

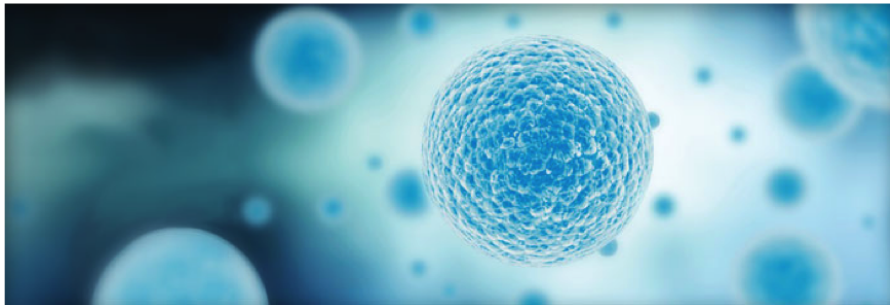
# ReasearchTalk

Samantha A. Alger

5/1/2017

# The role of plants in bee virus transmission

Samantha Alger



# It's Official!



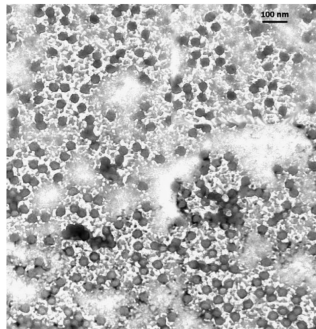
Rusty Patched Bumble Bee • *Bombus affinis*

First bee in the continental U.S. to be listed  
under the Endangered Species Act

Xerces Society

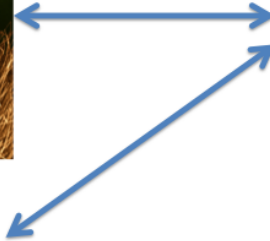
# RNA Viruses

Deformed Wing Virus (DWV)  
Black Queen Cell Virus (BQCV)  
Israeli Acute Paralysis Virus (IAPV)





# Transmission Routes



# Research Questions

## Part I.

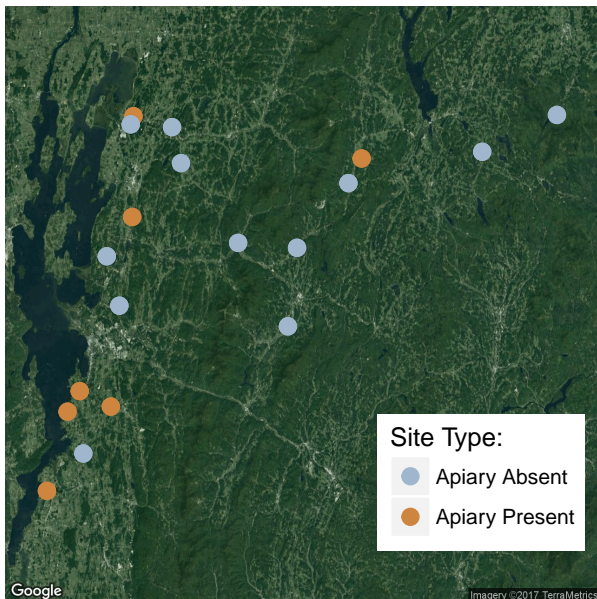
What is the prevalence of RNA viruses in bumble bees?

Is there evidence for disease spillover from managed honey bees?

## Part II.

Can flowers act as bridges in disease transmission?

