Q2 are also available. (a) Development rate function (DR), (b) adults produced per female function (EN).

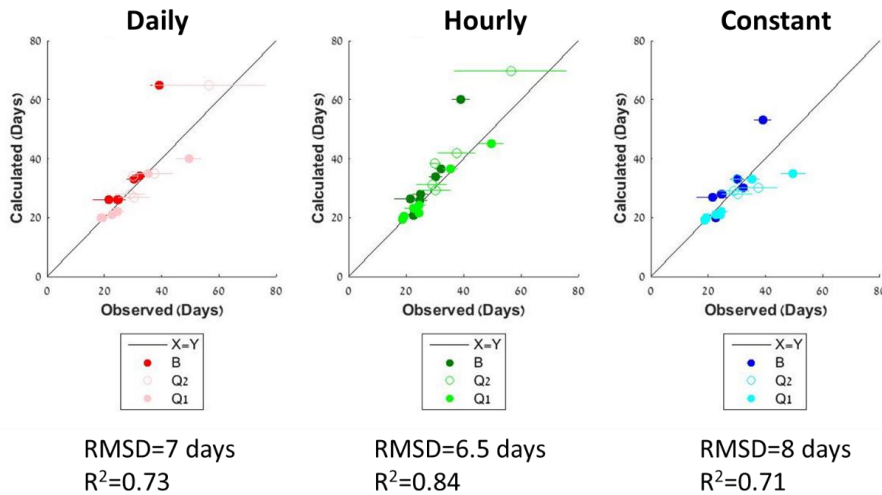


Figure 9. Model simulations (calculated days) predict well the field developmental period (observed days). The hourly model seems best. Optimization by field data makes only minor changes in the *DR* and *EN* functions.

Three locations in the Mediterranean climate region were selected, with different climate characteristics: **Montpellier**, France (43°36'42.84" N, 3°52'37.92" E) in the central part of the Mediterranean with cold winters and mild summers; **Seville**, Spain (37°22'38" N, 5°59'13" W) in the western part of the Mediterranean with mild winters and hot summers and, **Beit-Jamal**, Israel (31°43'30" N 34°58'35" E) in the eastern part of the Mediterranean, with mild winters and mild to hot summers. In addition, the Montpellier location differ significantly from Seville and Beit-Jamal in the current pest status of *B. tabaci*. In contrast to the latter two locations, *B. tabaci* populations in the south of France are considered to be restricted in their distribution, to be mostly in protected conditions and to cause relatively minimal economic problems in open-fields



Figure 10. Sites chosen for simulation of future scenarios

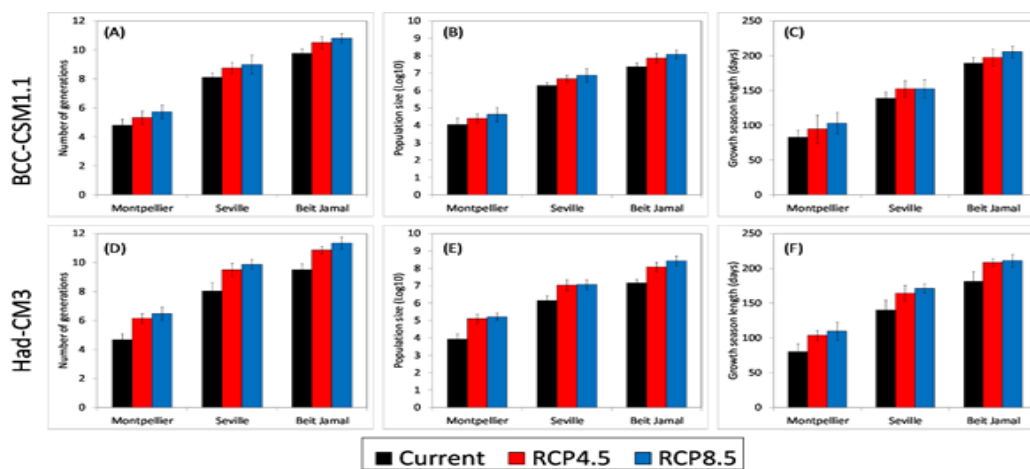


Figure 11. Results from the population dynamics model: (a, d) number of generations, (b, e) annual maximal populations size (Log10), and, (c, f) growth season length (number of days between the end of the first and last generations). Bars represent mean value and error bars represent one standard deviation computed from means of 150 values for each simulated year.

