

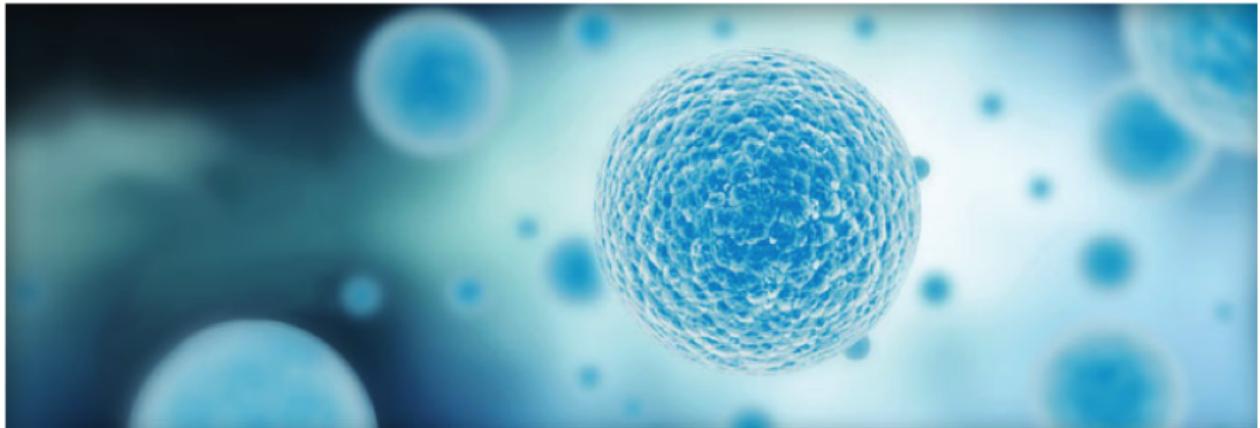
ReasearchTalk

Samantha A. Alger

5/1/2017

The role of plants in bee virus transmission

Samantha Alger



It's Official!



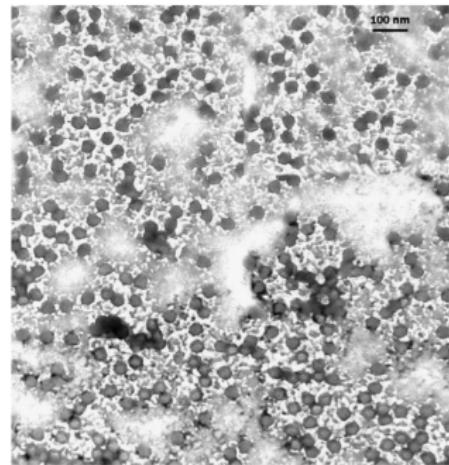
Rusty Patched Bumble Bee • *Bombus affinis*

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

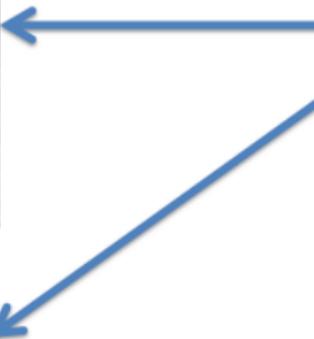
Xerces Society

RNA Viruses

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



Transmission Routes



Research Questions

Part I.

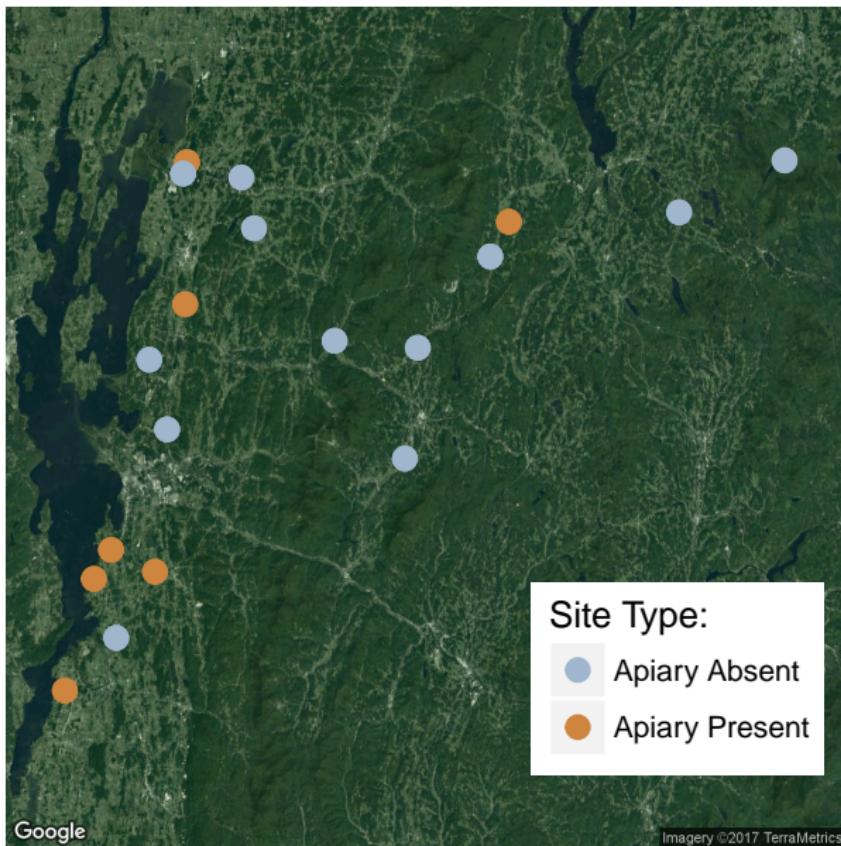
What is the prevalence of RNA viruses in bumble bees?

