RC 159-5: Evaluation of three differents to coltrol red slime

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Introduction

Tissue culture tube with callus in Bldg. 001, Rm. 331 after six months are beginning to be contaminated with a red slime. Consequently, it became imperitive that we find a way to control the bacteria. Evidently PPm wasn't working. Maybe at a higher concenation. A series of experiments were planned to evaluate different antibiotics that we have used in the past ro control the bacteria.

summary

The following is a summary of the treatments (antibiotics and no antibiotics) by bacterial concentration.

```
## # A tibble: 5 x 3
## # Groups:   Trt [2]
##   Trt          concBac Total_mean
##   <fct>        <fct>        <dbl>
## 1 antibiotic   -4            17.2
## 2 antibiotic   -3            81.2
## 3 noantibiotic -4            26.8
## 4 noantibiotic -3            90
## 5 noantibiotic 0              0
```

analysi of variance for total area

```
##
## Call:
## lm(formula = count ~ Trt + concBac + Trt * concBac, data = RC159_5Data,
##     na.action = na.omit)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -28.000  -3.875   0.000   3.000  33.000
##
## Coefficients: (1 not defined because of singularities)
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  17.250      6.543   2.637   0.0187 *
## Trtnoantibiotic               9.500      9.252   1.027   0.3208
## concBac-3                    64.000      9.252   6.917 4.92e-06 ***
## concBac0                    -26.750      9.252  -2.891   0.0112 *
## Trtnoantibiotic:concBac-3    -0.750     13.085  -0.057   0.9550
## Trtnoantibiotic:concBac0         NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 13.08 on 15 degrees of freedom
## Multiple R-squared:  0.9094, Adjusted R-squared:  0.8853
```

```
## F-statistic: 37.66 on 4 and 15 DF,  p-value: 1.175e-07
```

```
## Note: model has aliased coefficients
##       sums of squares computed by model comparison
```

```
## Anova Table (Type II tests)
##
## Response: count
##              Sum Sq Df F value    Pr(>F)
## Trt           333.1  1  1.9453    0.1834
## concBac     25279.6  2 73.8234 1.723e-08 ***
## Trt:concBac     0.6  1  0.0033    0.9550
## Residuals    2568.2 15
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

pair wise t test diff vs PlantId

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  RC159_5Data$count and RC159_5Data$Trt
##
##              antibiotic
## noantibiotic 0.57
##
## P value adjustment method: holm
```

summary

```
## `summarise()` regrouping output by 'Trt' (override with `.groups` argument)
```

```
## # A tibble: 4 x 3
## # Groups:   Trt [2]
##   Trt          concBac Total_mean
##   <fct>        <fct>        <dbl>
## 1 antibiotic   -4            17.2
## 2 antibiotic   -3            81.2
## 3 noantibiotic -4            26.8
## 4 noantibiotic -3            90
```

analysi of variance for colony count

```
##
## Call:
## lm(formula = count ~ Trt + concBac + Trt * concBac, data = RC159_5Data,
##     na.action = na.omit)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -28.000  -4.625  -2.125   4.750  33.000
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)                17.250      7.315   2.358   0.0362 *
## Trtnoantibiotic             9.500     10.345   0.918   0.3765
```

```
## concBac-3                   64.000     10.345   6.187 4.68e-05 ***
## Trtnoantibiotic:concBac-3   -0.750     14.630  -0.051   0.9600
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.63 on 12 degrees of freedom
## Multiple R-squared:  0.8655, Adjusted R-squared:  0.8319
## F-statistic: 25.74 on 3 and 12 DF,  p-value: 1.633e-05
```

```
## Anova Table (Type II tests)
##
## Response: count
##              Sum Sq Df F value   Pr(>F)
## Trt           333.1  1  1.5562    0.236
## concBac     16192.6  1 75.6588 1.58e-06 ***
## Trt:concBac     0.6  1  0.0026    0.960
## Residuals    2568.3 12
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

pair wise t test count vs Trt

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  RC159_5Data$count and RC159_5Data$Trt
##
##              antibiotic
## noantibiotic 0.63
##
## P value adjustment method: holm
```

pair wise t test count vs concBac

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  RC159_5Data$count and RC159_5Data$concBac
##
##    -4
## -3 4.2e-07
##
## P value adjustment method: holm
```