Three-cornered Alfalfa Hopper and Other Potential Vectors of Red Blotch

Houston Wilson[1], Kelsey McCalla[2], Alexis Billings[2], Monica Cooper[3], Kent Daane[2]

[1]Dept. Entomology, UC Riverside
[2]Dept. Enviro. Sci., Policy and Management, UC Berkeley
[3]UC Cooperative Extension

Grapevine Red Blotch Virus (GRBV)

Background and Timeline

Grapevine Red Blotch Virus (GRBV)

- Geminiviridae, characterized in 2012
- (Krenz et al. 2012, Al Rwahnih et al. 2013, Sudarshana et al. 2015)

Symptoms

- Reddening of leaf veins, blotchy red areas on leaf

Impacts

- Reduced crop vigor, yield and quality, delayed maturation of fruit

Geography

- First reported 2008 @ Oakville Station (Calvi 2011)
- Widespread in North America (Krenz et al. 2014)
- Archival samples contain virus (Al Rwahnih et al. 2015)

Spread

- Humans? Nursery stock? Insects? (Poojari et al. 2013)

Photo: http://www.princeofpinot.com/article/1575/UC IPM

Grapevine Red Blotch Virus (GRBV)

Background and Timeline

Daane / Wilson Research Group

1. Survey insects and plants for virus (2015-2017)
2. Transmission experiments (2015-2018)
3. Threecornered Alfalfa Hopper (TCAH) studies (2017-2020)

Grapevine Red Blotch Virus (GRBV)

Background and Timeline

Daane / Wilson Research Group

1. Survey insects and plants for virus (2015-2017)
2. Transmission experiments (2015-2018)
3. Threecornered Alfalfa Hopper (TCAH) studies (2017-2020)

Grapevine Red Blotch Virus (GRBV)

Plant and Insect Surveys

- Can we find the virus outside of vineyards?
- What insects carry the virus?
- Association between insects and positive plants?

Grapevine Red Blotch Virus (GRBV)

Plant and Insect Surveys

- Can we find the virus outside of vineyards?
- What insects carry the virus?
- Association between insects and positive plants?

Plant Hosts of Red Blotch Virus

Family	Genus/Species	n	% Positive
Adoxaceae	*Sambucus spp.*	0/4	0
Apiaceae	*Conium maculatum*	0/2	0
	Foeniculum vulgarum	0/1	0
Apocynaceae	*Vinca major*	0/17	0
Araliaceae	*Hedera helix*	0/2	0
Asteraceae	*Artemisia spp.*	0/3	0
	Baccharis pilularis	0/11	0
	Calendula sp.	0/1	0
	Taraxacum officinale	0/2	0
Betulaceae	*Alnus spp.*	0/14	0
Brassicaceae	*Brassica spp.*	0/4	0
	Raphanus raphanistrum	0/1	0
Convulvulaceae	*Convolvulus arvensis*	0/1	0
Cucurbitaceae	*Marah sp.*	0/4	0
Ericaceae	*Arbutus menziesii*	0/9	0
	Archtostaphylos spp.	0/11	0
Fabaceae	*Vicia faba*	0/6	0
	Vigna sp.	0/4	0

Plant Hosts of Red Blotch Virus

Family	Genus/Species	n	% Positive
Fagaceae	*Quercus agrifolia*	0/35	0
	Quercus douglassi	0/2	0
	Quercus lobata	0/2	0
Juglandaceae	*Juglans sp.*	0/8	0
Lauraceae	*Umbellularia californica*	0/14	0
Malvaceae	*Malva parviflora*	0/3	0
Oleaceae	*Fraxinus latifolia*	0/11	0
	Olea europaea	0/11	0
Poaceae	*Avena sativa*	0/8	0
Rosaceae	*Heteromeles arbutifolia*	0/40	0
	Prunus spp.	0/10	0
	Rosa spp.	0/5	0
	Rubus spp.	0/28	0
Salicaceae	*Salix spp.*	0/23	0
Sapindaceae	*Acer sp.*	0/2	0
	Aesculus californica	0/10	0
Vitaceae	*Vitis californica x vinifera*	18/68	26
	Vitis vinifera	19/20	95

Plant Hosts of Red Blotch Virus

Additional ground covers from Cieniwicz et al. 2019

Family	**Genus/Species**	**Common namen**
Fabaceae	*Vicia faba*	Fava bean
	Vicia Americana	Purple vetch
	Trifolium spp.	Red/white clover
	Pisium sativa	Field peas
Poaeceae	Various species	Mixed grasses

Grapevine Red Blotch Virus (GRBV)

Plant and Insect Surveys

- Can we find the virus outside of vineyards?
- What insects carry the virus?
- Association between insects and positive plants?

Insects Positive for Red Blotch Virus

Family	Genus/Species	Mean ±SEM	n	% Positive
Aphididae		9.8 ±1.2	0/122	0
Berytidae		2.7 ±1.1	0/7	0
Cicadellidae	*Acanalonia* sp.	1.0 ±0.0	0/3	0
	Aceratagallia spp.	4.0 ±1.1	0/55	0
	Acinopterus angulatus	1.3 ±0.1	2/26	8
	Alconeura sp.	2.0 ±0.0	0/2	0
	Colladonus coquilletti	1.3 ±0.2	4/6	67
	Colladonus montanus reductus	1.0 ±0.0	1/2	50
	Colladonus sp.	1.0 ±0.0	1/2	50
	Deltocephalus fuscinervosus	2.5 ±0.4	0/66	0
	Dikraneura rufula	1.0 ±0.0	0/3	0
	Dikrella californica	1.0 ±0.0	0/2	0

Insects Positive for Red Blotch Virus

Family	Genus/Species	Mean ±SEM	n	% Positive
Cicadellidae (cont'd)	*Empoasca* spp.	3.7 ±0.8	0/41	0
	Erythroneura elegantula	5.3 ±0.6	0/156	0
	Erythroneura variabilis	3.7 ±0.5	0/66	0
	Euscelidius schenkii	1.4 ±0.3	0/12	0
	Graphocephala atropunctata	1.0 ±0.0	0/2	0
	Macrosteles quadrilineatus	1.0 ±0.0	0/4	0
	Osbornellus sp.	2.0 ±0.0	0/2	0
	Scaphytopius spp.	1.1 ±0.1	9/19	47
	Thamnotettix zelleri	2.0 ±0.4	0/8	0
Cixiidae	*Melaniolarus* sp.	2.2 ±0.4	0/10	0
Delphacidae		1.2 ±0.1	1/21	5
Lygaeidae	*Nysius raphanus*	5.2 ±3.1	0/24	0
Membracidae	*Spissistilus festinus*	1.7 ±0.2	6/38	16
Miridae	*Lygus spp.*	3.8 ±0.5	1/99	1
Pentatomidae		1.5 ±0.5	0/2	0
Psyllidae		1.6 ±0.3	0/18	0
Rhopalidae	*Boisea rubrolineata*	4.0 ±0.0	0/2	0
Tingidae	*Corythuca* sp.	7.2 ±2.7	0/14	0

Insects Positive for Red Blotch Virus

Additional positives from Cieniwicz et al. 2019

Family	**Genus/Species**
Aphididae	
Cicadellidae	*Osbornellus borealis*
	Empoasca sp.
	Graphocephala atropunctata
Cixiidae	*Melaniolarus* sp.
Phylloxeridae	

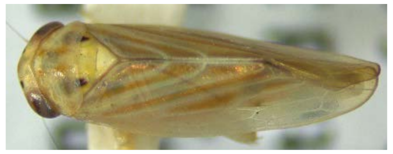
Grapevine Red Blotch Virus (GRBV)

Plant and Insect Surveys

- Can we find the virus outside of vineyards?
- What insects carry the virus?
- Association between insects and positive plants?

Lygus **spp.**

Acinopterus angulatus



Colladonus coquilletti

Colladonus montanus

Spissistilus festinus

Scaphytopius **spp.**

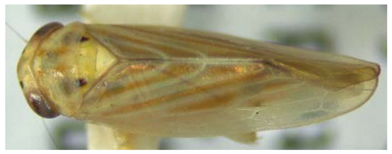
Key Questions

- How high are populations?
- How frequently do they test positive?
- Are they ever found on *Vitis*?


Lygus spp.

- High abundance
- 1% positive
- Not on grape vines


Acinopterus angulatus


Colladonus coquilletti


Colladonus montanus

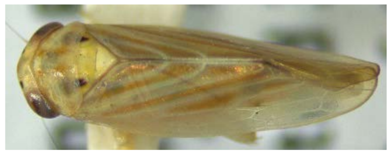

Spissistilus festinus


Scaphytopius spp.

Lygus spp.

Acinopterus angulatus

- Low abundance
- 8% positive
- Not on grape vines



Colladonus coquilletti

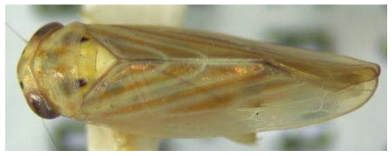
Colladonus montanus

Spissistilus festinus

Scaphytopius spp.

Lygus spp.

Acinopterus angulatus



Colladonus coquilletti

Colladonus montanus

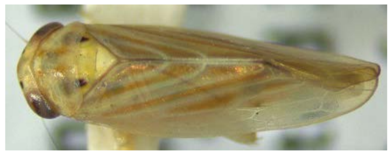
- Low abundance
- 50-67% positive
- Not on grape vines

Spissistilus festinus

Scaphytopius spp.

Lygus spp.

Acinopterus angulatus



Colladonus coquilletti

Colladonus montanus

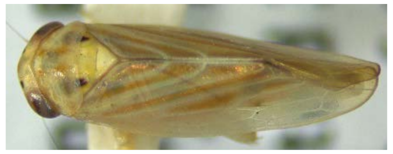
Spissistilus festinus

- Low abundance
- 16% positive
- Sometimes on grape vines

Scaphytopius spp.

Lygus spp.

Acinopterus angulatus



Colladonus coquilletti

Colladonus montanus

Spissistilus festinus

Scaphytopius spp.

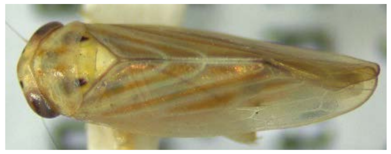
- High abundance
- 47% positive
- Frequently on grape vines

Candidate Rank

Lygus spp.

Acinopterus angulatus

Very Low



Colladonus coquilletti

Colladonus montanus

Low

Spissistilus festinus

Medium

Scaphytopius spp.

High

Grapevine Red Blotch Virus (GRBV)

Plant and Insect Surveys

Results

Key Points:

- Multiple species tested positive
  - This DOES NOT mean that they are a vector

- Differences in…
  - Abundance
  - Frequency of positive GRBV
  - Activity in vine canopy

- Lab vs. Field Transmission
  - Transmission *efficiency* is key

Grapevine Red Blotch Virus (GRBV)

Background and Timeline

Daane / Wilson Research Group

1. **Survey insects and plants for virus (2015-2017)**
2. **Transmission experiments (2015-2018)**
3. **Threecornered Alfalfa Hopper (TCAH) studies (2017-2019)**

OPEN ACCESS Freely available online

PLOS | ONE

A Leafhopper-Transmissible DNA Virus with Novel Evolutionary Lineage in the Family *Geminiviridae* Implicated in Grapevine Redleaf Disease by Next-Generation Sequencing

Sudarsana Poojari[1], **Olufemi J. Alabi**[1], **Viacheslav Y. Fofanov**[2], **Rayapati A. Naidu**[1]*

1 Department of Plant Pathology, Washington State University, Irrigated Agriculture Research and Extension Center, Prosser, Washington, United States of America,
2 Eureka Genomics, Sugar Land, Texas, United States of America

Abstract

A graft-transmissible disease displaying red veins, red blotches and total reddening of leaves in red-berried wine grape (*Vitis vinifera* L.) cultivars was observed in commercial vineyards. Next-generation sequencing technology was used to identify etiological agent(s) associated with this emerging disease, designated as grapevine redleaf disease (GRD). High quality RNA extracted from leaves of grape cultivars Merlot and Cabernet Franc with and without GRD symptoms was used to prepare cDNA libraries. Assembly of highly informative sequence reads generated from Illumina sequencing of cDNA libraries, followed by bioinformatic analyses of sequence contigs resulted in specific identification of taxonomically disparate viruses and viroids in samples with and without GRD symptoms. A single-stranded DNA virus, tentatively named Grapevine redleaf-associated virus (GRLaV), and *Grapevine fanleaf virus* were detected only in grapevines showing GRD symptoms. In contrast, *Grapevine rupestris stem pitting-associated virus, Hop stunt viroid, Grapevine yellow speckle viroid 1, Citrus exocortis viroid* and *Citrus exocortis Yucatan viroid* were present in both symptomatic and non-symptomatic grapevines. GRLaV was transmitted by the Virginia creeper leafhopper (*Erythroneura ziczac* Walsh) from grapevine-to-grapevine under greenhouse conditions. Molecular and phylogenetic analyses indicated that GRLaV, almost identical to recently reported Grapevine Cabernet Franc-associated virus from New York and Grapevine red blotch-associated virus from California, represents an evolutionarily distinct lineage in the family *Geminiviridae* with genome characteristics distinct from other leafhopper-transmitted geminiviruses. GRD significantly reduced fruit yield and affected berry quality parameters demonstrating negative impacts of the disease. Higher quantities of carbohydrates were present in symptomatic leaves suggesting their possible role in the expression of redleaf symptoms.