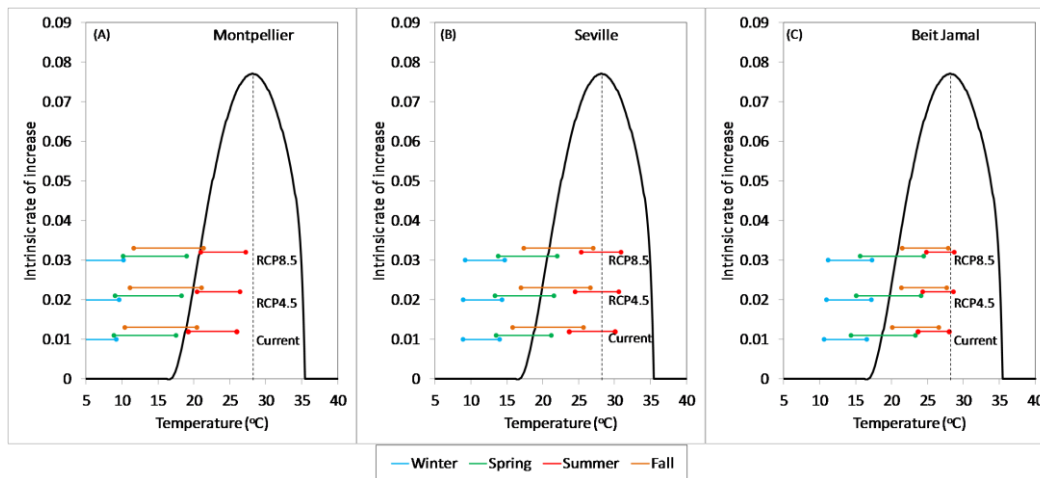


Figure 12. Daily temperature range (horizontal bars represent mean plus/minus one standard deviation of daily temperature) for each season and climate scenario in relation to the insect's thermal performance curves.

Recent studies on *B. tabaci* (as well as other ectotherms) response to climate change generated future temperature conditions using current climate surface temperature to which a delta was added, representing the mean change in temperature derived from climate models. Although these altered data series are able to capture the mean change, the actual future temperature will most probably differ from these means due to natural variability. It is important to consider this variability because of the non-linearity of the insect's population dynamic response, which causes the mean of responses to be different from the response to the mean. We found that running the model for the mean of the 1500 temperature time series, leads to substantial underestimation (up to ~40%) of the population sizes, compared to the mean of model simulations for each of the temperature series separately. This implies that predictions based on mean anomalies are relatively conservative and it is better to apply stochastic tools, such as the weather generator presented here, to resolve complex responses to climate change while taking natural variability into account. It is also important to note that the KNN methodology was applied here to atmospheric data (NCEP/NCAR), enabled generating the required variability in the forcing conditions instead of the outcome (temperature) which seems to be better representing the actual variability.

Work package 5: Establish a network of researchers.

SWIPE participants met four times during the project: at the beginning, 15 consortium members, representing all countries, met in Krakow, Poland for 2-days kick off meeting, on May 2013 (16 members) for 2 days in Crete, Greece on May 2014 (18 members) for 3 days in Antalya, Turkey and on May 2015 (13 members) for 3 days in Naples, Italy. During the meetings the participants and their expertise were introduced, and details of the protocols were discussed in order to insure a tightly coordinated work. As initially planned, whiteflies were collected in five countries and shipped for analyses in different partners' laboratory.

Bacon SJ, Aebi A, Calanca P, Bacher S. 2014. Quarantine arthropod invasions in Europe: the role of climate, hosts and propagule pressure. *Diversity and Distributions* 20, 84–94.

Bacon SJ, Bacher S, Aebi A. 2012. Gaps in border controls are related to quarantine alien insect invasions in Europe. *PLoS ONE* 7(10): e47689.



