

# T. mopan X T. dimidiata

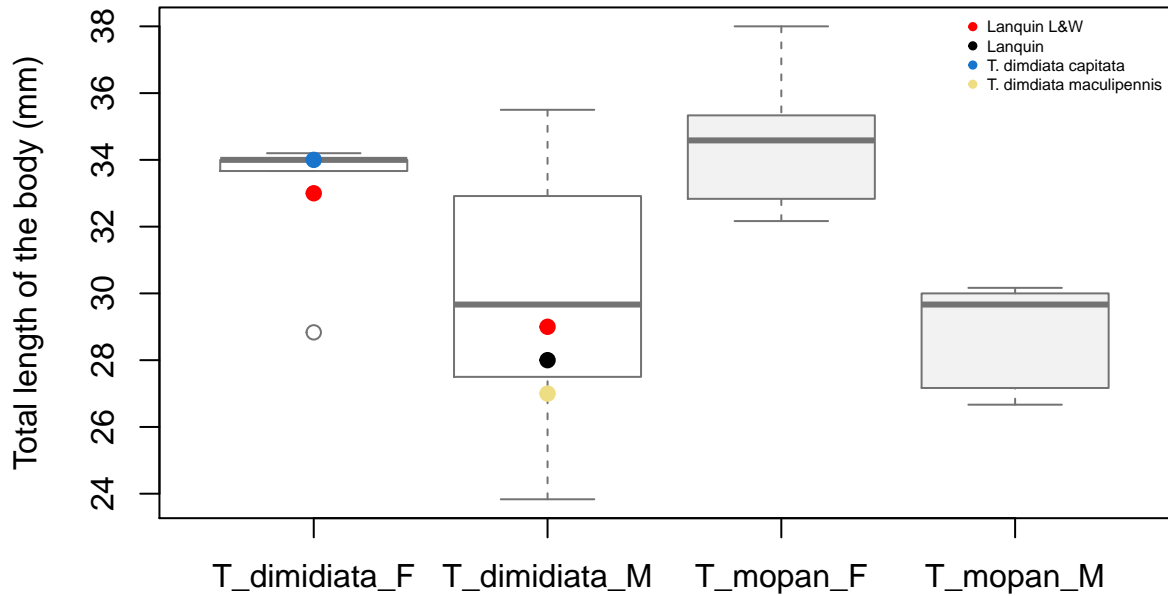
*Silvia Justí*

2/26/2018

```
data<-read.csv("measures_mopan.csv", header=T)
Lanquin<-data[3, ]
Capitata <- data[20,]
Macullipennis <-data[21,]
T_dim_F<-subset(data, Species=='T_dimidiata_F')
T_mop_F<-subset(data, Species=='T_mopan_F')
T_dim_M<-subset(data, Species=='T_dimidiata_M')
T_mop_M<-subset(data, Species=='T_mopan_M')

boxplot(data$TL ~ data$Species, ylab = "Total length of the body (mm)",
        border= c("gray45", "gray45", "gray45", "gray45"),
        col=c("white", "white", "gray95", "gray95" ),
        main = "Comparison of total length of the body")
stripchart(Lanquin$TL, vertical=TRUE, add=TRUE,
           method="stack", col='black', pch=19, at = 2)
stripchart(29, vertical=TRUE, add=TRUE,
           method="stack", col='red', pch=19, at = 2)
stripchart(33, vertical=TRUE, add=TRUE,
           method="stack", col='red', pch=19, at = 1)
stripchart(Capitata$TL, vertical=TRUE, add=TRUE,
           method="stack", col='dodgerblue3', pch=19, at = 1)
stripchart(Macullipennis$TL, vertical=TRUE, add=TRUE,
           method="stack", col='lightgoldenrod', pch=19, at = 2)
legend("topright", legend = c("Lanquin L&W", "Lanquin", "T. dimidiata capitata",
                             "T. dimidiata maculipennis"),
       col = c('red', 'black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")
```

## Comparison of total length of the body

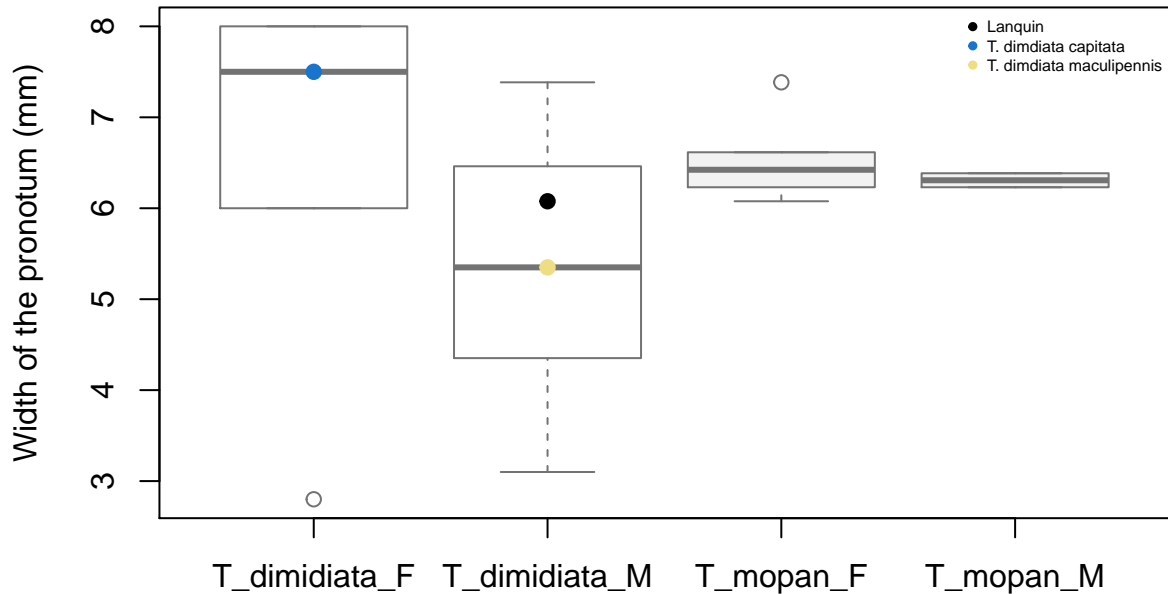


```

boxplot(data$WOP ~ data$Specie, ylab = "Width of the pronotum (mm)",
        border= c("gray45", "gray45", "gray45", "gray45"),
        col=c("white", "white", "gray95", "gray95" ),
        main = "Comparison of width of the pronotum ")
stripchart(Lanquin$WOP, vertical=TRUE, add=TRUE,
           method="stack", col='black', pch=19, at = 2)
stripchart(Capitata$WOP, vertical=TRUE, add=TRUE,
           method="stack", col='dodgerblue3', pch=19, at = 1)
stripchart(Macullipennis$WOP, vertical=TRUE, add=TRUE,
           method="stack", col='lightgoldenrod', pch=19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

## Comparison of width of the pronotum

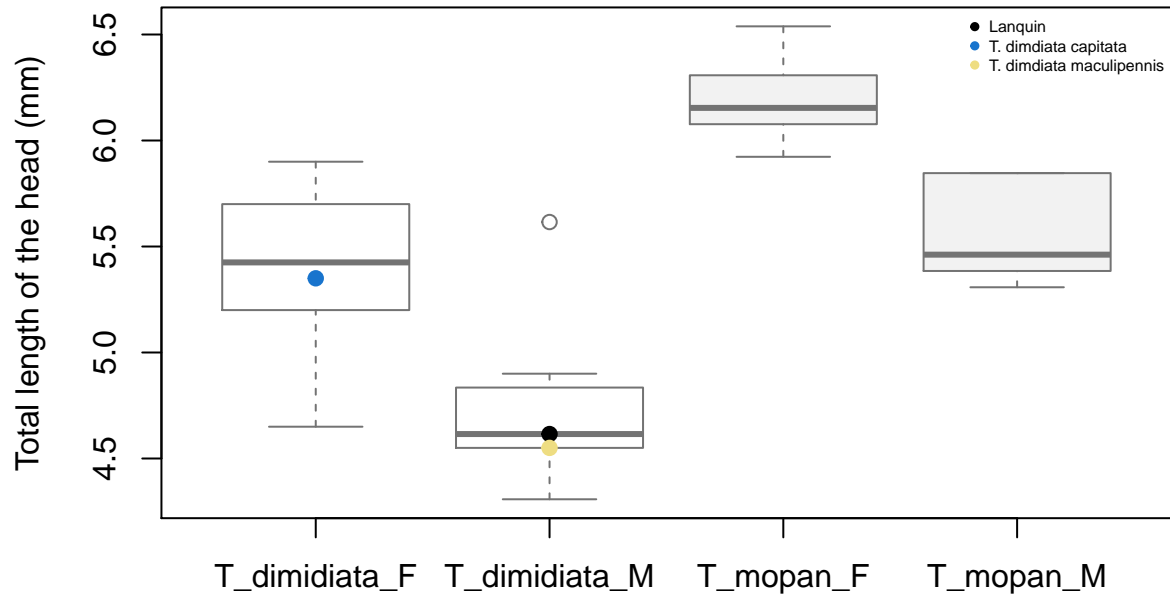