Citation: Poojari S, Alabi OJ, Fofanov VY, Naidu RA (2013) A Leafhopper-Transmissible DNA Virus with Novel Evolutionary Lineage in the Family *Geminiviridae* Implicated in Grapevine Redleaf Disease by Next-Generation Sequencing. PLoS ONE 8(6): e64194. doi:10.1371/journal.pone.0064194

Editor: Darren P. Martin, Institute of Infectious Disease and Molecular Medicine, South Africa

Received February 13, 2013; **Accepted** April 10, 2013; **Published** June 5, 2013

Funding: This work was supported, in part, by Washington State University's Agricultural Research Center in the College of Agricultural, Human, and Natural Resource Sciences, Wine Advisory Committee of the Washington Wine Commission, USDA-Northwest Center for Small Fruits Research, USDA-NIFA Specialty Crop Research Initiative (Award Number 2009-51181-06027), Washington State Department of Agriculture Nursery Assessment Funds, Washington State Commission on Pesticide Registration and USDA-APHIS National Clean Plant Network. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have the following interests to report: Viacheslav Y. Fofanov is employed by Eureka Genomics. There are no patents, products in development or marketed products to declare. This does not alter the authors' adherence to all the PLOS ONE policies on sharing data and materials, as detailed online in the guide for authors.

* E-mail: naidu.rayapati@wsu.edu

Introduction

Nearly seventy viruses and other infectious sub-cellular obligate parasites, collectively referred to as graft-transmissible agents (GTAs), have been documented in grapevines (*Vitis* spp.) [1], [2]. Among all diseases caused either directly or indirectly by these GTAs, grapevine leafroll disease is considered as the most economically important disease affecting plant vigor and longevity and causing significant losses in fruit yield and impacting berry quality attributes [3], [4], [5]. Other virus diseases, such as rugose wood complex, fanleaf infectious degeneration and fleck complex, represent a group of disorders distributed widely in several grape-growing countries around the world [1], [2]. Besides these 'traditional' virus diseases, which can cause significant problems to grape production, other diseases due to GTAs have limited geographic distribution causing relatively less economic damage to grape production.

In addition to viruses, several viroids belonging to the family *Pospiviroidae* are ubiquitous in cultivated grapevines [6], [7], [8], [9]. They are *Hop stunt viroid* (HpSVd, genus *Hostuviroid*), *Grapevine yellow speckle viroid 1* (GYSVd-1, genus *Apscaviroid*) and 2 (GYSVd-2, genus *Apscaviroid*), *Citrus exocortis viroid* (CEVd, genus *Pospiviroid*) and *Australian grapevine viroid* (AGVd, genus *Apscaviroid*). Although these viroids are found in symptomless grapevines, GYSVd-1 has been implicated in vein-banding and yellow speckle symptoms, likely due to a synergistic interaction between GYSVd-1 and *Grapevine fanleaf virus* (GFLV, genus *Nepovirus*, family *Comoviridae*) [10], [11].

Besides their negative impacts on yield and quality of grapes, the introduction and subsequent spread of viruses and other GTAs to healthy vineyards is of great concern for sanitation and grapevine

PLOS ONE | www.plosone.org 1 June 2013 | Volume 8 | Issue 6 | e64194

Grapevine Red Blotch Virus (GRBV)

Transmission Experiments – WSU

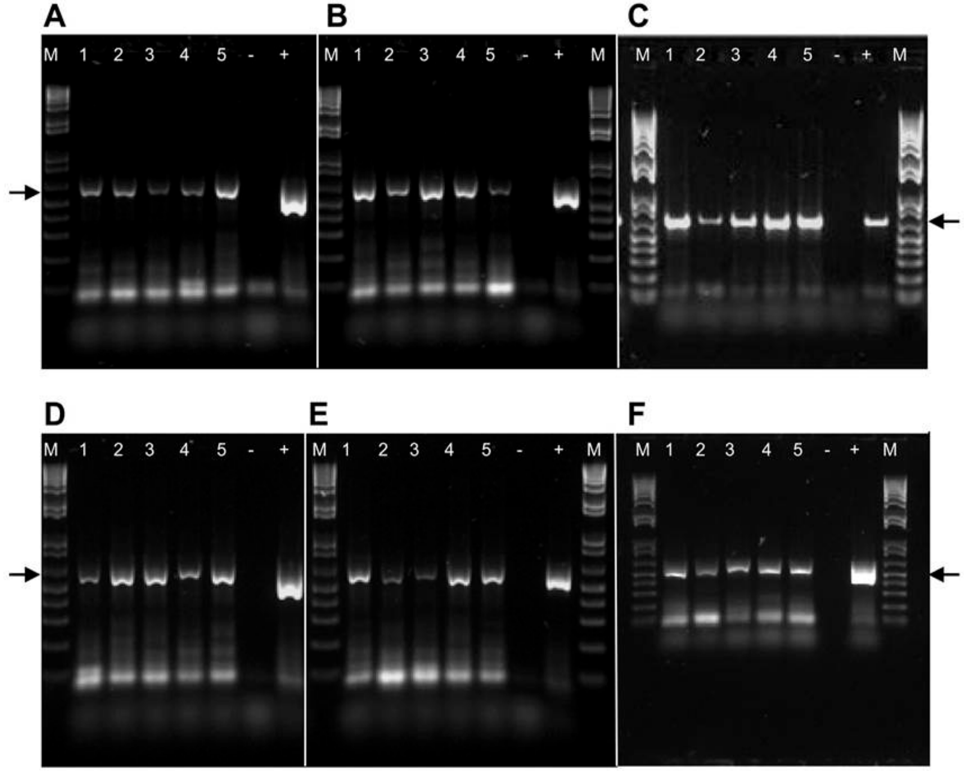


Figure 5. Detection of Grapevine redleaf-associated virus (GRLaV) in grapevines inoculated with viruliferous Virginia creeper leafhoppers. An agarose gel (0.8%) showing amplification of partial IR and CP regions of GRLaV from (A) Cabernet Franc, (B) Chardonnay, (C) Merlot, (D) Pinot Noir, (E) Pixie and (F) Sangiovese. Lanes 1 to 5 represent individual grapevines, '+' represents positive control for GRLaV, '−' represents healthy control negative for GRLaV, and 'M' represents 1 kb plus DNA ladder (Invitrogen). Arrows represent ~550 bp DNA band specific to GRLaV.
doi:10.1371/journal.pone.0064194.g005

Methods

- 50 insects / plant
- 6 cultivars (A-F)
- 48 hr Acquisition AP
- 48 hr Inoculation AP
- PCR tests in 4 wks

Our initial goal was to repeat this work and then test similar insects (e.g., WGLH), and common vineyard pests

Grapevine Red Blotch Virus (GRBV)

Transmission Experiments

Focus on Common/Abundant Candidates

Common Name	Species
Western grape leafhopper	*Erythroneura elegantula*
Variegated leafhopper	*Erythroneura variabilis*
Virginia creeper leafhopper	*Erythroneura ziczac*
Grape whitefly	*Trialeurodes vittatas*
Grape mealybug	*Pseudococcus maritimus*
Vine mealybug	*Planococcus ficus*
Blue-green sharpshooter	*Graphocephala atropunctata*
Foliar phylloxera	*Daktulosphaira vitifoliae*
Threecornered alfalfa hopper	*Spissistilus festinus*

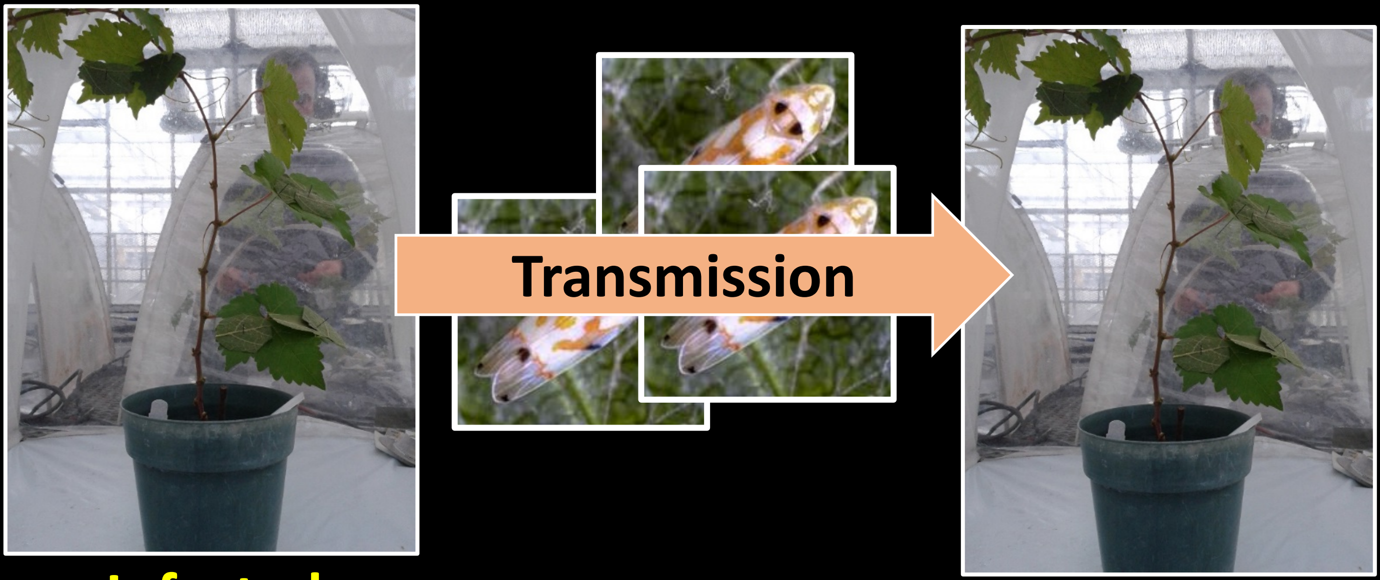
Grapevine Red Blotch Virus (GRBV)

Transmission Experiments

Focus on Common/Abundant Candidates

Experimental Setup

- Potted vines caged in greenhouse
- Cohorts of 10-100 individuals/species
- 3-10 replicates/trial



Transmission

Infected

Healthy

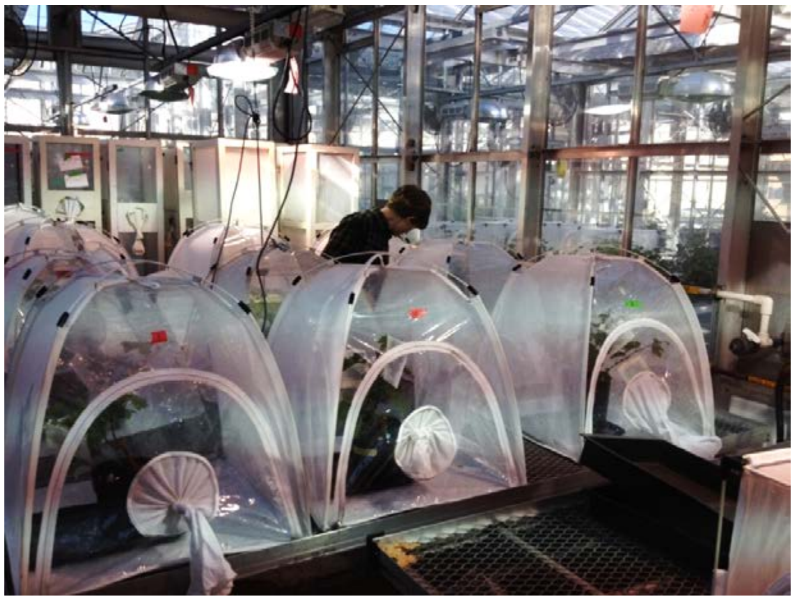
Grapevine Red Blotch Virus (GRBV)

Transmission Experiments

Focus on Common/Abundant Candidates

Experimental Setup

- 48-72 hr Acquisition (AAP)
- 48-72 hr Inoculation (IAP)



Grapevine Red Blotch Virus (GRBV)

Transmission Experiments

Focus on Common/Abundant Candidates

Experimental Setup

- Vines held for 2 years to observe symptoms and test with PCR

Grapevine Red Blotch Virus (GRBV)

Transmission Experiments

Focus on Common/Abundant Candidates

Experimental Setup

Some variations and repeat experiments

- "Bouquets" of mature leaves from field vines
- Longer AAP/IAP (5 days)
- Paired infected/healthy vines

Grapevine Red Blotch Virus (GRBV)

Transmission Experiments – Results

Family	Species Tested	Acquires	Transmits
Cicadellidae	*Erythroneura elegantula*	No*	No
	Erythroneura variabilis	No	No
	Erythroneura ziczac	Yes	No
	Graphocephala atropunctata	No	No
Aleyrodidae	*Trialeurodes vittatus*	No	No
Pseuodococcidae	*Pseudococcus maritimus*	No	No
	Planococcus ficus	Yes	No
Phylloxeridae	*Daktulosphaira vitifoliae*	Yes	No
Membracidae	*Spissistilus festinus*	Yes	No

*** Yes in field collections**

Grapevine Red Blotch Virus (GRBV)

2018-2020 – Field Transmission Exp. – UCB

- Worries over virus titer led to field and lab inoculations
- Focus on TCAH and *Scaphytopius*

Methods

- 48hrs AAP in the field
- Insects brought to lab + placed on clean plants for 48 hrs IAP
- Check vines regularly for symptoms and PCR evaluations for 2 years

Grapevine Red Blotch Virus (GRBV)

