Predictive Modeling and Mitigation of the Effects of Climate Change on the Infestation Patterns of a Migratory Crop Pest Insect.

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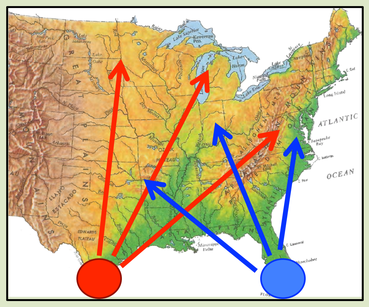
Fall armyworm (FAW)
***Spodoptera frugiperda* (J. E. Smith)**

- Western Hemisphere Noctuid moth
- Major economic pest of:
  - corn, sorghum, turf grasses, cotton
- Long-distance migration
  - Annual migrations across U.S.

- Infestation range extends from Canada to Mexico.
- Does not survive freezing winters.
- Overwintering populations in TX and FL responsible for most infestations in the U.S.



Advantages of FAW as a model organism for migration studies:

- Annual migration allows detection of recurring pattern changes.
- Have genetic method to identify overwintering origin of migrants.

Project rationale

Objective: Develop FAW migration as a bio-indicator of climate change.

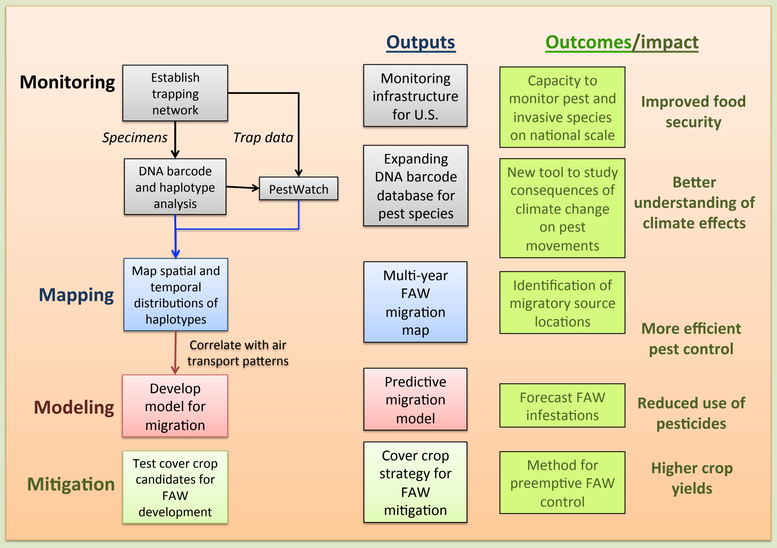
Hypothesis: Changes in seasonal wind patterns due to climate change will alter the direction and/or timing of FAW migration.

Approach:

1. Use multi-year FAW migration information to develop predictive migratory model based on air transport systems.
2. Predict migration pathways under different climate scenarios.
3. Establish regional/national system to monitor migration.

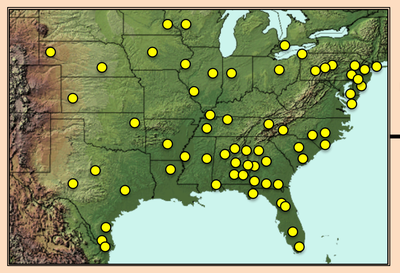
Impact: Forecasting the timing and direction of pest migration will make pest management more efficient and facilitate preemptive strategies.

Project flow chart



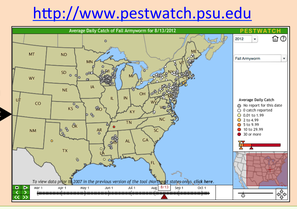
Specific Aim-1 Monitoring

1. Organize a national FAW monitoring and reporting network



Data stored in PestWatch

http://www.pestwatch.psu.edu



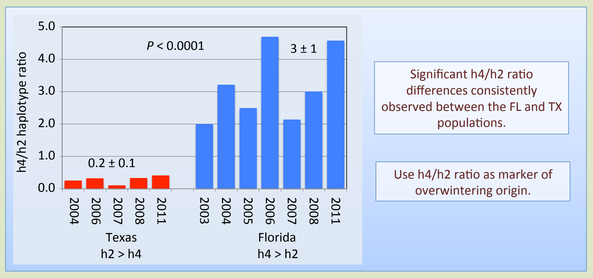
PestWatch, a publically accessible online database with interactive maps displaying data from the autonomous monitoring of migratory Lepidopteran pests. It has been maintained for over 10 years, with over 600 monitoring sites in 29 states.