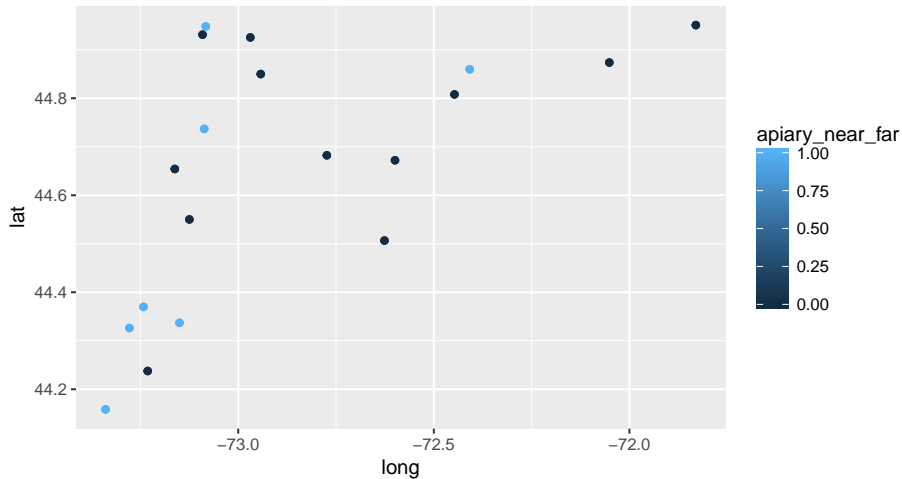
# Part I: Survey



# Code for Map

```
1  ──  
2  ──  
3  ──  
4  library(ggmap) ──  
5  ──  
6  # make preliminary plot to check it out ──  
7  # color according to apiary near/far: ──  
8  ggplot(spatDat, aes(x = long, y = lat, group = apiary_near_far)) +  
9  · geom_point(aes(colour = apiary_near_far)) ──  
10 ──  
11 ──
```

## Code for Map



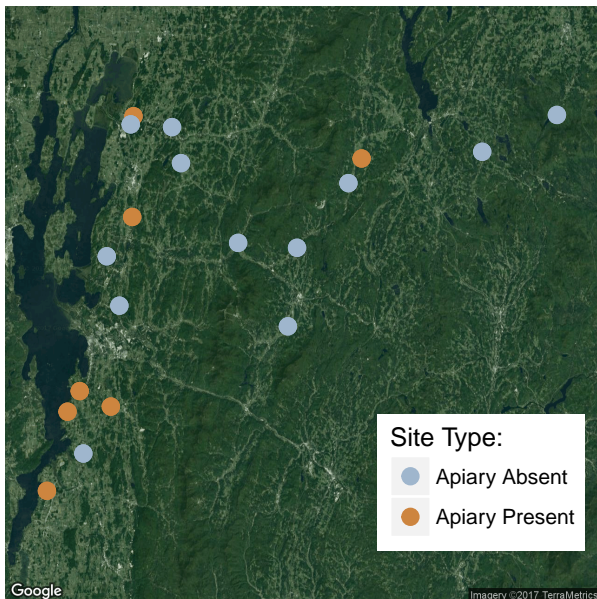
# Code for Map

```
14  ↵
15  #Now we need a map to overlay these points:↵
16  ↵
17  # Use the dataframe lat and long to make the bounding box↵
18  # adding or subtracting 0.5 for aesthetics:↵
19  bbox <- c(min(spatDat$long) - 0.1,↵
20  ..... min(spatDat$lat) - 0.1,↵
21  ..... max(spatDat$long) + 0.1,↵
22  ..... max(spatDat$lat) + 0.1↵
23  )↵
24  ↵
25  # get the base map ↵
26  vt <- get_map(location = bbox, source = "google", maptype = "satellite")↵
27  ↵
```

# Code for Map

```
33 #set colors for the map points:
34 colors <- c("slategray3", "tan3")
35 # use ggmap to plot the points on the vt basemap
36 ggmap(vt) +
37   geom_point(data = spatDat, aes(x = long,
38     ..... y = lat,
39     ..... color = (spatDat$apiary)),
40   ..... size=3) +
41   theme( # theme removing grids etc.
42     .... legend.position=c(.8, .2),
43     .... panel.grid.major = element_blank(), # remove major grid
44     .... panel.grid.minor = element_blank(), # remove minor grid
45     .... axis.text = element_blank(),
46     .... axis.title = element_blank(),
47     .... axis.ticks = element_blank()
48   ) + scale_color_manual(values=colors, name="Site Type", labels=c("Apiary Absent",
49     "Apiary Present"))
```

