**Annual Report Format for Feed the Future Innovation Labs with Competitive Subawards**

1. Research Project Reports
   * + 1. Project Title:
       2. Location: USA (University of Virginia)
       3. Description: The project developed an epidemiological model to study the spread and impact of *T. absoluta*. In this phase, we completed the study of possible spread of *T. absoluta* in South and Southeast Asia region.
       4. Collaborators:

* Abhijin Adiga, Young Yun Chung Baek, Madhav Marathe, Joseph McNitt, Henning Mortveit: Virginia Tech, USA
* Thierry Brévault and Anaïs Chailleux, Cirad-Biopass, Dakar, Senegal
* Nicolas Desneux, French National Institute for Agricultural Research (INRA), France
* Mateus Ribeiro de Campos, INRA, France
  + - 1. Achievements

**Assessment of threat of *T. absoluta* to North America (Workplan Objective 2):** The MoU between USDA-APHIS and UVA has been initiated to access PestID. This is due to the recent move of the team of the Biocomplexity Institute of Virginia Tech to Univ. of Virginia.

**Multipathway model to study the spread of *T. absoluta*: case study of Southeast Asia (Workplan Objective 3):**

We developed a network-based propagation model to study the spread of invasive species. We applied it to study the possible spread of T. absoluta in the region of South East Asia. This stochastic, spatially-explicit model captures the pathways of natural and human-mediated spread. It was applied to study the invasion dynamics of T. absoluta with focus on the region of South and Southeast Asia comprising of 10 countries: Bangladesh, Myanmar, Vietnam, Laos, Cambodia, Thailand, Malaysia, Indonesia and Philippines. Our analysis with respect to historical invasion records indicate two possibilities of spread of T. absoluta in Bangladesh, one where trade is the dominant pathway and the other where it is not. Novel machine learning techniques were applied for parameterization, capturing variability in model outcomes and sensitivity analysis.



Figure . Outline of the process used for analyzing the multi-pathway spread. A novel unsupervised learning method was used to cluster simulation outputs of models that are a good match with the ground truth. The relationship between model parameters and the clusters are inferred by casting the problem as a classification problem with model parameters as the feature vectors and cluster indices as classes.

**Analysis of international and domestic trade (Objective 2 Activity 3)**: We are further analyzing international trade networks corresponding to four solanaceous crops obtained using the Food and Agricultural Organization trade database using Moore-Shannon network reliability. The work will be submitted as an invited paper in Journal of Network Science.

**Integrating Physiologically-based Demographic models with multipathway models: case study of Senegal and India (Workplan Objective 4):** In this ongoing work, we have been applying the developed models to Senegal and India. Currently, we are in the phase of implementation of the model which involves (i) identification and curation of datasets (ii) country-specific modifications to model implementation.

* 1. Lessons learned: Covered in individual tasks.

* + - 1. Location: Senegal
      2. Description: Study of
      3. Collaborators:
* Thierry Brévault, research entomologist, Cirad-Biopass, Dakar, Senegal
* Anaïs Chailleux, research entomologist, Cirad-Biopass, Dakar Senegal
* Arame Ndiaye, molecular biologist, postdoc, Biopass, Dakar, Senegal
* Philippe Correa, Master student, UCAD, Dakar, Senegal
* Modou Kane, Master student, UCAD, Dakar, Senegal
  + - 1. Achievements

**Routes of introduction (Workplan 6.1)**

After microsatellite markers development, 1250 specimens were extracted and 800 specimens have been firstly genotyped. After the first readings (problems of missing data due to some loci that could not or poorly been amplified), 572 specimens from 14 countries (13 Argentina, 8 Colombia, 4 France, 5 Greece, 6 Italy, 19 Mayotte, 39 Kenya, 35 Tanzania, 55 Niger, 97 Algeria, 36 Tunisia, 16 Togo, 40 Burkina Faso, 196 Senegal) were finally used for analyzes using only 9 microsatellite loci frow the 12 previously selected. Preliminary analyzes showed that genetic diversity is higher in Africa compared to Europe or to native areas. We found genetic homogeneity in some countries (Argentina, Colombia, Algeria and Tunisia) and two genetic lineages in other countries (Mayotte, Niger, Togo, Senegal). In Senegal, we found three populations. More analyzes are needed to determine the genetic flow (i.e. exchanges) between populations. The estimated genetic differentiation highlights important intra-African gene flows but also gene flows from Argentina to different African countries. Providing definitive answer, needs to complete the genotyping for the last samples (mainly Niger and Algeria) in order to finalize the population genetics analyzes.

