

# Havi Fecundity Analysis

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## Load Libraries

```
pacman::p_load(ggplot2, readxl, ggbeeswarm, readr, dplyr, tidyr, tidyverse, devtools,
               cowplot, knitr, emmeans, ggpmisc, lme4, lmerTest, RColorBrewer, viridis, install = FALSE)
```

## Load Data

```
aphid_count <- read_excel("data/fecundity_assay_count.xlsx") %>%
  filter(alate_alive_r1 != "control") %>%
  mutate(nymphs_r1 = as.numeric(nymphs_r1), nymphs_r2 = as.numeric(nymphs_r2))
```

```
## Warning: There was 1 warning in `mutate()`.
## i In argument: `nymphs_r2 = as.numeric(nymphs_r2)`.
## Caused by warning:
## ! NAs introduced by coercion
```

```
# === Pivot to long format ===
aphid_long <- aphid_count %>%
  pivot_longer(cols = c(starts_with("nymphs_r"), starts_with("alate_alive_r")),
              names_to = c(".value", "round"), names_pattern = "(.*)_r(\\d)")
```

## Calculations

Calculating how many aphids are in each group as a new data frame

## survival

```
# === Survival summary ===
survival_summary <- aphid_long %>%
  group_by(treatment, block, round) %>%
  summarise(alive_n = sum(alate_alive == "Yes", na.rm = TRUE), dead_n = sum(alate_alive ==
    "No", na.rm = TRUE), total = alive_n + dead_n, survival_pct = 100 * alive_n/total,
    .groups = "drop")

# Optional: Treatment-level survival averages
survival_by_treatment <- survival_summary %>%
  group_by(treatment, round) %>%
  summarise(mean_survival = mean(survival_pct), se_survival = sd(survival_pct)/sqrt(n()),
    .groups = "drop")
```

## fecundity

```
fecundity_by_block <- aphid_long %>%
  filter(alate_alive == "Yes") %>%
  group_by(treatment, block, round) %>%
  summarise(mean_fecundity = mean(nymphs, na.rm = TRUE), sd_fecundity = sd(nymphs,
    na.rm = TRUE), n = n(), .groups = "drop")

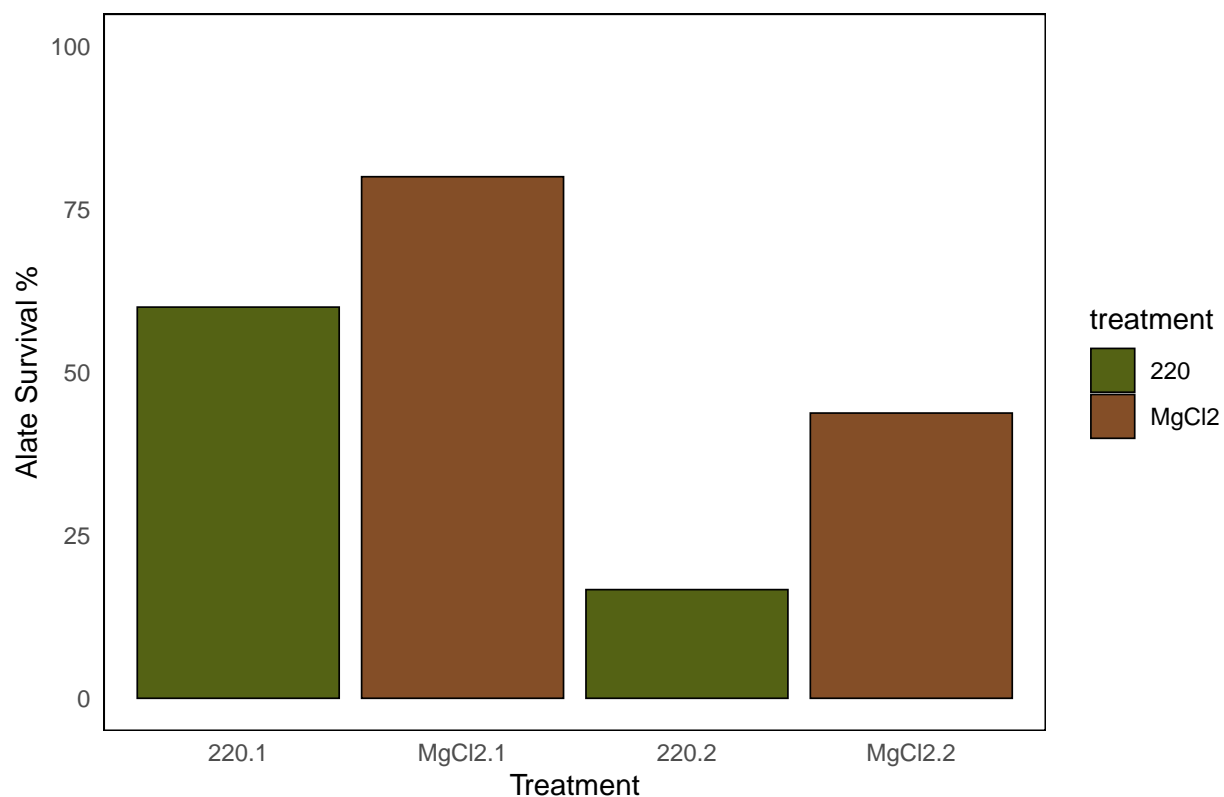
fecundity_by_treatment <- fecundity_by_block %>%
  group_by(treatment, round) %>%
  summarise(mean_nymphs = mean(mean_fecundity), se_nymphs = sd(mean_fecundity)/sqrt(n()),
    .groups = "drop")
```

## Plot aphid survival

```
survival_summary_block2 <- survival_summary %>%
  filter(block == 2)
ggplot(data = survival_summary_block2, aes(x = interaction(treatment, round), y = survival_pct,
  fill = treatment)) + geom_col(color = "black", size = 0.3) + labs(x = "Treatment",
  y = "Alate Survival %", title = "Aphid Survival on #220 or buffer plants - Block 2") +
  scale_fill_manual(values = c("#546214", "#844e27")) + ylim(0, 100) + theme_minimal() +
  theme(legend.position = "right", panel.background = element_rect(fill = "white"),
    panel.grid = element_blank(), panel.grid.minor.x = element_blank(), plot.title = element_text(h
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

## Aphid Survival on #220 or buffer plants – Block 2



## Plot aphid fecundity

```
fecundity_by_block_block2 <- fecundity_by_block %>%
  filter(block == 2)
ggplot(data = fecundity_by_block_block2, aes(x = interaction(treatment, round), y = mean_fecundity,
  fill = treatment)) + geom_col(color = "black", size = 0.3) + geom_errorbar(aes(ymin = mean_fecundity -
  sd_fecundity, ymax = mean_fecundity + sd_fecundity), width = 0.2, color = "black",
  position = position_dodge(width = 0.8)) + labs(x = "Treatment", y = "Nymphs per Alate",
  title = "Aphid Fecundity on #220 or buffer plants - Block 2") + scale_fill_manual(values = c("#54627f",
  "#844e27")) + ylim(0, 50) + theme_minimal() + theme(legend.position = "right",
  panel.background = element_rect(fill = "white"), panel.grid = element_blank(),
  panel.grid.minor.x = element_blank(), plot.title = element_text(hjust = 0.5))
```

# Aphid Fecundity on #220 or buffer plants – Block 2