Is there evidence for disease spillover from managed honey bees?

Part II.

Can flowers act as bridges in disease transmission?

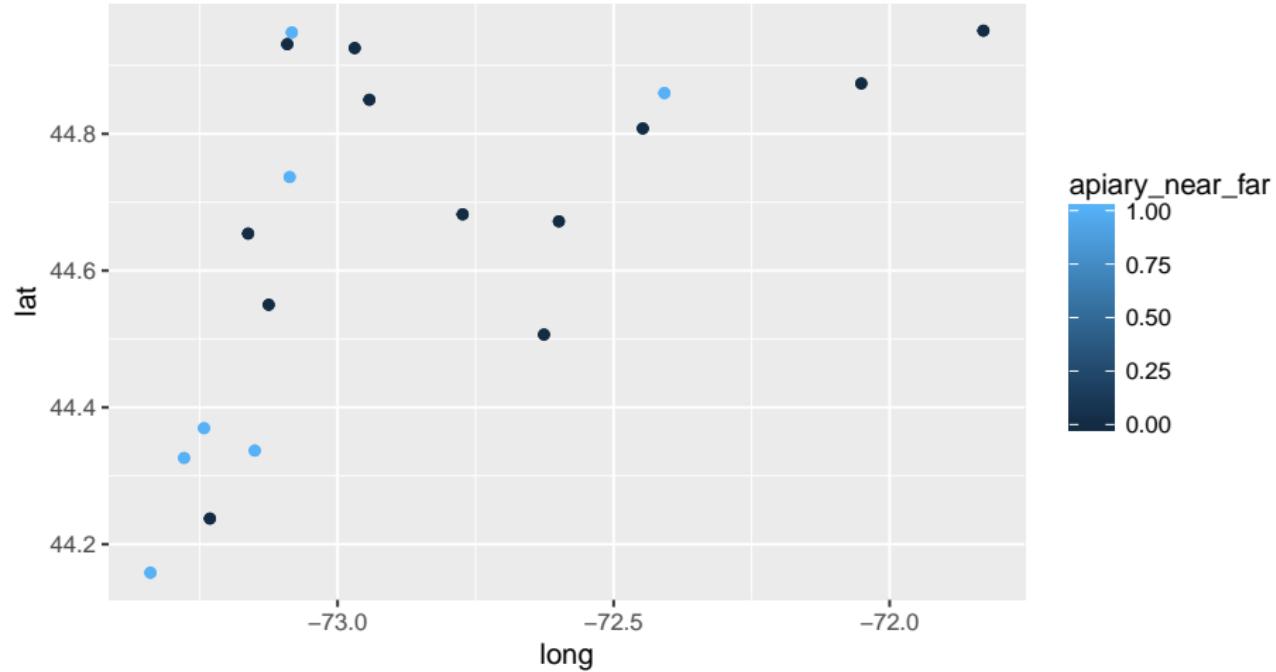
Part I: Survey



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