```

boxplot(data$HL ~ data$Specie, ylab = "Total length of the head (mm)",
        border= c("gray45", "gray45", "gray45", "gray45"),
        col=c("white", "white", "gray95", "gray95" ),
        main = "Comparison of length of the head ")
stripchart(Lanquin$HL, vertical=TRUE, add=TRUE,
           method="stack", col='black', pch=19, at = 2)
stripchart(Capitata$HL, vertical=TRUE, add=TRUE,
           method="stack", col='dodgerblue3', pch=19, at = 1)
stripchart(Macullipennis$HL, vertical=TRUE, add=TRUE,
           method="stack", col='lightgoldenrod', pch=19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

## Comparison of length of the head

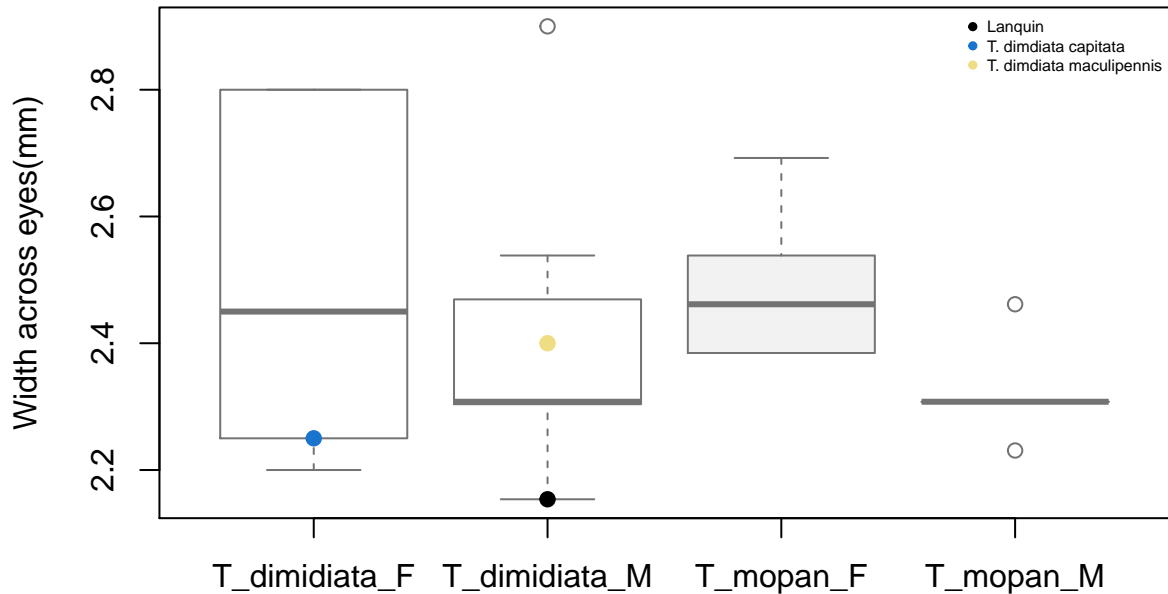


```

boxplot(data$WAE ~ data$Specie, ylab = "Width across eyes(mm)",
        border= c("gray45", "gray45", "gray45", "gray45"),
        col=c("white", "white", "gray95", "gray95" ),
        main = "Comparison of width across eyes")
stripchart(Lanquin$WAE, vertical=TRUE, add=TRUE,
           method="stack", col='black', pch=19, at = 2)
stripchart(Capitata$WAE, vertical=TRUE, add=TRUE,
           method="stack", col='dodgerblue3', pch=19, at = 1)
stripchart(Macullipennis$WAE, vertical=TRUE, add=TRUE,
           method="stack", col='lightgoldenrod', pch=19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

## Comparison of width across eyes

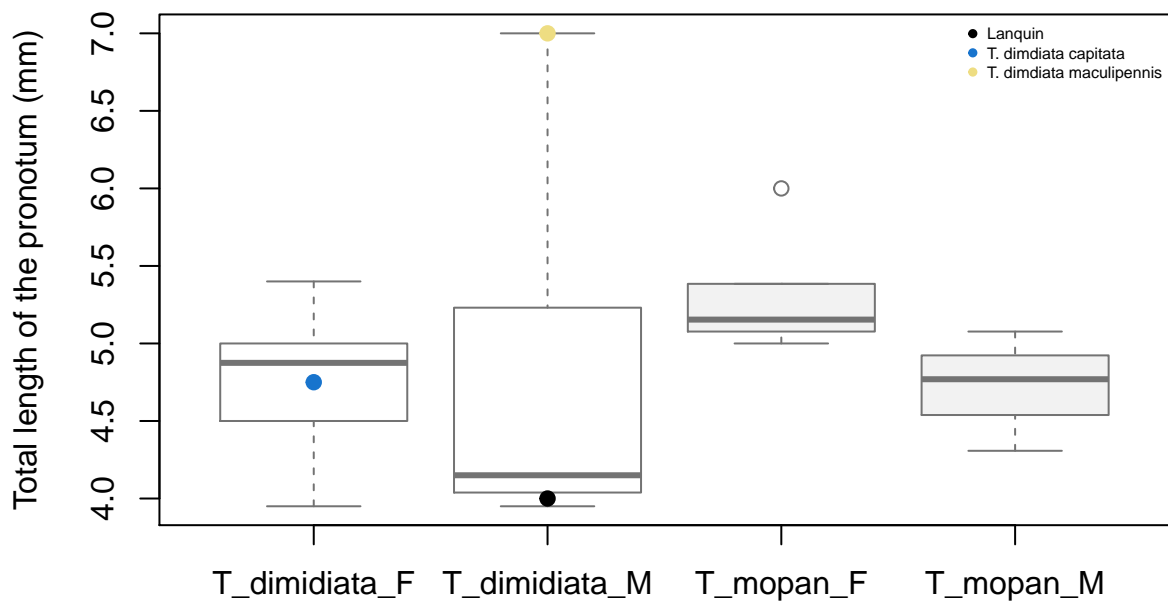


