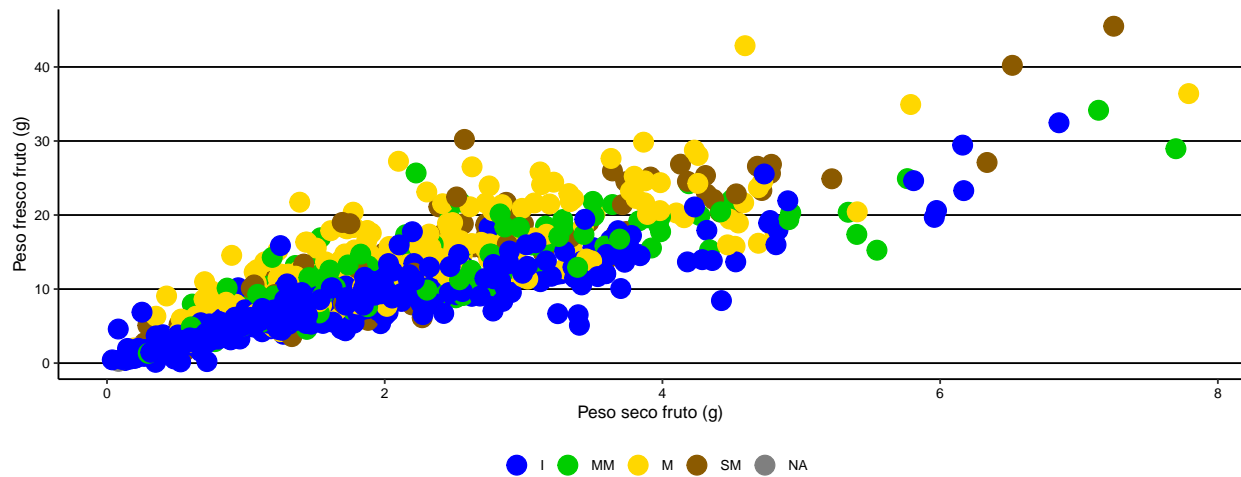


## Peso seco

### Carga de datos y conversión de variables

### Gráfico de dispersión



### Se ajusta el modelo

```
##  
## Call:  
## lm(formula = psf ~ pff, data = datospeso)  
##  
## Coefficients:  
## (Intercept)      pff  
##      0.1749      0.1657
```

### Modelo

```
##  
## Call:  
## lm(formula = psf ~ pff, data = datospeso)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max   
## -2.68401 -0.26222 -0.07354  0.22012  2.85114   
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)      
## (Intercept)  0.17491    0.03283   5.328 1.19e-07 ***  
## pff          0.16571    0.00281  58.983 < 2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.6162 on 1164 degrees of freedom
```

```
## Multiple R-squared:  0.7493, Adjusted R-squared:  0.7491
## F-statistic:  3479 on 1 and 1164 DF,  p-value: < 2.2e-16
```

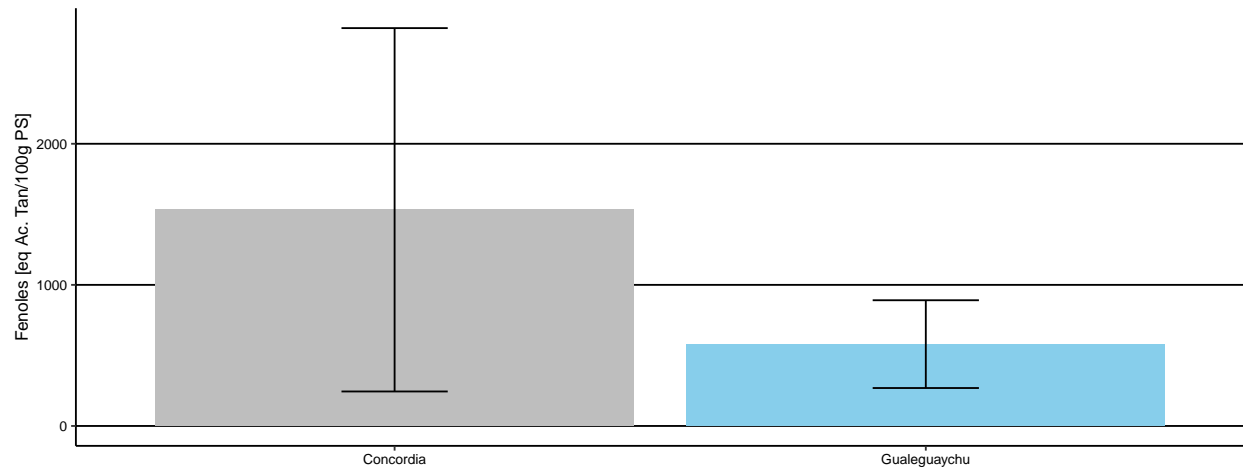
## Análisis univariado

### Fenoles

#### Tabla descriptiva por población

```
## # A tibble: 2 x 4
##   site          n Mean    sd
##   <fct>      <int> <dbl> <dbl>
## 1 Concordia      64 1532. 1288.
## 2 Gualeguaychu   38  580.  311.
```

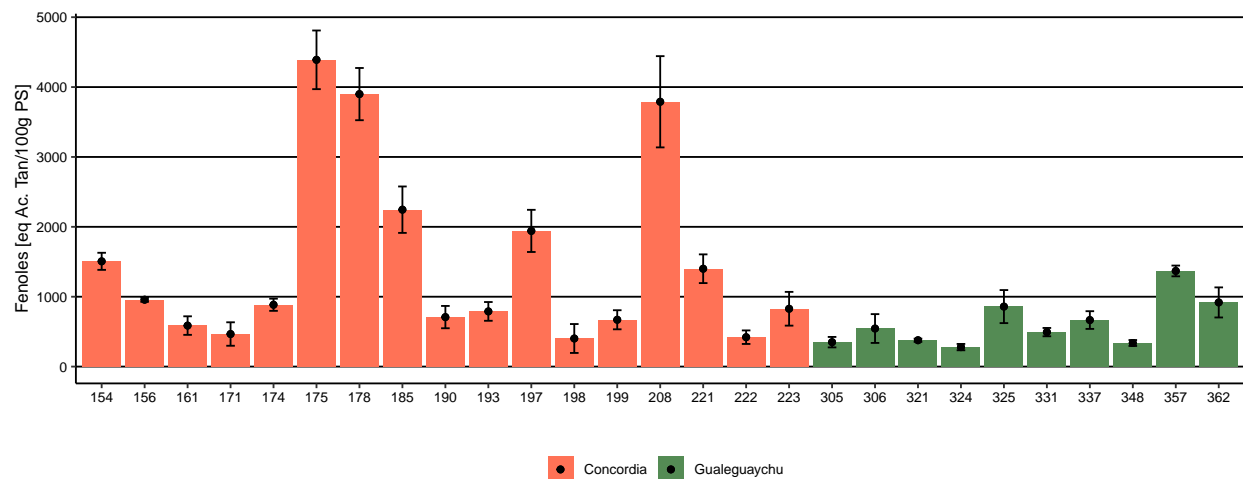
#### Gráfico por población



#### Tabla descriptiva por fenotipo

```
## # A tibble: 27 x 5
## # Groups:   site [2]
##   site    phenotype      n Mean    sd
##   <fct>    <fct>    <int> <dbl> <dbl>
## 1 Concordia 154      4 1507. 122.
## 2 Concordia 156      4  957.  29.8
## 3 Concordia 161      4  587.  133.
## 4 Concordia 171      4  466.  168.
## 5 Concordia 174      3  885.   87.0
## 6 Concordia 175      4 4390. 420.
## 7 Concordia 178      4 3900. 374.
## 8 Concordia 185      4 2245. 332.
## 9 Concordia 190      4  708.  160.
## 10 Concordia 193      4  790.  134.
## # i 17 more rows
```

## Gráficos por fenotipo



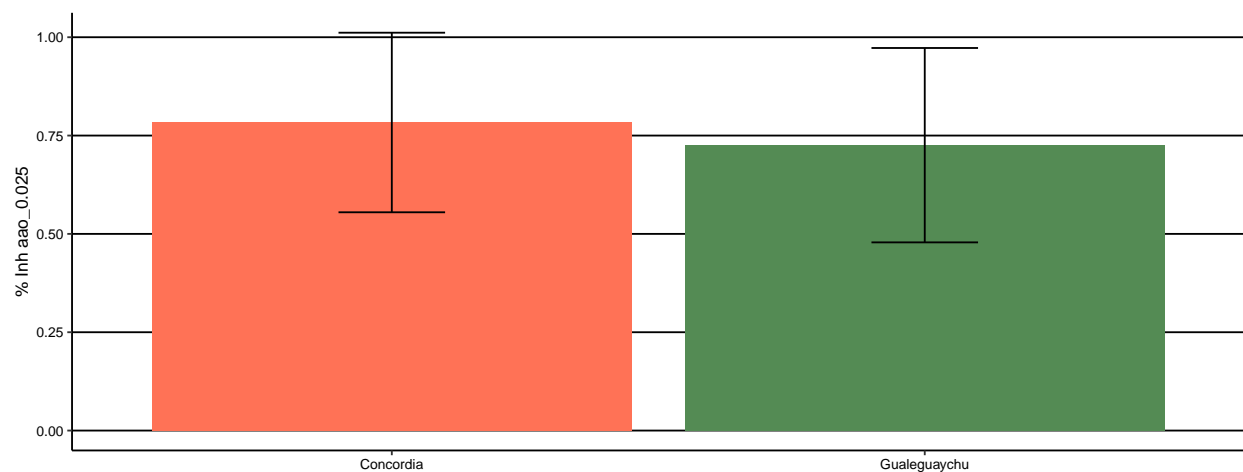
## AAO

0.025

####Tabla descriptiva por población

```
## # A tibble: 2 x 4
##   site      n Mean  sd
##   <fct>    <int> <dbl> <dbl>
## 1 Concordia    64 0.783 0.228
## 2 Gualeguaychu  38 0.726 0.247
```

