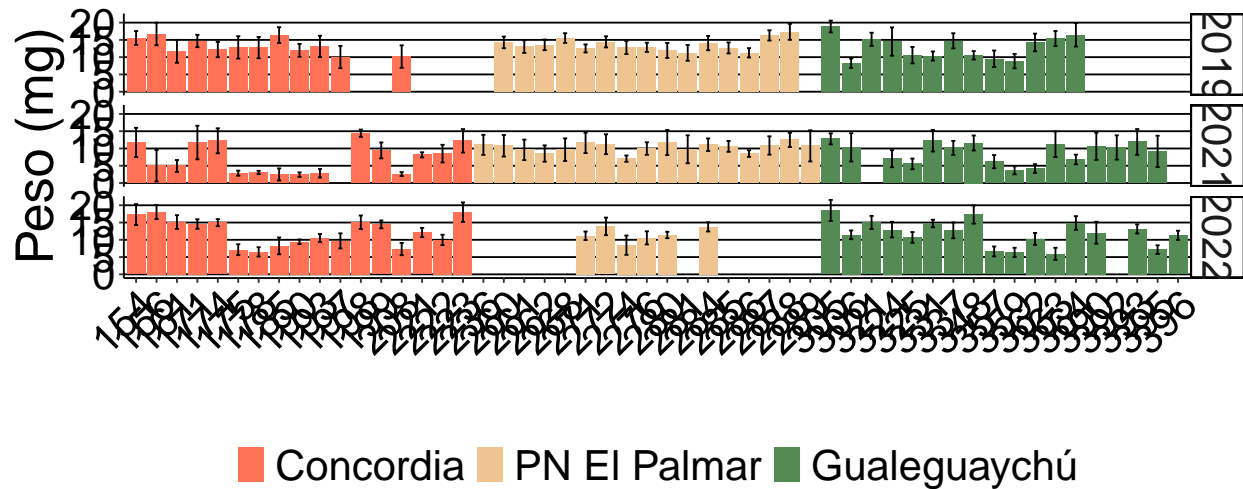


Variables reproductivas

Estimación de coeficientes de correlación intraclase (CCI)

Peso seco de botones florales en fases C/D (PSFL)



Resumen

```
## Bootstrap Progress:
## Permutation Progress for year :
## Permutation Progress for site :
## Permutation Progress for phenotype :

##
## Repeatability estimation using the lmm method
##
## Call = rptGaussian(formula = PSFL ~ (1 | year) + (1 | site) + (1 | phenotype), grname = c("year", "s
##
## Data: 1178 observations
## -----
##
## year (3 groups)
##
## Repeatability estimation overview:
##      R      SE   2.5% 97.5% P_permut  LRT_P
## 0.296 0.113 0.177 0.378 0.667      0
##
## Bootstrapping and Permutation test:
```

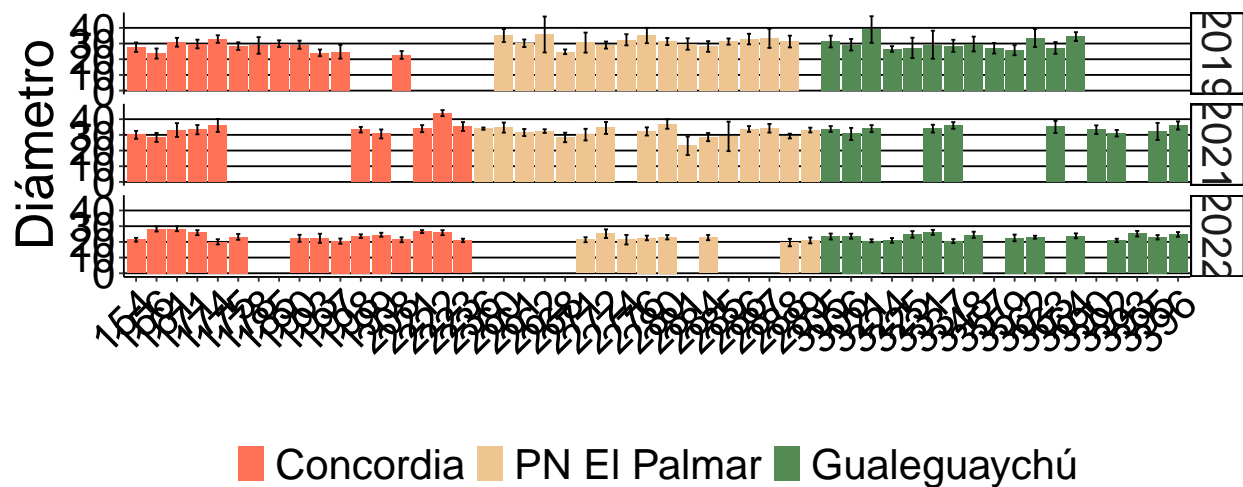
```

##           N   Mean Median   2.5% 97.5%
## boot           3  0.296  0.341 0.1771  0.378
## permut          3  0.352  0.296 0.0148  0.737
##
## Likelihood ratio test:
## logLik full model = -3043.276
## logLik red. model = -3255.274
## D  = 424, df = 1, P = 1.65e-94
##
## -----
##
##
## site (3 groups)
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
## 0.00482 0.0194 0.000409 0.0355    0.667  0.397
##
## Bootstrapping and Permutation test:
##           N   Mean Median   2.5% 97.5%
## boot           3  0.015 0.00818 0.000409 0.0355
## permut          3  0.148 0.00482 0.000241 0.4166
##
## Likelihood ratio test:
## logLik full model = -3043.276
## logLik red. model = -3043.31
## D  = 0.0687, df = 1, P = 0.397
##
## -----
##
##
## phenotype (52 groups)
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
## 0.257 0.0474 0.209 0.295    0.667    0
##
## Bootstrapping and Permutation test:
##           N   Mean Median   2.5% 97.5%
## boot           3  0.245  0.227 0.2092  0.295
## permut          3  0.329  0.257 0.0128  0.707
##
## Likelihood ratio test:
## logLik full model = -3043.276
## logLik red. model = -3239.608
## D  = 393, df = 1, P = 1.09e-87
##
## -----
##
##
## Residual
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P

```

```
## 0.442 0.0459 0.412 0.493 NA NA
##
## Bootstrapping and Permutation test:
## N Mean Median 2.5% 97.5%
## boot 3 0.444 0.423 0.412 0.493
## permut 3 NA NA NA NA
##
## Likelihood ratio test:
## logLik full model = -3043.276
## logLik red. model = NA
## D = NA, df = NA, P = NA
##
## -----
```

Diámetro máximo de polen (DMAP)