```

boxplot(data$LOP ~ data$Species, ylab = "Total length of the pronotum (mm)",
        border = c("gray45", "gray45", "gray45", "gray45"),
        col = c("white", "white", "gray95", "gray95"),
        main = "Comparison of length of the pronotum ")
stripchart(Lanquin$LOP, vertical = TRUE, add = TRUE,
           method = "stack", col = 'black', pch = 19, at = 2)
stripchart(Capitata$LOP, vertical = TRUE, add = TRUE,
           method = "stack", col = 'dodgerblue3', pch = 19, at = 1)
stripchart(Macullipennis$LOP, vertical = TRUE, add = TRUE,
           method = "stack", col = 'lightgoldenrod', pch = 19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

## Comparison of length of the pronotum

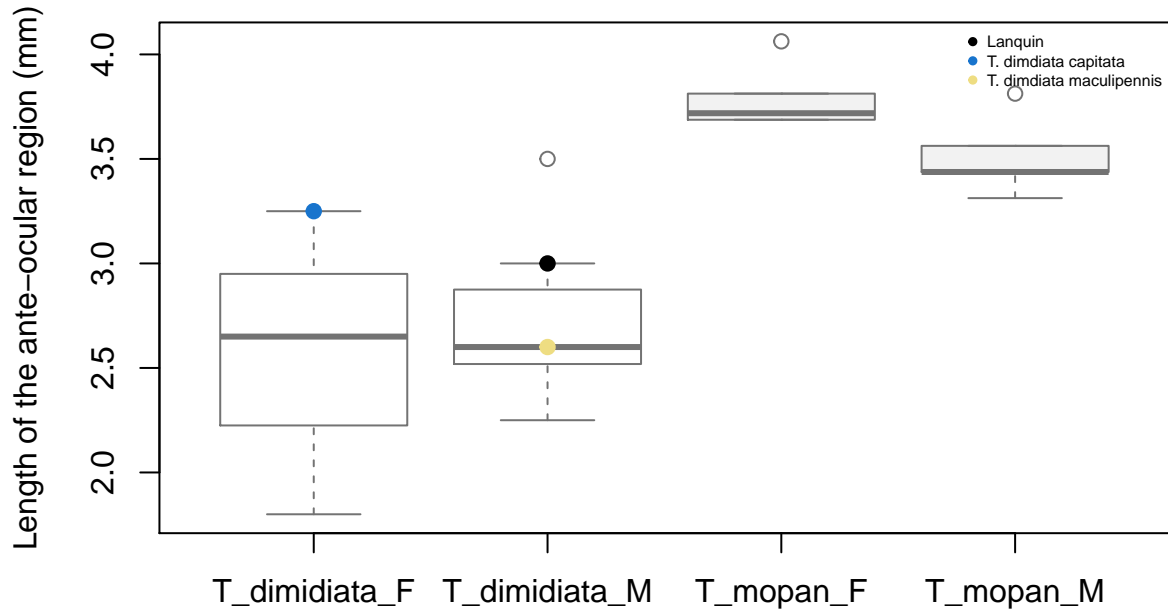


```

boxplot(data$AOR ~ data$Species, ylab = "Length of the ante-ocular region (mm)",
        border= c("gray45", "gray45", "gray45", "gray45"),
        col=c("white", "white", "gray95", "gray95" ),
        main = "Comparison of length of the ante-ocular region ")
stripchart(Lanquin$AOR, vertical=TRUE, add=TRUE,
           method="stack", col='black', pch=19, at = 2)
stripchart(Capitata$AOR, vertical=TRUE, add=TRUE,
           method="stack", col='dodgerblue3', pch=19, at = 1)
stripchart(Macullipennis$AOR, vertical=TRUE, add=TRUE,
           method="stack", col='lightgoldenrod', pch=19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

## Comparison of length of the ante-ocular region

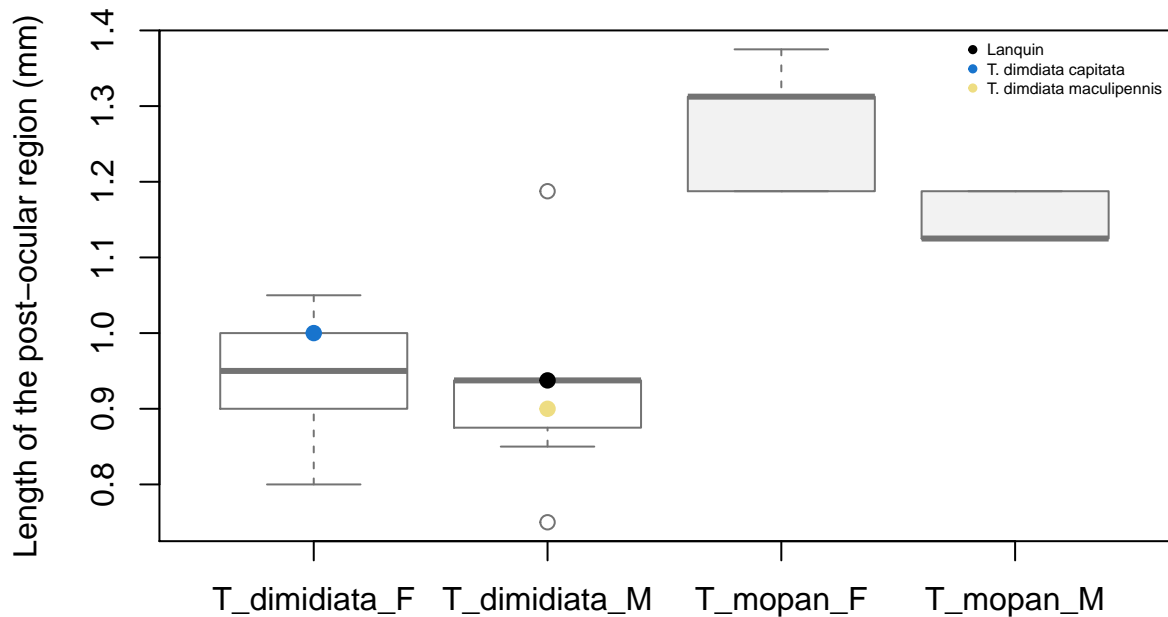