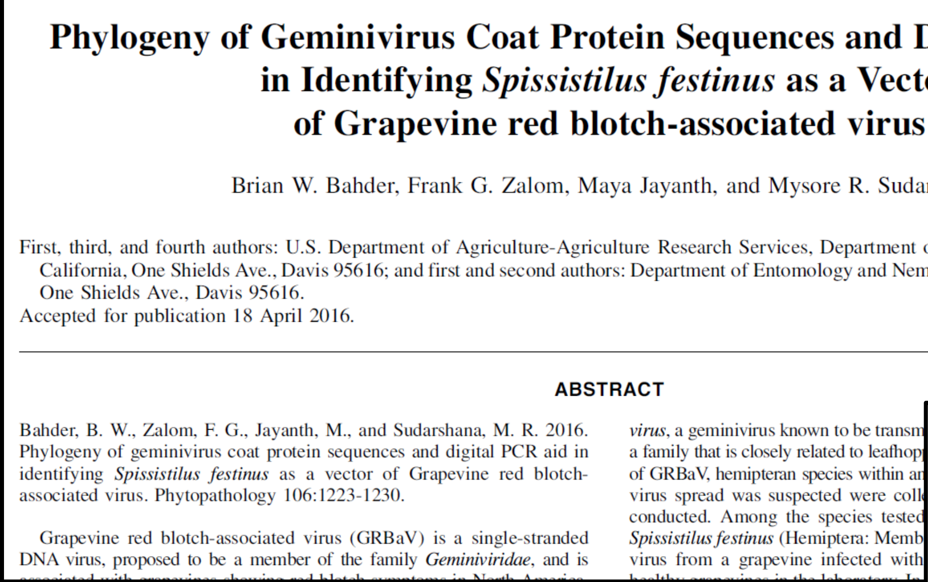
Background and Timeline

Daane / Wilson Research Group

1. Survey insects and plants for virus (2015-2017)
2. Transmission experiments (2015-2018)
3. Threecornered Alfalfa Hopper (TCAH) studies (2017-2019)

Grapevine Red Blotch Virus (GRBV)

TCAH as Vector – Addressing Grower Concerns



Phylogeny of Geminivirus Coat Protein Sequences and Digital PCR Aid in Identifying *Spissistilus festinus* as a Vector of Grapevine red blotch-associated virus

Brian W. Bahder, Frank G. Zalom, Maya Jayanth, and Mysore R. Sudarshana

First, third, and fourth authors: U.S. Department of Agriculture-Agriculture Research Services, Department of Plant Pathology, University of California, One Shields Ave., Davis 95616; and first and second authors: Department of Entomology and Nematology, University of California, One Shields Ave., Davis 95616.

Accepted for publication 18 April 2016.

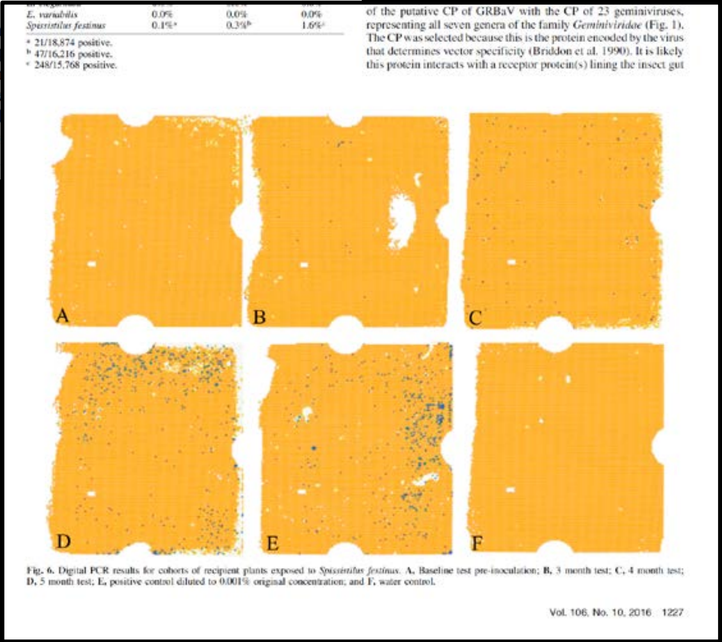
ABSTRACT

Bahder, B. W., Zalom, F. G., Jayanth, M., and Sudarshana, M. R. 2016. Phylogeny of geminivirus coat protein sequences and digital PCR aid in identifying *Spissistilus festinus* as a vector of Grapevine red blotch-associated virus. Phytopathology 106:1223-1230.

Grapevine red blotch-associated virus (GRBaV) is a single-stranded DNA virus, proposed to be a member of the family *Geminiviridae*, and is

virus, a geminivirus known to be transm
a family that is closely related to leafhop
of GRBaV, hemipteran species within an
virus spread was suspected were coll
conducted. Among the species tested
Spissistilus festinus (Hemiptera: Memb
virus from a grapevine infected with

Fig. 3. *Spissistilus festinus* adult **A,** male and **B,** female feeding on alfalfa plants.



E. variabilis	0.0%	0.0%	0.0%
Spissistilus festinus	0.1%[a]	0.3%[b]	1.6%[c]

[a] 21/18,874 positive.
[b] 47/16,216 positive.
[c] 248/15,768 positive.

of the putative CP of GRBaV with the CP of 23 geminiviruses, representing all seven genera of the family *Geminiviridae* (Fig. 1). The CP was selected because this is the protein encoded by the virus that determines vector specificity (Briddon et al. 1990). It is likely this protein interacts with a receptor protein(s) lining the insect gut

Fig. 6. Digital PCR results for cohorts of recipient plants exposed to *Spissistilus festinus*. **A,** Baseline test pre-inoculation; **B,** 3 month test; **C,** 4 month test; **D,** 5 month test; **E,** positive control diluted to 0.001% original concentration; and **F,** water control.

Grapevine Red Blotch Virus (GRBV)

TCAH Ecology

Distribution

- Widely distributed in US
- Especially southern regions
- Present in North Coast – but not a pest of grapes

Pest Status?

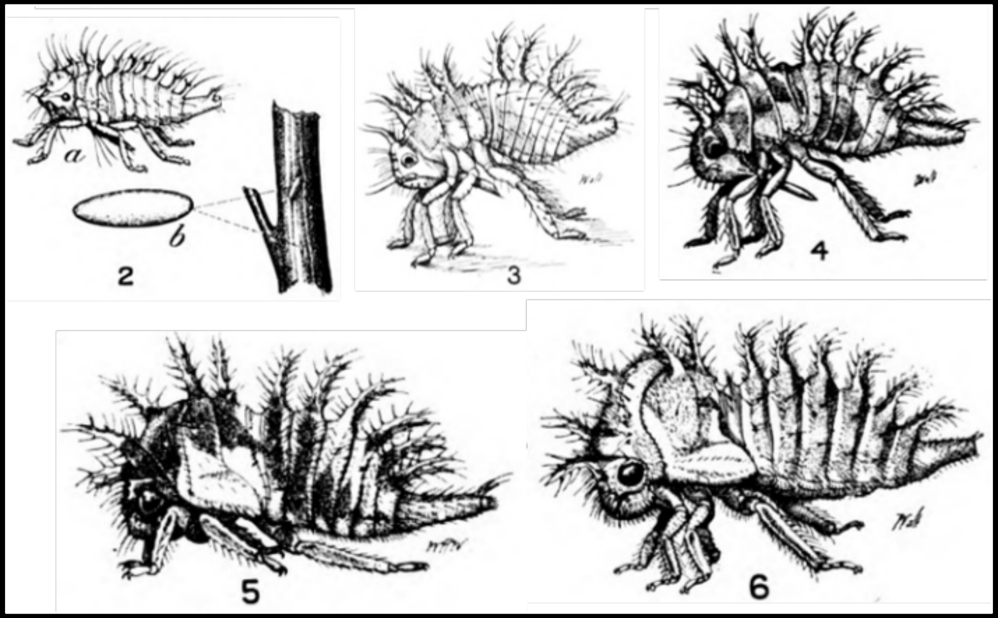
- <u>Legumes</u> – soybean, peanut, alfalfa

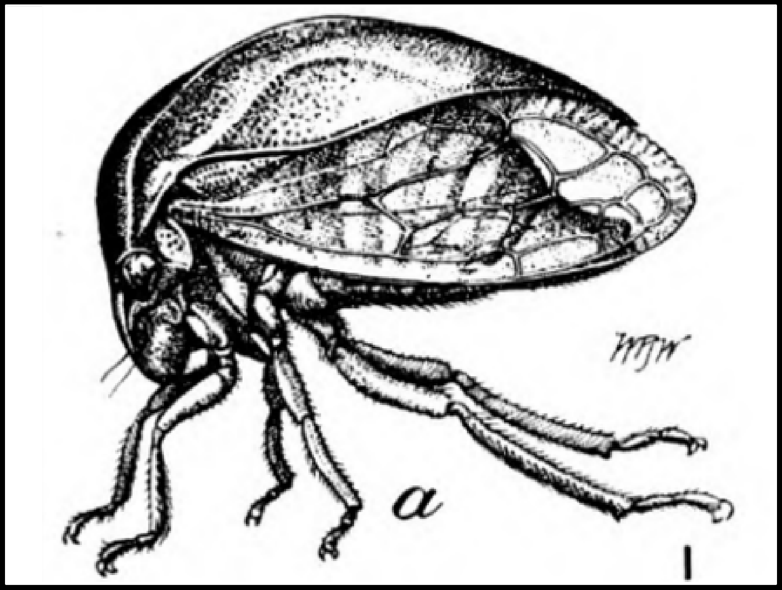
Grapevine Red Blotch Virus (GRBV)

TCAH Ecology

Life Cycle – General

- Adults → Eggs → 5 nymphal instars → Adults
- 2-4 generations/year
- Preference for legumes – but can develop on other species
- Overwinter in adult stage in sheltered areas



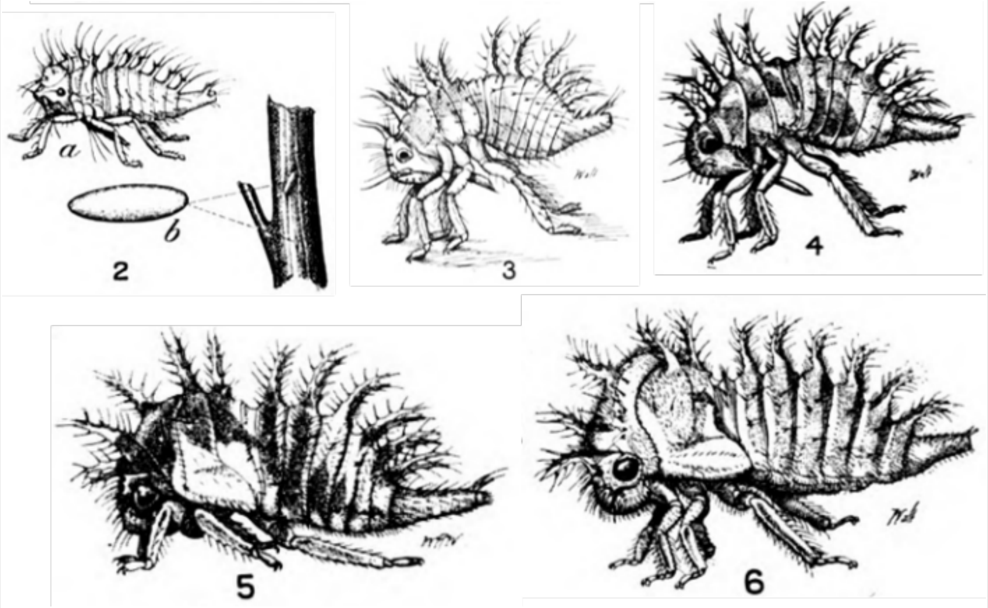


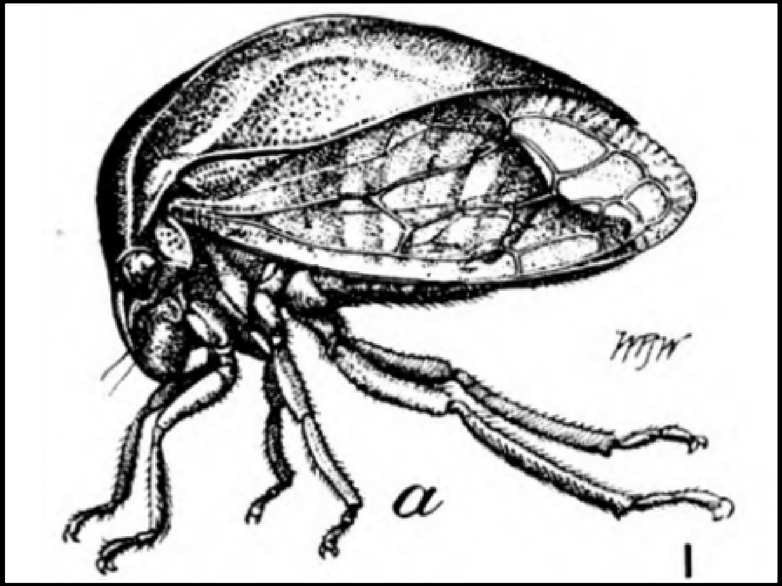
Grapevine Red Blotch Virus (GRBV)

TCAH Ecology

Life Cycle – Vineyards

- Adults appear on ground covers in the spring
- Feed/reproduce on ground covers (likely legumes)
- Petiole girdling later in season
- 2 generations/year