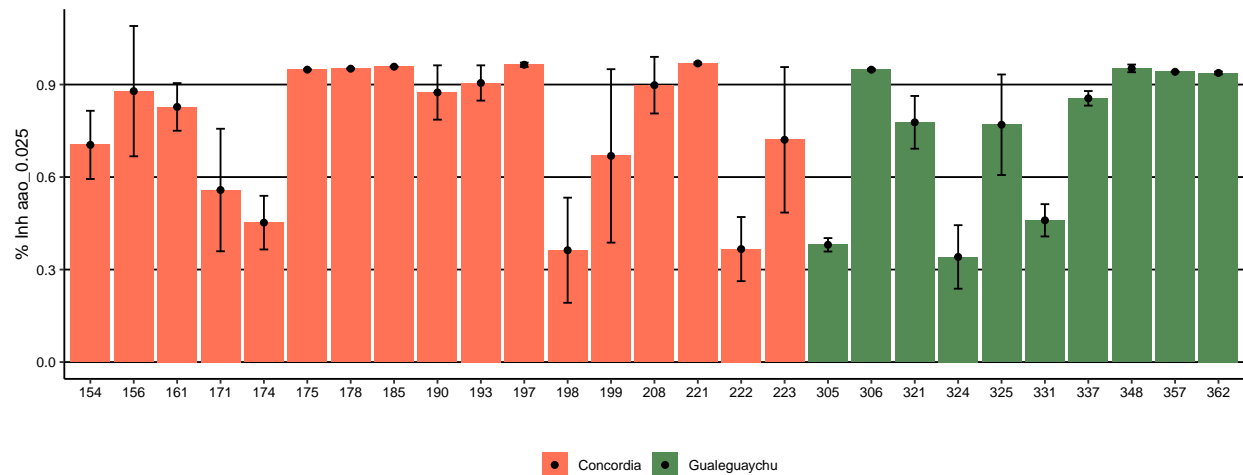
## Gráfico por población



## Tabla descriptiva por fenotipo

```
## # A tibble: 27 x 5
## # Groups:   site [2]
##   site      phenotype    n Mean      sd
##   <fct>    <fct>    <int> <dbl>  <dbl>
## 1 Concordia 154      4 0.704 0.111
## 2 Concordia 156      4 0.879 0.211
## 3 Concordia 161      4 0.827 0.0772
## 4 Concordia 171      4 0.558 0.199
## 5 Concordia 174      3 0.452 0.0870
## 6 Concordia 175      4 0.948 0.00187
## 7 Concordia 178      4 0.951 0.00160
## 8 Concordia 185      4 0.958 0.00114
## 9 Concordia 190      4 0.874 0.0881
## 10 Concordia 193      4 0.905 0.0572
## # i 17 more rows
```

## Gráficos por fenotipo

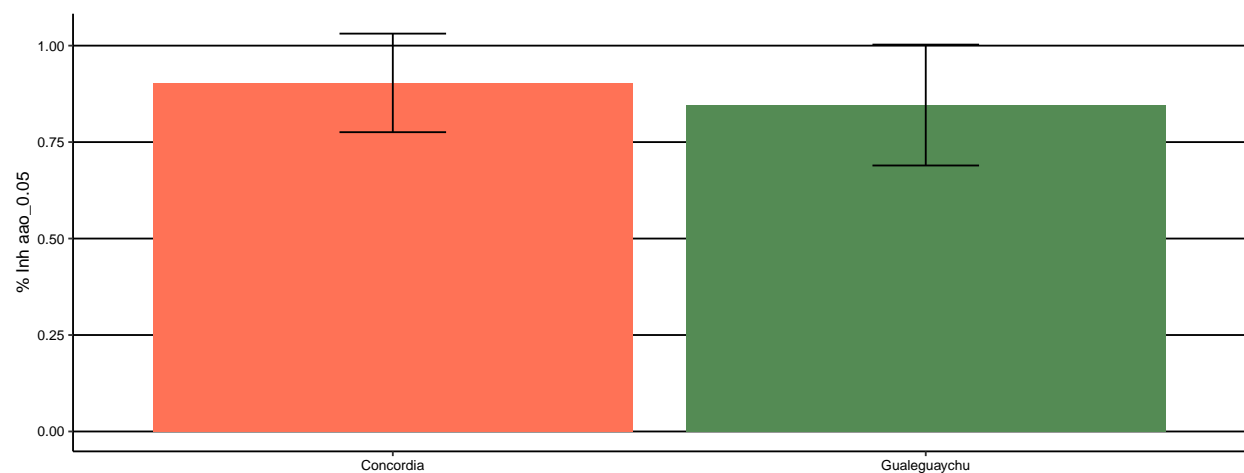


0.050

## Tabla descriptiva por población

```
## # A tibble: 2 x 4
##   site      n Mean      sd
##   <fct>    <int> <dbl>  <dbl>
## 1 Concordia    63 0.903 0.128
## 2 Gualeguaychu  38 0.846 0.157
```

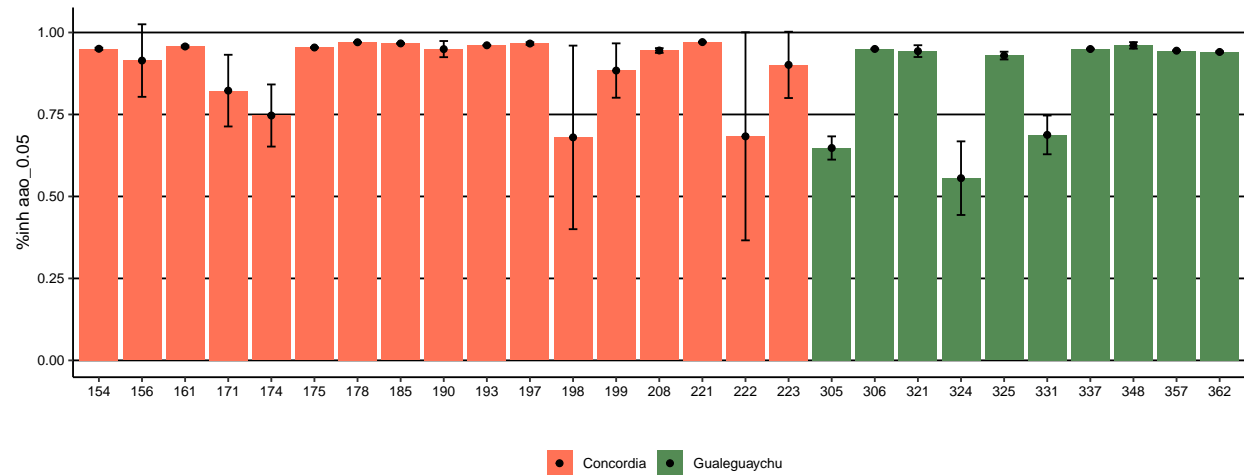
## Gráfico por población



### Tabla descriptiva por fenotipo

```
## # A tibble: 27 x 5
## # Groups:   site [2]
##   site    phenotype    n  Mean    sd
##   <fct>    <fct>    <int> <dbl>  <dbl>
## 1 Concordia 154      4 0.950 0.00315
## 2 Concordia 156      4 0.914 0.111
## 3 Concordia 161      4 0.957 0.00312
## 4 Concordia 171      4 0.823 0.109
## 5 Concordia 174      3 0.747 0.0947
## 6 Concordia 175      4 0.954 0.00145
## 7 Concordia 178      4 0.970 0.000801
## 8 Concordia 185      3 0.967 0.00139
## 9 Concordia 190      4 0.949 0.0246
## 10 Concordia 193      4 0.961 0.00108
## # i 17 more rows
```

### Gráficos por fenotipo

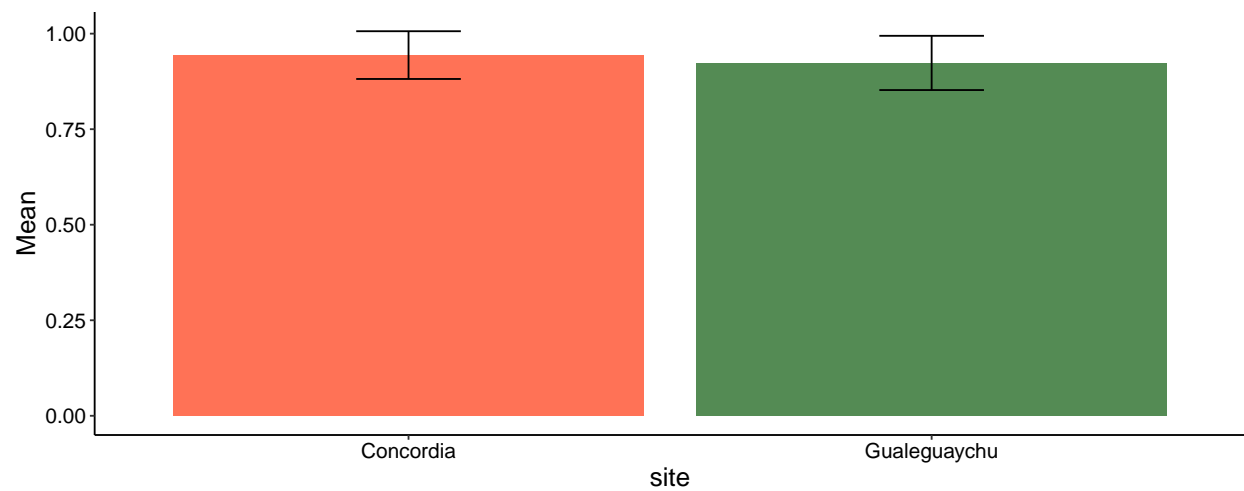


0.100

### Tabla descriptiva por población

```
## # A tibble: 2 x 4
##   site          n Mean    sd
##   <fct>      <int> <dbl> <dbl>
## 1 Concordia     63 0.944 0.0625
## 2 Gualeguaychu  38 0.923 0.0710
```