Resumen

```
## Bootstrap Progress:
## Permutation Progress for year :
## Permutation Progress for site :
## Permutation Progress for phenotype :

##
## Repeatability estimation using the lmm method
##
## Call = rptGaussian(formula = DMAP ~ (1 | year) + (1 | site) + (1 | phenotype), grname = c("year", "s
##
## Data: 1130 observations
## -----
##
## year (3 groups)
##
## Repeatability estimation overview:
## R SE 2.5% 97.5% P_permut LRT_P
```

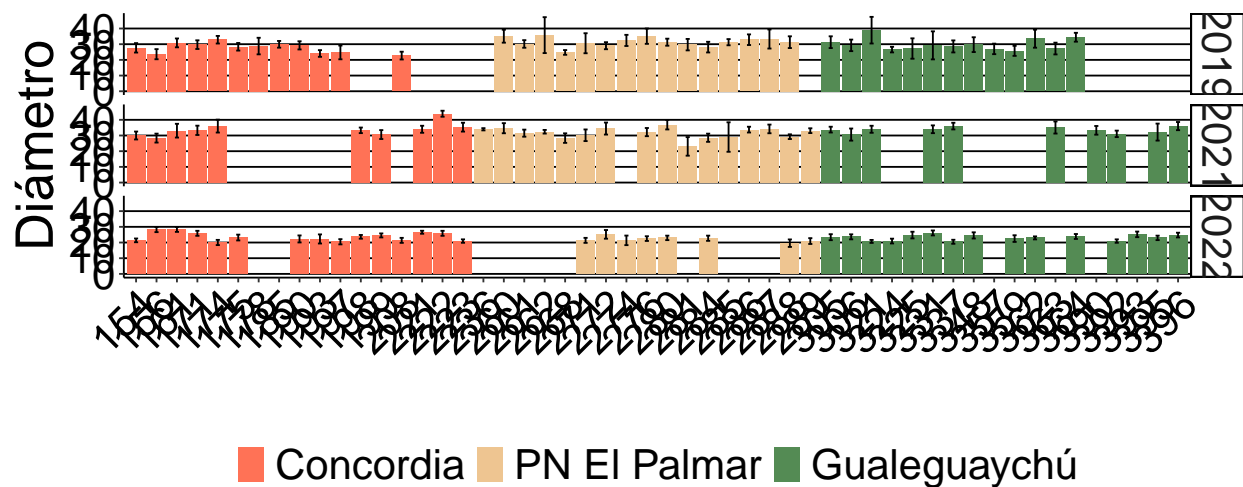
```

##    0.547  0.117  0.389  0.596    0.667    0
##
## Bootstrapping and Permutation test:
##          N    Mean Median   2.5% 97.5%
## boot      3  0.514  0.564 0.3894  0.596
## permut     3  0.459  0.547 0.0297  0.815
##
## Likelihood ratio test:
## logLik full model = -3198.259
## logLik red. model = -3547.919
## D  = 699, df = 1, P = 2.1e-154
##
## -----
##
##
## site (3 groups)
##
## Repeatability estimation overview:
##      R      SE   2.5% 97.5% P_permut  LRT_P
##      0 0.000146      0 0.00024      1    0.5
##
## Bootstrapping and Permutation test:
##          N    Mean Median   2.5% 97.5%
## boot      3 8.42e-05      0      0 0.00024
## permut     3 1.12e-01      0      0 0.31994
##
## Likelihood ratio test:
## logLik full model = -3198.259
## logLik red. model = -3198.259
## D  = 1.27e-07, df = 1, P = 0.5
##
## -----
##
##
## phenotype (52 groups)
##
## Repeatability estimation overview:
##      R      SE   2.5% 97.5% P_permut  LRT_P
##      0.102 0.0329 0.0778 0.133    0.667    0
##
## Bootstrapping and Permutation test:
##          N    Mean Median   2.5% 97.5%
## boot      3 0.0976 0.0795 0.07782  0.133
## permut     3 0.1887 0.1020 0.00832  0.443
##
## Likelihood ratio test:
## logLik full model = -3198.259
## logLik red. model = -3281.782
## D  = 167, df = 1, P = 1.63e-38
##
## -----
##
##
## Residual

```

```
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
##    0.351 0.0844 0.327 0.478      NA      NA
##
## Bootstrapping and Permutation test:
##      N    Mean Median    2.5% 97.5%
## boot     3 0.388 0.356 0.327 0.478
## permut     3    NA    NA    NA    NA
##
## Likelihood ratio test:
## logLik full model = -3198.259
## logLik red. model = NA
## D = NA, df = NA, P = NA
##
## -----
```

Diámetro mínimo de polen (DMIP)



Resumen

```
## Bootstrap Progress:
## Permutation Progress for year :
## Permutation Progress for site :
## Permutation Progress for phenotype :

##
## Repeatability estimation using the lmm method
##
## Call = rptGaussian(formula = DMIP ~ (1 | year) + (1 | site) + (1 | phenotype), grname = c("year", "site", "phenotype"))
##
## Data: 1130 observations
## -----
##
## year (3 groups)
```

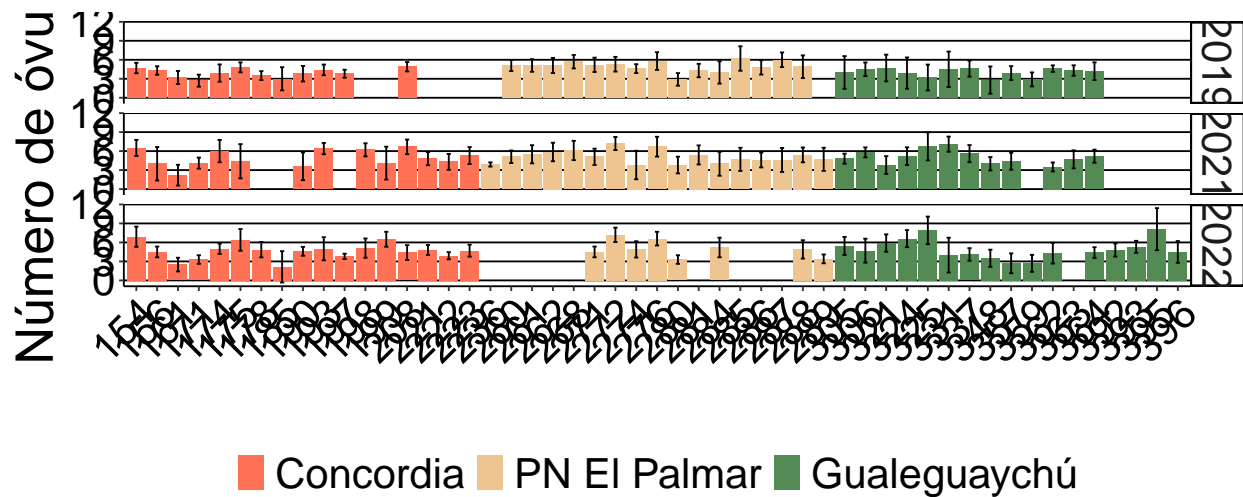
```

##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
##    0.391 0.239 0.281 0.711    0.667      0
##
## Bootstrapping and Permutation test:
##      N    Mean Median    2.5% 97.5%
## boot      3 0.459 0.372 0.2809 0.711
## permut     3 0.378 0.391 0.0244 0.719
##
## Likelihood ratio test:
## logLik full model = -3198.896
## logLik red. model = -3416.192
## D = 435, df = 1, P = 8.14e-97
##
## -----
##
##
## site (3 groups)
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
##    5.16e-10 1.1e-09 3.79e-11 1.9e-09    0.667      1
##
## Bootstrapping and Permutation test:
##      N    Mean  Median    2.5% 97.5%
## boot      3 7.30e-10 1.63e-10 3.79e-11 1.90e-09
## permut     3 1.42e-01 5.16e-10 6.36e-11 4.04e-01
##
## Likelihood ratio test:
## logLik full model = -3198.896
## logLik red. model = -3198.896
## D = -1.32e-07, df = 1, P = 1
##
## -----
##
##
## phenotype (52 groups)
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
##    0.166 0.0718 0.0679 0.195    0.667      0
##
## Bootstrapping and Permutation test:
##      N    Mean Median    2.5% 97.5%
## boot      3 0.144 0.174 0.06793 0.195
## permut     3 0.241 0.166 0.00831 0.539
##
## Likelihood ratio test:
## logLik full model = -3198.896
## logLik red. model = -3310.774
## D = 224, df = 1, P = 6.86e-51
##
## -----

