**Metadata for Disease\_Pos\_global\_publish.csv**

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Description: Records of which individual bees from four focal host species (*Apis mellifera*, *Bombus impatiens*, *Eucera pruinosa*, and *Lasioglossum* spp.) were positive when tested for the viral positive strand for deformed wing virus (DWV), black queen cell virus (BQCV), and sacbrood virus (SBV), and additional co-variate data included for each sample. All bees were collected in or adjacent to winter squash fields. All samples were randomly selected from PollinatorComm2015\_2016\_publish.csv.

Header descriptions

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| Sample | Unique sample number for each individual in the study. These sample numbers match those found in PollinatorComm2015\_2016\_publish.csv |
| Transect.ID | Unique transect ID that indicates the site, year of collection, transect A B C or D, visit number to the site, and net or pan trap collected. All individuals collected from the same transect share a transect ID. These unique IDs match those found in PollinatorComm2015\_2016\_publish.csv |
| Individual.ID | Includes the transect ID with a sequential number for each sample. These unique IDs match those found in PollinatorComm2015\_2016\_publish.csv |
| Year | Year of sample collection, either 2015 or 2016 |
| Site | Unique site code for each of the 14 sites |
| VisitNumber | Visit number to the site, each site was visited twice for this study. The first and second visit are indicated by “1” and “2”, respectively. |
| Lat | Latitude coordinate for the Site |
| Long | Longitude coordinate for the Site |
| Collected | Categorical variable for the type of flowers that the bee was collected from, either “squash” flowers or a mixture of native and weed “flowers” along the hedgerows of the squash field. |
| Transect | Pollinators were sampled along 4 randomly placed transects at each site, and labeled “A”, “B”, “C”, or “D”. Transects were sampled via hand nets in alphabetical order. Transects A, B, and C were always within the squash field, and transect D was always located within a nearby hedgerow that often contained native and weedy plant species. |
| NetorPan | Categorical variable indicating the method of collection for each bee sample.  Net = hand net  Pan = pan trap |
| DateCollected | Date the sample was collected. |
| Type | Either “APIS” to indicate a managed, *Apis mellifera* sample, or “NON” to indicate a native bee and non-*Apis* sample. |
| SpeciesCode | Species identity code  APME = *Apis mellifera*  BOIM = *Bombus impatiens*  LASI = *Lasioglossum* spp.  PEPR = *Eucera pruinosa* (species was previously named *Peponapis pruinosa*) |
| GenusCode | Genus identity code  APIS = *Apis mellifera*  BOMB = *Bombus impatiens*  LASI = *Lasioglossum* spp.  PEPO = *Eucera pruinosa* (species was previously named *Peponapis pruinosa*) |
| Sex | Sex of the bee sampled.  F = female  M = male |
| RNA conc. | RNA concentration (ng/µl) obtained from the Broad Range Qubit kit after RNA extraction for each sample. Samples with “too high” had > 600 ng/µl, and samples with “Sample too low” had < 5 ng/µl, both of which were outside of the range of detection for the kit used. All samples included in the data set amplified the 18S rRNA gene used as a control, indicating sufficient RNA for detection of viral RNA. |
| Virus\_Type | Categorical variable for the three viruses studied.  DWV = deformed wing virus  BQCV = black queen cell virus  SBV = sacbrood virus |
| Virus | Samples found to be positive (1) or negative (0) for the presence of the virus listed in the Virus\_Type column. |
| Richness | Species richness per site (both visits combined) |
| EstRich\_Asyp | Estimated species richness at the asymptote of the rarefaction curve for each site. |
| EstRich\_46 | Estimated species richness for each site at the lowest number of individuals (46 pollinators) collected at any site based on the rarefaction curve. |
| EstRich\_183 | Estimated species richness for each site at the second lowest number of individuals (183 pollinators) collected at any site based on the rarefaction curve. |
| EstRich\_338 | Estimated species richness for each site at the average number of individuals (338 pollinators) collected at any site based on the rarefaction curve. |
| Abundance | Total number of pollinators collected at each site (both visits combined) |
| Diversity | Simpson diversity index (1-D) at each site (both visits combined) |
| APME\_ABUND | Number of *Apis mellifera* samples collected at each site (both visits combined) |
| BOIM\_ABUND | Number of *Bombus impatiens* samples collected at each site (both visits combined) |
| LASI\_ABUND | Number of *Lasioglossum* spp. samples collected at each site (both visits combined) |
| PEPR\_ABUND | Number of *Eucera pruinosa* samples collected at each site (both visits combined). This species was previously named *Peponapis pruinosa.* |