```

boxplot(data$POR~ data$Species, ylab = "Length of the post-ocular region (mm)",
        border= c("gray45", "gray45", "gray45", "gray45"),
        col=c("white", "white", "gray95", "gray95" ),
        main = "Comparison of length of the post-ocular region ")
stripchart(Lanquin$POR, vertical=TRUE, add=TRUE,
           method="stack", col='black', pch=19, at = 2)
stripchart(Capitata$POR, vertical=TRUE, add=TRUE,
           method="stack", col='dodgerblue3', pch=19, at = 1)
stripchart(Macullipennis$POR, vertical=TRUE, add=TRUE,
           method="stack", col='lightgoldenrod', pch=19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

## Comparison of length of the post-ocular region

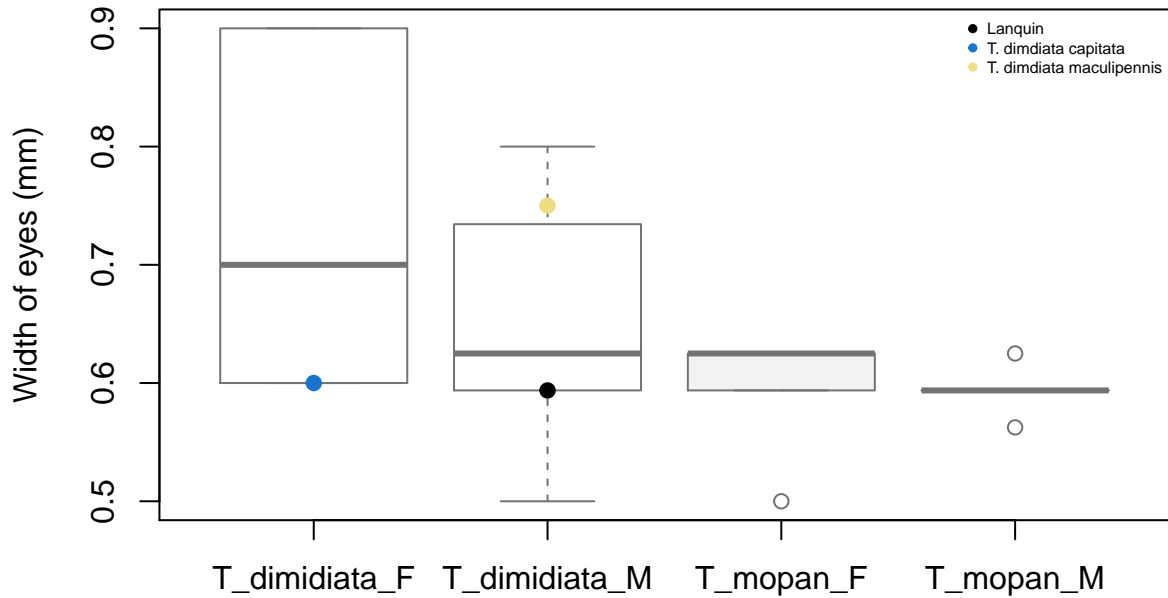


```

boxplot(data$WE ~ data$Species, ylab = "Width of eyes (mm)",
        border = c("gray45", "gray45", "gray45", "gray45"),
        col = c("white", "white", "gray95", "gray95"),
        main = "Comparison of width of eyes ")
stripchart(Lanquin$WE, vertical = TRUE, add = TRUE,
           method = "stack", col = 'black', pch = 19, at = 2)
stripchart(Capitata$WE, vertical = TRUE, add = TRUE,
           method = "stack", col = 'dodgerblue3', pch = 19, at = 1)
stripchart(Macullipennis$WE, vertical = TRUE, add = TRUE,
           method = "stack", col = 'lightgoldenrod', pch = 19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")
    
```