2. Improve efficiency of species identification of captures

- Initial screen by morphology using classic taxonomic keys.
- DNA barcode analysis to confirm species identification.
- Genetic markers to identify FAW subpopulation.

Specific Aim-2 Mapping

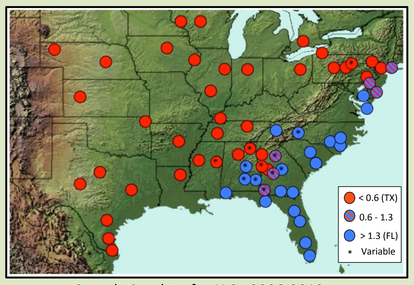
Developed haplotype method to map FAW migration from TX and FL



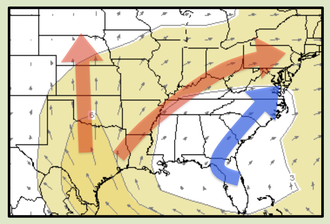
Significant h4/h2 ratio differences consistently observed between the FL and TX populations.

Use h4/h2 ratio as marker of overwintering origin.

Mapping proof-of-concept



Cumulative data for U.S., 2006-2012



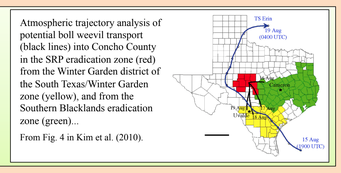
Correspondence between wind direction and ratio distribution supports notion that both can be used to model FAW migration.

Specific Aim-3 Modeling

Develop predictive FAW migration model

The HYSPLIT (HYbrid Single-Particle Lagrangian Integrated Trajectory) model is a complete system for computing simple air parcel trajectories to complex dispersion and deposition simulations.

HYSPLIT has been used to model Boll weevil migration, with simulations compared to field trap results. *(Westbrook et al. 2011, Int. J. Biometeorol. 55: 585-93; Kim et al. 2010, J R Soc Interface 7: 677–686)*



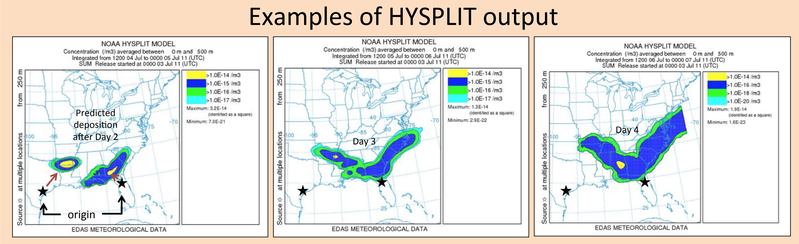
Atmospheric trajectory analysis of potential boll weevil transport (black lines) into Concho County in the SRP eradication zone (red) from the Winter Garden district of the South Texas/Winter Garden zone (yellow), and from the Southern Blacklands eradication zone (green)...

From Fig. 4 in Kim et al. (2010).

Use similar strategy for FAW

- HYSPLIT will simulate the distribution of FAW populations.
- The simulation will be compared to observed haplotype distributions.
- HYSPLIT variables will be adjusted to compensate for discrepancies between the projected and observed patterns.
- **The optimized FAW migration model will predict the migration pathways expected under different climate change scenarios.**

Examples of HYSPLIT output



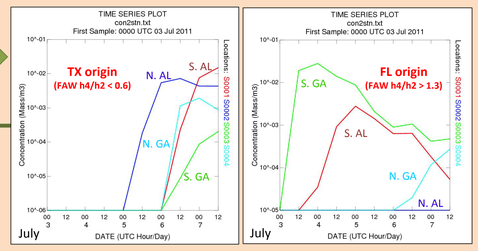
Predicted movements based on air transport systems from origin (★) in TX and FL

