## Visualizing data from microplate OD600

#### El Park

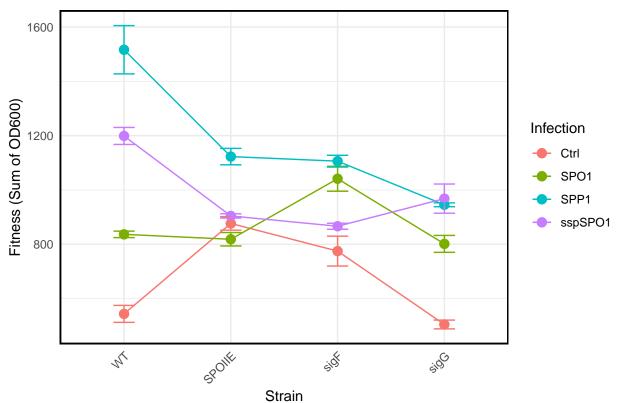
#### 24 March, 2025

Load and wrangle data

```
#load data, change date
data<-read.csv("../data/202502280D600.csv")</pre>
design<-read.csv("../reference/202502280D600Design.csv", header=FALSE)
source("C:/Users/parke/OneDrive - Indiana University/GitHub/ASG-fitness-effects/microplate_fitness_assa
Visualize data
# Order strain categories (if needed)
custom_order <- c("WT", "SPOIIE", "sigF", "sigG") # Adjust as needed</pre>
od.summary <- od.long %>%
  group_by(Media, Strain, Infection) %>%
  summarize(
   Fitness = sum(total.OD, na.rm = TRUE), # Sum total OD600 for fitness
   SE = sd(total.OD, na.rm = TRUE) / sqrt(n()) # Standard error across replicates
## 'summarise()' has grouped output by 'Media', 'Strain'. You can override using
## the '.groups' argument.
od.summary$Strain <- factor(od.summary$Strain, levels = custom_order)
od.summaryLB<-od.summary%>%
  filter(grepl("LB", Media))
od.summaryDSM<-od.summary%>%
  filter(grepl("DSM", Media))
# Plot
LB<-ggplot(od.summaryLB, aes(x = Strain, y = Fitness, color = Infection, group = Infection)) +
  geom_point(size = 3) + # Dots for each infection
  geom_errorbar(aes(ymin = Fitness - SE, ymax = Fitness + SE), width = 0.2) + # Standard error bars
  geom_line() + # Lines connecting points of the same infection
  theme_minimal() +
  labs(title = "Fitness Across Strains and Infections in LB",
       x = "Strain",
       y = "Fitness (Sum of OD600)") +
  theme(axis.text.x = element text(angle = 45, hjust = 1),
   panel.border = element_rect(color = "black", fill = NA, size = 1))
```

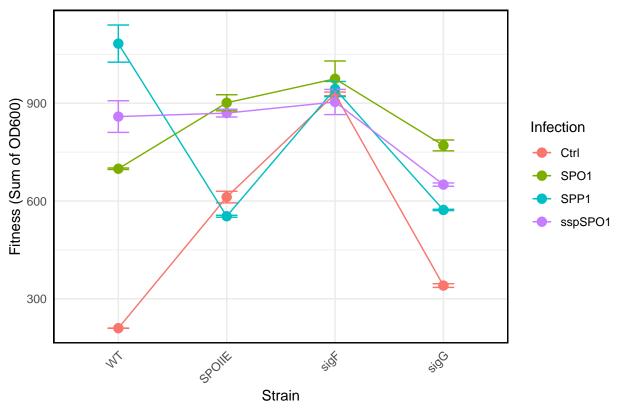
```
## Warning: The 'size' argument of 'element_rect()' is deprecated as of ggplot2 3.4.0.
## i Please use the 'linewidth' argument instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
DSM<-ggplot(od.summaryDSM, aes(x = Strain, y = Fitness, color = Infection, group = Infection)) +
  geom_point(size = 3) + # Dots for each infection
  geom_errorbar(aes(ymin = Fitness - SE, ymax = Fitness + SE), width = 0.2) + # Standard error bars
  geom_line() + # Lines connecting points of the same infection
  theme minimal() +
  labs(title = "Fitness Across Strains and Infections in DSM",
      x = "Strain",
       y = "Fitness (Sum of OD600)") +
   theme(axis.text.x = element_text(angle = 45, hjust = 1),
   panel.border = element rect(color = "black", fill = NA, size = 1))
setwd('../Output')
ggsave("20250228_VisLB.png", plot=LB, width = 10, height = 6, dpi = 300)
ggsave("20250228_VisDSM.png", plot=DSM, width = 10, height = 6, dpi = 300)
```