## Comparison of width of eyes

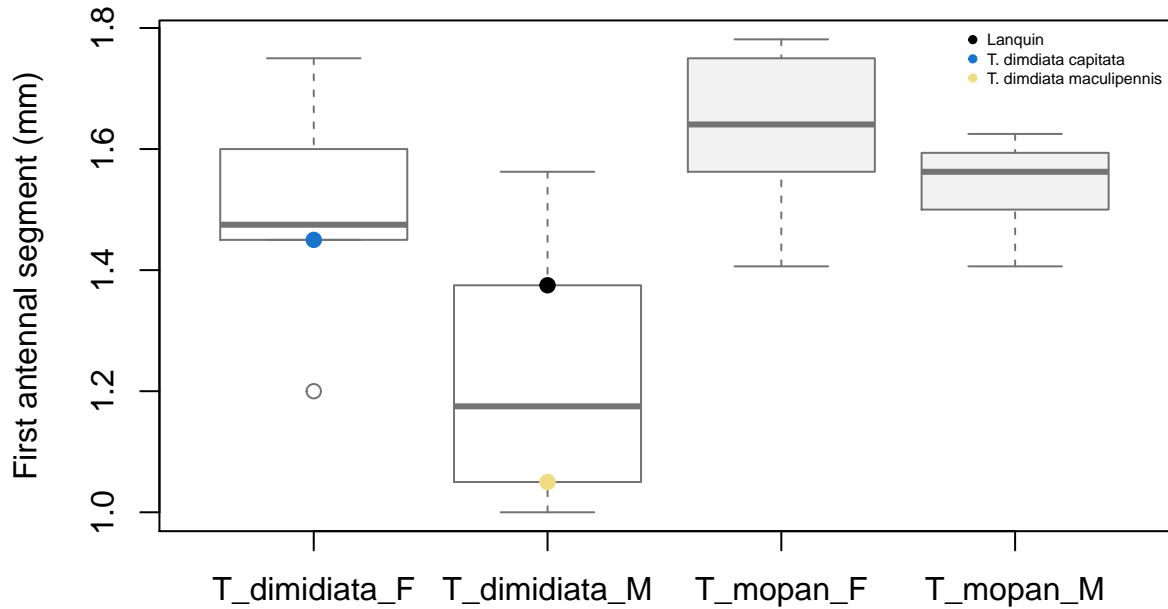


```

boxplot(data$A1 ~ data$Species, ylab = "First antennal segment (mm)",
        border= c("gray45", "gray45", "gray45", "gray45"),
        col=c("white", "white", "gray95", "gray95" ),
        main = "First antennal segment")
stripchart(Lanquin$A1, vertical=TRUE, add=TRUE,
           method="stack", col='black', pch=19, at = 2)
stripchart(Capitata$A1, vertical=TRUE, add=TRUE,
           method="stack", col='dodgerblue3', pch=19, at = 1)
stripchart(Macullipennis$A1, vertical=TRUE, add=TRUE,
           method="stack", col='lightgoldenrod', pch=19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

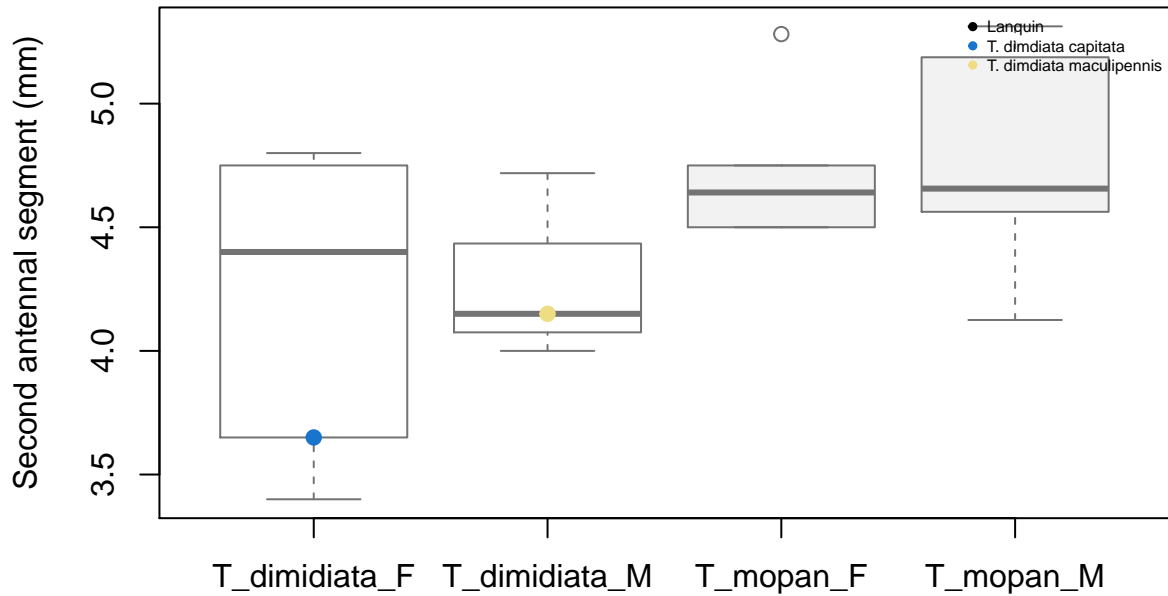
## First antennal segment



```

boxplot(data$A2 ~ data$Species, ylab = "Second antennal segment (mm)",
        border = c("gray45", "gray45", "gray45", "gray45"),
        col = c("white", "white", "gray95", "gray95"),
        main = "Second antennal segment")
stripchart(Lanquin$A2, vertical = TRUE, add = TRUE,
           method = "stack", col = 'black', pch = 19, at = 2)
stripchart(Capitata$A2, vertical = TRUE, add = TRUE,
           method = "stack", col = 'dodgerblue3', pch = 19, at = 1)
stripchart(Macullipennis$A2, vertical = TRUE, add = TRUE,
           method = "stack", col = 'lightgoldenrod', pch = 19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")
    