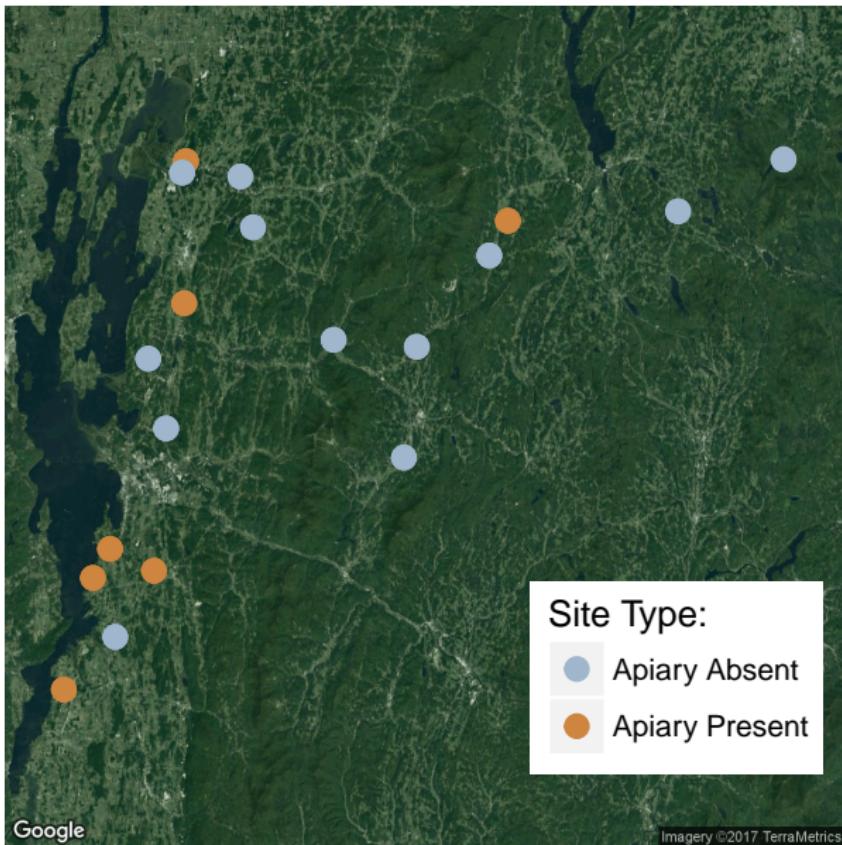
Code for Map

```
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",
"Apiary Present"))
```

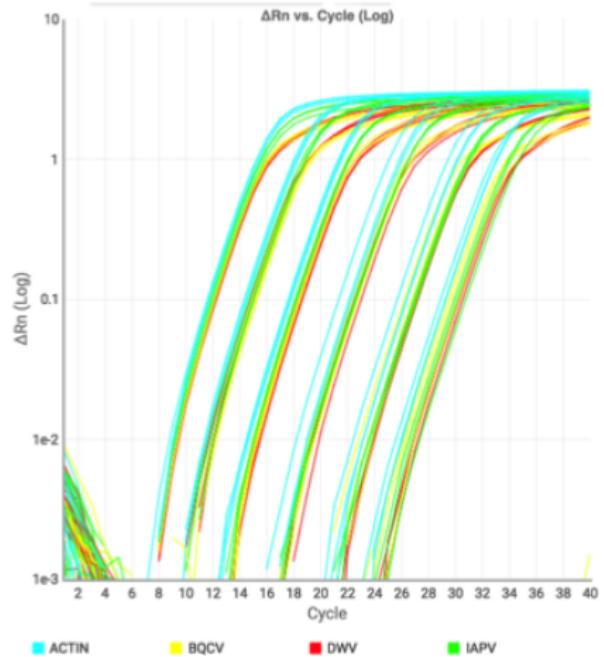
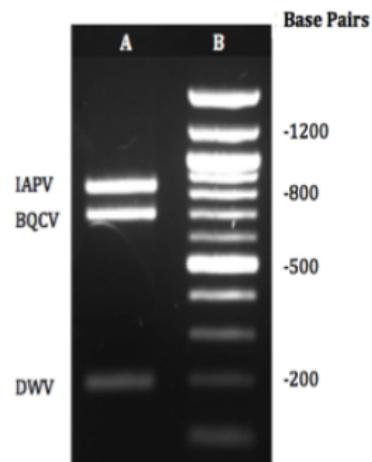
Final Map