# Final Map

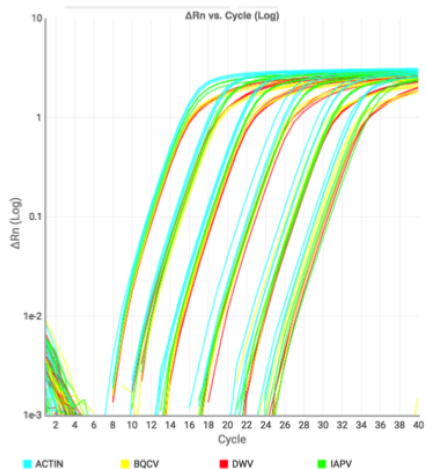
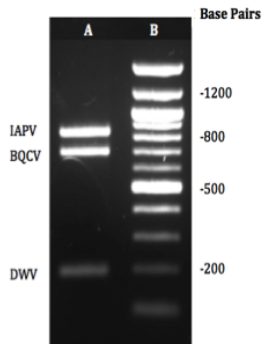




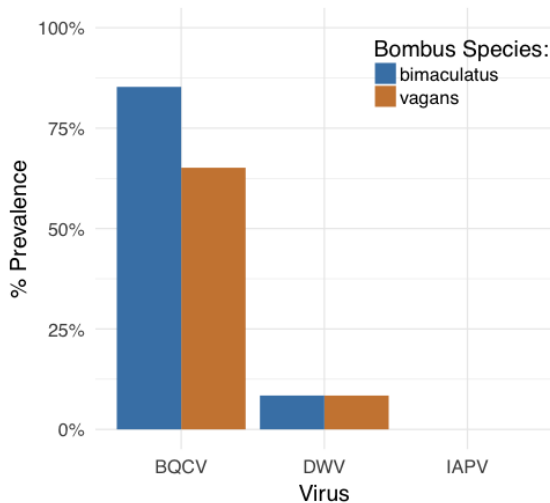
# Part I: Survey



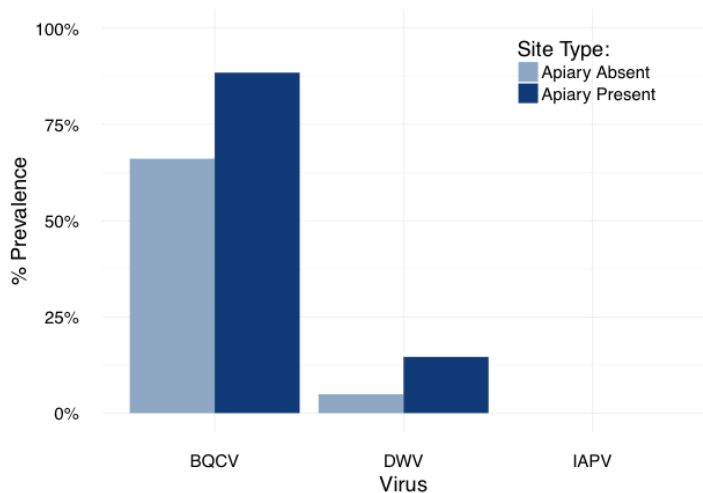
# QPCR



## BQCV More Prevalent in *bimaculatus*



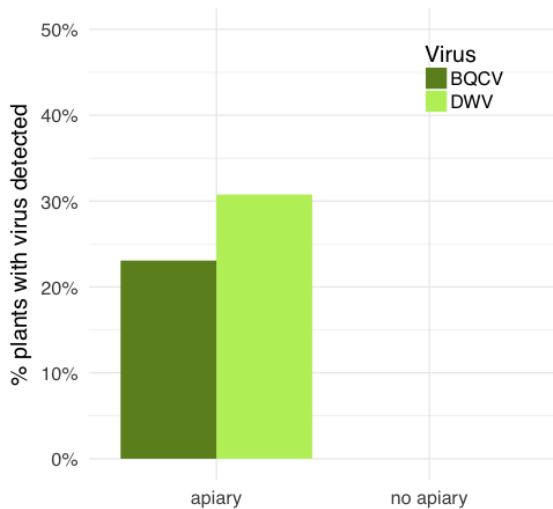
# Viruses More Prevalent in Bumble Bees near Apiaries