4. Deliverables

Please report on deliverables (from M1 to M36). Explain any changes, difficulties encountered and solutions adopted (Comments column).

Deliverable name	Partner responsible	Date delivered	Comments
Climatologic characteristics	Morin	7/2013	Completed
Kick-off meeting	Zchori-Fein	7/2012	Completed
Database analysis	Mouton	05/2015	Readjusted
Whitefly collection	Tsagkarakou	10/2013	Completed
Symbiont sequence and annotation	Silva	10/2013	Completed
Symbiont determination	Zchori-Fein	8/2014	Completed
Population genetic structure	Mouton	7/2015	In process
Parasitoid association	Beitia	7/2015	Completed
Virus association	Akbas	7/2015	Partially completed
Pesticide resistance association	Tsagkarakou	7/2015	Completed
Risk assessment models	Morin	7/2015	Completed
Heat resistance	Mouton	7/2015	Completed
Sequence analysis	Silva	7/2015	Almost completed
Determination of invasion routes	Aebi	7/2015	Partially completed
Final meeting	Zchori-Fein	5/2015	Completed
Publish manuscripts	All groups		In progress
Draft recommendations	Zchori-Fein		In progress



5. General description of the cooperation over the duration of the project

Factual description, specifying the input of each participant. Describe the added value of doing the work in a transnational project.

The SWIPE project was designed in five work packages that were highly interconnected. As such, results obtained in WP1 (genetic groups and symbiotic contents) were used to design specific experiments conducted in WP3 (Tasks 3.1, 3.2, 3.3). Similarly, the genome analysis conducted in Task 3.4 set the basis for the experiments conducted in Task 3.2. Finally, all the results obtained in WP1-WP3 will be important for future refinements of the model developed in WP4. Close collaboration among the different SWIPE partner was an absolute must for achieving the goals set for the project:

- 1) Insect samples were collected by partners in two consecutive years from specific host plants in their own countries (i.e. Giorgini in IT, Tsagkarakou in GR, Morin in IS, Akbas in TU, and Beitia in SP). Half of these samples were shipped to Zchori-Fein in IS and half to Mouton in FR for symbiont and genetic analyses respectively.
- 2) Tsagkarakou performed insecticide resistance experiments on samples collected by Beitia (SP) and Erdogan (TU).
- 3) Giorgini (IT) and Beitia (SP) jointly designed and performed experiments based on the results provided by Silva (SP).
- 4) The team at Lyon worked together with Aebi (Switzerland) to conduct the invasion risk analysis.
- 5) Most importantly, partners from Turkey, Spain, Greece and Israel (Fidan, Degirmenci Karacaoglu, Beitia, Tsagkarakou and Morin) 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 was summarized and incorporated into the model by Morin (IS), and facilitated the development of a tool that can predict whitefly population outbreaks.

6. Dissemination activities (including list of scientific publications)

List of publications derived from this project, including those in preparation, in review and in press

Published in reviewed Journals

- Santos-Garcia, D, Farnier PA, Beitia F, Zchori-Fein E, Vavre F, Mouton L, Moya A, Latorre A, Silva FJ. 2012. Complete genome sequence of *Candidatus Portiera aleyrodidarum* BT-QVLC, an obligate symbiont that supplies amino acids and carotenoids to *Bemisia tabaci*. *Journal of Bacteriology* 194: 6654-6655.
- Santos-Garcia, D., P-A. Rollat-Farnier, F. Beitia, E. Zchori-Fein, F. Vavre, L. Mouton, A. Moya, A. Latorre and F.J. Silva. 2014. The genome of *Cardinium* cBtQ1 provides insights into genome reduction, symbiont motility and its settlement in *Bemisia tabaci*. *Genome Biology and Evolution*, 6: 1013–1030.
- Santos-Garcia, D, Silva FJ, Moya A, Latorre A. 2014. No exception to the rule: *Candidatus Portiera aleyrodidarum* cell wall revisited. *FEMS Microbiol. Lett.* 360:132-136.
- Terraz G, Gueguen G, Arno J, Fleury, Mouton L. 2014. Nuclear and cytoplasmic differentiation among Mediterranean populations of *Bemisia tabaci*: testing the biological relevance of cytotypes. *Pest Management Science*, 70: 1503-1513.