**Biological control (Workplan 6.2)**

1. Finding alternatives to synthetic pesticides is a major challenge. Biological control through conservation of native natural enemies of the tomato leaf miner is a way forward as a strategy accessible to small farmers in Senegal.
2. A field experiment was led in the experimental station of the Senegalese Research Institute in Sangalkam, Senegal. Four-month field monitoring (from March to July 2018) was conducted by Philippe Correa (Master student) to investigate the potential of the combination of biocontrol and net house (Photo 1). Previously, we identified a predatory mirid bug, *Nesidiocoris tenuis* (Heteroptera: Miridae), as a very promising biological control agent (withstanding high temperatures) and we identified two wild insectary plant species (*Physalis angulata* and *Ceratotheca sesamoides)*. In this new study, we monitored the spontaneous colonization and establishment of *N. tenuis* and other pest natural enemies of non-sprayed (i) open field crops and (ii) net houses with two different mesh sizes. Results showed that the predator colonized the open field and was able to colonize the net house with the bigger mesh size, but too late to protect efficiently the crop. However, net houses were interesting at first to delay crop infestation by *Tuta absoluta* moths. In addition, this experiment allowed us to identify the acariphagous species, *Stethorus* sp., as a predator of spider mites. In March 2019, we started a new experiment conducted by Modou Kane (Master student), in which *N. tenuis* was introduced into the net houses with tomato seedlings (Photo 2) and insectary plants. This experiment is in progress.

**Photo 1.** Tomato plants under net house. 2018 experiment, Sangalkam, Senegal.

1. We also started to evaluate the suitability of the two wild insectary plants for the development of *N. tenuis* under laboratory conditions. This experiment is led by Massamba Diakhaté (Post-Master student).

**Photo 2.** Transfer of *Ephestia kuehniella* sterilized eggs to feed *N. tenuis* just after transplanting. 2019 experiment, Sangalkam, Senegal.

* 1. Lessons Learned

1. The release of indigenous predatory bugs such as *N. tenuis* along with insectary plants is very promising for tomato crop protection in net houses.
   * + 1. Location: France
       2. Description: Physiologically based demographic models (PBDMs) of species have been used to capture the weather-driven biology of the species in species relevant interacting in its food chain or web. (Ponti et al. 2015). The capture these processes using observed daily weather or climate scenarios to drive model dynamics across time and geographic space, and to map the results via a geographic information system. The dynamics of speciescan be captured using the same resource acquisition from the demographics parameters of the species under study (Gutierrez & Ponti 2013). When the requisite biological data are not available, the model structure provides a useful guide for identifying the data gaps (Ponti et al 2015) facilitating precise gathering of the missing data to characterize the biodemographic functions. Therefore, due to the high potential of *Tuta absoluta* to invade new areas (Desneux et al 2011; Campos et al 2017), PBDM development providing information of some shortcomings in *T. absoluta* biology is important to obtain further reach resolution of this pest.
       3. Collaborators:

* Nicolas Desneux, French National Institute for Agricultural Research (INRA), France
* Mateus Ribeiro de Campos, INRA, France
* Philippe Bearez, INRA, France
* Antonio Biondi, University of Catania, Italy
* Luigi Ponti, Agenzia nazionale per le nuove tecnologie, l’energia e lo sviluppo economico sostenibile (ENEA), Centro Ricerche Casaccia, Italy
* Andrew Gutierrez, Center for the Analysis of Sustainable Agricultural Systems Global (CASAS Global), USA
* Abhijin Adiga, Virginia Tech, USA
  + - 1. Achievements:

(i) Thermal requirements: Updated results are provided in the figures.

