STATISTICAL REPORT

**Unhealthy Brood Disorder: The UBO trait is strongly correlated with decreased virus, *Nosema*, and chalkbrood loads.**

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* Finish Stats
* Add Methods
* Add Results

**STATISTICAL METHODS**

***Nosema:*** The

To determine if chalkbrood cells and chalkbrood spore type were influenced by UBO score, we conducted a GLM with chalkbrood spore count described by chalkbrood type, UBO score, and their interaction. As chalkbrood spore count was skewed right, a Poisson distribution was used with a link “log” function.

***RNA Viruses:*** The

All data analyses were conducted in R (v4.2.3) (R Core Team 2019). Significance for all models was determined by conducting type II Wald chi-square tests using the "Anova" function in the CAR package (v3.1-0) (Fox and Weisberg 2019).

**RESULTS:**

**Nosema:** The

**Chalkbrood:** The

**RNA Viruses:** The

**FIGURES:**

**Figure 1:** Prevalence and intensity of chalkbrood as a function of UBO score and spore type. Percent UBO score is shown on the x axis. Black chalkbrood (infective) spores are shown in green and white spores are shown in orange. Green and purple lines represent lines of best fit for white and black spores, respectively. The hatched black line represents the line of best fit for all spores, regardless of type.

**Figure 2:** *Nosema* prevalence and load by month and high and low UBO score. High UBO represents colonies scoring 60% or higher (blue) and low UBO represent colonies that scored less than 60% (orange). **(A)** *Nosema* prevalence (infected colonies/total colonies) by UBO score over time (months). Error bars represent a confidence interval generated by sampling from a binomial distribution parametrized by the number of infected (1) and uninfected (0) colonies for each UBO group at each month. **(B)** *Nosema* load (spores/bee) by UBO score over time (month). Error bars represent standard error.

**Figure 3:** *Nosema* load (spores/bee) by percent UBO score for June, July, August, and September. Green regression lines represent the line of best fit generated by a linear model.

**Figure 4:** Virus prevalence and load by virus and UBO status (low and high). High UBO is represented by blue and Low UBO by orange. **(A)** Virus prevalence represents the number of infected samples over the total number of samples for each virus and UBO group multiplied by 100. Blue bars represent low UBO colonies, while orange bars represent high UBO colonies. Error bars represent a confidence interval generated by sampling from a binomial distribution parametrized by the number of infected (1) and uninfected (0) colonies for each virus and UBO group. **(B)** Virus load represents genome copies/bee and was log10 transformed. Horizontal black lines represent the median. Black dots represent outliers.

**Figure 5:** Virus load (genome copies/bee) by UBO score for 6 different viruses: BQCV, DWV-A, DWV-B, IAPV, LSV, and SBV. Green regression lines represent the line of best fit generated by a linear model.

**Figure 1**

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**Figure 2**

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**Figure 3**

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**Figure 4**

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**Figure 5**

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