- Mouton L, Gnankiné O, Henri H, Terraz G, Ketoh G, Martin T, Fleury F, Vavre F. 2015. Detection of genetically isolated entities within the Mediterranean species of *Bemisia tabaci*: new insights into the systematics of this worldwide pest. *Pest Management Science*, 71: 452-458.
- Rollat-Farnier PA, Santos-Garcia D, Rao Q, Sagot MF, Silva FJ, Henri H, Zchori-Fein E, Latorre A, Moya A, Barbe V, Liu SS, Wang XW, Vavre F, Mouton L. 2015. Two host clades, two bacterial arsenals: evolution through gene losses in facultative endosymbionts. *Genome Biology and Evolution*, 6: 1013-1030.
- Rao Q, Rollat-Farnier PA, Zhong HZ, Santos-Garcia D, Silva FJ, Moya A, Zhu DT, Klein C, Vavre F, Sagot MF, Liu SS, Mouton L, Wang XW. 2015 Genome reduction and metabolic complementation of the dual endosymbionts in the whitefly *Bemisia tabaci*. *BMC Genomics*, 16: 226.
- Santos-Garcia, D, Vargas-Chavez C, Moya A, Latorre A, Silva FJ. 2015. Genome evolution in the primary endosymbiont of whiteflies sheds light on their divergence. *Genome Biol. Evol.* 7:873-888.
- Zidon R, Tsueda H, Morin E, Morin S. 2015. Projecting pest population dynamics under global warming: the combined effect of inter- and intra-annual variations. *Ecol. Appl.* (in-press) <http://dx.doi.org/10.1890/15-1045.1>
- Ilias A, Lagnel J, Kapaintadaki D, Roditakis E, Tsigenopoulos K, Vontas J and A Tsagkarakou 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.
- Giorgini M, Beitia F, Mouton L, Parrella G, Silva F, Tsagkarakou A, Vavre F, Zchori-Fein E et al. Distribution of *Bemisia tabaci* genetic variants and their bacterial endosymbionts in the Mediterranean area (in prep.).
- Guz N, Atlihan R, Karut S., Karacaoglu M, Akbas B, Degirmenci K, Erdogan C, Fidan H, Gurkan MO, Morin S and Zchori-Fein E. Development and survival of *Bemisia tabaci* reared on *Solanum nigrum* in field conditions (in Prep.).
- Cass B.N., Farnier P.A., Van Leuven J.T., Hackett J.D., Mouton L., Vavre F., Hunter M.S. Genome of *Rickettsia* endosymbiont suggests candidate mechanisms for fitness benefit to whitefly host (in Prep.).
- Terraz G., Andrieux T., Vavre F., Fleury F., Mouton L. Field and experimental evidences of horizontal transfer of *Rickettsia* within the *Bemisia tabaci* complex species (in Prep.).

Dissemination of results and knowledge transfer

Abstracts in scientific meetings

- Ilias, A., D. E. Kapantaidaki, E. Sioziou, E. Morou, E. Roditakis, J. Vontas, A. Tsagkarakou (2013) Characterization of neonicotinoid resistance in *Bemisia tabaci* from Greece. 1st International Whitefly Symposium (poster presentation)
- Gauthier, N., M. Peterschmitt, A. Tsagkarakou (2013) Population genetics of *Bemisia tabaci* from Mediterranean countries 1st International Whitefly Symposium 20-24 May Kolymbari – Greece (oral presentation)
- Gnankiné O, Mouton L, Martin T, Ketoh G, Vavre F, Fleury F. (2013) Identification of mutations in the para sodium 1 channel gene (*kdr*) and in Acetylcholinesterase gene (*Ace-1^R*) of *Bemisia tabaci* (Hemiptera: Aleyrodidae) from western Africa associated with