A close up of a map

Description automatically generated

**Figure 1**. Development rate of *Tuta absoluta* eggs to adults and temperatures were correlated with experimental data Campos et al (straight line) and from literature (dash line) on figure 1A. The data from Campos et al and literature was combined on figure 1B. The data was fitted in non-linear regression at equation y = ax + b with *P* < 0.05.

(ii) Updates for age-specific fertility of *T. absoluta* female is presented in the figure 2.

![A close up of a map

Description automatically generated]()

**Figure 2**. Age-specific oviposition of *Tuta absoluta* female on six constant temperatures. The data distribution on temperature x age (days) x eggs/female/day was plotted on three-dimension (A) and the statistical analysis in (B) where eggs/female/day and age (days) data fitted the nonlinear regression model in equation exponential decay at *P* < 0.05.

(iii) Diapause experiments

 **Figure 3**. All 4369 samples were obtained from *Tuta absoluta* diapause induction (A). The samples were plotted in 3 dimensions (temperature [°C] × minutes day length [photoperiod] × degrees-days). The multiple linear regression was proceeded generating the equation *DDTe* = 259.679 - (17.092 \* Temperature) - (0.000836 \* Minutes day length) *r*2 = 0.751 and *P* < 0.001. Diapause percentage (%) was calculated following degree-days threshold (*DDTe*) and compared with degree-days observed on larvae and pupae of *Tuta absoluta* exposed in four temperatures, six photoperiods and four different times intervals (B).

1. East Africa Invasive Groundnut Leafminer DNA Sequencing Project

b) Targeted sample collection locations – Ethiopia, Uganda, Kenya, Malawi, South Africa, India, Australia

Description: The project objective is to confirm the species and identify the possible origin of an invasive pest of groundnuts in East Africa, Groundnut leafminer (GLM).  GLM is a high-impact pest of groundnuts, a staple crop in much of Africa. The pest had been identified on the basis of morphological characters as *Aproaerema modicella* (Lepidoptera: Gelechiidae), after being detected in 1998 on groundnut in Uganda (Page *et al.*, 2000).  *A. modicella* is endemic in South and SE Asia and more prominently in South India, where it severely damages groundnuts and has been a pest for more than 20 years (Amin and Mohammad, 1980; Shanower *et al.*, 1993).  However, when Buthelezi et al. (2012) sequenced the mtDNA CO1 of groundnut leafminer specimens collected from six sites in South Africa and compared them with reference sequences in BOLD (Barcode of Life Database), the sequences of 70% of the South African specimens matched with *A. simplexella*. *Aproaerema simplexella* (Walker) had never been reported in Africa. *A. simplexella* is known to be a pest of soybean (and not of groundnuts) in Australia. Our objective is to confirm the species, and thereby identify the possible origin, of groundnut leafminer populations in East Africa.

* + - 1. Collaborators:

- Ethiopia: Dr. Muluken Goftishu Muleta, Assistant Professor of Entomology, College of Agriculture and Environmental Sciences, Haramaya University

- Uganda: Dr. Moses Biruma (Program leader, oilcrops) and Mr. Dennis Gayi (entomologist), NaSARRI (National Semi Arid Resources Research Institute)

- Kenya: Dr. Muo Kasina, Director, National Sericulture Research Centre, Industrial Crops Research Institute, KALRO (Kenya Agricultural & Livestock Research Organization)

- Malawi: Dr. Donald Kachigamba (entomologist) and Mrs. Trust Donga (entomologist)

LUANAR (Lilongwe University of Agriculture & Natural Resources)

- South Africa: Dr. Godfery E. Zharare (Head of Department of Agriculture), University of Zululand, KwaDlangezwa. Dr. N. Makhosi Buthelezi, Mangosuthu U. of Technology, buthelezim@mut.ac.za.