### Gráfico por población

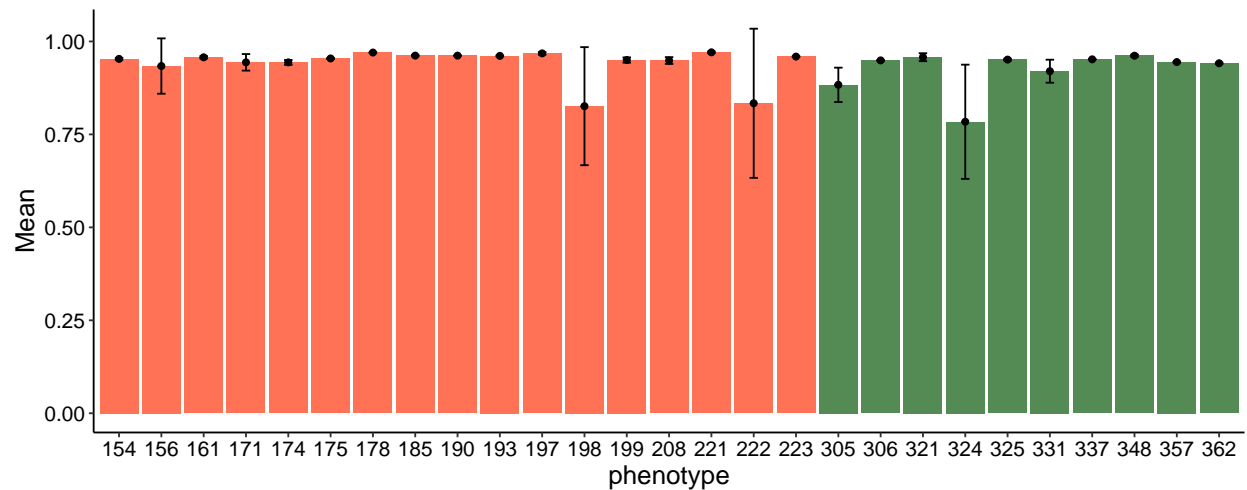


### Tabla descriptiva por fenotipo

```
## # A tibble: 27 x 5
## # Groups:   site [2]
##   site    phenotype      n Mean    sd
```

```
##      <fct>      <fct>      <int> <dbl>      <dbl>
##  1 Concordia 154          4 0.953 0.00249
##  2 Concordia 156          4 0.934 0.0744
##  3 Concordia 161          4 0.957 0.00312
##  4 Concordia 171          4 0.944 0.0222
##  5 Concordia 174          3 0.944 0.00650
##  6 Concordia 175          4 0.954 0.00145
##  7 Concordia 178          4 0.970 0.000801
##  8 Concordia 185          3 0.962 0.00182
##  9 Concordia 190          4 0.962 0.000858
## 10 Concordia 193          4 0.961 0.00106
## # i 17 more rows
```

## Gráficos por fenotipo

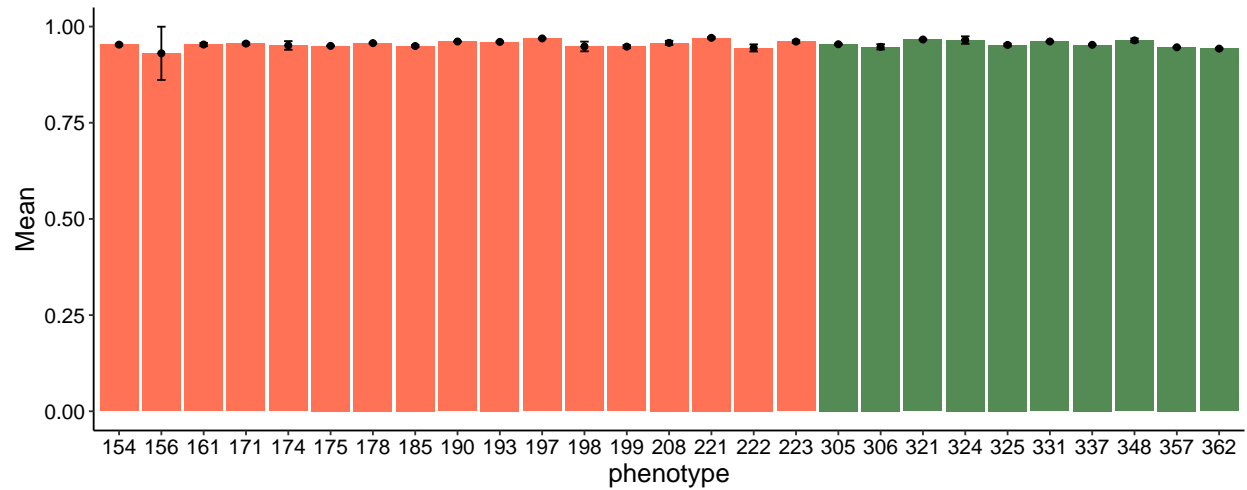


0.250

####Tabla descriptiva por población

```
## # A tibble: 2 x 4
##   site      n Mean    sd
##   <fct>  <int> <dbl>  <dbl>
## 1 Concordia    63 0.954 0.0184
## 2 Gualeguaychu  38 0.956 0.00901
```

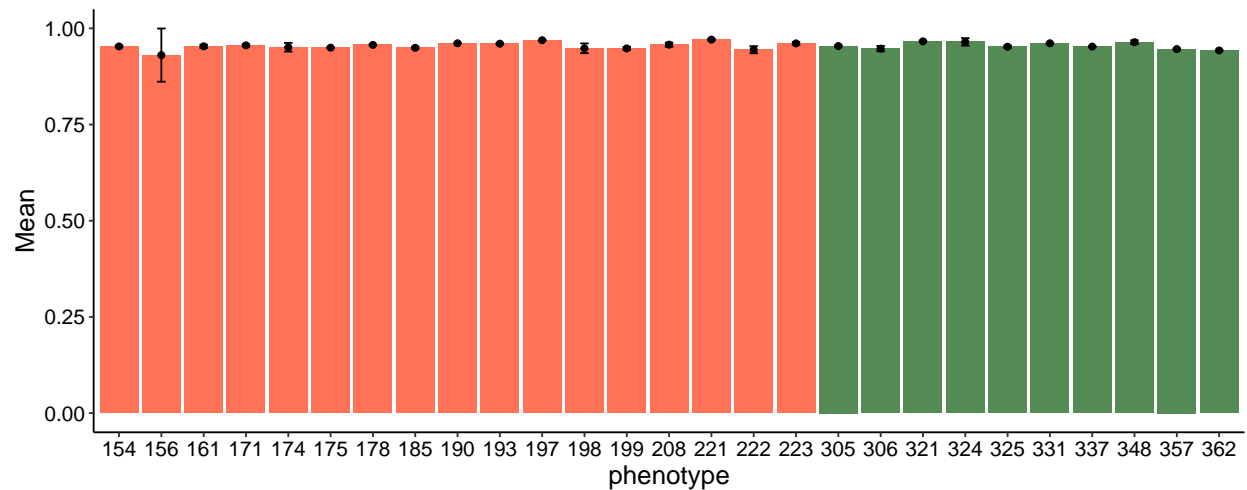
## Gráfico por población



### Tabla descriptiva por fenotipo

```
## # A tibble: 27 x 5
## # Groups:   site [2]
##   site    phenotype     n Mean      sd
##   <fct>    <fct>   <int> <dbl>   <dbl>
## 1 Concordia 154         4 0.953 0.00249
## 2 Concordia 156         4 0.930 0.0692
## 3 Concordia 161         4 0.953 0.00417
## 4 Concordia 171         4 0.956 0.00280
## 5 Concordia 174         3 0.951 0.0112
## 6 Concordia 175         4 0.950 0.000922
## 7 Concordia 178         4 0.957 0.00113
## 8 Concordia 185         3 0.949 0.00277
## 9 Concordia 190         4 0.961 0.000429
## 10 Concordia 193        4 0.960 0.00145
## # i 17 more rows
```

### Gráficos por fenotipo



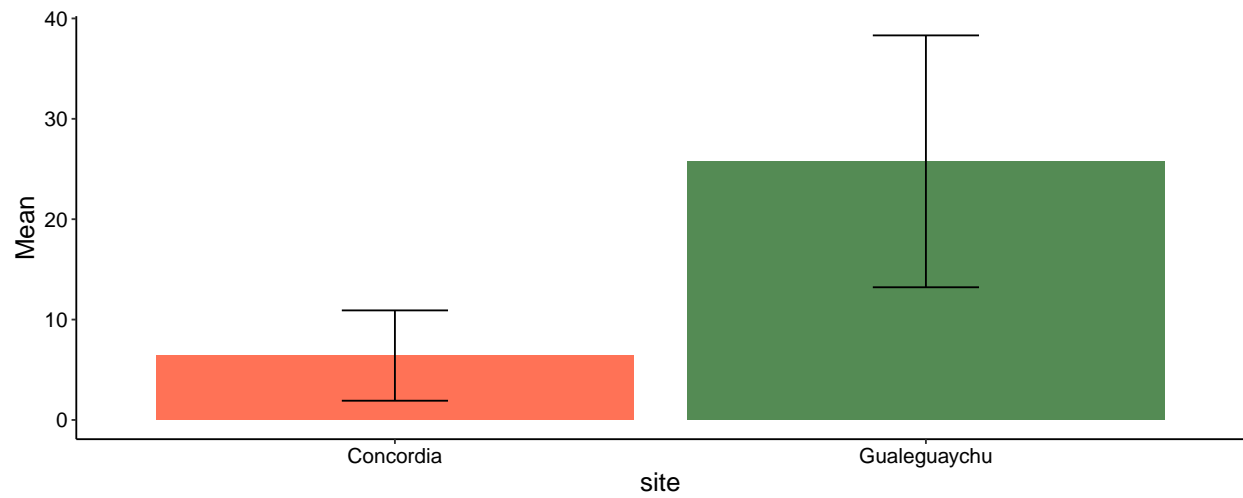


## Clorofila a

### Tabla descriptiva por población

```
## # A tibble: 2 x 4
##   site      n Mean  sd
##   <fct>    <int> <dbl> <dbl>
## 1 Concordia     63  6.42  4.50
## 2 Gualeguaychu   37 25.8  12.5
```