```

```
##
##
## Residual
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
##    0.443  0.173    0.22  0.544      NA     NA
##
## Bootstrapping and Permutation test:
##      N    Mean Median    2.5% 97.5%
## boot     3  0.397  0.432    0.22  0.544
## permut     3     NA     NA     NA     NA
##
## Likelihood ratio test:
## logLik full model = -3198.896
## logLik red. model = NA
## D = NA, df = NA, P = NA
##
## -----
```

Número de óvulos por flor



Resumen

```
## Bootstrap Progress:
## Permutation Progress for year:
## Permutation Progress for site:
## Permutation Progress for phenotype:

##
## Repeatability estimation using glmer method
##
## Call = rptPoisson(formula = NO ~ (1 | year) + (1 | site) + (1 | phenotype), grname = c("year", "site")
##
## Data: 1184 observations
```

```

## -----
##
## year (3 groups)
##
## Repeatability estimation overview:
##           R      SE    2.5%  97.5% P_permut
## Org      NA      NA      NA      NA      NA
## Link 0.0116 0.0143 0.00108 0.0249    0.333
##
##
## Bootstrapping:
##           N    Mean  Median    2.5%  97.5%
## Org        3      NA      NA      NA      NA
## Link        3 0.0096 0.00162 0.00108 0.0249
##
## Permutation test:
##           N    Mean  Median    2.5%  97.5% P_permut
## Org        3      NA      NA      NA      NA      NA
## Link        3 0.00419 0.000956 4.78e-05 0.0111    0.333
##
## Likelihood ratio test:
## logLik full model = -2365.942
## logLik red. model = -2370.112
## D = 8.34, df = 1, P = 0.00194
##
## -----
##
##
## site (3 groups)
##
## Repeatability estimation overview:
##           R      SE    2.5%  97.5% P_permut
## Org      NA      NA      NA      NA      NA
## Link 0.00224      0      0      0    0.333
##
##
## Bootstrapping:
##           N    Mean  Median    2.5%  97.5%
## Org        3      NA      NA      NA      NA
## Link        3      0      0      0      0
##
## Permutation test:
##           N    Mean  Median    2.5%  97.5% P_permut
## Org        3      NA      NA      NA      NA      NA
## Link        3 0.000745      0      0 0.00212    0.333
##
## Likelihood ratio test:
## logLik full model = -2365.942
## logLik red. model = -2365.971
## D = 0.0575, df = 1, P = 0.405
##
## -----
##
##

```



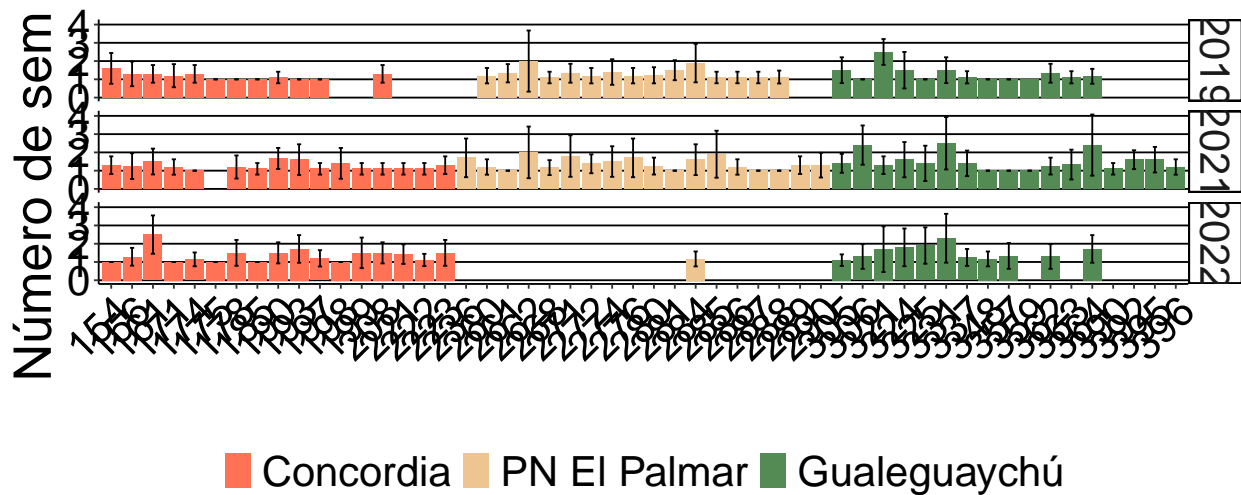
```

## phenotype (51 groups)
##
## Repeatability estimation overview:
##      R      SE   2.5%  97.5% P_permut
## Org      NA      NA      NA      NA      NA
## Link 0.125 0.0162 0.131 0.162 0.333
##
##
## Bootstrapping:
##      N   Mean Median   2.5%  97.5%
## Org      3      NA      NA      NA      NA
## Link      3 0.146 0.145 0.131 0.162
##
## Permutation test:
##      N   Mean Median   2.5%  97.5% P_permut
## Org      3      NA      NA      NA      NA      NA
## Link      3 0.0425 0.00269 0.000134 0.119 0.333
##
## Likelihood ratio test:
## logLik full model = -2365.942
## logLik red. model = -2408.118
## D = 84.4, df = 1, P = 2.07e-20
##
## -----
##
##
## Overdispersion
##
## Repeatability estimation overview:
##      R      SE   2.5%  97.5% P_permut
## Org      NA      NA      NA      NA      NA
## Link      0 0.0213 0.829 0.867      NA
##
##
## Bootstrapping:
##      N   Mean Median   2.5%  97.5%
## Org      3      NA      NA      NA      NA
## Link      3 0.844 0.836 0.829 0.867
##
## Permutation test:
##      N   Mean Median   2.5%  97.5% P_permut
## Org      3      NA      NA      NA      NA      NA
## Link      3      NA      NA      NA      NA      NA
##
## Likelihood ratio test:
## logLik full model = -2365.942
## logLik red. model = -2365.942
## D = 1.5e-09, df = 1, P = 0.5
##
## -----
##
##
## Residual
##