#### Fitness Across Strains and Infections in LB



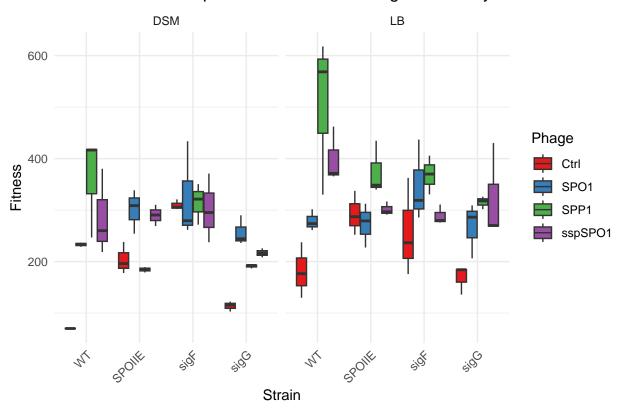
DSM

### Fitness Across Strains and Infections in DSM



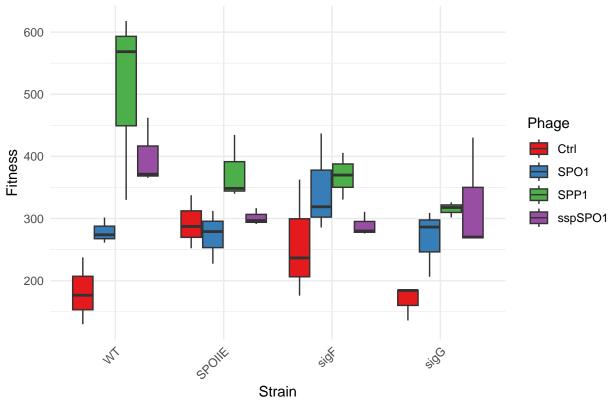
```
#Prep datasets per media
custom order <- c("WT", "SPOIIE", "sigF", "sigG")</pre>
od.long$Strain <- factor(od.long$Strain, levels = custom_order)</pre>
od.longLB<-od.long%>%
 filter(grepl("LB", Media))
od.longDSM<-od.long%>%
  filter(grepl("DSM", Media))
# Plot
All <-ggplot(od.long, aes(x = Strain, y = total.OD, fill = Infection)) +
  geom_boxplot(aes(group = interaction(Strain, Infection)),
               position = position_dodge(width = 0.8)) +
  facet_wrap(~Media)+
  theme_minimal() +
  scale_fill_brewer(palette = "Set1") + # Adjust colors as needed
  labs(title="Fitness Effects of Sporulation Mutants during Infection by Media",x = "Strain", y = "Fitn
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
LBBW<-ggplot(od.longLB, aes(x = Strain, y = total.OD, fill = Infection)) +
  geom_boxplot(aes(group = interaction(Strain, Infection)),
               position = position_dodge(width = 0.8)) +
  theme_minimal() +
  scale_fill_brewer(palette = "Set1") + # Adjust colors as needed
  labs(title="Fitness Effects of Sporulation Mutants during Infection in LB",x = "Strain", y = "Fitness
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```

## Fitness Effects of Sporulation Mutants during Infection by Media



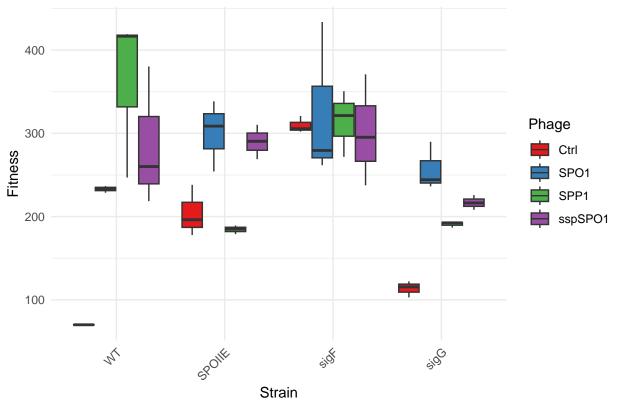
LBBW





DSMBW





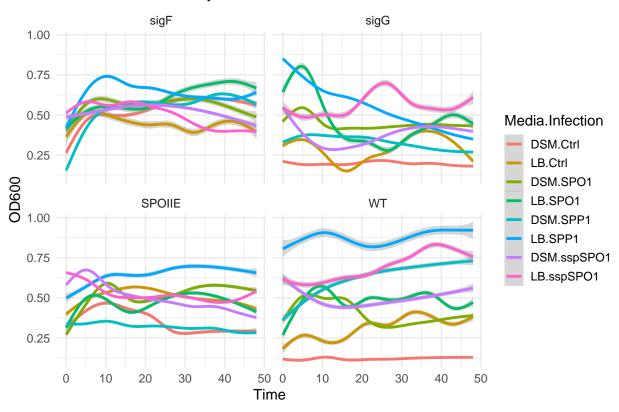
Plot OD for ref

```
#plot and sort by treatment
d<-ggplot(OD.long, aes(x = Time, y = OD600, colour = interaction(Media, Infection))) +
    #geom_line() +
    theme_minimal() + geom_smooth()+
    labs(title = "OD600 over Time by Strain", x = "Time", y = "OD600", colour = "Media.Infection") +
    theme(legend.key.size = unit(0.5, 'cm'), legend.position = "right")+
    facet_wrap(~Strain)
ggsave("20250228_Strains.png", plot = d, width = 6, height = 4, dpi = 300)

## 'geom_smooth()' using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'
print(d)</pre>
```

## 'geom\_smooth()' using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'

### OD600 over Time by Strain



```
#plot and sort by infection
s <- ggplot(OD.long, aes(x = Time, y = OD600, colour = interaction(Strain, Media))) +
    theme_minimal() +
    geom_smooth() +
    labs(title = "OD600 over Time by Treatment", x = "Time", y = "OD600", colour = "Strain") +
    theme(legend.key.size = unit(0.5, 'cm'), legend.position = "right") +
    facet_wrap(~Infection)
ggsave("20250228_Infection.png", plot = s, width = 6, height = 4, dpi = 300)

## 'geom_smooth()' using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'
print(s)</pre>
```

## 'geom\_smooth()' using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'

# OD600 over Time by Treatment