### Gráfico por población



### Tabla resumen por fenotipo

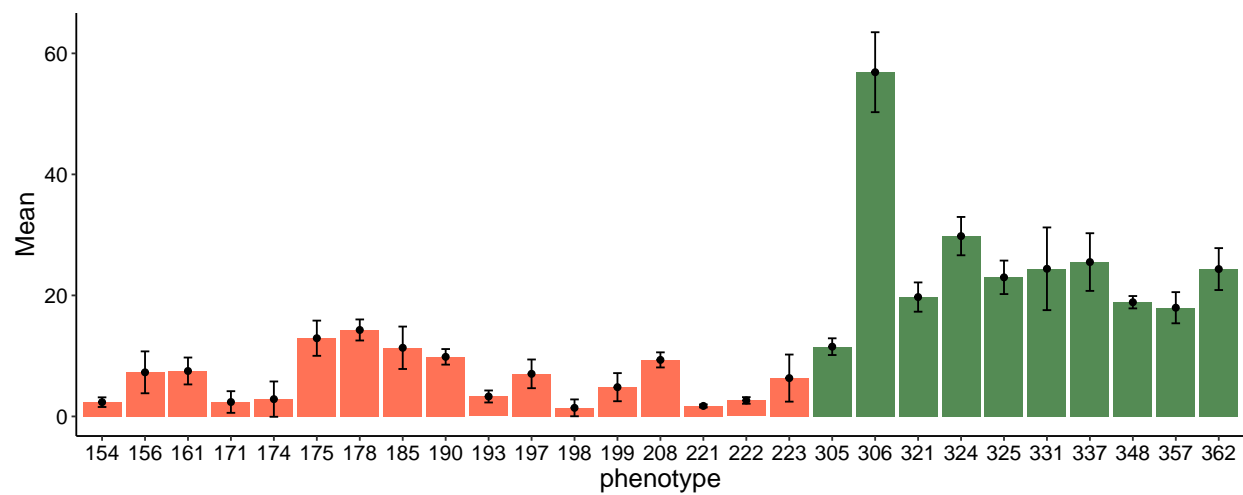
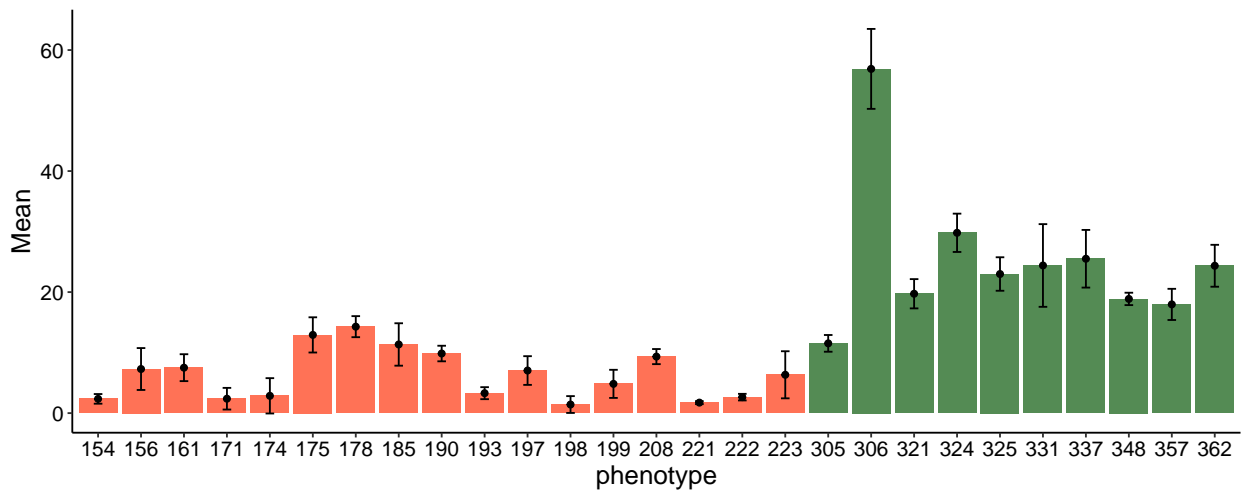


Gráfico resumen por fenotipo



Clorofila b

Tabla descriptiva por población

## NULL

Gráfico por población

## NULL

Tabla resumen por fenotipo

## NULL

Gráfico resumen por fenotipo

## NULL

Carotenoides

Tabla descriptiva por población

```
## # A tibble: 2 x 4
##   site          n Mean    sd
##   <fct>      <int> <dbl> <dbl>
## 1 Concordia     63  15.5  6.32
## 2 Gualeguaychu  37  15.4  4.64
```

Gráfico por población

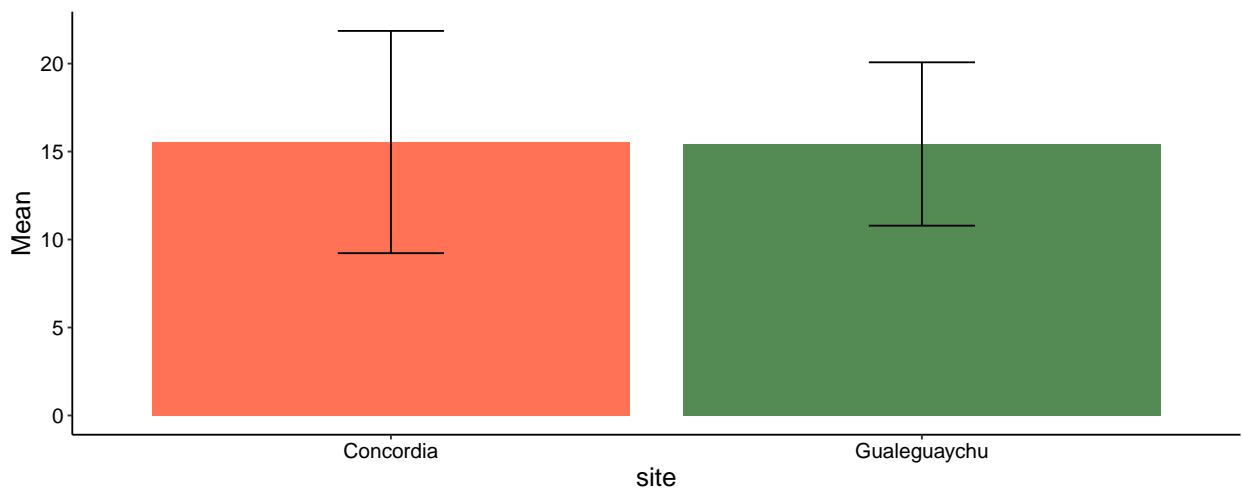
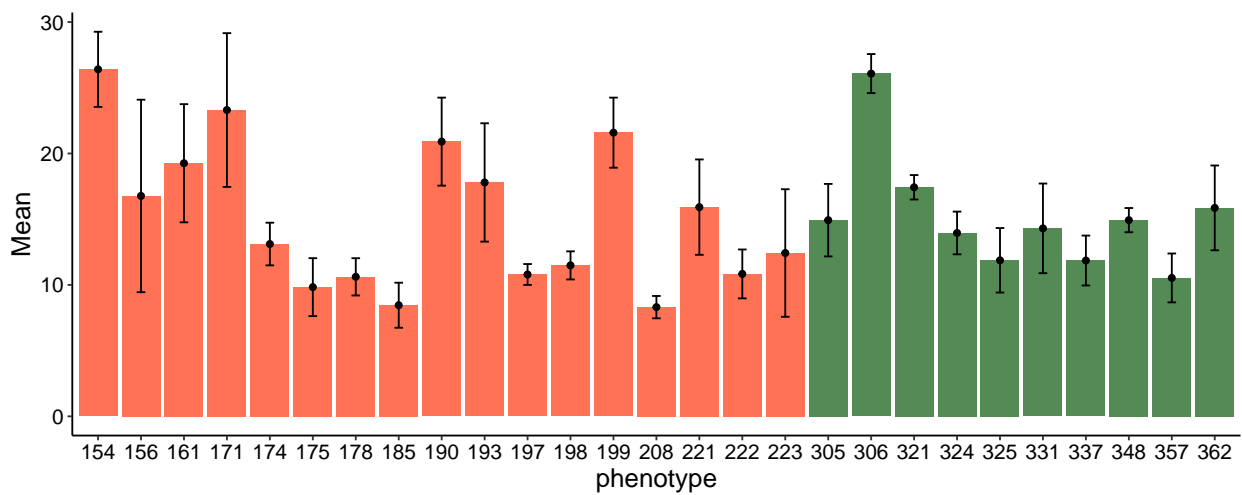
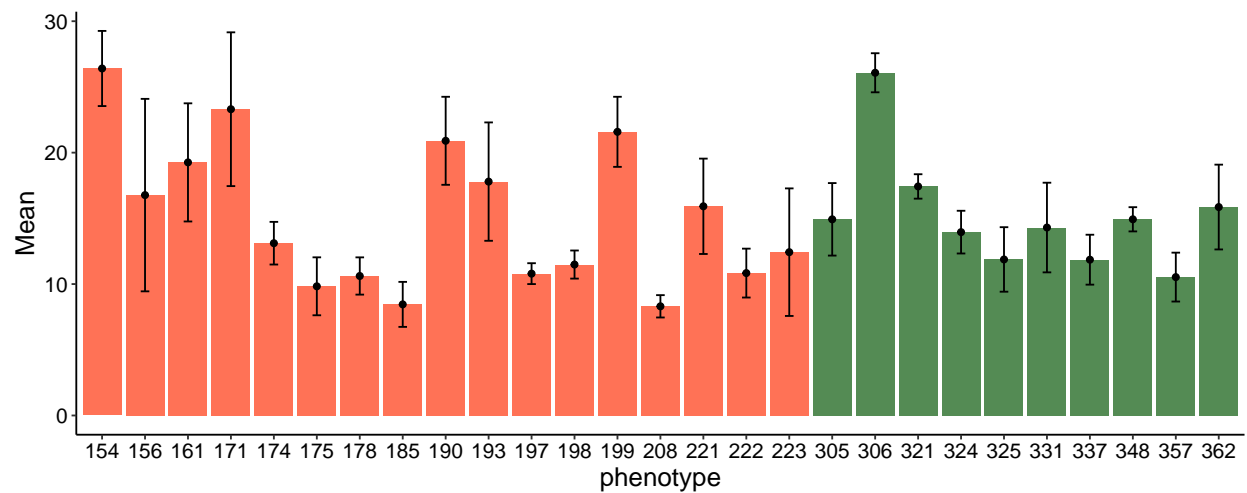