- resistance to pyrethroid and organophosphate. 1st International Whitefly Symposium, 20-24 May, Kolymbari – Greece Crete (poster)
- Mouton L. (2012) Evolution of multiple infections with vertically transmitted symbionts. Earth and Life Institute, Université Catholique de Louvain, Louvain, Belgium. June 2012. (oral presentation)
- Mouton L. (2013) Diversité des communautés de bactéries endosymbiotiques chez *Bemisia tabaci* et conséquences écologiques sur les populations d'hôte. 6^{ème} journées du Réseau BAPOA (Biologie Adaptative des Pucerons et Organismes Associés). CIRAD, Montpellier, France. October 2013. (oral presentation)
- Rollat-Farnier PA, Wang XW, Santos-Garcia D, Zchori-Fein E, Liu SS, Sagot MF, Silva FJ, Vavre F, Mouton L. (2013) Evolution of *Hamiltonella defensa* genomes in phloemophagous insects. First international whitefly symposium, Crete, Greece. May 2013. (oral presentation)
- Santos-Garcia D, Beitia F, Mouton L, Moya A, Latorre A, Silva FJ. (2012) Whitefly endosymbiont metagenomes. GDRE - Comparative Genomics. Lyon, France, November 2012. (oral presentation)
- Santos-Garcia D, Farnier PA, Beitia F, Zchori-Fein E, Vavre F, Mouton L, Moya A, Latorre A, Silva FJ. (2013) The genome of “*Candidatus Portiera aleyrodidarum*” BT-QVLC, an obligate symbiont that supplies amino acids and carotenoids to *Bemisia tabaci*. 1st International Whitefly Symposium, Crete, Greece. May 2013. (oral presentation)
- Santos-Garcia D, Farnier PA, Beitia F, Zchori-Fein E, Vavre F, Mouton L, Moya A, Latorre A, Silva FJ. (2013) *Cardinium* and *Bemisia tabaci*: is it a mutualistic relationship? 1st International Whitefly Symposium, Crete, Greece. May 2013. (oral presentation)
- Santos-Garcia D, Vargas-Chavez C, Moya A, Latorre A, Silva FJ. Genome evolution in the primary endosymbionts of whiteflies. 4th Meeting of the Spanish Society for Evolutionary Biology. SESBE 2013. Barcelona (Spain). November 27-29, 2013. (Poster)
- Terraz G, Gueguen G, Fleury F, Mouton L. (2013) Nuclear and cytoplasmic differentiation among Mediterranean populations of *B. tabaci*: a test for endosymbiont induced incompatibilities. First international whitefly symposium, Crete, Greece. May 2013. (oral presentation)
- Zidon, R, Morin, S and Morin, E (2013) Utilizing a stochastic weather generator to study effects of climatic conditions on insect population dynamics. 1st International Whitefly Symposium 20-24 May Kolymbari – Greece. (poster presentation)
- Zidon, R, Morin, S and Morin, E (2013) Utilizing a stochastic weather generator to study effects of climatic conditions on insect population dynamics: *Bemisia tabaci* as a case study. 41st annual meeting of the Israeli society of ecology and environmental sciences, Rehovot, Israel. (oral presentation)
- Morin, S and Morin, E (2014) Predicting agricultural pest response to future climate change based on IPCC scenarios. French-Israeli Colloquium on Climate Change Constraints On Agriculture. March 2014. Agriculture Research Organization, Bet Dagan, Israel. (oral presentation).
- Gafni R, Zidon, R, Morin, S and Morin, E (2014) A model for predicting *Bemisia tabaci* population dynamics based on environmental temperatures. The annual meeting of the Israeli Entomological Society. October 2014. Agriculture Research Organization, Bet Dagan, Israel. (oral presentation).