- India: Dr. Jagdish Jaba (entomologist), International Crops Research Institute for the Semi-arid Tropics (ICRISAT), Patancheru. Dr. R. Asokan Principal Scientist (Agricultural Entomology) Division of Biotechnology, Indian Institute of Horticultural Research (IIHR), Bangalore. Dr. P. R. Shashank, (Agril. Entomology)

Scientist (ARS), Insect Taxonomy Laboratory, National Pusa Collection (NPC), Division of Entomology,

Indian Agricultural Research Institute (ICAR), New Delhi.

- Australia: Dr. Andreas Zwick (entomologist), Australian National Insect Collection, Commonwealth Scientific and Industrial Research Organization (CSIRO), Acton, ACT

- United States: Dr. J.B. van Kretschmar and Dr. G.R. Pallipparambil, North Carolina State University (NCSU) Center for Integrated Pest Management (CIPM)

e) Achievements

1. India: Co-PI for the project, Dr. Pallipparambil, visited India for a preliminary meeting with the collaborators and to collect GLM samples. Although this field visit was in August-September 2018 i.e. before the reported period of performance, some of the related discussions and follow-up work were completed between October 2018 and March 2019. The first destination for the visit was International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) where the Co-PI established contact with the only entomologist at the location; GLM samples were collected from two locations (1) ICRISAT campus, Patancheru, Hyderabad, Telangana and (2) Raichur, Karnataka. The Co-PI next visited the Indian Agricultural Research Institute (IARI) in Delhi to consult with a microlepidopteran taxonomist regarding the development of a framework to collect GLM samples worldwide and transfer to an integrated molecular-morphological identification approach. The final visit was to the ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, regarding discussions to process some of the samples collected in India.Processing samples that were collected from Karnataka and Telangana, India. Establishing GLM research collaborations with multiple premier national and international agricultural institutes in India. Development of a framework to collect GLM samples worldwide and transfer to an integrated molecular-morphological identification approach.
2. South Africa: Co-PI for the project, JBvK, visited South Africa in December 2018 to meet collaborators and collect GLM samples. JBvK met the Head of the Dept. of Agriculture of the University of Zululand; the senior author of two research papers referenced for this project (Buthelezi et al., 2012, 2016); and, a U. of Zululand graduate student working with GLM. GLM samples were collected from groundnuts in Manguzi. Reinforced current collaboration. Identified additional collaborators for the current GLM project and for future projects. Identified prospective research objectives for future GLM projects. Connected collaborator who wants training in genitalic dissections of GLM with collaborator in India who has expertise in such dissections. Collaborator agreed to send GLM adults to collaborator in India for morphological characterization. Obtained GLM specimens for DNA analysis.
3. Ethiopia, Kenya, Malawi, Indonesia: Collection efforts in these countries heretofore have failed to find GLM and/or remain pending.
4. Lab analyses: Collaborators were identified to take over lab analyses from JBvK.JBvK isolated total DNA from specimens collected from soybeans in Uganda, and from groundnuts in Uganda, and India. Dr. Logu Ponnusamy isolated total DNA from specimens collected from groundnuts in South Africa. The mtCO1 gene was amplified and sequenced. The sequences were aligned and compared to reference sequences at GenBank. Sequences from the African specimens had highest identity with GenBank *A. simplexella* sequences. Sequences from the Indian specimens sent to NCSU had highest identity with *Anarsia* spp. Indian collaborators acknowledged *Anarsia* spp. to be pests of groundnuts in India. However, Indian collaborators found all other samples collected from groundnuts at other Indian locations to have highest identity with *A. simplexella*. These results challenge the reported identity of GLM in India to be *A. modicella*. They also challenge the identification of GLM in Africa as *A. modicella*, and support the identification by Buthelezi et al. (2012, 2016) of GLM in Africa as *A. simplexella*.
   * + 1. Capacity Building (one summary paragraph)
       2. Lessons Learned
       3. Presentations and Publications: All publications are peer-reviewed unless explicitly mentioned.
     1. Sylla, S., Brévault, T., Monticelli, L. S., Diarra, K., & Desneux, N. (2019). Geographic variation of host preference by the invasive tomato leaf miner Tuta absoluta: implications for host range expansion. Journal of Pest Science, 1-10.
     2. S. Venkatramanan, S. Wu, B. Shi, A. Marathe, M. Marathe, S. Eubank, L. Sah, A. Giri, L. Colavito, K. Nitin, V. Sridhar, R. Asokan, R. Muniappan, G. Norton, and A. Adiga, “Modeling commodity flow in the context of invasive species spread: Study of Tuta absoluta in Nepal,” Crop Protection, 2019
5. Human and Institutional Capacity Development**5**
   1. Short-term training
      1. Use the following table to report all short-term training.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Country of Training** | **Date of Training Activity** | **Brief Purpose of Training** | **Who was Trained 6** | **Number Trained 7**  **M F Total** | | |
| UK | Cambridge,  13 Dec | A talk “Using network reliability to understand international food trade dynamic” by Stephen Eubank in “International Workshop on Complex Networks and their Applications” | researchers |  |  |  |
| Senegal | Feb 21 | field demonstration of combined use of net houses and pest predators for Tuta absoluta management | farmers and partners from ISRA (Senegalese Agricultural Research Institute)agroecological crop protection. | 20 | 5 | 25 |
| France | Nov. 15 | Talk by Mateus Campos “Thermal requirement and diapause induction on *T. absoluta*.” | PhD and Masters students | 3 | 5 | 8 |