```

```
## Repeatability estimation overview:
##           R      SE    2.5%  97.5% P_permut
## Org      NA      NA      NA      NA      NA
## Link  0.861 0.0203 0.00139 0.0399      NA
##
##
## Bootstrapping:
##           N    Mean Median    2.5%  97.5%
## Org        3      NA      NA      NA      NA
## Link       3    0.02 0.0184 0.00139 0.0399
##
## Permutation test:
##           N    Mean Median    2.5%  97.5% P_permut
## Org        1      NA      NA      NA      NA      NA
## Link       1      NA      NA      NA      NA      NA
##
## Likelihood ratio test:
## logLik full model = -2365.942
## logLik red. model = NA
## D = NA, df = NA, P = NA
##
## -----
```

Número de semillas por fruto



```
## Bootstrap Progress:
## Permutation Progress for year:
## Permutation Progress for site:
## Permutation Progress for phenotype:

##
## Repeatability estimation using glmer method
##
## Call = rptPoisson(formula = NS ~ (1 | year) + (1 | site) + (1 | phenotype), grname = c("year", "site"))
##
```

```

## Data: 988 observations
## -----
##
## year (3 groups)
##
## Repeatability estimation overview:
##           R      SE  2.5% 97.5% P_permut
## Org      NA      NA      NA      NA      NA
## Link 0.00212      0      0      0      0.667
##
##
## Bootstrapping:
##           N      Mean Median  2.5% 97.5%
## Org      3      NA      NA      NA      NA
## Link     3      0      0      0      0
##
## Permutation test:
##           N      Mean Median  2.5% 97.5% P_permut
## Org      3      NA      NA      NA      NA      NA
## Link     3 0.00232 0.00212 0.000993 0.00381 0.667
##
## Likelihood ratio test:
## logLik full model = -1222.769
## logLik red. model = -1222.965
## D = 0.393, df = 1, P = 0.265
##
## -----
##
##
## site (3 groups)
##
## Repeatability estimation overview:
##           R      SE  2.5% 97.5% P_permut
## Org      NA      NA      NA      NA      NA
## Link 0.00348 0.00697      0 0.0115 0.333
##
##
## Bootstrapping:
##           N      Mean Median  2.5% 97.5%
## Org      3      NA      NA      NA      NA
## Link     3 0.00402      0      0 0.0115
##
## Permutation test:
##           N      Mean Median  2.5% 97.5% P_permut
## Org      3      NA      NA      NA      NA      NA
## Link     3 0.00116      0      0 0.0033 0.333
##
## Likelihood ratio test:
## logLik full model = -1222.769
## logLik red. model = -1223.354
## D = 1.17, df = 1, P = 0.14
##
## -----
##

```

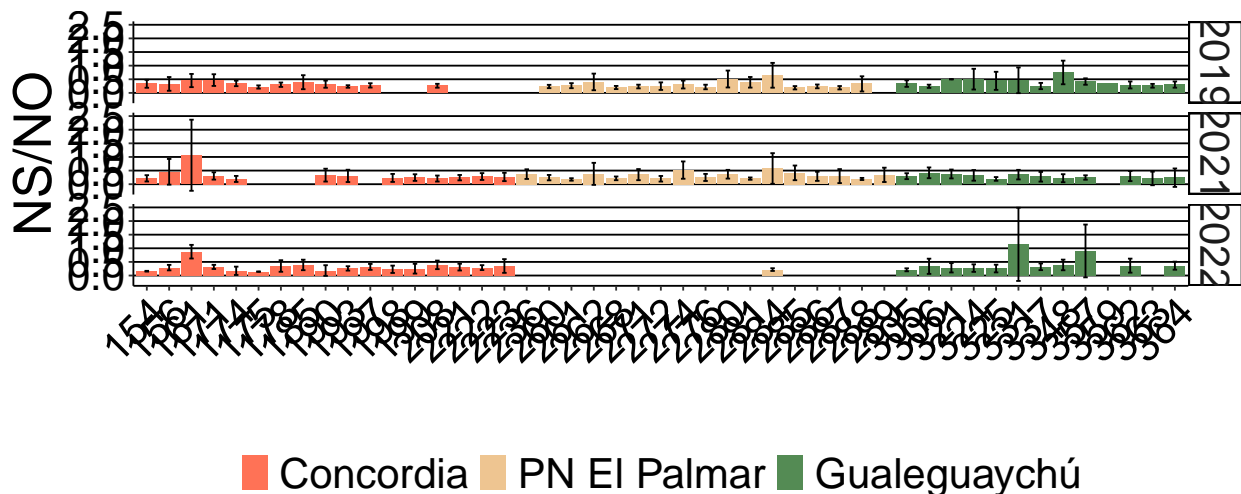
```

##
## phenotype (52 groups)
##
## Repeatability estimation overview:
##           R      SE      2.5% 97.5% P_permut
## Org      NA      NA      NA      NA      NA
## Link 1.87e-14 0.00304 7.33e-16 0.005    0.667
##
##
## Bootstrapping:
##           N      Mean  Median      2.5% 97.5%
## Org      3      NA      NA      NA      NA
## Link     3 0.00176 1.47e-14 7.33e-16 0.005
##
## Permutation test:
##           N      Mean  Median      2.5% 97.5% P_permut
## Org      3      NA      NA      NA      NA      NA
## Link     3 0.00225 1.87e-14 9.35e-16 0.00643    0.667
##
## Likelihood ratio test:
## logLik full model = -1222.769
## logLik red. model = -1222.769
## D = -1.36e-11, df = 1, P = 1
##
## -----
##
##
## Overdispersion
##
## Repeatability estimation overview:
##           R      SE      2.5% 97.5% P_permut
## Org      NA      NA      NA      NA      NA
## Link     0      0.01 0.984      1      NA
##
##
## Bootstrapping:
##           N      Mean  Median      2.5% 97.5%
## Org      3      NA      NA      NA      NA
## Link     3 0.994      1 0.984      1
##
## Permutation test:
##           N      Mean  Median      2.5% 97.5% P_permut
## Org      3      NA      NA      NA      NA      NA
## Link     3      NA      NA      NA      NA      NA
##
## Likelihood ratio test:
## logLik full model = -1222.769
## logLik red. model = -1222.769
## D = 1.44e-09, df = 1, P = 0.5
##
## -----
##
##
## Residual

