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| title: “RC 159-5.1: 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 two new 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: 6 x 3  
## # Groups: Trt [3]  
## Trt concBac Total\_mean  
## <fct> <fct> <dbl>  
## 1 with anti. -4 18   
## 2 with anti. -3 57.2  
## 3 without anti. -4 22.7  
## 4 without anti. -3 181   
## 5 without anti. 0 17   
## 6 without bac. 0 1.5

### 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   
## -83.000 -7.667 -0.750 4.125 162.000   
##   
## Coefficients: (3 not defined because of singularities)  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 18.000 26.958 0.668 0.5152   
## Trtwithout anti. 4.667 41.179 0.113 0.9114   
## Trtwithout bac. -10.833 73.002 -0.148 0.8841   
## concBac-3 39.250 38.124 1.030 0.3207   
## concBac0 -5.667 62.256 -0.091 0.9288   
## Trtwithout anti.:concBac-3 119.083 56.117 2.122 0.0522 .  
## Trtwithout bac.:concBac-3 NA NA NA NA   
## Trtwithout anti.:concBac0 NA NA NA NA   
## Trtwithout bac.:concBac0 NA NA NA NA   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 53.92 on 14 degrees of freedom  
## Multiple R-squared: 0.6763, Adjusted R-squared: 0.5607   
## F-statistic: 5.849 on 5 and 14 DF, p-value: 0.004029

## 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 17768 2 3.0561 0.079190 .   
## concBac 41055 2 7.0617 0.007576 \*\*  
## Trt:concBac 13090 1 4.5031 0.052158 .   
## Residuals 40696 14   
## ---  
## 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   
##   
## with anti. without anti.  
## without anti. 0.21 -   
## without bac. 0.44 0.13   
##   
## 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 with anti. -4 18   
## 2 with anti. -3 57.2  
## 3 without anti. -4 22.7  
## 4 without anti. -3 181

### 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   
## -83.000 -10.958 0.000 5.167 162.000   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 18.000 30.402 0.592 0.5658   
## Trtwithout anti. 4.667 46.440 0.100 0.9218   
## concBac-3 39.250 42.995 0.913 0.3809   
## Trtwithout anti.:concBac-3 119.083 63.288 1.882 0.0866 .  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 60.8 on 11 degrees of freedom  
## Multiple R-squared: 0.6235, Adjusted R-squared: 0.5208   
## F-statistic: 6.072 on 3 and 11 DF, p-value: 0.01081

## Anova Table (Type II tests)  
##   
## Response: count  
## Sum Sq Df F value Pr(>F)   
## Trt 17575 1 4.7537 0.05184 .  
## concBac 32967 1 8.9168 0.01238 \*  
## Trt:concBac 13090 1 3.5405 0.08660 .  
## Residuals 40669 11   
## ---  
## 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   
##   
## with anti.  
## without anti. 0.097   
##   
## 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 0.023  
##   
## P value adjustment method: holm