Verification of HYSPLIT simulations using haplotypes

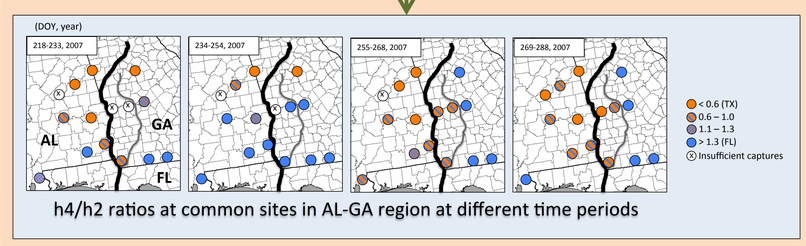
HYSPLIT can simulate contributions from TX and FL to a given region and time

Predicted h4/h2 based on simulation:

Region	FAW proportion	h4/h2
N. AL	TX FAW >> FL FAW	< 0.6
S. AL	TX FAW ≤ FL FAW	mixed
N. GA	TX FAW ≥ FL FAW	mixed
S. GA	TX FAW << FL FAW	> 1.3



Can test simulations against observed h4/h2 for given time and place



h4/h2 ratios at common sites in AL-GA region at different time periods

Specific Aim-4 Mitigation

Develop strategies to mitigate changes and/or expansion of the FAW migratory range due to climate change

Observations:

- Decreased FL corn acres in the 1980s correlated with declines in FAW infestations in other southeastern states (Pair and Westbrook, 1995).
- Sunn hemp and cowpeas linked to high FAW larval mortality (Meagher et al., 2004).
- Sorghum-sudangrass is a popular cover crop and a good host for FAW.

Hypothesis: Replacing sorghum-sudangrass with sunn hemp or cowpea will reduce FAW infestations and migratory populations.

Objective: Increase use of sunn hemp and/or cowpeas by cost-benefit analyses that takes into account effects on pest and beneficial insect populations in monoculture and polyculture field plots.

Sunn hemp

Cowpeas

Sorghum-sudan

Approach: Compare populations of FAW, natural enemies, and pollinators supported by above cover crop plantings.

YEARS 1-2 accomplishments

Established national FAW monitoring network.

- Trapping network from Mexico to Canada
- >140 FAW collection/monitoring sites
- 29 states + Mexico + Canada
- >125 cooperators.

Improved specimen identification methods

- DNA barcode database for FAW and related species. *(Nagoshi et al. 2011, Journal of Insect Sci. 11: 154)*.
- Improved genetic methods to characterize FAW subpopulations. *(Nagoshi 2012, Annals of the ESA 105: 351-358).*

Haplotype distribution map to infer migration pathways.

- Haplotype data from approx. 3000 samples. *(Nagoshi et al. 2012, Ecology and Evolution 2: 1458-1467)*

Outcomes/Impact to date

- Increased reports concerning FAW to PestWatch from 94 in 2010, to 203 in 2011 and 151 as of July 2012.
- Adoption of haplotype methods by scientists in Argentina (CONICET) to study South American FAW populations.
- Training of Argentine scientist in the U.S. in 2011 and 2012 on FAW haplotyping methods.
- Request by USDA-APHIS to establish DNA barcode database for Spodoptera species considered a high invasive risk to U.S. agriculture.
- Consultations by U.S. seed companies with project scientists in 2011 and 2012 on survey strategies for and high risk areas of establishment in the U.S. of a Bt-resistance trait recently found in Puerto Rico FAW.

YEAR 3 goals

- Refine and expand FAW monitoring network.
- Expand barcode database.
- Update PestWatch to improve information sharing and dissemination.
- Assess automated trapping systems to increase monitoring efficiency.
- Continue h4/h2spatial distribution mapping to third year.
- Begin preliminary modeling using the first two years of migration data.
- Begin first year of field study comparisons of sunn hemp, cowpeas, and sorghum varieties.