# Viruses detected on plants collected only in apiaries!



# Research Questions

## Part I.

What is the prevalence of RNA viruses in bumble bees?

**-BQCV is most common, followed by DWV**

Is there evidence for disease spillover from managed honey bees?

**-Yes, bumble bees are more likely to be infected when caught near an apiary and when the apiary has high viral loads**

## Part II.

Can flowers act as bridges in disease transmission?





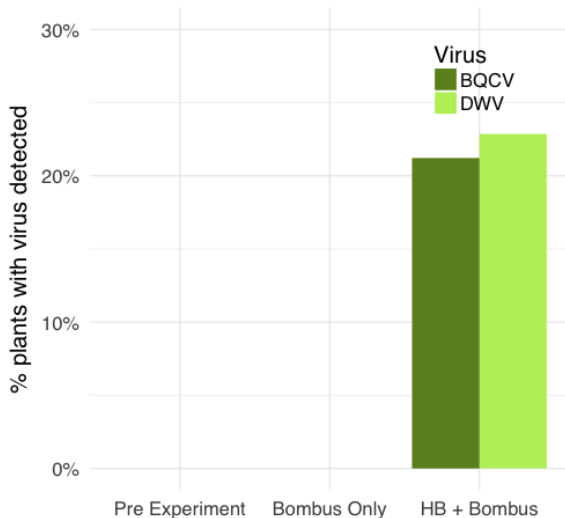




# Experimental Setup

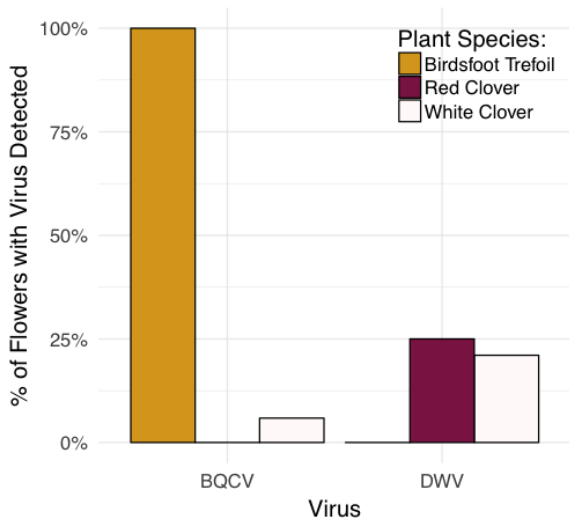


# Viruses detected only on plants visited by honeybees



# Does plant species matter?





# Conclusions

## Part I.

What is the prevalence of RNA viruses in bumble bees?

**-BQCV is most common, followed by DWV**

Is there evidence for disease spillover from managed honey bees?

**-Yes, bumble bees are more likely to be infected when caught near an apiary and when the apiary has high viral loads**

## Part II.

Can flowers act as bridges in disease transmission?

**-Bees can deposit viruses on flowers**

**-Plant species and virus matter!**



## Questions for future work...

- Can bees become infected after visiting an infected flower?
- Are there differences in how viruses are shed?  
(Fecally vs. Orally)
- Does floral morphology matter?

# Implications

- BQCV is common in bumble bees and its effects should be studied
- Reducing honey bee viral loads (mite management) could lessen spillover of DWV
- Recommendations for 'pollinator friendly' habitat

# Contributors and Collaborators

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