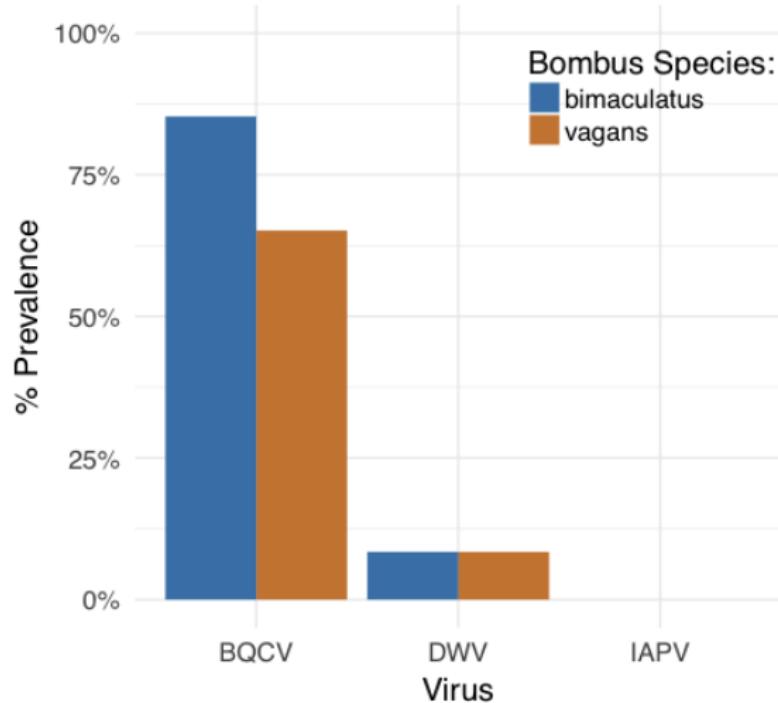
Part I: Survey



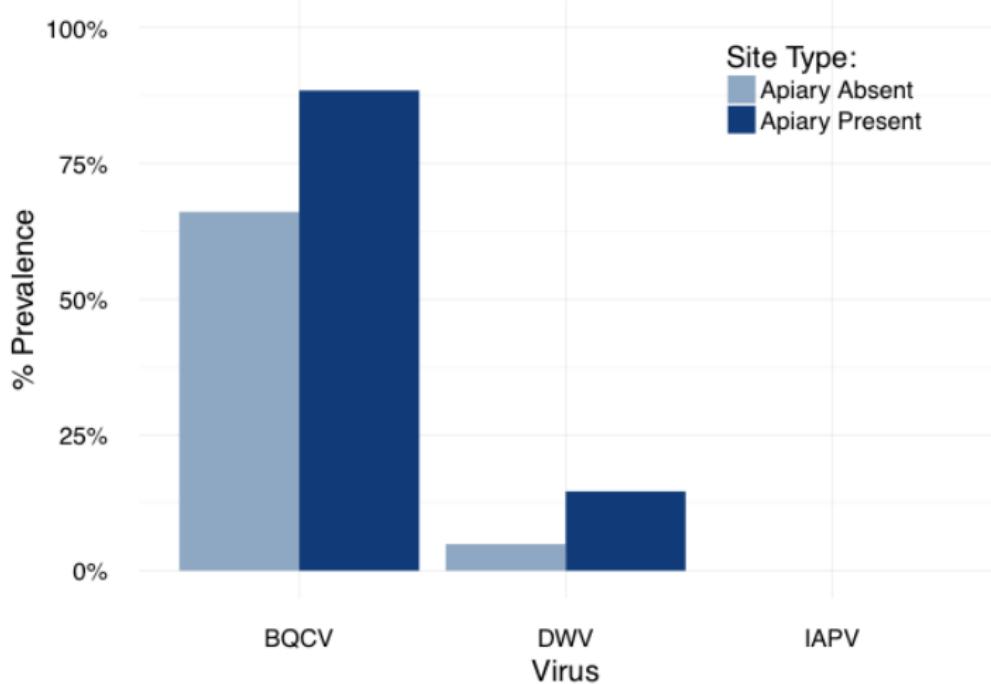
QPCR



BQCV More Prevalent in *bimaculatus*



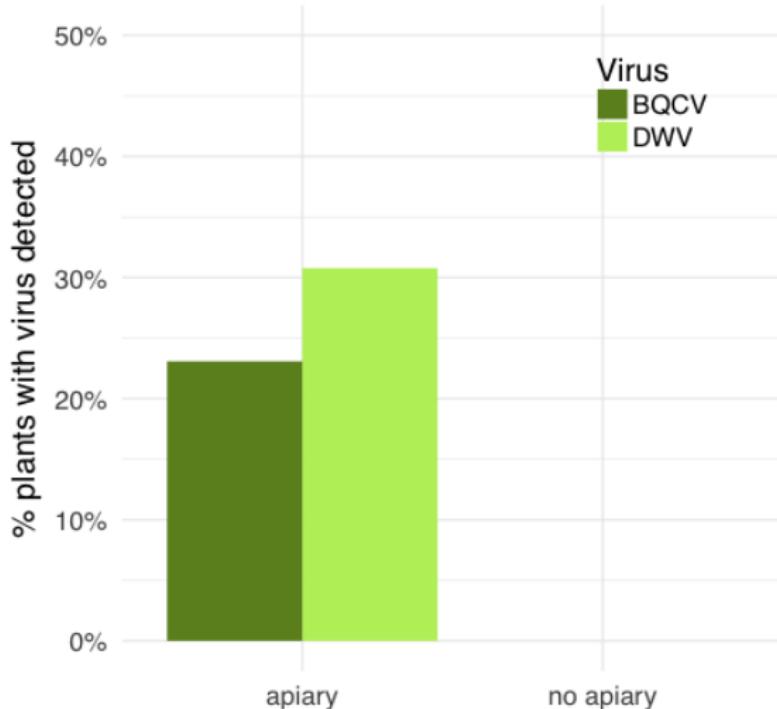
Viruses More Prevalent in Bumble Bees near Apiaries