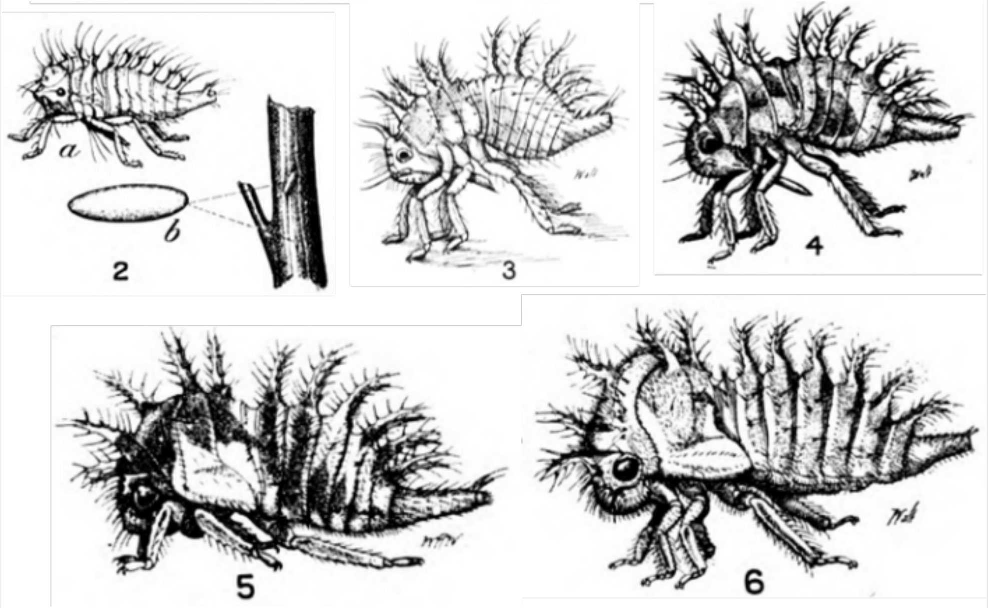


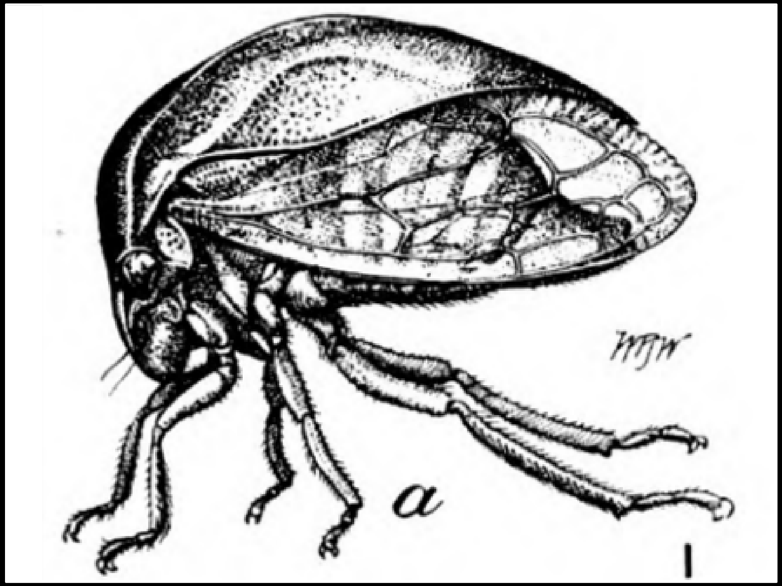
Grapevine Red Blotch Virus (GRBV)

TCAH Ecology

Key Questions

- When and how much activity in vine canopy?
- Overwinter in natural habitats? Vineyard edge activity?





Grapevine Red Blotch Virus (GRBV)

TCAH Ecology

Key Questions

- When and how much activity in vine canopy?
- Overwinter in natural habitats? Vineyard edge activity?

Fig. 1. Map illustrating two red blotch disease epidemics in a 1.5-ha Cabernet Sauvignon and a 2.0-ha Cabernet franc vineyard within 10 years post-planting in California, and the proximity of these vineyards to the Napa River and riparian habitat. In the Cabernet Sauvignon vineyard, red overlay indicates diseased vines in 2017 at the onset of the study and orange indicates new GRBV infections in 2018. In the Cabernet franc vineyard, red overlay indicates initial disease incidence recorded previously for 2014 to 2016 (Cieniewicz et al. 2017a). Purple and orange indicate new infections in 2017 and 2018, respectively. White grids indicate areas where insect survey was conducted in 2015 and 2016 in the Cabernet franc (Cieniewicz et al. 2018b) and in 2017 and 2018 in the Cabernet Sauvignon (this study).

Cieniwicz et al. 2019

Grapevine Red Blotch Virus (GRBV)

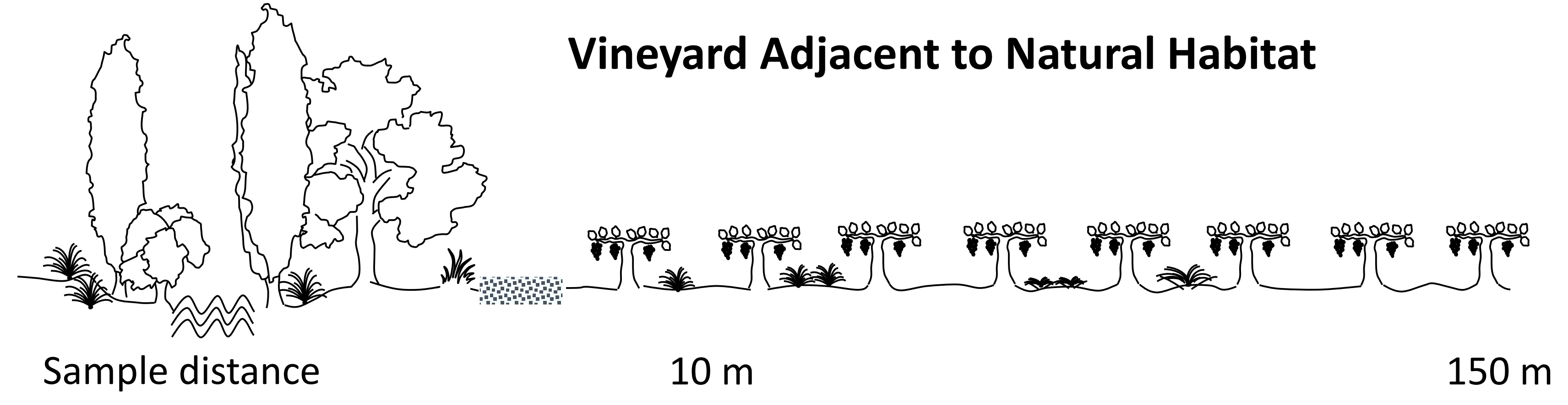
TCAH Ecology

Key Questions

- When and how much activity in vine canopy?
- Overwinter in natural habitats? Vineyard edge activity?

Transect Study (2017-2018)

- 5 vineyard sites
- Sampled 2x/month March – November (2017-2018)



Grapevine Red Blotch Virus (GRBV)

TCAH Transect Study

Sampling Methods

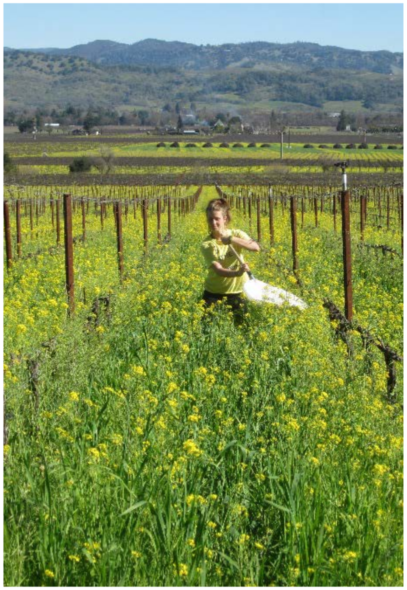
Grapevine Red Blotch Virus (GRBV)

TCAH Transect Study

Sampling Methods

Samples at Vineyard Edge and Interior

- **Ground covers –** Yellow sticky-traps (Mar-Nov)
- **Vine Canopy –** Yellow sticky-traps (Mar-Nov)
- **Petiole girdling –** 1-2x/month (June-Oct)



Grapevine Red Blotch Virus (GRBV)

TCAH Transect Study

Focal Organisms

Spissistilus festinus

Three-cornered Alfalfa Hopper

“TCAH”

Scaphytopius spp.

Sharp-nosed Leafhopper

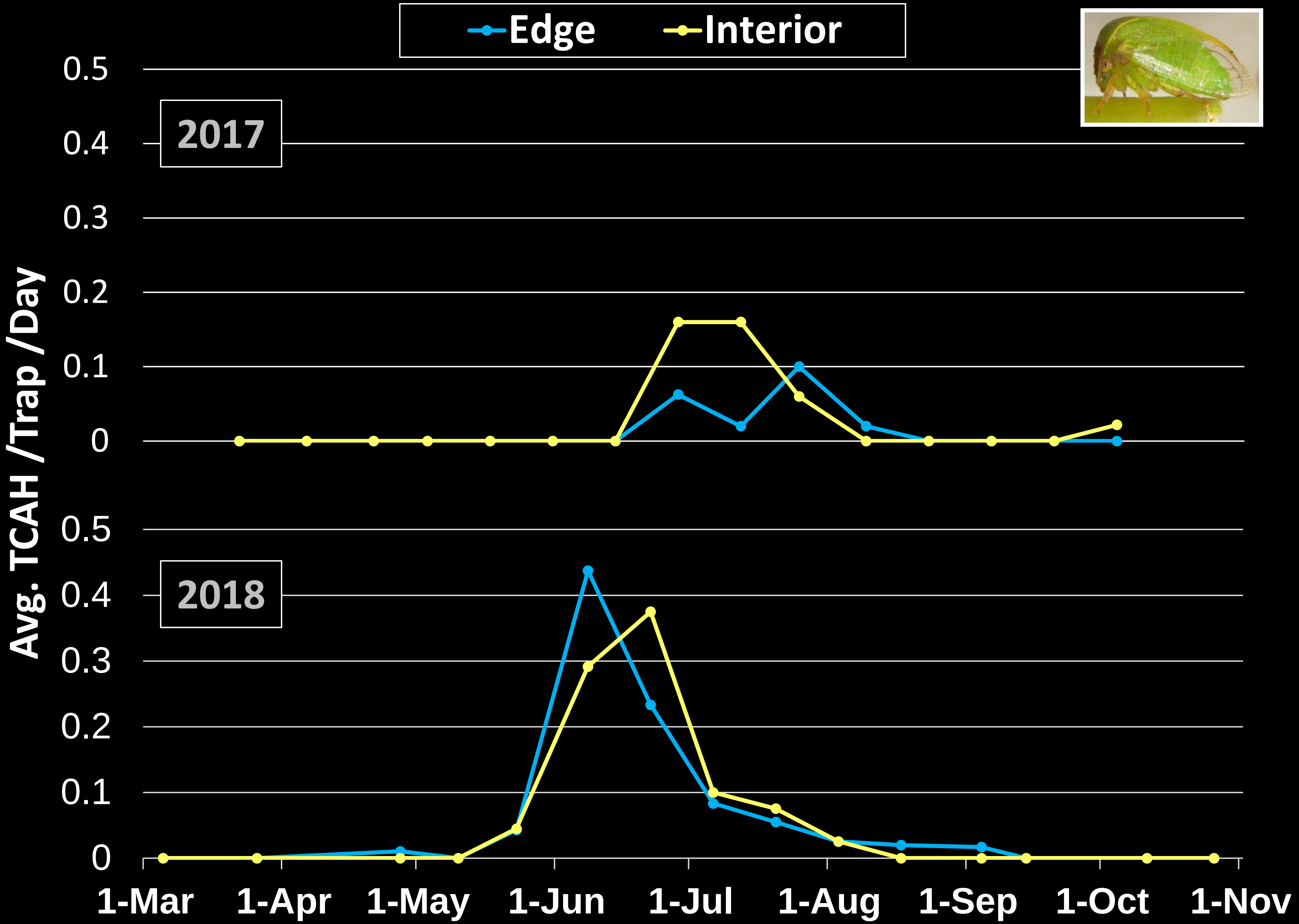
“Scaphy”