Tabla resumen por fenotipo



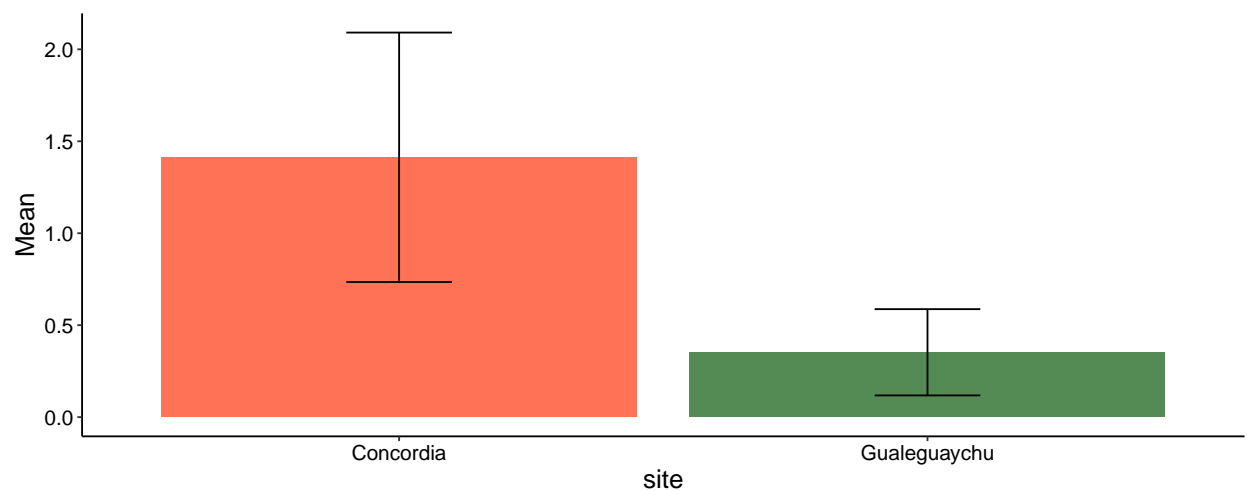
## Gráfico resumen por fenotipo



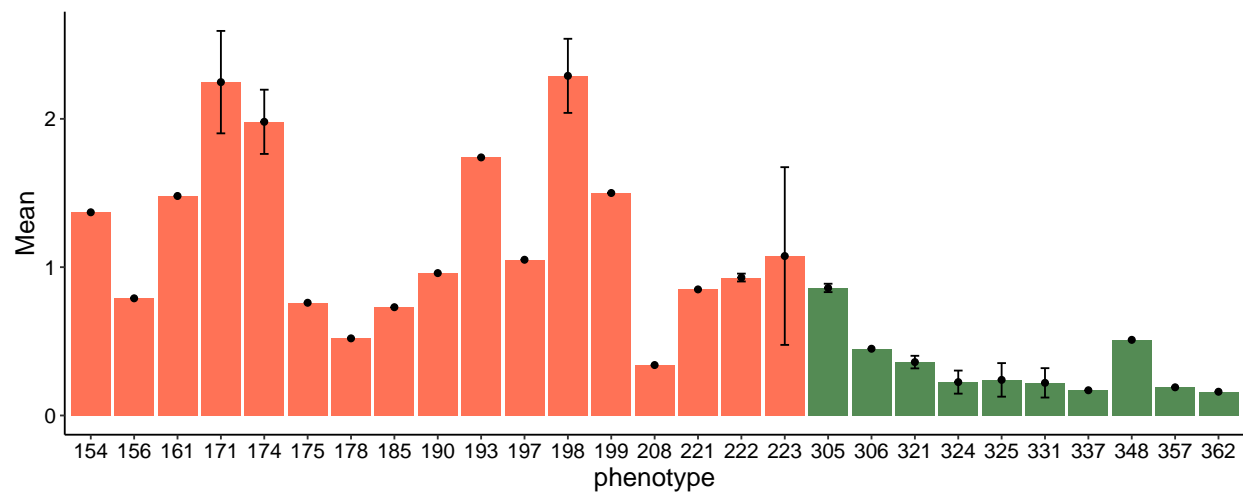
## Acidez Total Titulable (ATT)

```
## # A tibble: 2 x 4
##   site          n Mean    sd
##   <fct>      <int> <dbl> <dbl>
## 1 Concordia     29  1.41  0.678
## 2 Gualeguaychu  15  0.353 0.235
```

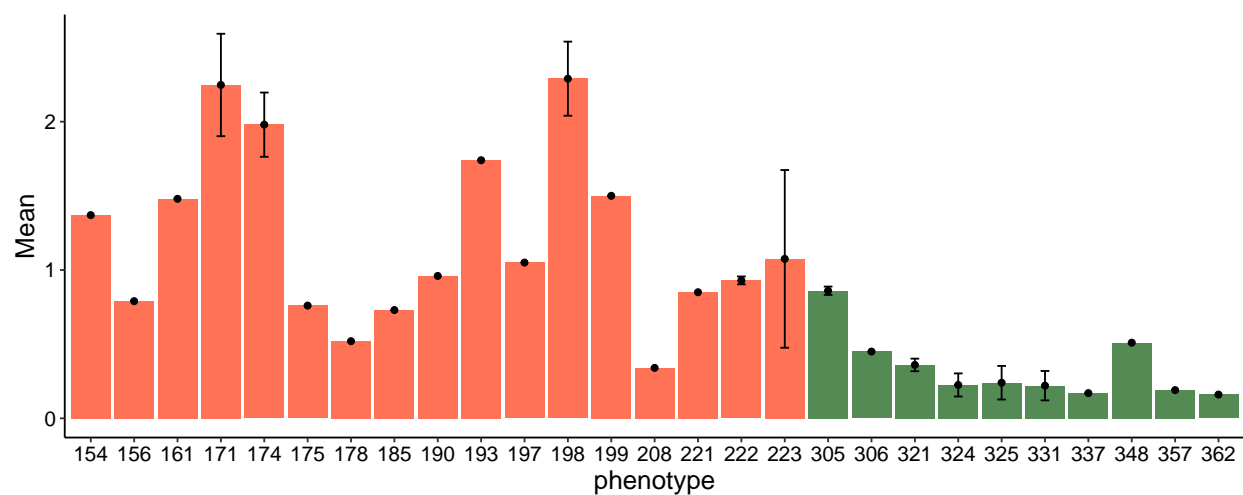
## Gráfico por población



## Tabla resumen por fenotipo



## Gráfico resumen por fenotipo



## Sólidos solubles

### Tabla descriptiva por población

```
## # A tibble: 2 x 4
##   site      n Mean  sd
##   <fct>    <int> <dbl> <dbl>
## 1 Concordia    29  9.58  2.15
## 2 Gualeguaychu 15  6.69  1.21
```

Gráfico por población

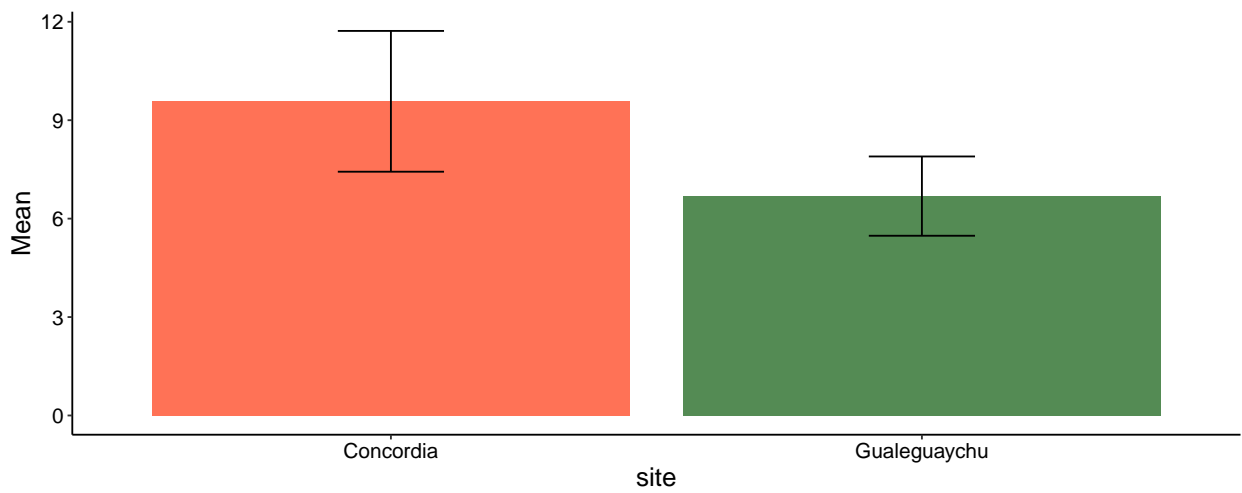
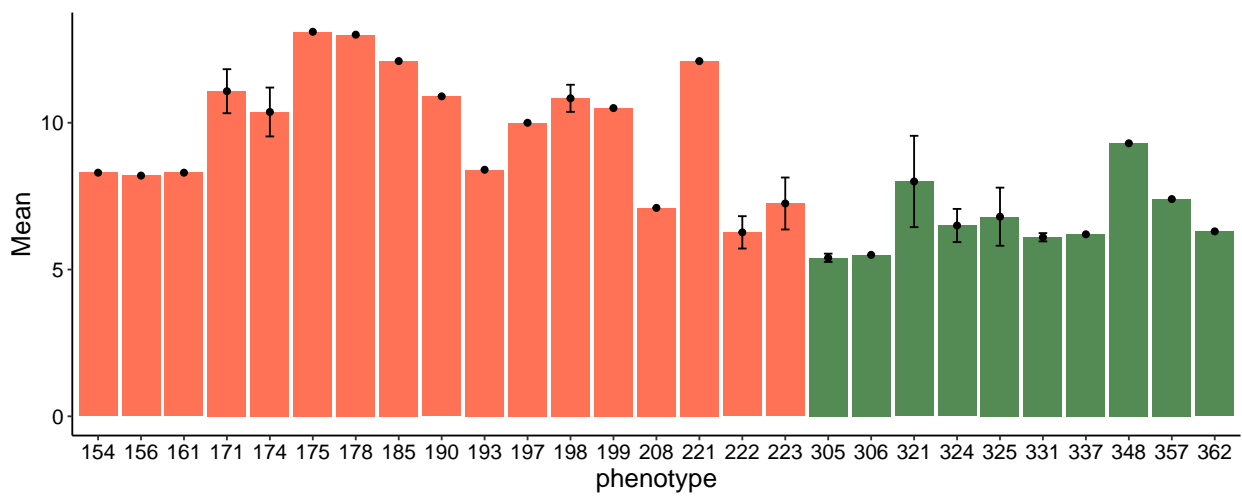
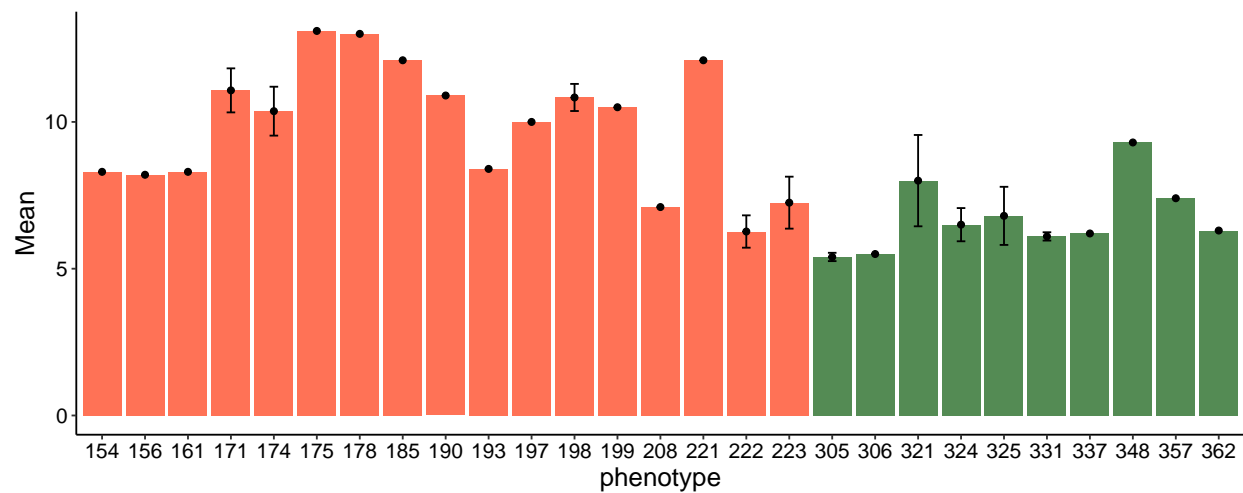