```

```
##
## Repeatability estimation overview:
##      R      SE      2.5% 97.5% P_permut
## Org      NA      NA      NA      NA      NA
## Link 0.994 0.00707 4.68e-15 0.0116      NA
##
##
## Bootstrapping:
##      N      Mean      Median      2.5% 97.5%
## Org      3      NA      NA      NA      NA
## Link      3 0.00408 9.36e-14 4.68e-15 0.0116
##
## Permutation test:
##      N      Mean Median      2.5% 97.5% P_permut
## Org      1      NA      NA      NA      NA      NA
## Link      1      NA      NA      NA      NA      NA
##
## Likelihood ratio test:
## logLik full model = -1222.769
## logLik red. model = NA
## D = NA, df = NA, P = NA
##
## -----
```

NS/NO



```
## Bootstrap Progress:
## Permutation Progress for year :
## Permutation Progress for site :
## Permutation Progress for phenotype :
```

```
##
## Repeatability estimation using the lmm method
##
## Call = rptGaussian(formula = (NS_NO_log) ~ (1 | year) + (1 | site) + (1 | phenotype), grname = c("ye
```

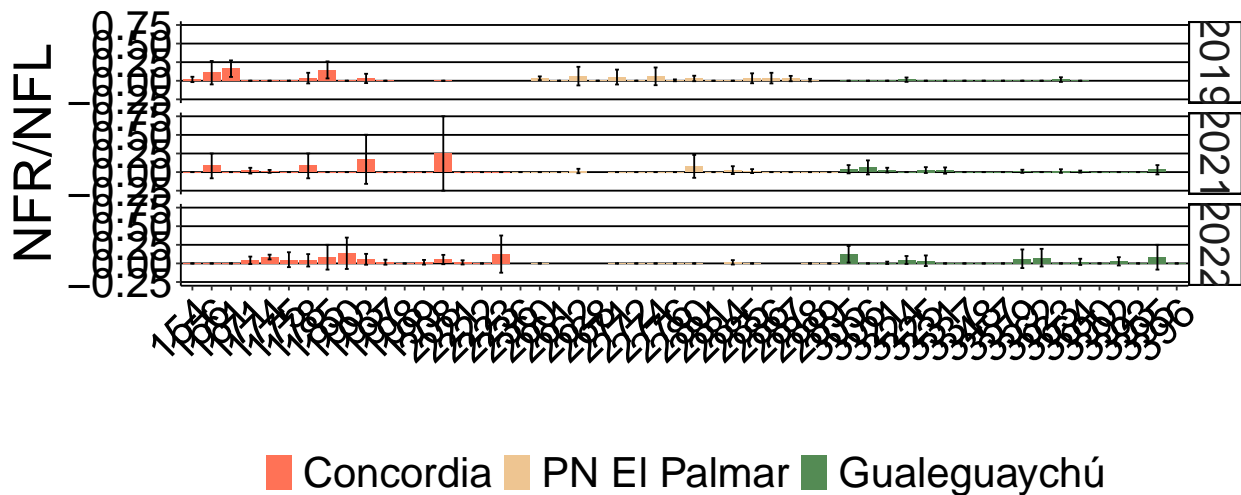
```

##
## Data: 879 observations
## -----
##
## year (3 groups)
##
## Repeatability estimation overview:
##      R      SE    2.5%  97.5% P_permut  LRT_P
## 0.00212 0.00336 0.000187 0.00656    0.667  0.288
##
## Bootstrapping and Permutation test:
##      N    Mean  Median    2.5%   97.5%
## boot    3 0.00348 0.00373 0.000187 0.00656
## permut   3 0.31223 0.00212 0.001639 0.88642
##
## Likelihood ratio test:
## logLik full model = 349.8305
## logLik red. model = 349.6741
## D = 0.313, df = 1, P = 0.288
##
## -----
##
##
## site (3 groups)
##
## Repeatability estimation overview:
##      R      SE    2.5%  97.5% P_permut  LRT_P
##      0      0      0      0          1      1
##
## Bootstrapping and Permutation test:
##      N    Mean  Median    2.5%   97.5%
## boot    3 0.000 0.00000 0.000000 0.000
## permut   3 0.314 0.00894 0.000447 0.886
##
## Likelihood ratio test:
## logLik full model = 349.8305
## logLik red. model = 349.8305
## D = -6.81e-11, df = 1, P = 1
##
## -----
##
##
## phenotype (47 groups)
##
## Repeatability estimation overview:
##      R      SE    2.5%  97.5% P_permut  LRT_P
## 0.0999 0.0112 0.116 0.135    0.667    0
##
## Bootstrapping and Permutation test:
##      N    Mean  Median    2.5%   97.5%
## boot    3 0.128 0.1340 0.1161 0.135
## permut   3 0.364 0.0999 0.0242 0.927
##
## Likelihood ratio test:

```

```
## logLik full model = 349.8305
## logLik red. model = 329.4002
## D = 40.9, df = 1, P = 8.17e-11
##
## -----
##
##
## Residual
##
## Repeatability estimation overview:
##      R      SE    2.5%  97.5% P_permut  LRT_P
## 0.898 0.0116 0.859    0.88      NA     NA
##
## Bootstrapping and Permutation test:
##      N    Mean Median    2.5%  97.5%
## boot     3 0.868 0.866 0.859    0.88
## permut     3    NA    NA    NA     NA
##
## Likelihood ratio test:
## logLik full model = 349.8305
## logLik red. model = NA
## D = NA, df = NA, P = NA
##
## -----
```

NFL/NFR



```
## Bootstrap Progress:
## Permutation Progress for year :
## Permutation Progress for site :
## Permutation Progress for phenotype :

##
## Repeatability estimation using the lmm method
##
```

```

## Call = rptGaussian(formula = NFL_cm_log ~ (1 | year) + (1 | site) + (1 | phenotype), grname = c("year", "site", "phenotype"))
##
## Data: 534 observations
## -----
##
## year (3 groups)
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
## 0.0194 0.017 0.000833 0.0296    0.667  0.003
##
## Bootstrapping and Permutation test:
##      N    Mean Median    2.5% 97.5%
## boot    3 0.0115 0.00265 0.000833 0.0296
## permut   3 0.2072 0.01936 0.000968 0.5731
##
## Likelihood ratio test:
## logLik full model = -163.2479
## logLik red. model = -166.9907
## D = 7.49, df = 1, P = 0.00311
##
## -----
##
## site (3 groups)
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
## 0.12 0.0111 0.0102 0.0313    1 0.003
##
## Bootstrapping and Permutation test:
##      N    Mean Median    2.5% 97.5%
## boot    3 0.0206 0.0201 0.0102 0.0313
## permut   3 0.2816 0.1472 0.1214 0.5562
##
## Likelihood ratio test:
## logLik full model = -163.2479
## logLik red. model = -167.0384
## D = 7.58, df = 1, P = 0.00295
##
## -----
##
## phenotype (52 groups)
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
## 0.26 0.0788 0.275 0.408    0.667    0
##
## Bootstrapping and Permutation test:
##      N    Mean Median    2.5% 97.5%
## boot    3 0.324 0.281 0.275 0.408
## permut   3 0.354 0.260 0.013 0.776
##