Spissistilus festinus

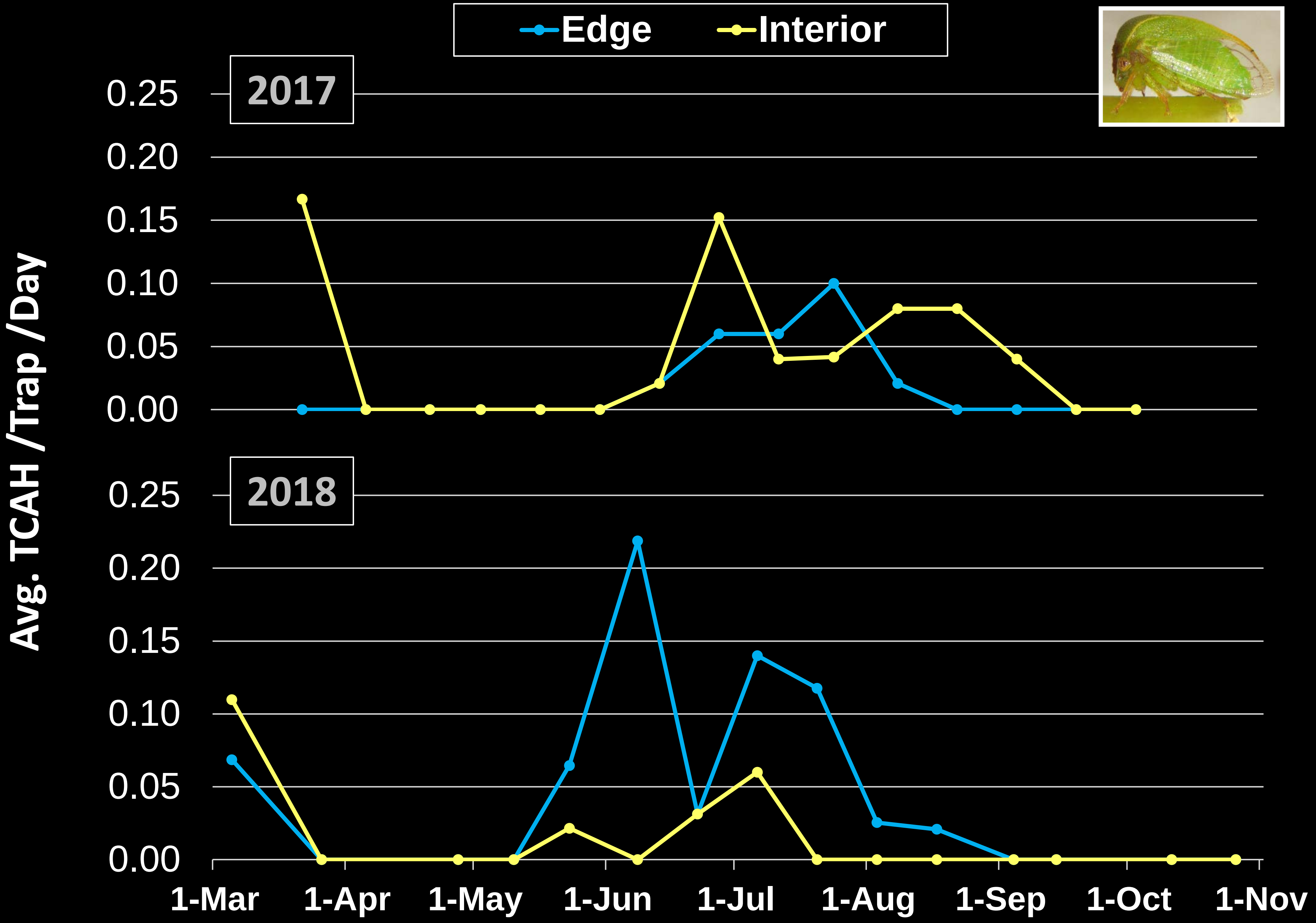
Three-cornered Alfalfa Hopper

"TCAH"

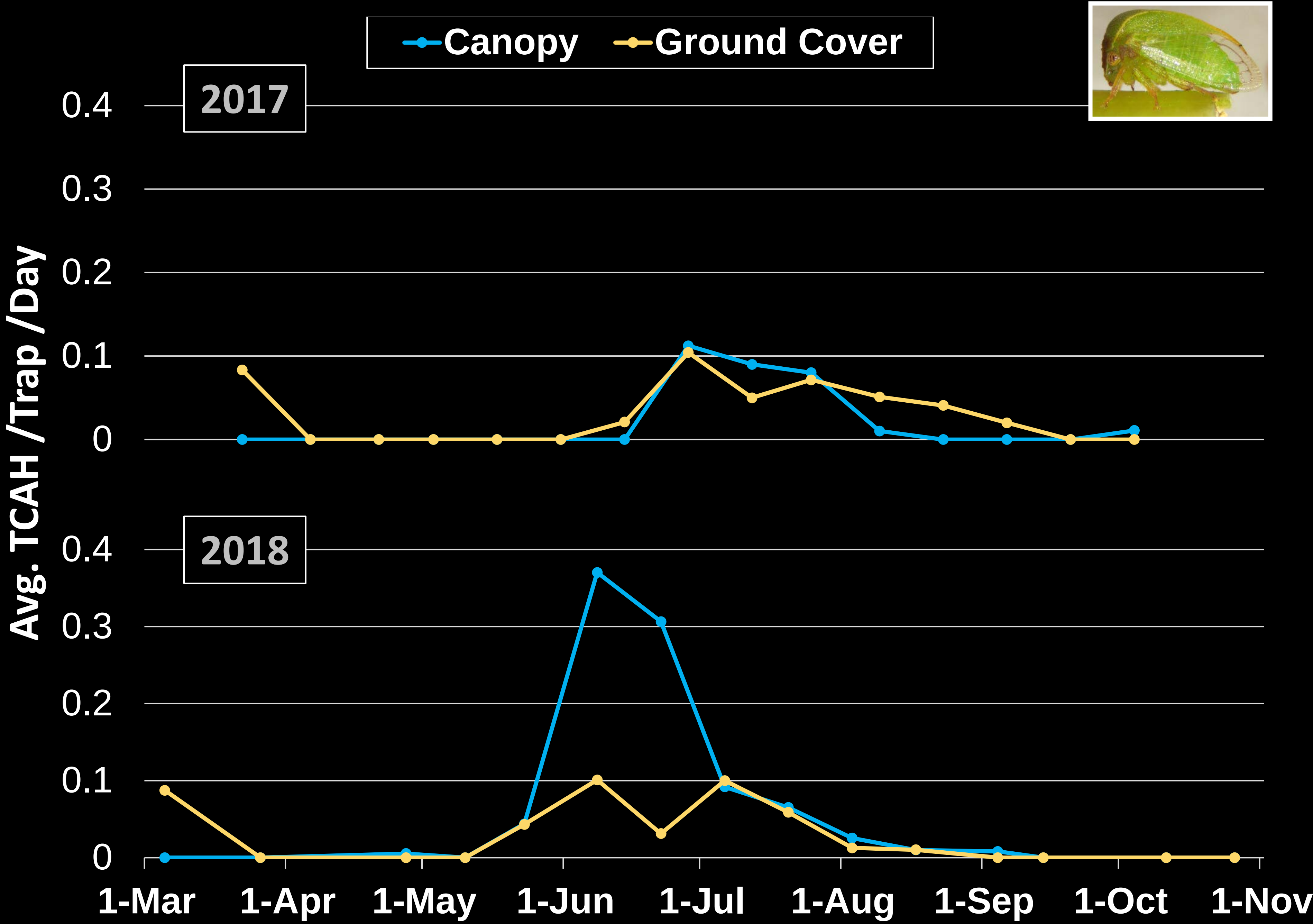
Vine Canopy – No differences between edge/interior



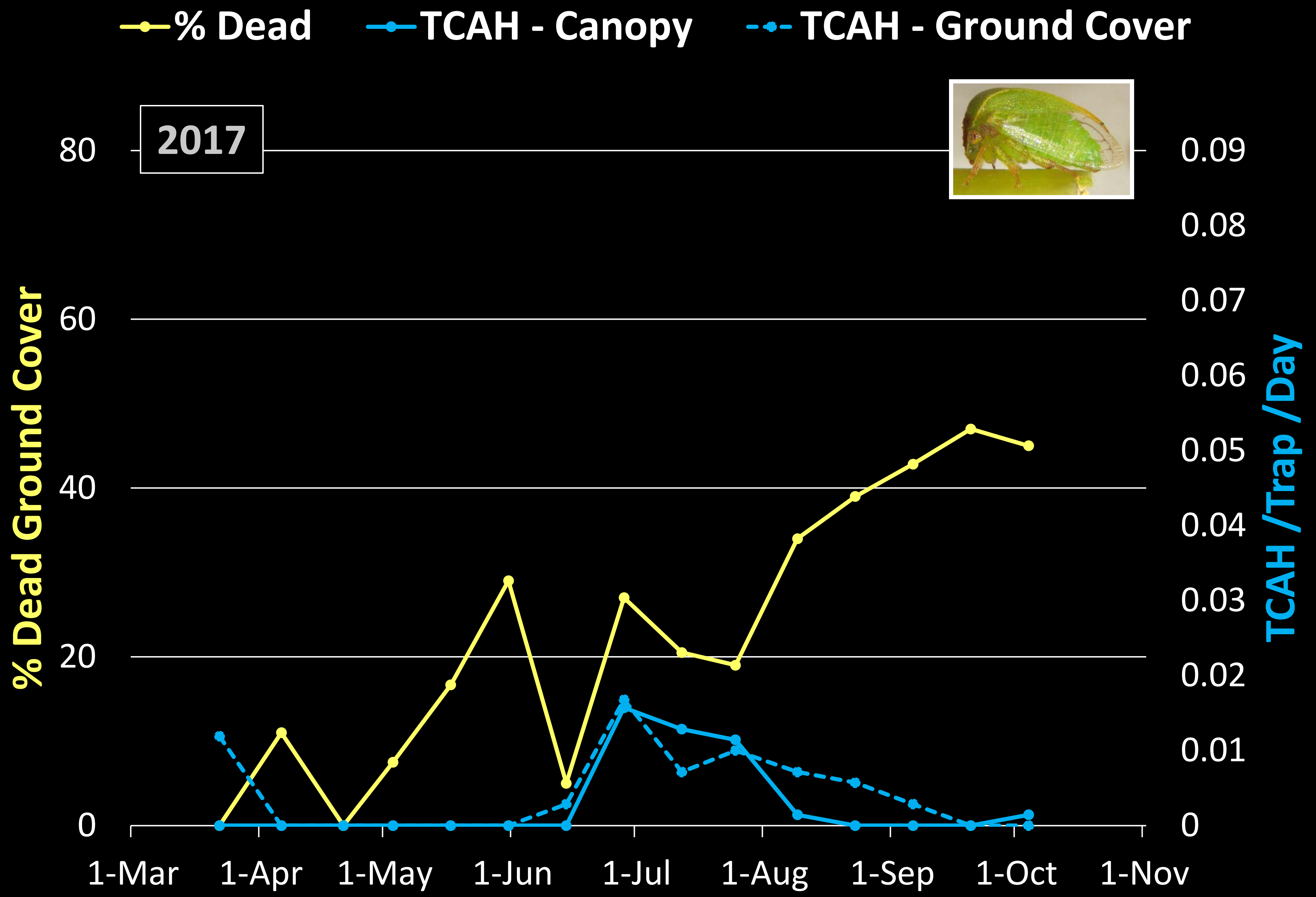
Ground Covers – No differences between edge/interior



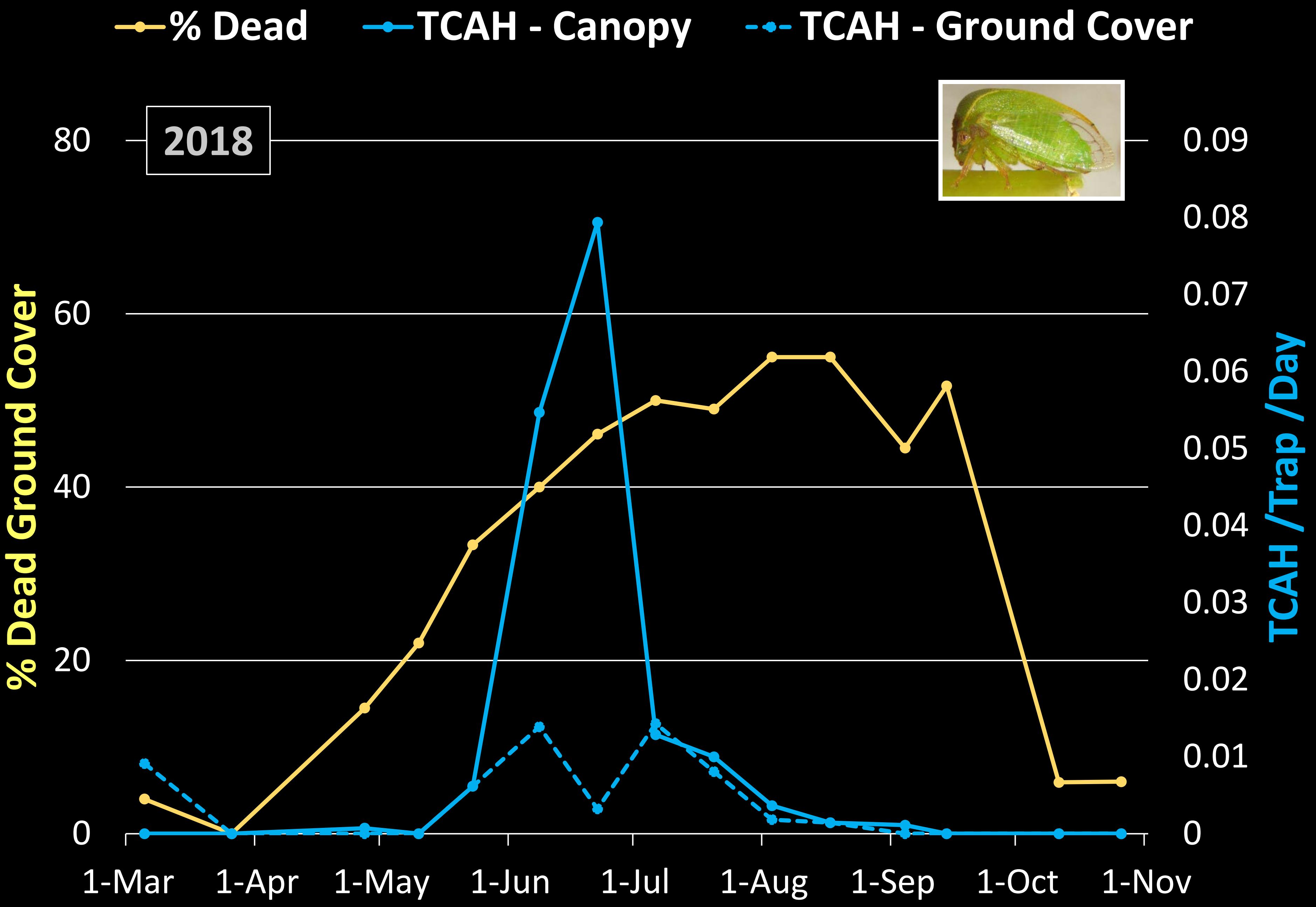
No consistent differences between canopy + ground covers