- Santos-Garcia, D, Vargas-Chavez, C, Reyes-Prieto, M, Moya, A, Latorre, A, Silva, F.J. (2014) Genome evolution in the primary endosymbiont of whiteflies. 15th International Symposium on Microbial Ecology (ISME15). Seoul (Korea). August 24-29 (Poster).
- Degirmenci K, Guz N, Akbas B, Erdogan C, Fidan H, Karacaoglu M., Kutuk H, Karut S, Gurkan MO, Zchori-Fein E. 2014. Tritrophic interactions between the *Bemisia tabaci*, its bacterial endosymbionts and TYLCV (Tomato yellow leaf curl virus). Proceedings of the 5th Plant Protection Congress of Turkey p.34, 3-5 February 2014, Antalya.
- Guz N, Degirmenci K, Akbas B, Erdogan C, Fidan H, Karacaoglu M, Kutuk H, Karut S, Gurkan MO, Zchori-Fein, E., 2014. Bacterial endosymbionts associated with *Bemisia tabaci* populations in Turkey. Proceedings of the 5th Plant Protection Congress of Turkey p.147, 3-5 February 2014, Antalya.
- Erdogan C, Guz N, Akbas B, Degirmenci K, Fidan H, Karacaoglu M, Kutuk H, Karut S, Gurkan MO, Tsagkarakou A, Zchori-Fein E. 2014. The insecticide resistance and endosymbiont status of *Bemisia tabaci* collected from different hosts. Proceedings of the 5th Plant Protection Congress of Turkey, p.27, 3-5 February 2014, Antalya.
- Santos-Garcia, D, Moya, A, Latorre, A, Silva, F.J. (2015) *Bemisia tabaci* QHC-VLC: a host for an endosymbiotic triumvirate. Microbial Eco-Genomics in Agriculture, Hagoshrim Kibbutz, Upper Galilee (Israel). May 18-20. (Poster).
- Tsagkarakou A, Kapantaidaki D, Stavrakaki M, Mouton L, Tsiamis G, Vontas J, Bourtzis K, Giorgini M, Zchori-Fein E. (2015) Genetic and symbiont diversity of *Bemisia tabaci* (Hemiptera: Aleyrodidae) from Mediterranean countries. 16 Panhellenic Entomological Congress, 20-23 October, Heraklion Greece

Significant external interactions in the project, Technology transfer, List of achieved degrees / patents / other outcomes in the project. Describe to what degree these results have been achieved as a result of cooperation between the partners in the project

Achieved degrees:

Name of student	Degree	Institute	Country	Remarks
Roni Gafni	MSc.	Hebrew University	Israel	
Santos García, Diego	PhD	University of Valencia	Spain	Some research in cooperation with partners 1, 9 and 13
Farnier Pierre-Antoine	PhD	University of Lyon	France	Some research in cooperation with partners 4 and 14
Terraz Gabriel	PhD	University of Lyon	France	Some research in cooperation with partners 2 and 14
Bondarenko Taisiia	MSc.	University of Lyon	France	



Follow up activities and plans for further exploitation of the results. What sort of follow-up activities should take place to ensure that the results of this project are applied to the fullest extent possible? Several actions need to be taken in order to promote the application of the results obtained as a part of the SWIPE project:

- 1) The model, currently based on *Solanum nigrum* data, should be calibrated to specific crops of interest such (e.g. cotton, tomatoes, beans, watermelons) and made available to relevant authorities (Ministries responsible for agriculture, extension agencies, grower associations etc.).
- 2) Each interested country could establish a website for farmers where the model predictions will be published and may help planning of crop rotation, planting time, and pest control.
- 3) We plan to write a report summarizing the risk assessment analysis and submit it to the relevant agencies in our respective countries and the EU.

Media and Communication to the general public

Beitia F, Sabater-Muñoz B, Tormos J, Santos-García D, Silva, FJ. 2015. Influencia del cambio climático y de las bacterias endosimbiontes en brotes poblacionales de la mosca blanca *Bemisia tabaci*. *Agrícola Vergel*, 382: 129-133.

Πρόγραμμα « ARIMNet – SWIPE: Predicting whitefly population outbreaks in changing environments» (2012-2015 ERA-NET). Newsletter of the Hellenic Entomological Society, September 2014, <http://www.entsoc.gr/site/phocadownload/deltio%20eee%20september%202014.pdf> (in Greek).