```

## Second antennal segment

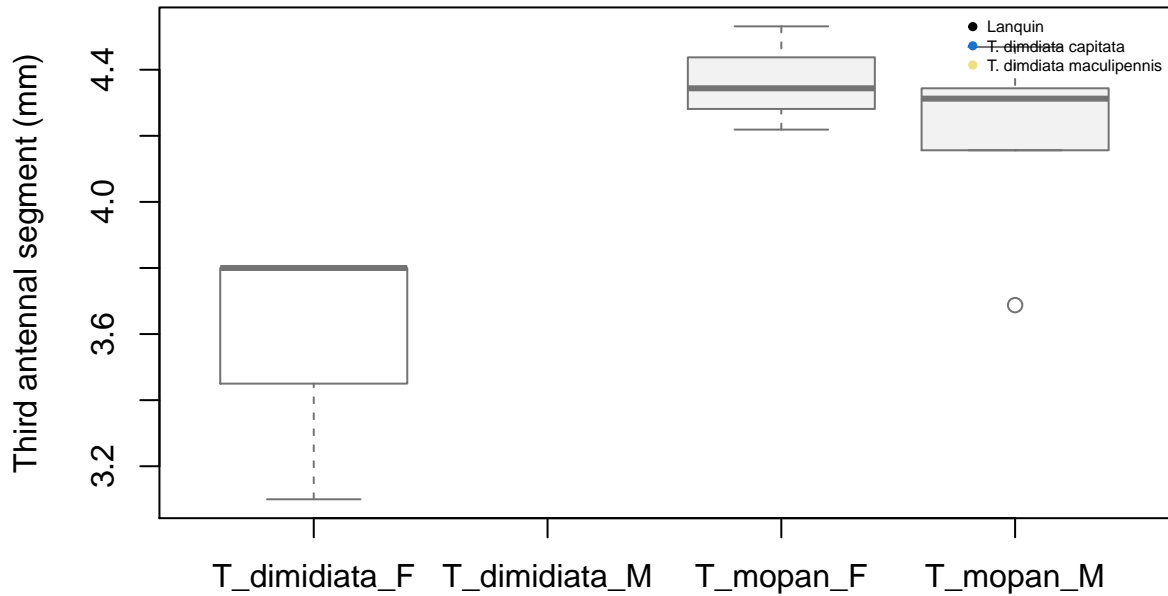


```

boxplot(data$A3 ~ data$Species, ylab = "Third antennal segment (mm)",
        border = c("gray45", "gray45", "gray45", "gray45"),
        col = c("white", "white", "gray95", "gray95"),
        main = "Third antennal segment")
stripchart(Lanquin$A3, vertical = TRUE, add = TRUE,
           method = "stack", col = 'black', pch = 19, at = 2)
stripchart(Capitata$A3, vertical = TRUE, add = TRUE,
           method = "stack", col = 'dodgerblue3', pch = 19, at = 1)
stripchart(Macullipennis$A3, vertical = TRUE, add = TRUE,
           method = "stack", col = 'lightgoldenrod', pch = 19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

## Third antennal segment

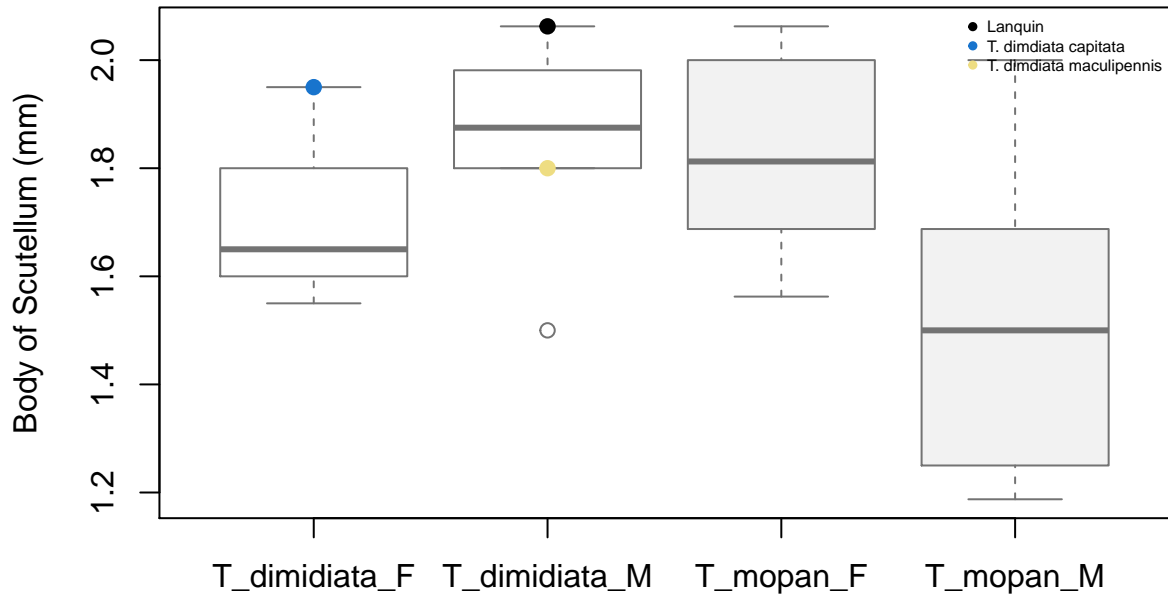


```

boxplot(data$BOS ~ data$Species, ylab = "Body of Scutellum (mm)",
        border = c("gray45", "gray45", "gray45", "gray45"),
        col = c("white", "white", "gray95", "gray95"),
        main = "Body of Scutellum")
stripchart(Lanquin$BOS, vertical = TRUE, add = TRUE,
           method = "stack", col = 'black', pch = 19, at = 2)
stripchart(Capitata$BOS, vertical = TRUE, add = TRUE,
           method = "stack", col = 'dodgerblue3', pch = 19, at = 1)
stripchart(Macullipennis$BOS, vertical = TRUE, add = TRUE,
           method = "stack", col = 'lightgoldenrod', pch = 19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

## Body of Scutellum

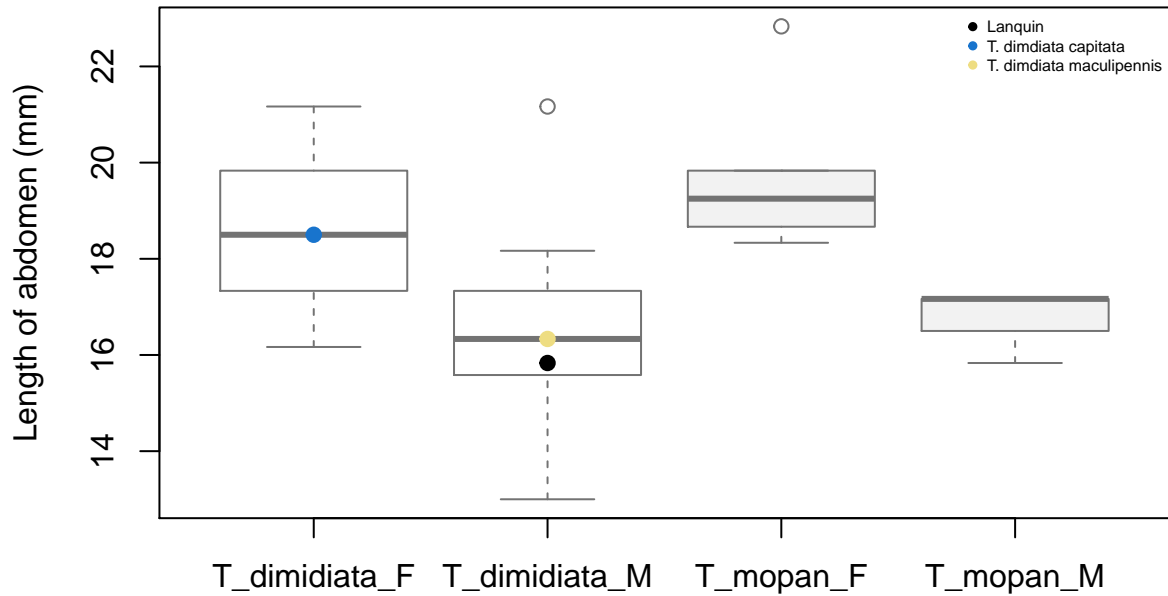