* 1. Long-term training
     1. Use the following table to report all U.S. citizens/permanent residents and third country nationals currently receiving Innovation Lab funds (regardless of percentage). Include post-docs and individuals being trained outside of the U.S.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Name**  **(first, last)** | **Gender** | **University** | **Degree** | **Major** | **Program**  **End Date 8**  **(month/year)** | **Degree Granted 9**  **(Y/N)** | **Home Country** |
| **Philippe CORREA** | **M** | **Université Cheikh Anta Diop (UCAD)** | **Cirad-Biopass laboratory** | **Plant biology** | **Pant protection** | **1/2018** | **10/2018** |
| **Modou KANE** | **M** | **Université Cheikh Anta Diop (UCAD)** | **Cirad-Biopass laboratory** | **Plant biology** | **Plant protection** | **1/2019** | **10/2019** |
| **Massamba Diakhaté** | **M** | **Université Cheikh Anta Diop (UCAD)** | **Ciard-Biopass laboratory** | **Plant biology** | **Plant protection** | **2/2019** |  |
| **Mateus Ribeiro de Campos** | **M** | **INRA** | **Postdoc** | **Entomology** | **01/2019** | **N** | **France** |
| Philippe Bearez | **M** | **INRA** | **PhD** | **Entomology** |  |  | **France** |
|  |  |  |  |  |  |  |  |

* + 1. For students who have completed their degree and returned to their home country, indicate if they are employed in their field and the name of the employer if known.

Joseph McNitt: Currently working by Epic Systems Corporation.

* 1. Institutional Development
     1. Description
     2. Partners

1. Innovation Transfer and Scaling Partnerships
   1. Plan of Action
      1. Steps taken
      2. Partnerships made
      3. Technologies ready to scale
      4. Technologies transferred
      5. Technologies scaled
2. Open Data Management Plan
   1. Provide a status report to include location of data made public
3. Future Directions
4. District level.
5. Provide names, institutional affiliation and country.
6. Link to relevant section of annual workplan.
7. Provide full citation for publications and indicate if peer-reviewed
8. This section is to serve as a compilation of all program training activities for the 12 month reporting period and not meant to duplicate the Capacity Building section under I(f)
9. Such as farmers, government officials, women entrepreneurs…
10. Disaggregate by gender if known.
11. Anticipated graduation date or end of program support.
12. Indicate if program support resulted in a degree.