```



```
## Likelihood ratio test:
## logLik full model = -163.2479
## logLik red. model = -214.2015
## D = 102, df = 1, P = 2.91e-24
##
## -----
##
##
## Residual
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
## 0.601 0.0962 0.542 0.712      NA      NA
##
## Bootstrapping and Permutation test:
##      N    Mean Median    2.5% 97.5%
## boot    3 0.644 0.686 0.542 0.712
## permut    3    NA    NA    NA    NA
##
## Likelihood ratio test:
## logLik full model = -163.2479
## logLik red. model = NA
## D = NA, df = NA, P = NA
##
## -----
```

NFL/cm

```
## Bootstrap Progress:
## Permutation Progress for year :
## Permutation Progress for site :
## Permutation Progress for phenotype :

##
## Repeatability estimation using the lmm method
##
## Call = rptGaussian(formula = (NFR_NFL_log) ~ (1 | year) + (1 | site) + (1 | phenotype), grname = c("))
##
## Data: 529 observations
## -----
##
## year (3 groups)
##
## Repeatability estimation overview:
##      R      SE    2.5% 97.5% P_permut  LRT_P
## 0 0.000761 3.46e-05 0.00148      1      1
##
## Bootstrapping and Permutation test:
##      N    Mean  Median    2.5% 97.5%
## boot    3 0.000737 0.000691 3.46e-05 0.00148
## permut    3 0.311112 0.000000 0.00e+00 0.88667
##
## Likelihood ratio test:
```

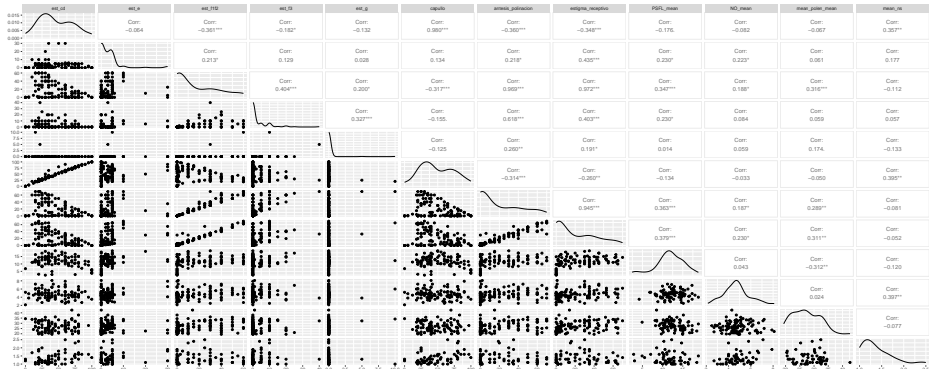
```

## logLik full model = 690.7281
## logLik red. model = 690.7281
## D = -1.05e-10, df = 1, P = 1
##
## -----
##
##
## site (3 groups)
##
## Repeatability estimation overview:
##      R      SE      2.5% 97.5% P_permut  LRT_P
## 0.0327 0.0496 0.000241 0.084    0.667 0.004
##
## Bootstrapping and Permutation test:
##      N      Mean Median      2.5% 97.5%
## boot      3 0.031 0.00482 0.000241 0.084
## permut     3 0.344 0.03266 0.013006 0.940
##
## Likelihood ratio test:
## logLik full model = 690.7281
## logLik red. model = 687.0945
## D = 7.27, df = 1, P = 0.00351
##
## -----
##
##
## phenotype (52 groups)
##
## Repeatability estimation overview:
##      R      SE      2.5% 97.5% P_permut  LRT_P
## 0 0.000687 5.01e-05 0.0013      1      1
##
## Bootstrapping and Permutation test:
##      N      Mean Median      2.5% 97.5%
## boot      3 0.000772 0.0010 5.01e-05 0.0013
## permut     3 0.316113 0.0167 8.36e-04 0.8859
##
## Likelihood ratio test:
## logLik full model = 690.7281
## logLik red. model = 690.7281
## D = -9.45e-10, df = 1, P = 1
##
## -----
##
##
## Residual
##
## Repeatability estimation overview:
##      R      SE      2.5% 97.5% P_permut  LRT_P
## 0.967 0.0504 0.914 0.998      NA      NA
##
## Bootstrapping and Permutation test:
##      N      Mean Median      2.5% 97.5%
## boot      3 0.968 0.995 0.914 0.998

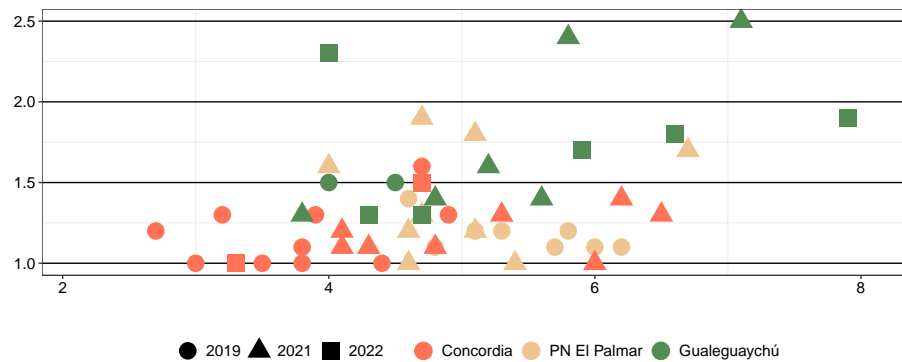
```

```
## permut      3      NA      NA      NA      NA
##
## Likelihood ratio test:
## logLik full model = 690.7281
## logLik red. model = NA
## D = NA, df = NA, P = NA
##
## -----
```