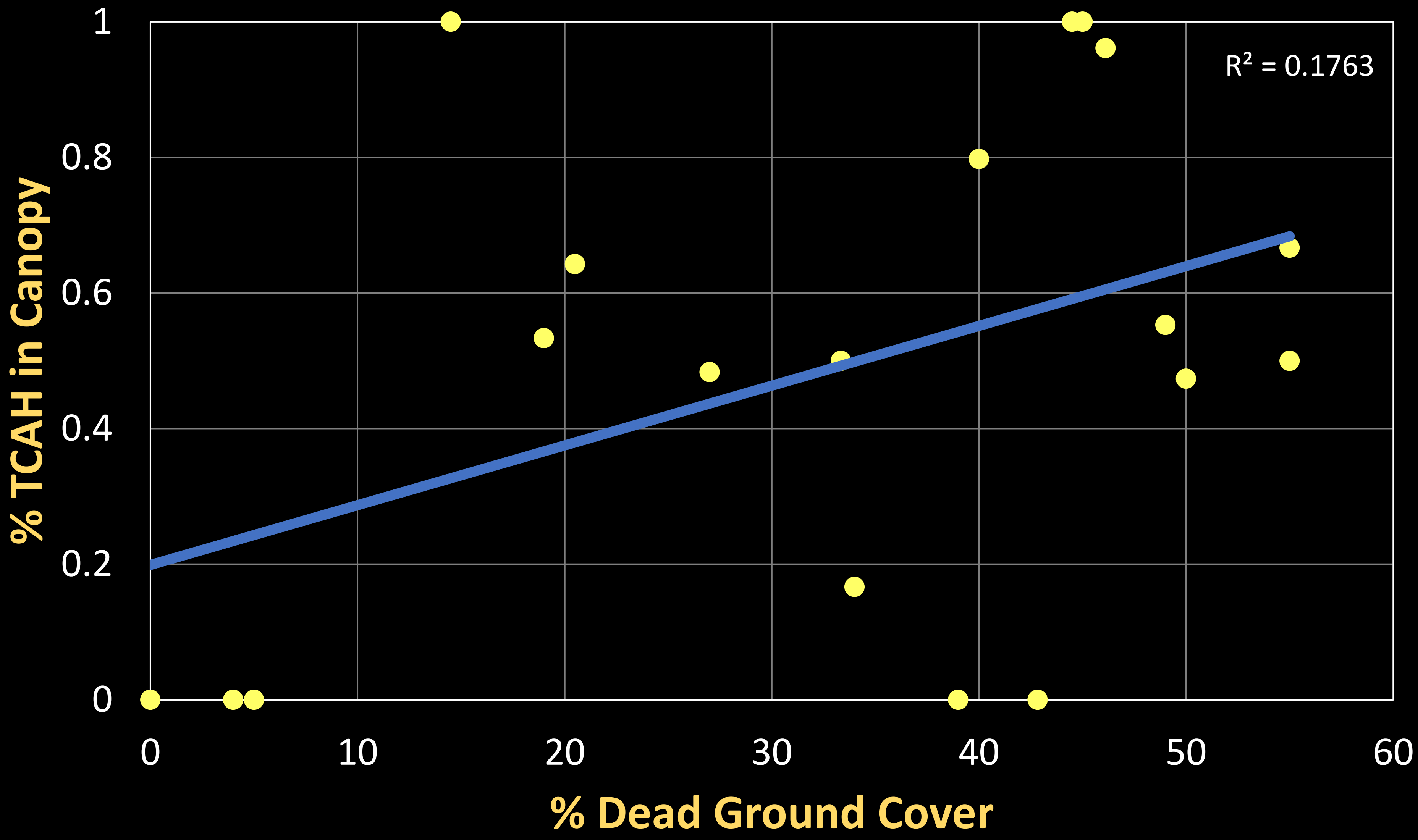
Ground cover quality decrease leads to vine canopy increase



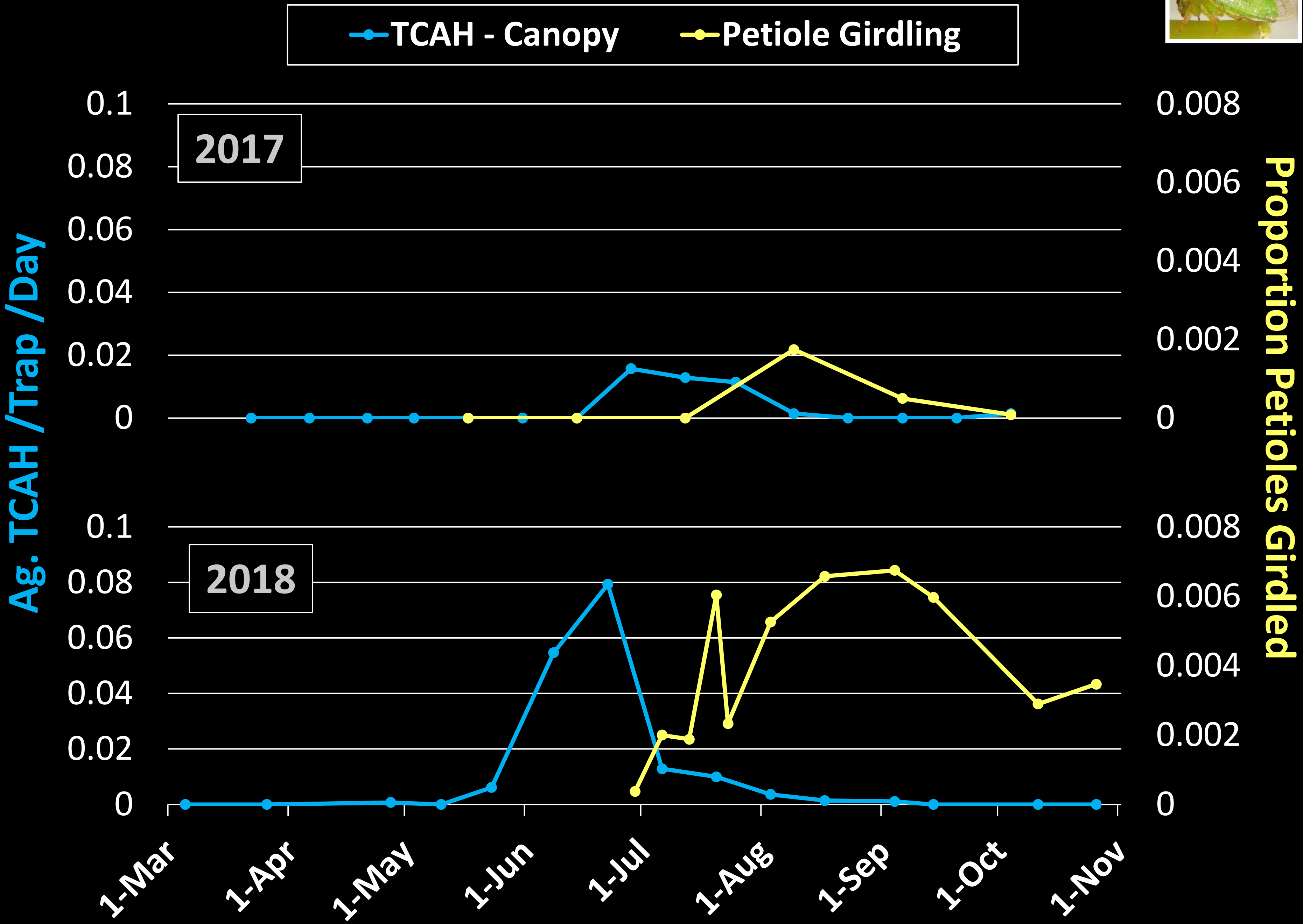
Ground cover quality decrease leads to vine canopy increase