```

boxplot(data$LA ~ data$Species, ylab = "Length of abdomen (mm)",
        border = c("gray45", "gray45", "gray45", "gray45"),
        col = c("white", "white", "gray95", "gray95"),
        main = "Length of abdomen")
stripchart(Lanquin$LA, vertical = TRUE, add = TRUE,
           method = "stack", col = 'black', pch = 19, at = 2)
stripchart(Capitata$LA, vertical = TRUE, add = TRUE,
           method = "stack", col = 'dodgerblue3', pch = 19, at = 1)
stripchart(Macullipennis$LA, vertical = TRUE, add = TRUE,
           method = "stack", col = 'lightgoldenrod', pch = 19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

## Length of abdomen

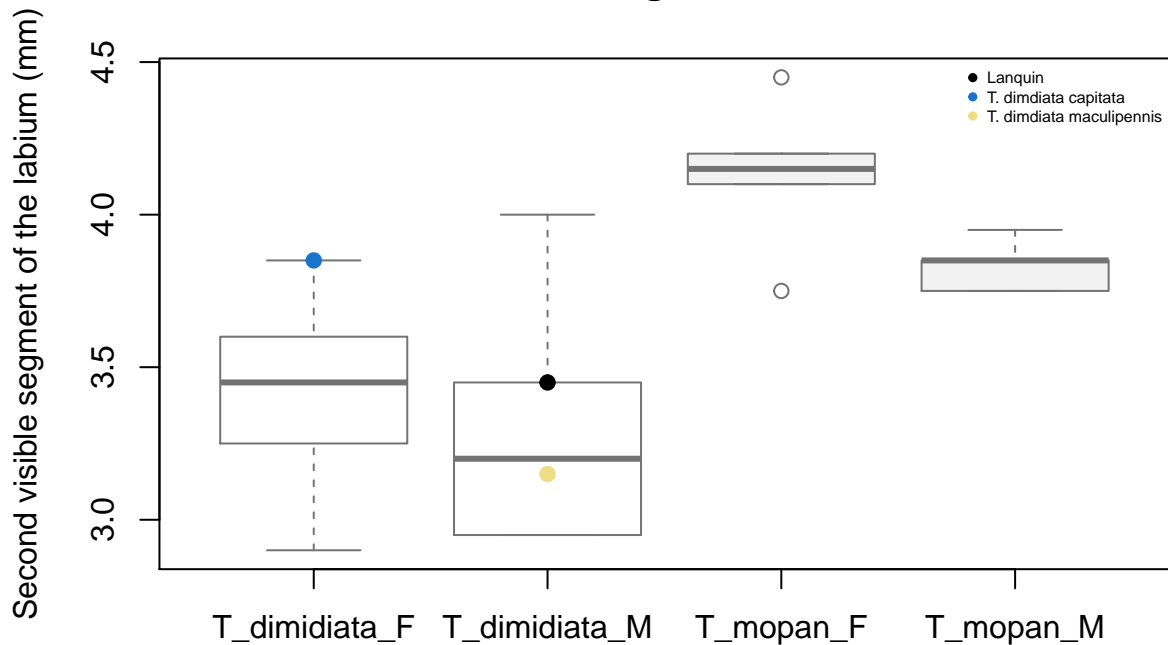


```

boxplot(data$R2 ~ data$Species, ylab = "Second visible segment of the labium (mm)",
        border = c("gray45", "gray45", "gray45", "gray45"),
        col = c("white", "white", "gray95", "gray95"),
        main = "Second visible segment of the labium")
stripchart(Lanquin$R2, vertical = TRUE, add = TRUE,
           method = "stack", col = 'black', pch = 19, at = 2)
stripchart(Capitata$R2, vertical = TRUE, add = TRUE,
           method = "stack", col = 'dodgerblue3', pch = 19, at = 1)
stripchart(Macullipennis$R2, vertical = TRUE, add = TRUE,
           method = "stack", col = 'lightgoldenrod', pch = 19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

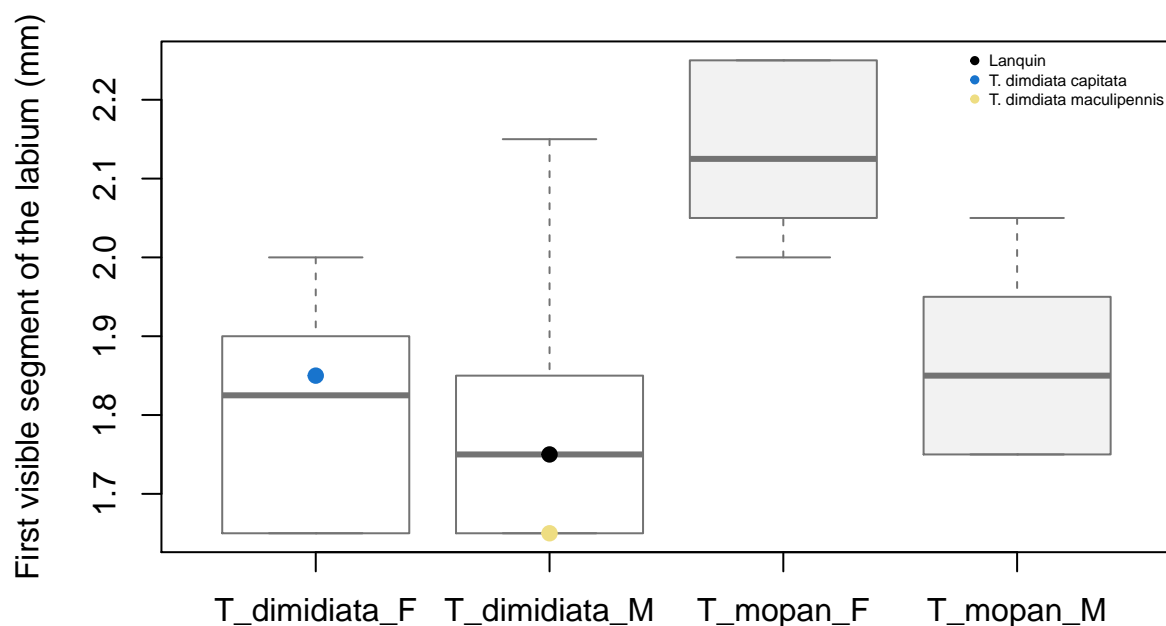
## Second visible segment of the labium



```

boxplot(data$R1 ~ data$Species, ylab = "First visible segment of the labium (mm)",
        border = c("gray45", "gray45", "gray45", "gray45"),
        col = c("white", "white", "gray95", "gray95"),
        main = "First visible segment of the labium")
stripchart(Lanquin$R1, vertical = TRUE, add = TRUE,
           method = "stack", col = 'black', pch = 19, at = 2)
stripchart(Capitata$R1, vertical = TRUE, add = TRUE,
           method = "stack", col = 'dodgerblue3', pch = 19, at = 1)
stripchart(Macullipennis$R1, vertical = TRUE, add = TRUE,
           method = "stack", col = 'lightgoldenrod', pch = 19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")
    