Correlaciones



Correlación N° de semillas y N° de óvulos



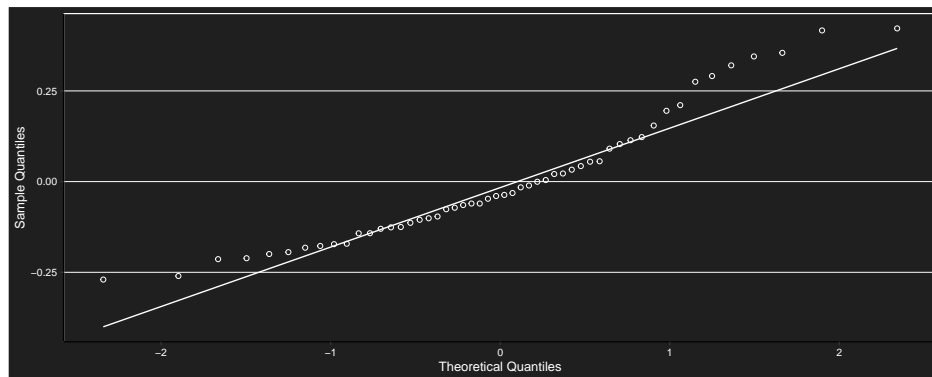
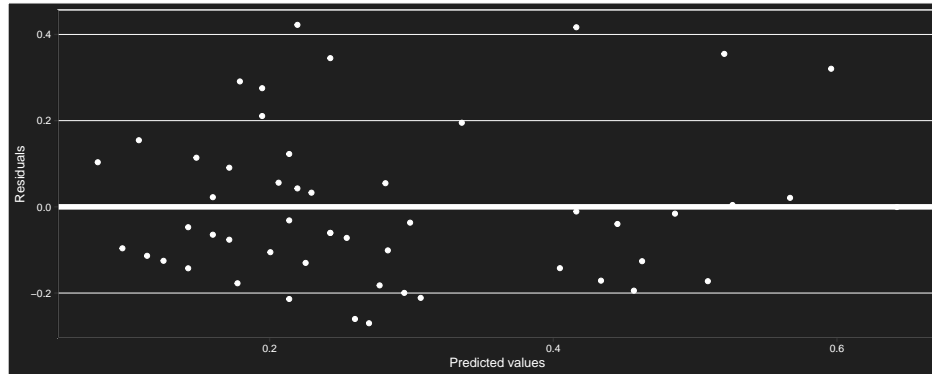
```
## [1] 0.3966561
```

Modelo

```
## Linear mixed model fit by REML ['lmerModLmerTest']
## Formula: log(mean_ns) ~ NO_mean + (1 | year) + (1 | site)
## Data: df_ovusem
## REML criterion at convergence: -14.8834
## Random effects:
## Groups Name Std.Dev.
## year (Intercept) 0.0000
## site (Intercept) 0.1514
## Residual 0.1832
```

```
## Number of obs: 52, groups:  year, 3; site, 3
## Fixed Effects:
## (Intercept)      NO_mean
##      0.01801      0.05795
## optimizer (nloptwrap) convergence code: 0 (OK) ; 0 optimizer warnings; 1 lme4 warnings
```

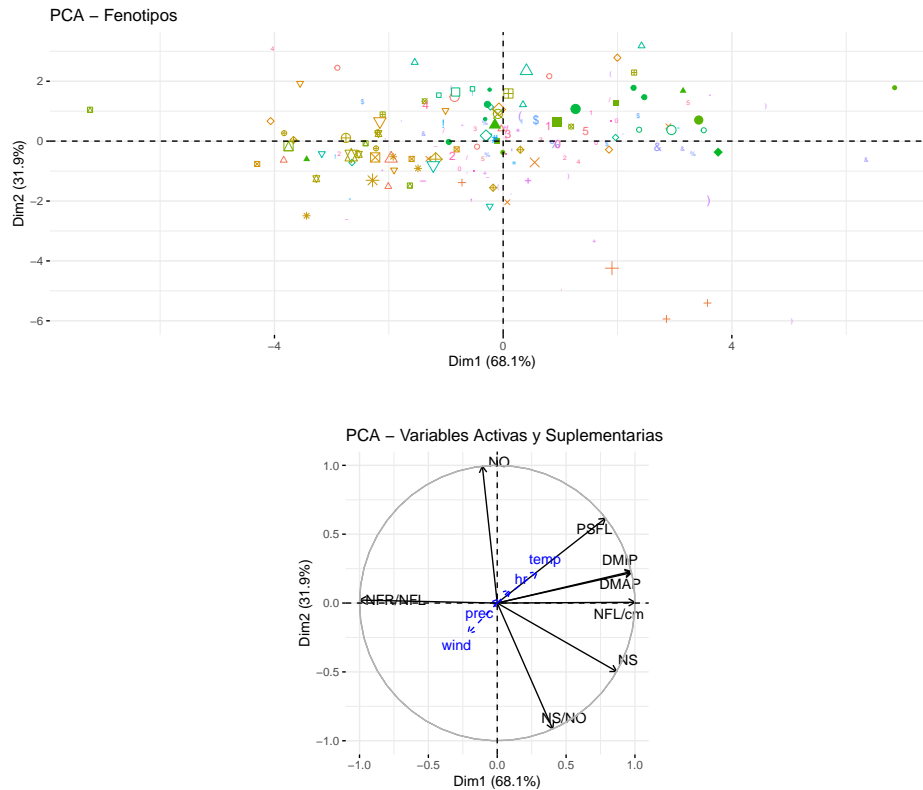
Verificación de supuestos



```
##
## Shapiro-Wilk normality test
##
## data:  e
## W = 0.93078, p-value = 0.004811
```

Análisis multivariado

Análisis de PCA con variables suplementarias



Resultado PCA

```
##
## Call:
## PCA(X = tabla_merged, quanti.sup = c(13:16), quali.sup = c(9:12),
##     graph = FALSE)
##
##
## Eigenvalues
##
```

	Dim.1	Dim.2	Dim.3	Dim.4	Dim.5	Dim.6	Dim.7	Dim.8
## Variance	5.445	2.555	0.000	0.000	0.000	0.000	0.000	0.000
## % of var.	68.063	31.937	0.000	0.000	0.000	0.000	0.000	0.000
## Cumulative % of var.	68.063	100.000	100.000	100.000	100.000	100.000	100.000	100.000

```
##
## Individuals (the 10 first)
##
```