Ground cover quality decrease leads to vine canopy increase



TCAH activity in vine canopy followed by girdling

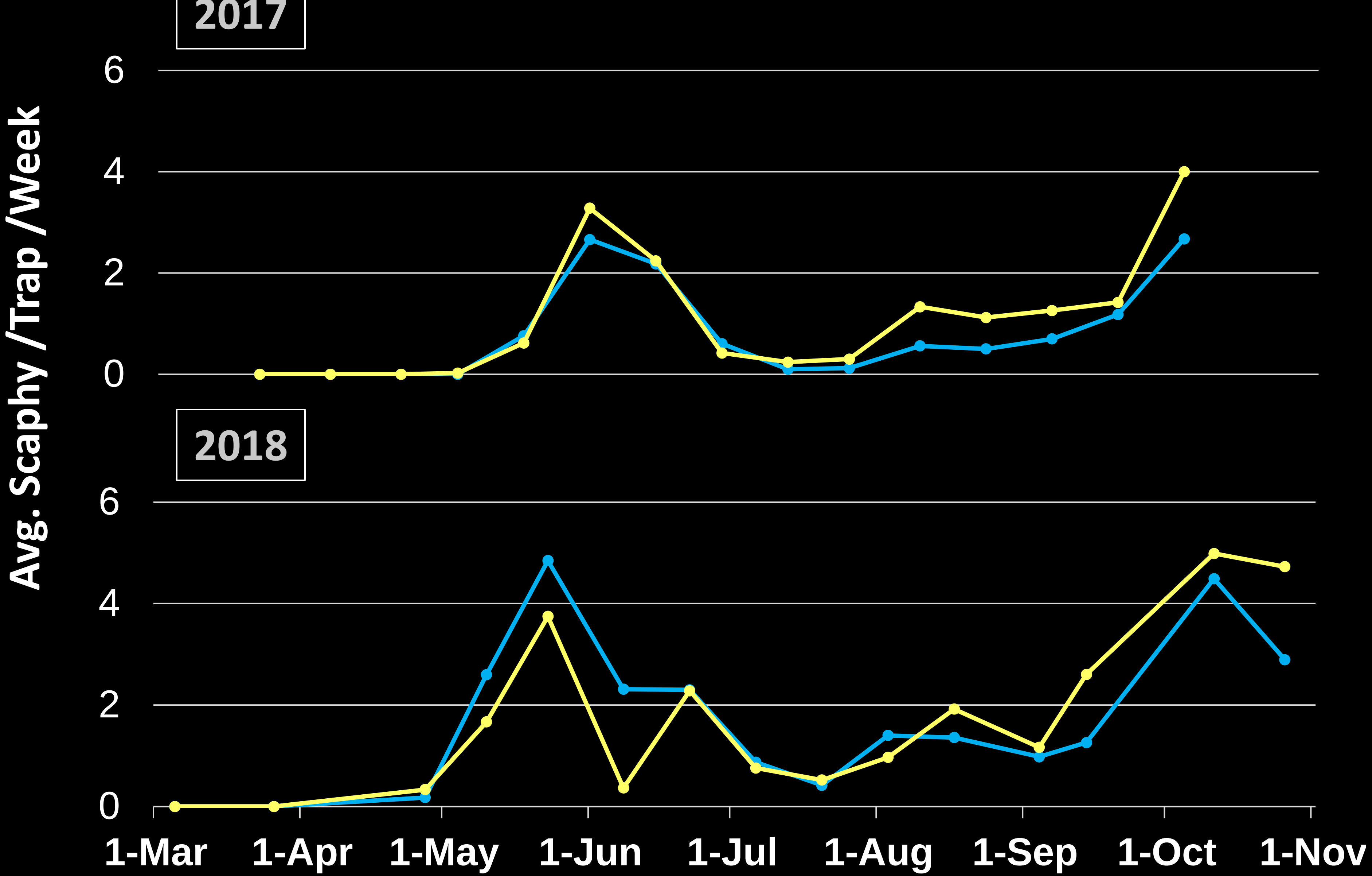


***Scaphytopius* sp.**

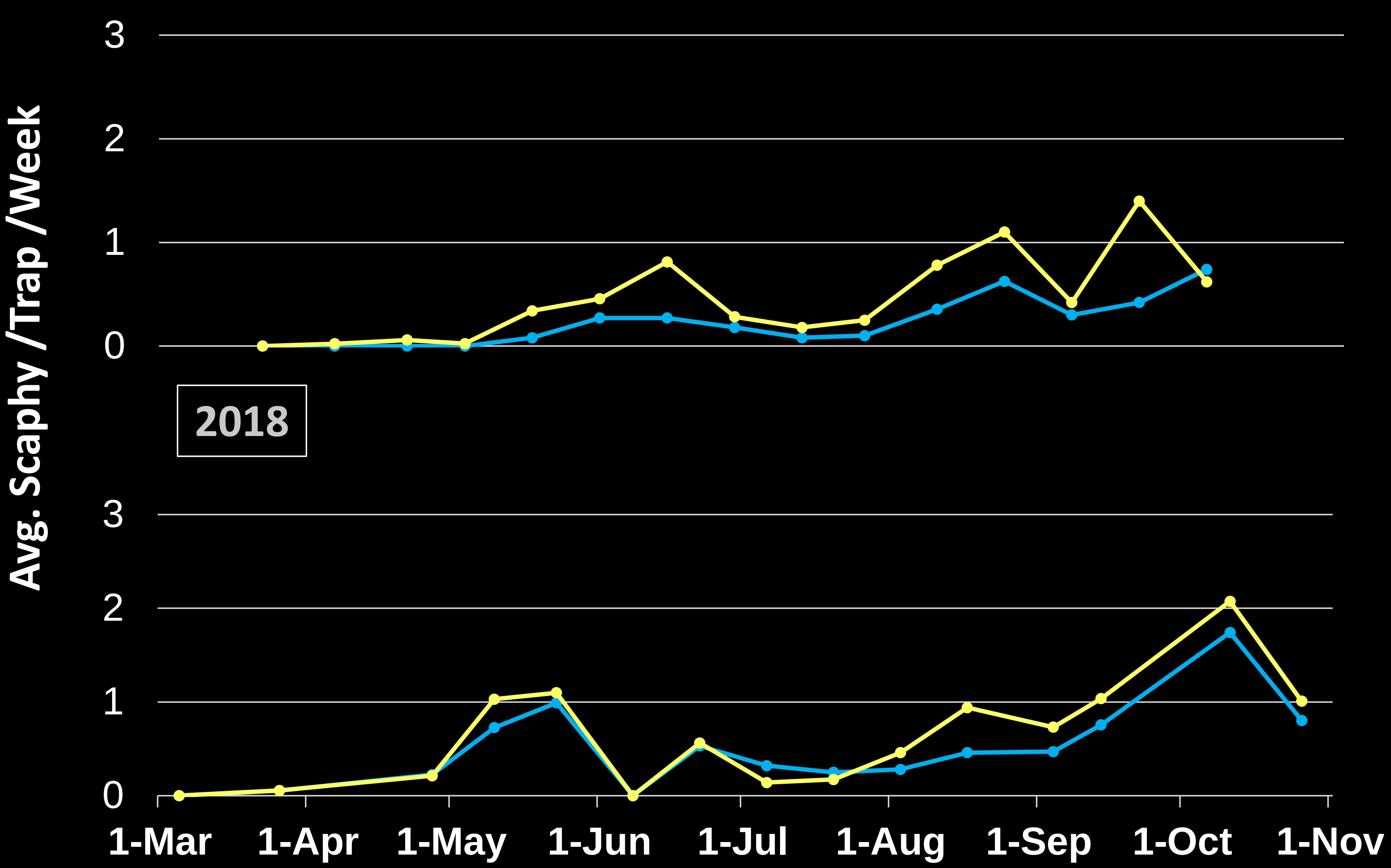
Sharp-nosed Leafhopper

“Scaphy”

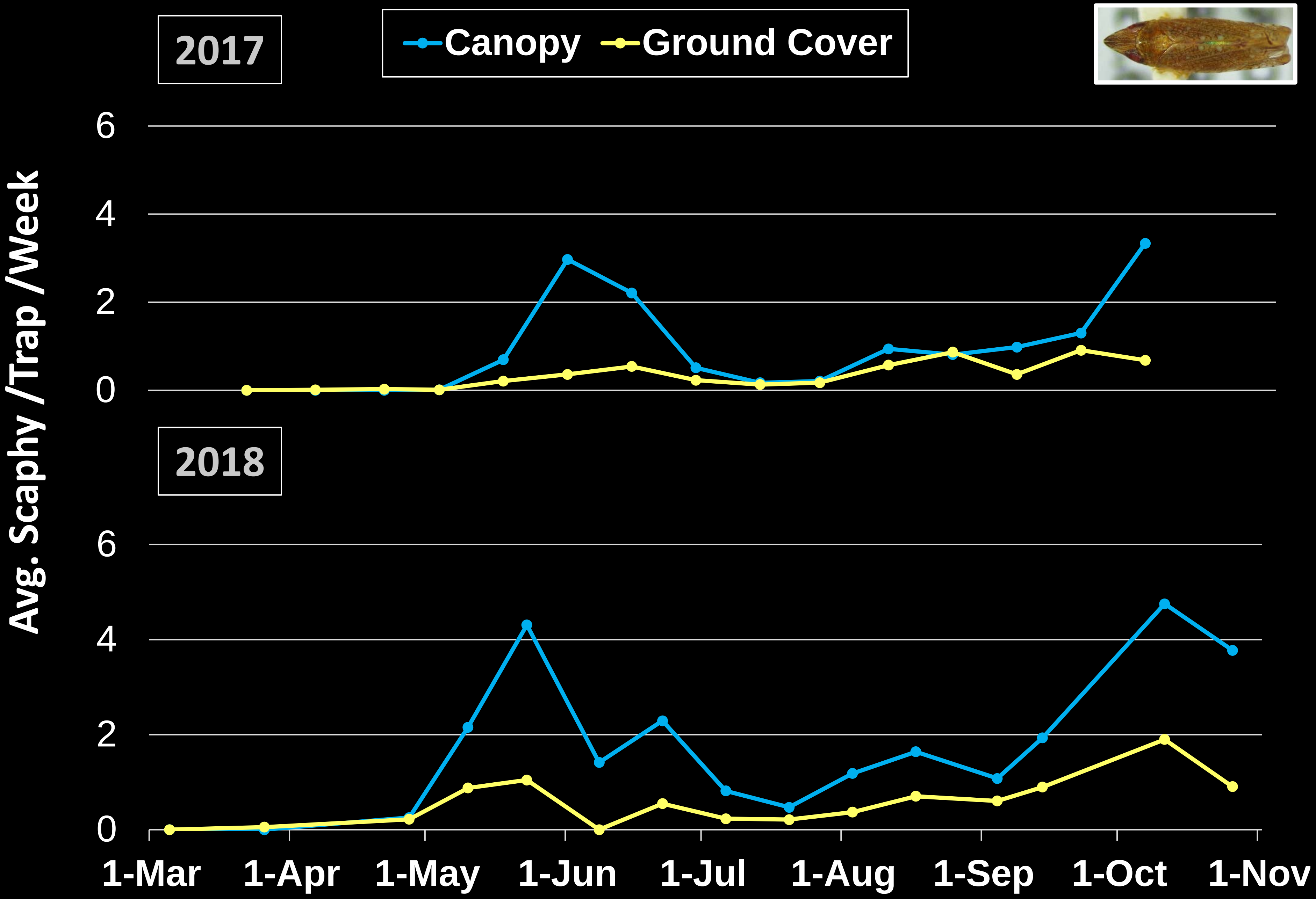
Vine Canopy – Densities slightly elevated at interior



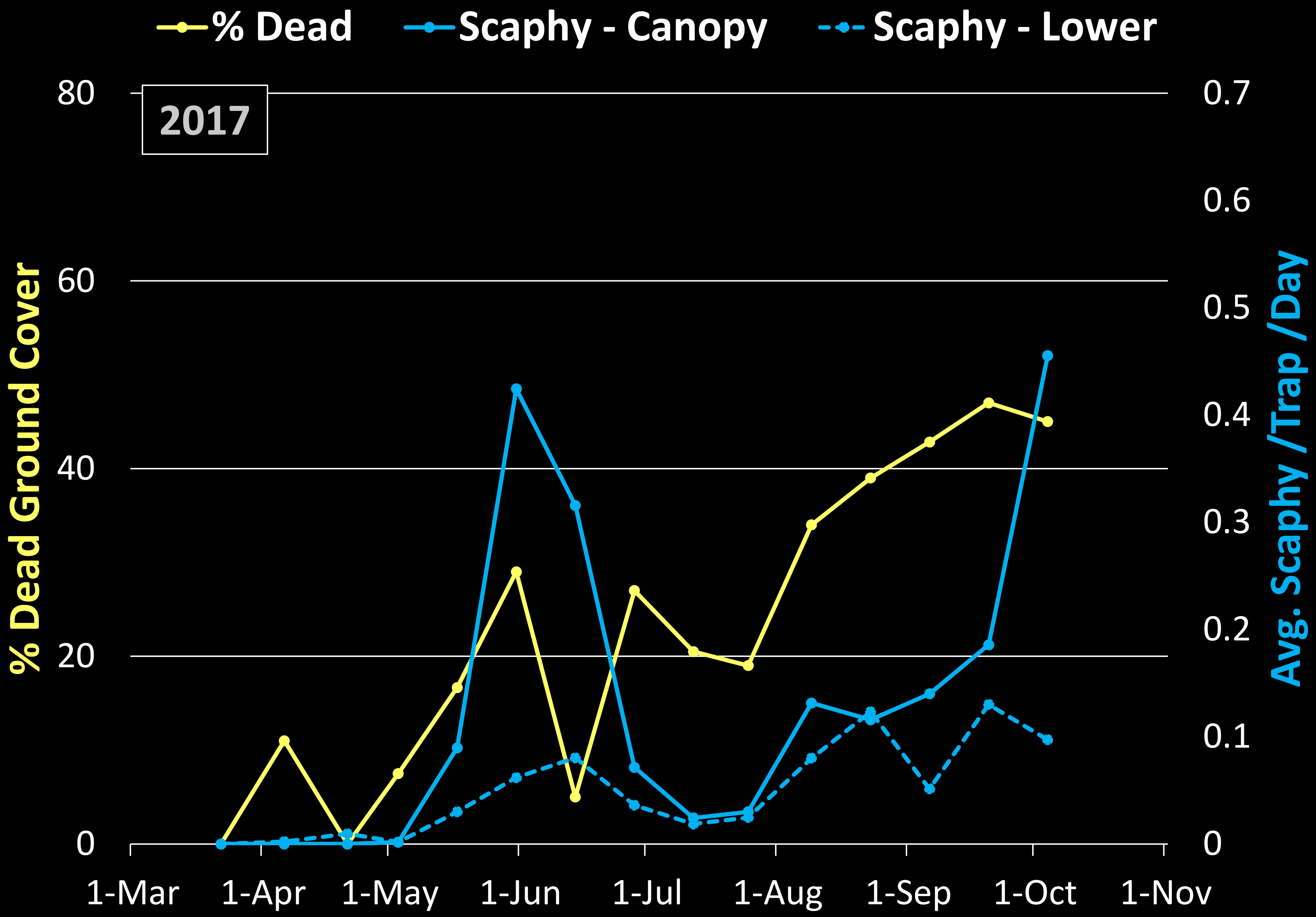
Ground Cover – Densities slightly elevated at interior



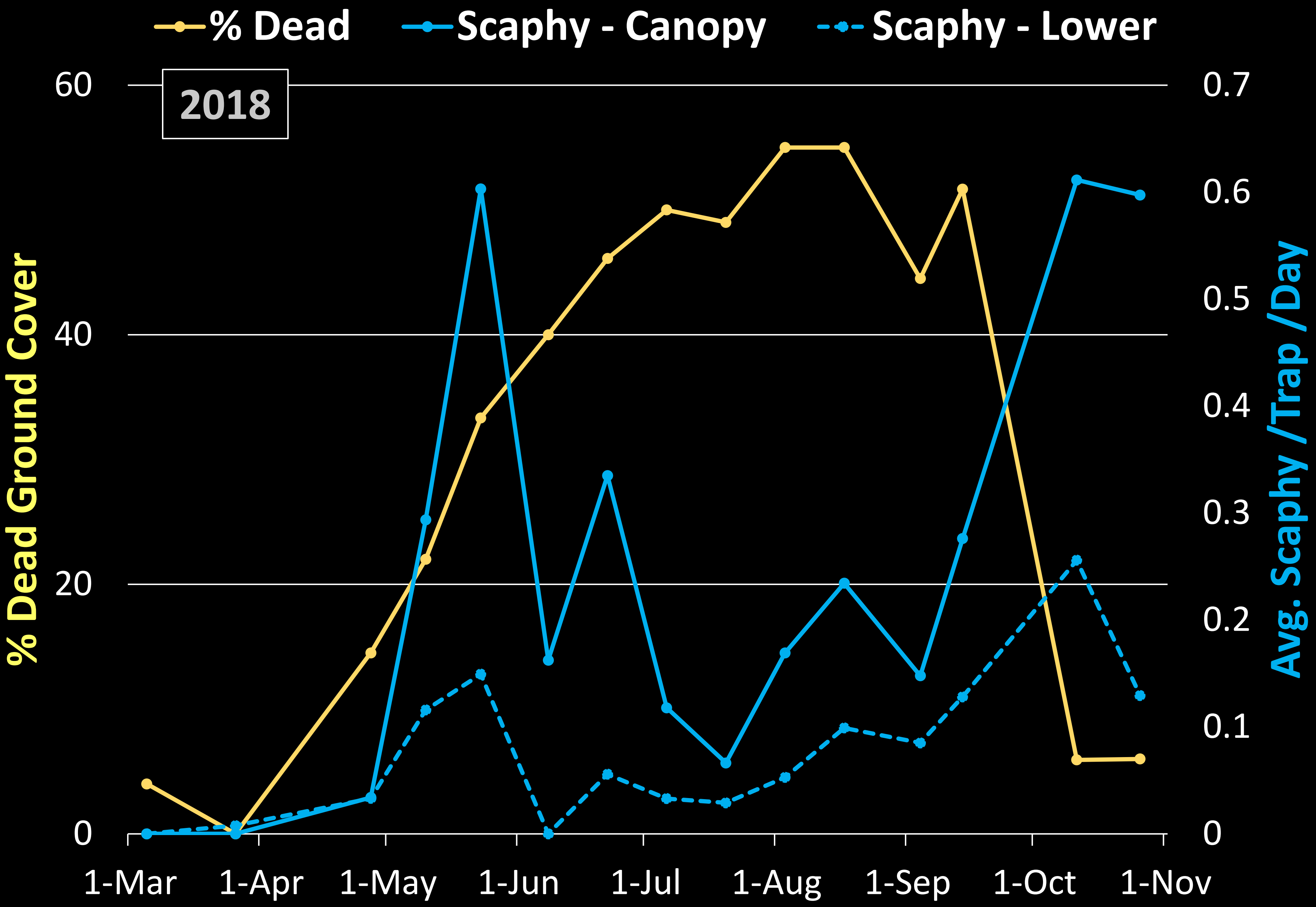
Consistently higher densities in the vine canopy