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?



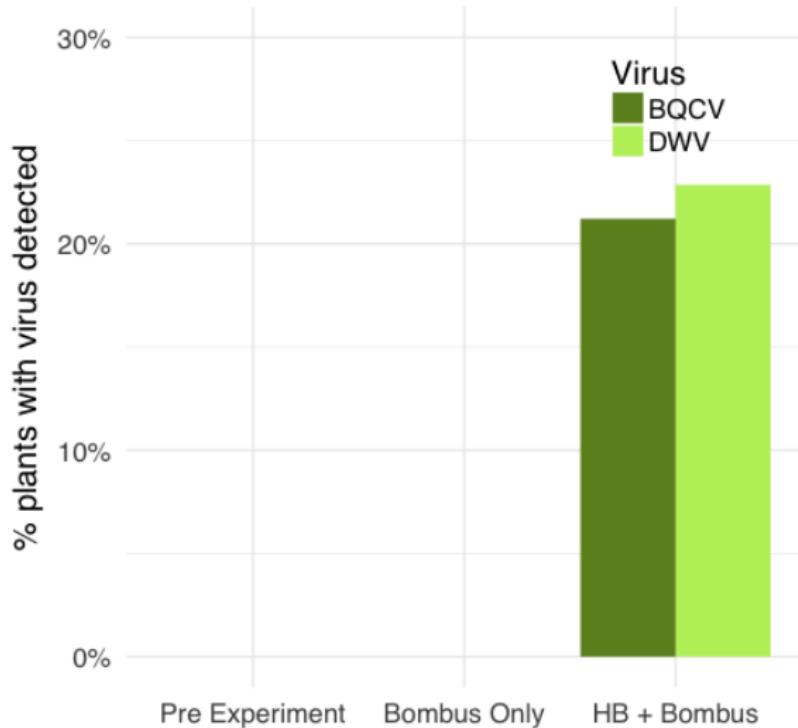




Experimental Setup

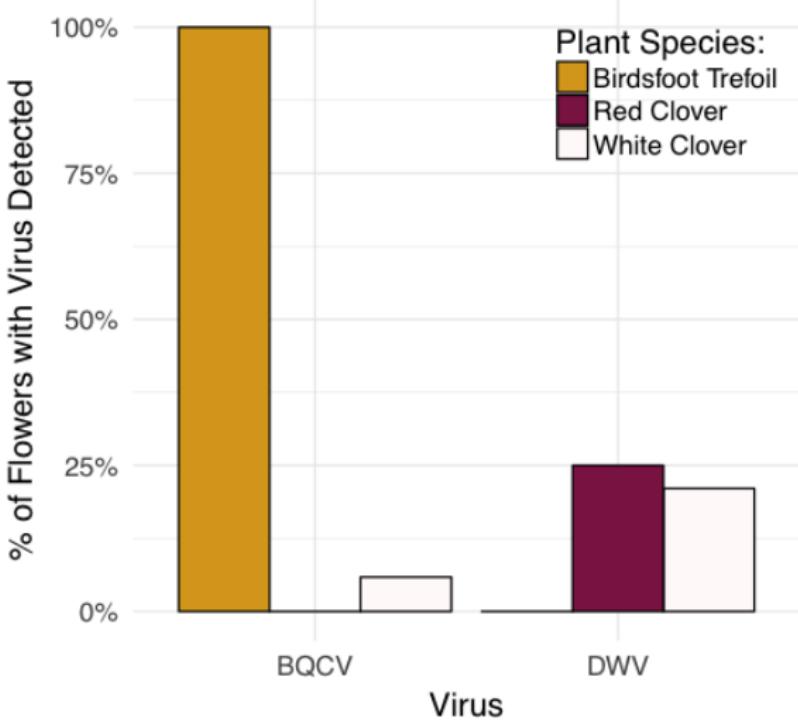


Viruses detected only on plants visited by honeybees



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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