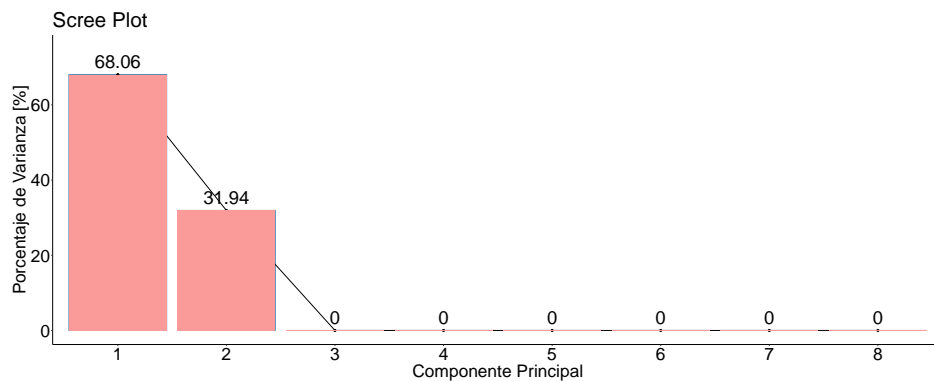
	Dist	Dim.1	ctr	cos2	Dim.2	ctr	cos2	Dim.3	ctr	cos2
## 1	0.493	-0.456	0.028	0.858	-0.185	0.010	0.142	0.000	0.000	0.000
## 2	3.891	-3.838	1.961	0.973	-0.637	0.115	0.027	0.000	0.000	0.000
## 3	1.560	-0.721	0.069	0.213	-1.384	0.543	0.787	0.000	0.000	0.000
## 4	2.043	0.073	0.001	0.001	-2.041	1.182	0.999	0.000	0.000	0.000
## 5	1.873	1.851	0.456	0.977	-0.285	0.023	0.023	0.000	0.000	0.000
## 6	1.436	-1.009	0.135	0.494	1.022	0.296	0.506	0.000	0.000	0.000

```

## 7      | 0.859 | -0.814 0.088 0.897 | -0.276 0.022 0.103 | 0.000 0.000 0.000 |
## 8      | 1.746 | -1.490 0.295 0.728 | -0.911 0.235 0.272 | 0.000 0.000 0.000 |
## 9      | 0.416 | 0.301 0.012 0.522 | -0.288 0.023 0.478 | 0.000 0.000 0.000 |
## 10     | 2.216 | -2.196 0.642 0.982 | 0.295 0.025 0.018 | 0.000 0.000 0.000 |
##
## Variables
##          Dim.1   ctr   cos2   Dim.2   ctr   cos2   Dim.3   ctr   cos2
## PSFL      | 0.787 11.378 0.620 | 0.617 14.892 0.380 | 0.000 0.000 0.000 |
## DMAP      | 0.975 17.471 0.951 | 0.221 1.907 0.049 | 0.000 0.000 0.000 |
## DMIP      | 0.973 17.403 0.948 | 0.229 2.050 0.052 | 0.000 0.000 0.000 |
## NO        | -0.108 0.214 0.012 | 0.994 38.683 0.988 | 0.000 0.000 0.000 |
## NS        | 0.868 13.829 0.753 | -0.497 9.668 0.247 | 0.000 0.000 0.000 |
## NS/NO     | 0.403 2.984 0.162 | -0.915 32.780 0.838 | 0.000 0.000 0.000 |
## NFL/cm    | 1.000 18.365 1.000 | 0.005 0.001 0.000 | 0.000 0.000 0.000 |
## NFR/NFL   | -1.000 18.357 1.000 | 0.022 0.018 0.000 | 0.000 0.000 0.000 |
##
## Supplementary continuous variables
##          Dim.1   cos2   Dim.2   cos2   Dim.3   cos2
## temp      | 0.291 0.084 | 0.227 0.051 | 0.000 0.000 |
## prec      | -0.047 0.002 | 0.007 0.000 | 0.000 0.000 |
## hr        | 0.093 0.009 | 0.096 0.009 | 0.000 0.000 |
## wind      | -0.213 0.046 | -0.222 0.049 | 0.000 0.000 |
##
## Supplementary categories (the 10 first)
##          Dist   Dim.1   cos2 v.test   Dim.2   cos2 v.test   Dim.3   cos2 v.test
## 2019      | 0.289 | 0.282 0.949 0.903 | -0.065 0.051 -0.304 | 0.000 0.000 0.000 |
## 2021      | 1.124 | 1.055 0.882 4.179 | 0.387 0.118 2.236 | 0.000 0.000 0.000 |
## 2022      | 1.545 | -1.493 0.934 -5.209 | -0.398 0.066 -2.026 | 0.000 0.000 0.000 |
## Concordia | 0.968 | -0.955 0.974 -3.387 | -0.158 0.026 -0.816 | 0.000 0.000 0.000 |
## PN El Palmar | 0.653 | 0.457 0.489 1.542 | 0.467 0.511 2.301 | 0.000 0.000 0.000 |
## Gualaguaychú | 0.561 | 0.496 0.781 1.844 | -0.262 0.219 -1.424 | 0.000 0.000 0.000 |
## 154       | 1.705 | -0.850 0.249 -0.636 | 1.478 0.751 1.613 | 0.000 0.000 0.000 |
## 156       | 2.044 | -1.960 0.919 -1.466 | -0.581 0.081 -0.634 | 0.000 0.000 0.000 |
## 161       | 4.650 | 1.903 0.167 1.423 | -4.243 0.833 -4.631 | 0.000 0.000 0.000 |
## 171       | 0.900 | 0.551 0.375 0.412 | -0.711 0.625 -0.776 | 0.000 0.000 0.000 |

```

Scree plot para ver la varianza explicada por cada Principal component



Contribuciones de las variables para CP1

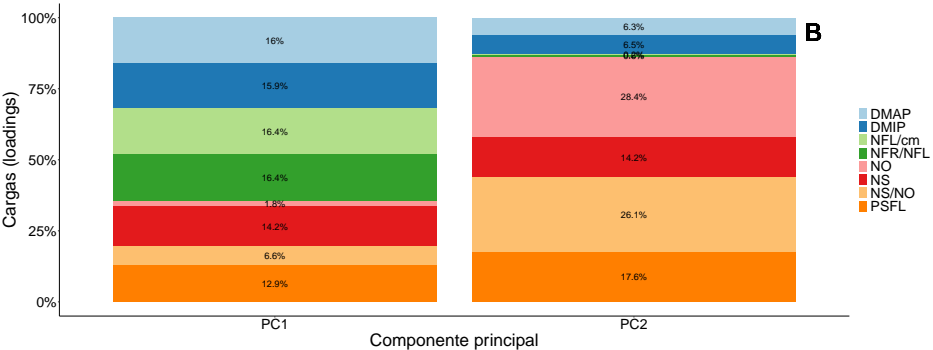
Contribuciones de las variables para CP2

##	NFL/cm	NFR/NFL	DMAP	DMIP	NS	PSFL	NS/NO	NO
##	18.3648058	18.3568335	17.4706790	17.4032081	13.8288115	11.3776648	2.9838846	0.2141126
##	NO	NS/NO	PSFL	NS	DMIP	DMAP	NFR/NFL	NFL/cm
##	38.683189931	32.780363172	14.891875690	9.668090235	2.050479768	1.906688384	0.018151563	0.001161

Contribución acumulada de cada variable a CP1 y CP2

##	NO	NS/NO	PSFL	NS	DMIP	DMAP	NFR/NFL	NFL/cm
##	38.89730	35.76425	26.26954	23.49690	19.45369	19.37737	18.37499	18.36597

Proporción de contribución de cada variable a PC1, PC2 y PC3



Biplots de PCA CP1 VS CP2