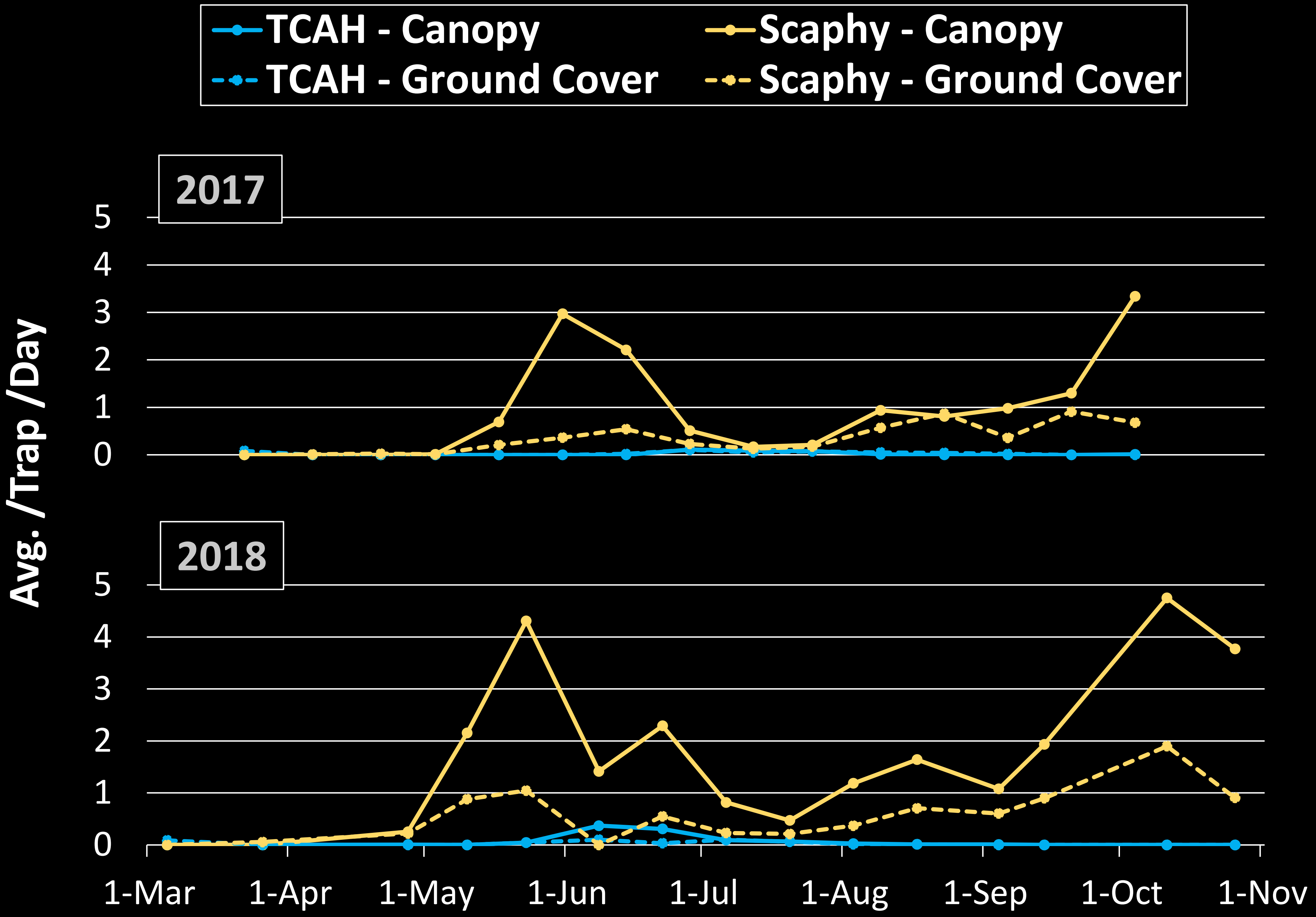
No response to ground cover quality



No response to ground cover quality



Much higher densities of *Scaphytopius* relative to TCAH



Grapevine Red Blotch Virus (GRBV)

Summary and Conclusions

Grapevine Red Blotch Virus (GRBV)

Summary and Conclusions

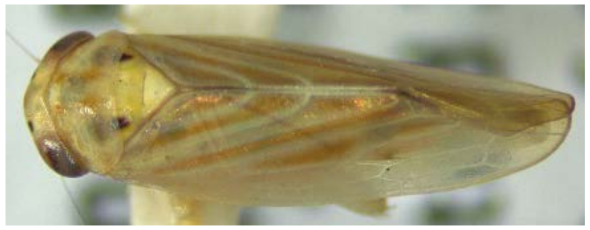
Surveyed potential plant reservoirs and insect vectors

- *Vitis* is sole positive plant host
- Cicadellids, TCAH and a few others tested positive
- Some species seem more promising than others

Scaphytopius spp.

Colladonus montanus

Spissistilus festinus



Colladonus coquilletti

Grapevine Red Blotch Virus (GRBV)

Summary and Conclusions

Transmission experiments with common vineyard insects

- Lots of experiments, lots of insects
- Some acquisition, but no transmission observed
- Rules out a lot of the most common insects

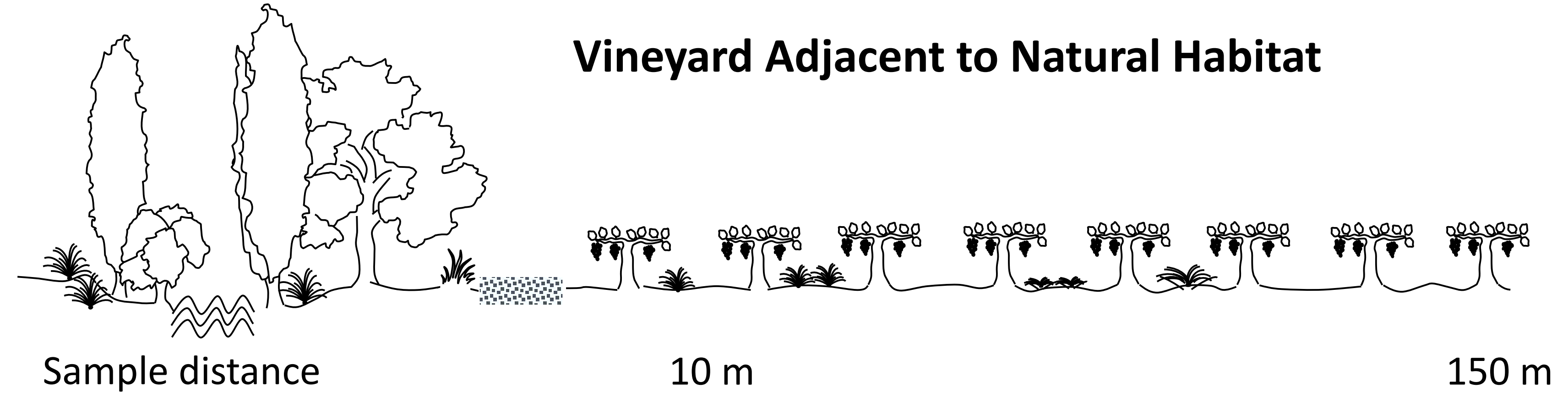
Family	Species Tested	Transmits
Cicadellidae	*Erythroneura elegantula*	No
	Erythroneura variabilis	No
	Erythroneura ziczac	No
	Graphocephala atropunctata	No
Aleyrodidae	*Trialeurodes vittatus*	No
Pseudodococcidae	*Pseudococcus maritimus*	No
	Planococcus ficus	No
Phylloxeridae	*Daktulosphaira vitifoliae*	No
Membracidae	*Spissistilus festinus*	No

Grapevine Red Blotch Virus (GRBV)

Summary and Conclusions

TCAH Seasonal Ecology

- Confirm 2 adult peaks/year
- Natural habitats don't seem to be a major source of TCAH
- Leguminous ground covers are important for TCAH
- Vine canopy activity Jun.-Aug. followed by girdling
- Canopy activity related to changes in ground cover quality

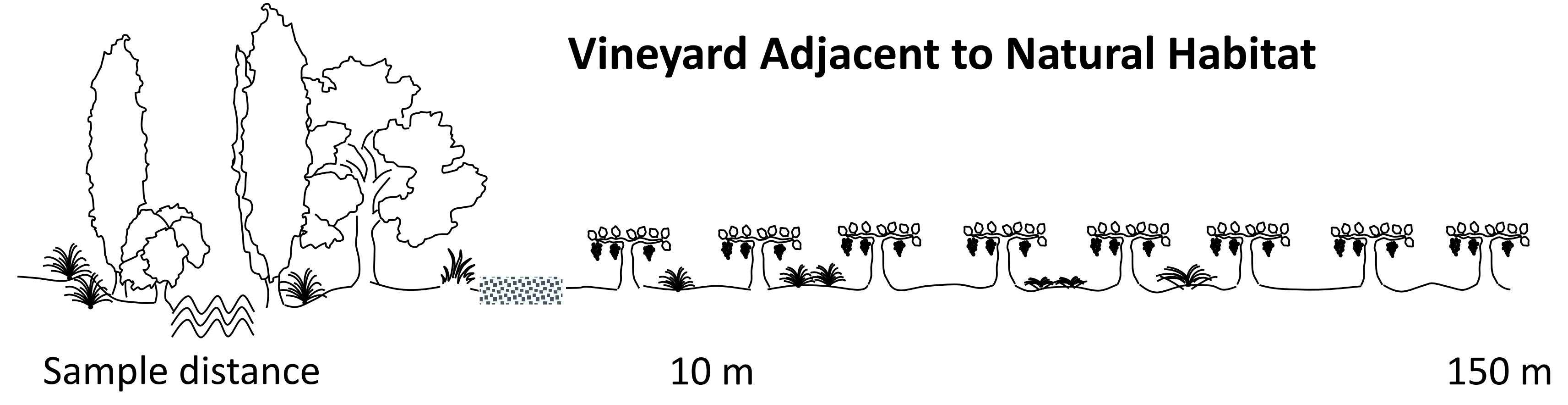


Grapevine Red Blotch Virus (GRBV)

Summary and Conclusions

What about *Scaphytopius*?

- Promising candidate vector
- Higher populations and affinity for grape vines
- Transmission studies currently in progress



Grapevine Red Blotch Virus (GRBV)

TCAH Management?

- No treatment thresholds or guidelines
  - No support for sprays
  - No support for ground cover management
    - Tradeoffs = soil quality, compaction, erosion

- Circumstantial evidence unconvincing
  - Generally low abundance
  - Low affinity for grape vine
  - Transmission efficiency unclear
  - Field transmission unconfirmed

- Broader candidate insect testing still incomplete

Grapevine Red Blotch Virus (GRBV)

Is Scaphytopius a Vector?

- We don't know yet!
    - Transmission unconfirmed
    - Experiments are in progress
    - Even if transmits, efficiency is still key

- Circumstantial evidence more convincing
    - Much higher densities
    - Strong affinity for grape vines
    - Paso Robles surveys – no TCAH, lots of Scaphy

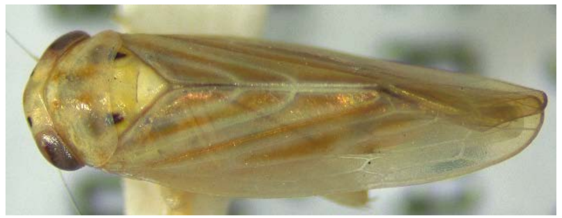
Grapevine Red Blotch Virus (GRBV)

Research in 2020 and Beyond

Daane / Wilson Research Group

1. Test more novel candidate vectors
2. Field transmission studies
3. Identify TCAH overwintering sites
4. TCAH transmission efficiency
5. Manipulate ground covers

Scaphytopius spp.



Caladonus coquilletti

Colladonus montanus

Thank You!

Houston Wilson
Houston.Wilson@UCR.edu

Kent Daane
KMDaane@Berkeley.edu

Acknowledgements:

[Funding] CDFA PD-GWSS, American Vineyard Foundation
[UCCE] Monica Cooper, Rhonda Smith, Lucia Varela, Lynn Wunderlich
[UC Berkeley/Davis] Deborah Golino, Brian Hogg (USDA), Kai Blaisdell, Jeremy Anderson, Kei-Lin Ooi, Armand Yazdani, Alexis Billings, Kelsey McCalla, Kristen Flores, Alonzo Ledesma, Jessica Maccaro
[Growers/PCAs] Numerous growers/PCAs throughout the North Coast

UNIVERSITY OF CALIFORNIA UCRIVERSIDE

Berkeley UNIVERSITY OF CALIFORNIA

UCCE University of California Cooperative Extension