Tabla resumen por fenotipo



## Gráfico resumen por fenotipo



## Relación ATT y SS

### Tabla descriptiva por población

```
## # A tibble: 2 x 4
##   site      n  Mean    sd
##   <fct>    <int> <dbl> <dbl>
## 1 Concordia    29 0.148 0.0621
## 2 Gualeguaychu 15 0.0557 0.0450
```

### Gráfico por población

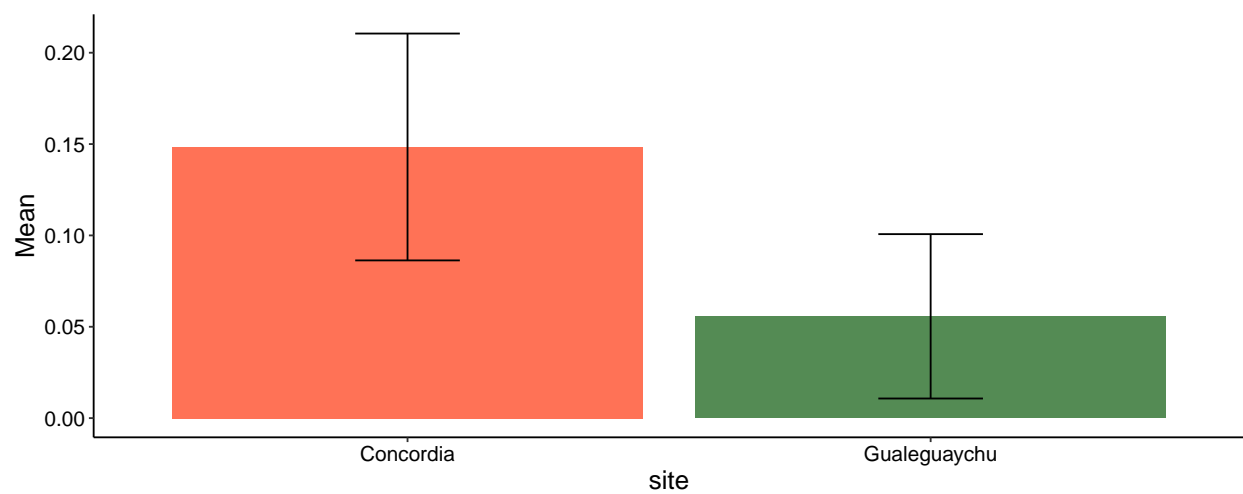


Tabla resumen por fenotipo

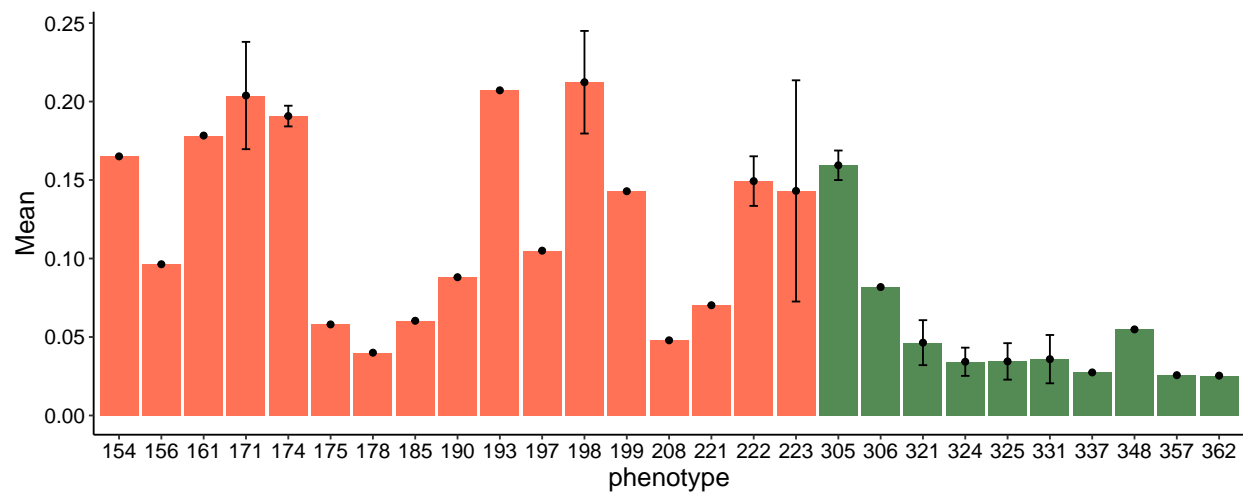
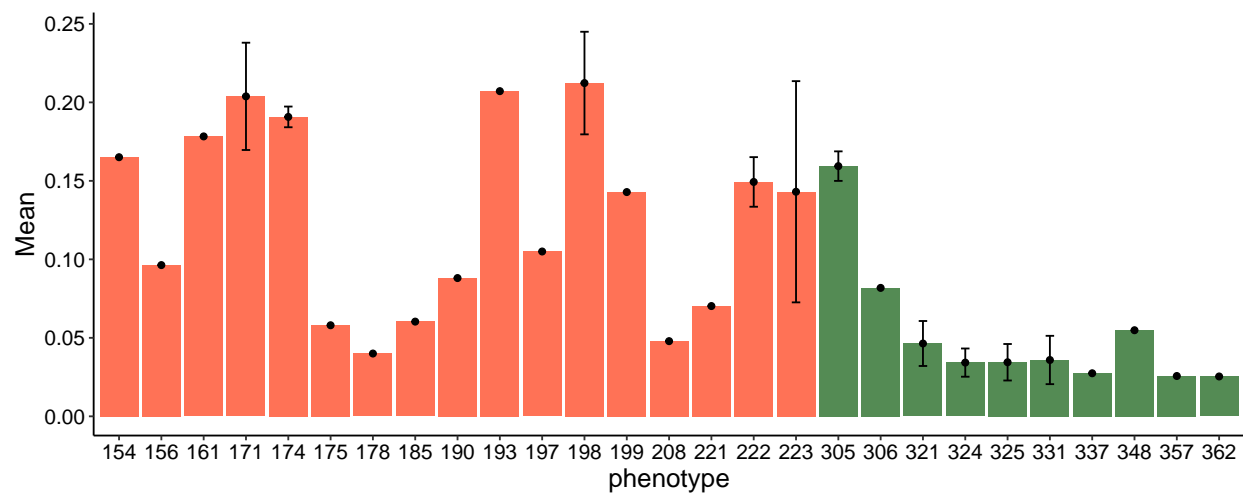
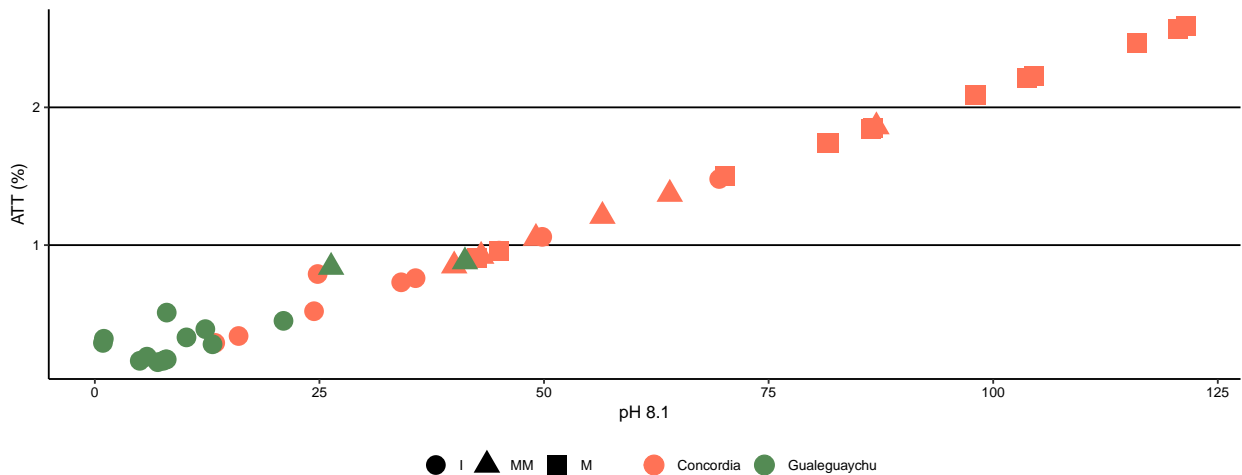
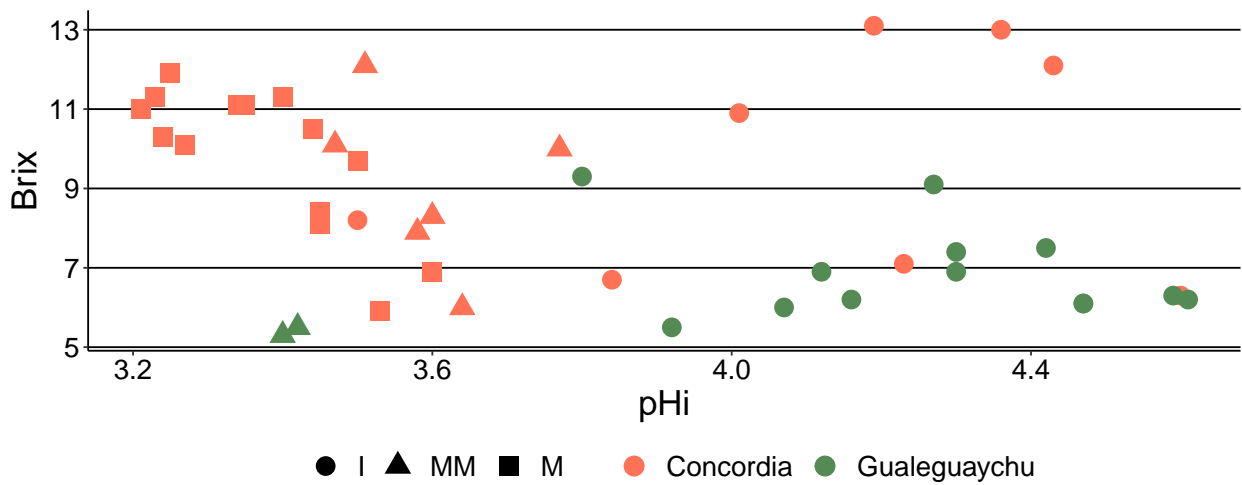
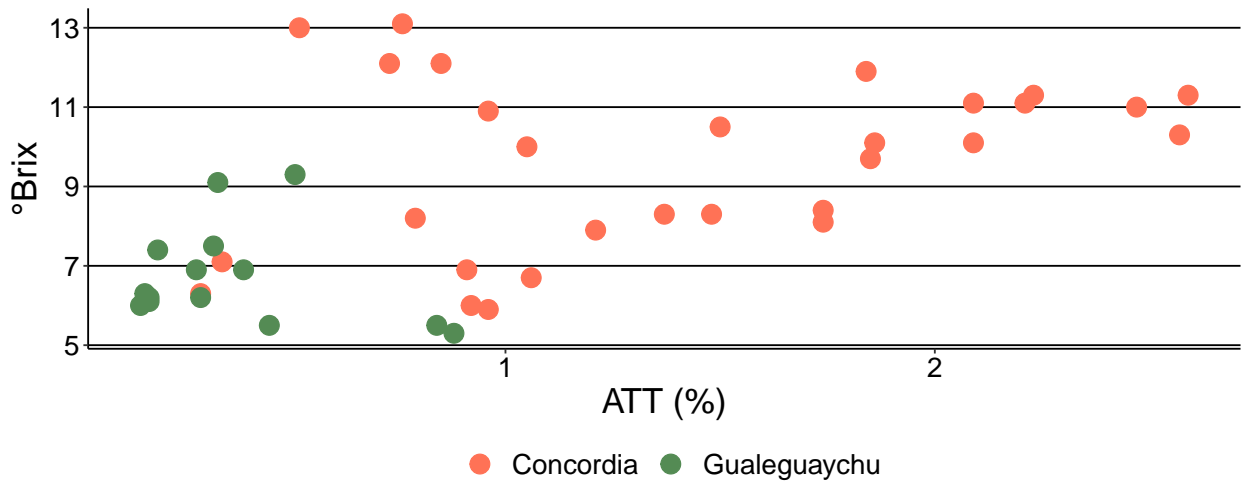