7. Impact statement: output and innovation contribution

We succeeded in developing a new modelling framework for projecting insect-pest population dynamics and supporting environmental decision-making under climate changes. The main scientific question addressed was how future changes in inter- and intra-temperature variability will affect the population dynamics of an insect-pest (*B. tabaci* as a study case), while taking into account genetic variability and symbiotic associations. We aimed to understand the various effects in the context of interactions between temperature patterns and the insect performance measures, and utilized stochastic modelling tools into which actual temperature variabilities were incorporated. The weather generator developed allows exploring the population 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, such as distinct intra-annual temperature patterns that lead to especially large or small population sizes. The ample additional data collected (species distribution patterns, symbiotic associations, resistance to environmental factors and more), could be incorporated into the model in the future. Together with the invasion risk assessment performed we believe that the modelling framework developed here 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.

סיכום עם שאלות מנחות

מטרות המחקר תוך התייחסות לתכנית העבודה

1. אפיון תנאי האקלים במהלך שלושת העשורים האחרונים (הושלם).
2. בחירת שני אתרי איסוף בכל מדינה שבהם חלה עליה מהותית בטמפרטורות (הושלם).
3. הערכת הפרמטרים של תולדות החיים של השדה (הושלם).
4. אפיון מכלולי ביוטופ-סימביונט (הושלם).
5. פיתוח דגם אקלימי (הושלם).

עיקרי התוצאות

1. *Portiera* מוסיפה לתזונת החרק קרוטנואידים וחומצות אמינו.
2. *Cardinium* מקנה לחרק עמידות כנגד צרעות טפיליות.
3. העונתיות משפיעה מאוד על דגם ההתפתחות של כע"ט ומראה הבדלים מרחביים.
4. הבדלים בביולוגיה של הפונדקאי מחייבים את כיול המודל לגידולים חקלאיים שונים.
5. אביב וסתיו חמימים צפויים לגרום לגידול האוכלוסייה.
6. קיימת אפשרות ליישום מסחרי של התוצאות בכפוף להתאמות.

מסקנות מדעיות וההשלכות לגבי יישום המחקר והמשכו

התוצאות תומכות בהשערה שביסוד פרוייקט SWIPE ומטרות המחקר הושגו כמעט במלואן. תועדו שינויים אקלימיים בפועל ואושרה תקפות המודל שנבנה. נתונים שנאספו בשדה ובמעבדה בישראל ובמדינות האחרות הוטמעו במודל וסייעו בפיתוח דגם ההתפרצויות.

בעיות שנתרו לפיתרון ו/או שינויים (טכנולוגיים, שיווקיים ואחרים) שחלו במהלך העבודה

הצוות הבינלאומי ערך שינויים אחדים בפרוטוקולים שנקבעו בתחילת המיזם. בעיקרו של דבר הוחלט לעבוד על צמח פונדקאי אחד, הוסכם על פרוטוקולים משותפים לניסויי השדה ונערכו התאמות בפרוטוקול המעבדה. השותף השוויצרי פרש, אך חלק מעבודתו נעשה על ידי הצוות הצרפתי.

הפצת הידע שנוצר בתקופת הדו"ח:

פרסומים בכתב: ציטוט ביבליוגרפי כמקובל בפרסום מאמר מדעי, אנא ראו לעיל "dissemination activity" (עמ' 18-19).

פרסום הדו"ח: אני ממליצה לא לפרסם את הדו"ח.

חסי – לא לפרסום

האם בכוונך להגיש תכנית המשך בתום תקופת המחקר הנוכחי? כן!



Coordination of the Agricultural Research
In the Mediterranean Area

בקשה לחסיון הדו"ח:

הדו"ח כולל מידע רב שנאסף על ידי השותפים למחקר במעבדות מצרפת, ספרד, יוון, תורכיה ואיטליה. בחוזה עליו אנחנו חתומים במסגרת תכנית ARIMNET (Consortium agreement) כתוב שהתוצאות שייכות בעיקרן למי שייצר אותן, ואין לנו זכות לפרסמן. יש לציין שחלקים גדולים של התוצאות המשותפות כבר פורסמו, ורב היתר נמצאים בשלבי כתיבה שונים.