Gráfico resumen por fenotipo





Dispersión Acidez y Sólidos Solubles

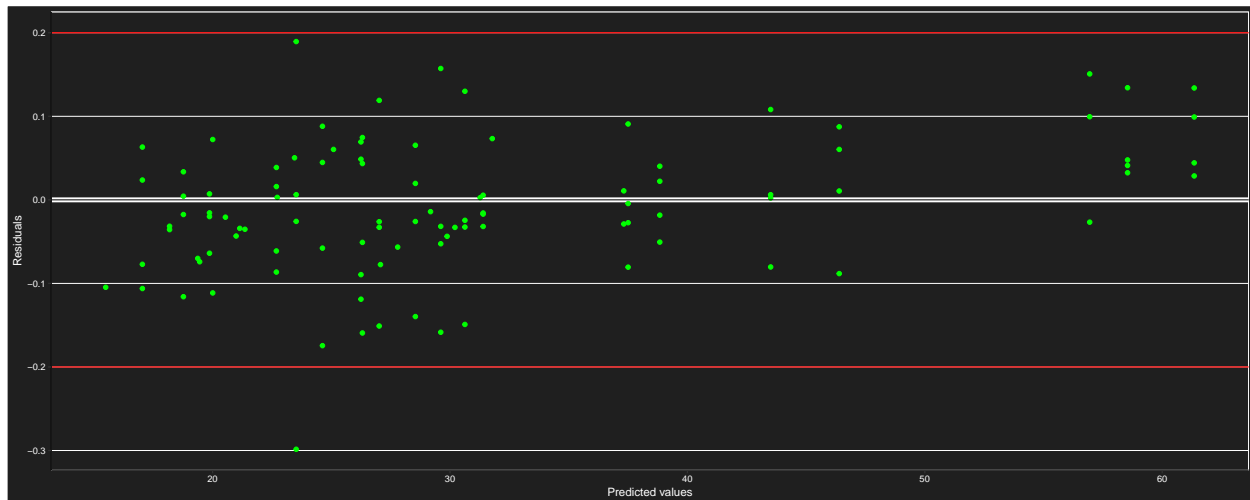


## Análisis de CCI

## Estadística inferencial

### Fenoles

### Supuestos del modelo



### Resumen del modelo

```
## Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
## Family: Gamma ( identity )
## Formula: sqrt(Fenoles) ~ (1 | site/phenotype/id)
## Data: database
##
##      AIC      BIC  logLik deviance df.resid
##    569.2    582.3  -279.6   559.2     97
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.8645 -0.3543 -0.1128  0.3094  1.3945
##
## Random effects:
## Groups              Name            Variance Std.Dev.
## id:(phenotype:site) (Intercept) 1.911e+01 4.371e+00
## phenotype:site      (Intercept) 7.009e+01 8.372e+00
## site                (Intercept) 9.410e-12 3.068e-06
## Residual                        2.091e-02 1.446e-01
## Number of obs: 102, groups:  id:(phenotype:site), 40; phenotype:site, 27; site, 2
##
## Fixed effects:
##              Estimate Std. Error t value Pr(>|z|)
## (Intercept)   39.354     4.068    9.673  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

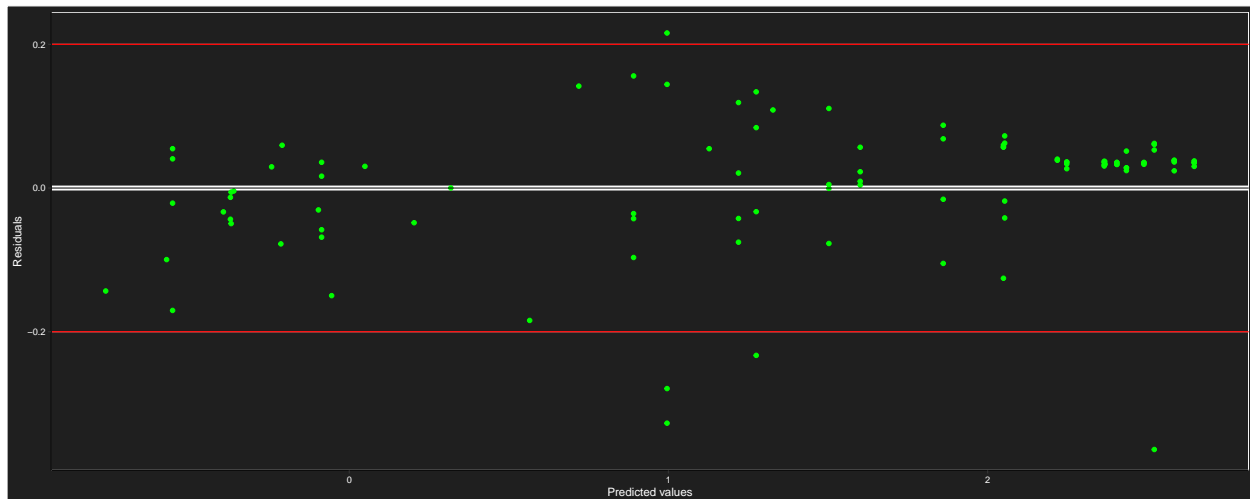
```
## optimizer (Nelder_Mead) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

### Componentes de varianza (%)

```
## [1] 1.122009
## [1] 33.91632
## [1] 64.96166
## [1] 1.686117e-05
```

### AAO

#### .025 Supuestos del modelo



#### Resumen del modelo

```
## Family: beta ( logit )
## Formula:      aao_0.025 ~ (1 | site/phenotype/id)
## Data: database
##
##      AIC      BIC   logLik deviance df.resid
##   -146.8   -133.7    78.4   -156.8     97
##
## Random effects:
##
## Conditional model:
## Groups          Name      Variance Std.Dev.
## id:phenotype:site (Intercept) 1.654e-01 4.067e-01
## phenotype:site    (Intercept) 1.241e+00 1.114e+00
## site              (Intercept) 7.648e-10 2.765e-05
## Number of obs: 102, groups: id:phenotype:site, 39; phenotype:site, 27; site, 2
```

```
##
## Dispersion parameter for beta family (): 15.1
##
## Conditional model:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.3919    0.2386   5.834 5.41e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Componentes de varianza (%)

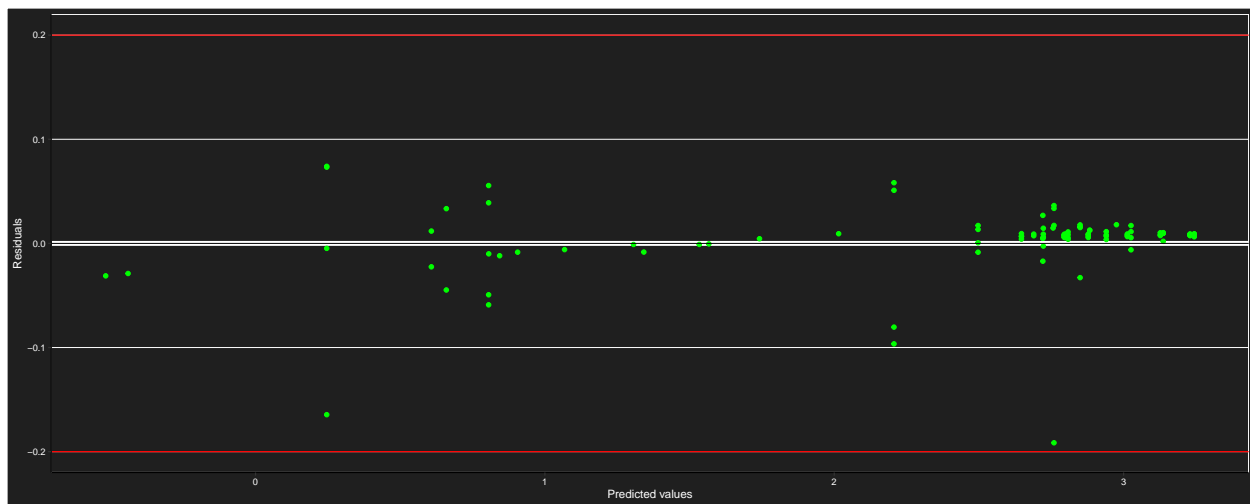
```
## [1] 1.122009
```

```
## [1] 33.91632
```

```
## [1] 64.96166
```

```
## [1] 1.686117e-05
```

.05 Supuestos del modelo



Resumen del modelo

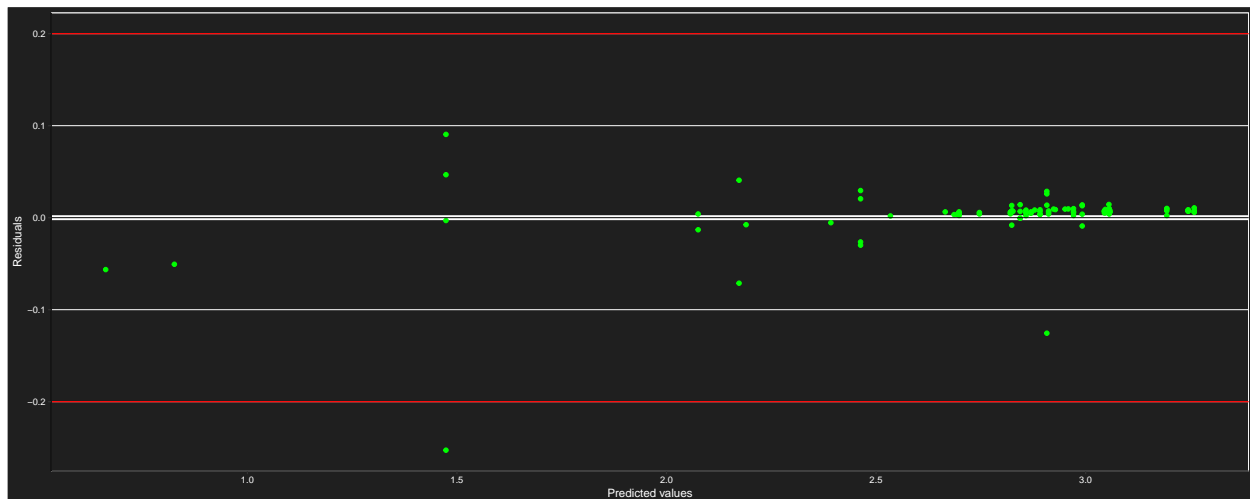
```
## Family: beta ( logit )
## Formula:      aao_0.05 ~ (1 | site/phenotype/id)
## Data: database
##
##      AIC      BIC   logLik deviance df.resid
##   -303.7   -290.6   156.8   -313.7      96
##
## Random effects:
##
## Conditional model:
## Groups          Name          Variance Std.Dev.
```

```
## id:phenotype:site (Intercept) 1.009e+00 1.004e+00
## phenotype:site (Intercept) 2.404e-01 4.903e-01
## site (Intercept) 1.799e-09 4.242e-05
## Number of obs: 101, groups: id:phenotype:site, 39; phenotype:site, 27; site, 2
##
## Dispersion parameter for beta family (): 75.3
##
## Conditional model:
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) 2.1893 0.2188 10.01 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Componentes de varianza (%)

```
## [1] 1.122009
## [1] 33.91632
## [1] 64.96166
## [1] 1.686117e-05
```

## 0.1 Supuestos del modelo

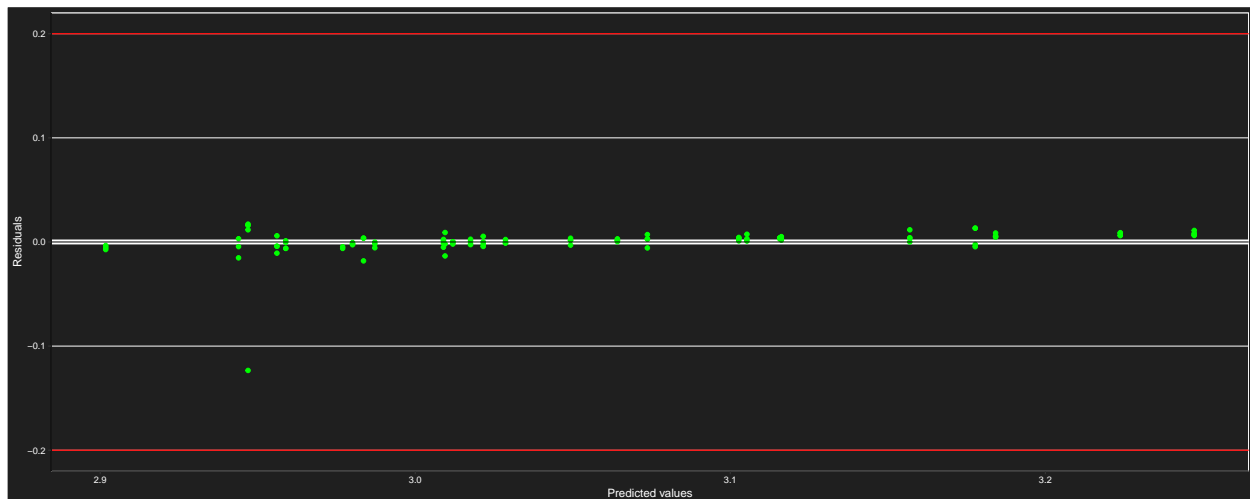


## Resumen del modelo

```
## Family: beta ( logit )
## Formula: aao_0.1 ~ (1 | site/phenotype/id)
## Data: database
##
## AIC BIC logLik deviance df.resid
## -398.5 -385.5 204.3 -408.5 96
##
```

```
## Random effects:
##
## Conditional model:
## Groups          Name          Variance Std.Dev.
## id:phenotype:site (Intercept) 3.711e-01 6.092e-01
## phenotype:site    (Intercept) 2.288e-02 1.513e-01
## site              (Intercept) 4.274e-11 6.537e-06
## Number of obs: 101, groups: id:phenotype:site, 39; phenotype:site, 27; site, 2
##
## Dispersion parameter for beta family (): 94.4
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.7310      0.1181   23.13  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## .25 Supuestos del modelo

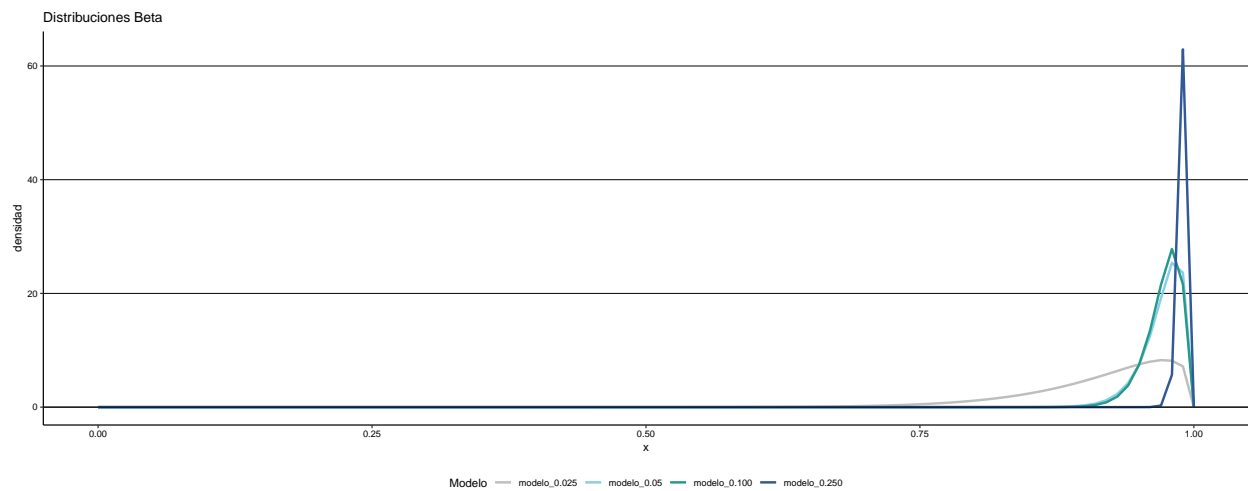


## Resumen del modelo

```
## Family: beta ( logit )
## Formula:          aao_0.25 ~ (1 | site/phenotype/id)
## Data: database
##
##      AIC      BIC   logLik deviance df.resid
##   -606.0   -592.9    308.0   -616.0      96
##
## Random effects:
##
## Conditional model:
## Groups          Name          Variance Std.Dev.
## id:phenotype:site (Intercept) 8.909e-10 2.985e-05
## phenotype:site    (Intercept) 1.606e-02 1.267e-01
## site              (Intercept) 4.370e-24 2.091e-12
## Number of obs: 101, groups: id:phenotype:site, 39; phenotype:site, 27; site, 2
```

```
##
## Dispersion parameter for beta family (): 378
##
## Conditional model:
##      Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.054      NaN    NaN    NaN
```

## Modelos de aao



Clorofila a

Clorofila b

Carotenoides

## Análisis multivariado