```

## First visible segment of the labium

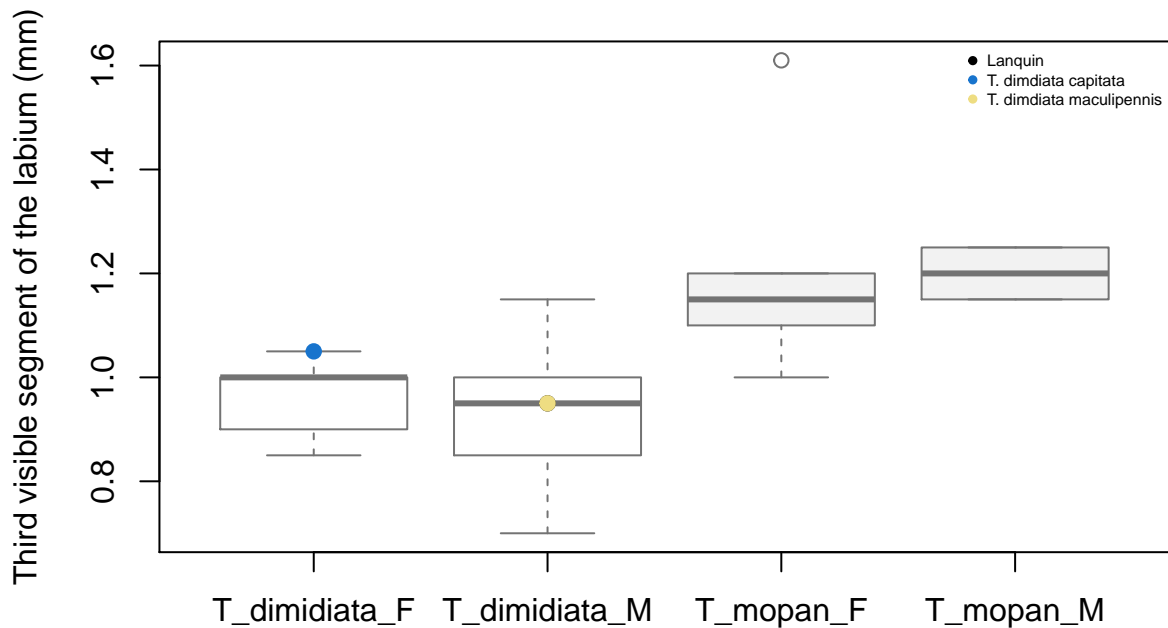


```

boxplot(data$R3 ~ data$Species, ylab = "Third visible segment of the labium (mm)",
        border = c("gray45", "gray45", "gray45", "gray45"),
        col = c("white", "white", "gray95", "gray95"),
        main = "Third visible segment of the labium")
stripchart(Lanquin$R3, vertical = TRUE, add = TRUE,
           method = "stack", col = 'black', pch = 19, at = 2)
stripchart(Capitata$R3, vertical = TRUE, add = TRUE,
           method = "stack", col = 'dodgerblue3', pch = 19, at = 1)
stripchart(Macullipennis$R3, vertical = TRUE, add = TRUE,
           method = "stack", col = 'lightgoldenrod', pch = 19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")
    
```



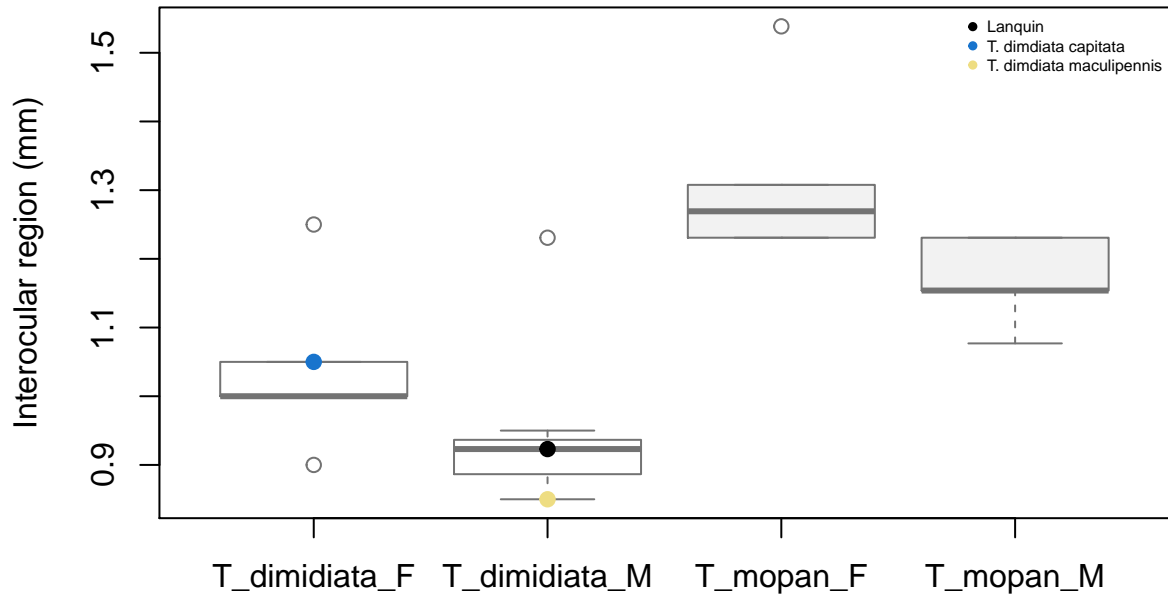
## Third visible segment of the labium



```

boxplot(data$S ~ data$Species, ylab = "Interocular region (mm)",
        border = c("gray45", "gray45", "gray45", "gray45"),
        col = c("white", "white", "gray95", "gray95"),
        main = "Interocular region")
stripchart(Lanquin$S, vertical = TRUE, add = TRUE,
           method = "stack", col = 'black', pch = 19, at = 2)
stripchart(Capitata$S, vertical = TRUE, add = TRUE,
           method = "stack", col = 'dodgerblue3', pch = 19, at = 1)
stripchart(Macullipennis$S, vertical = TRUE, add = TRUE,
           method = "stack", col = 'lightgoldenrod', pch = 19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimidiata capitata",
                              "T. dimidiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")
    
```

## Interocular region



```

boxplot(data$Scut ~ data$Species, ylab = "Total legh of scutellum (mm)",
        border= c("gray45", "gray45", "gray45", "gray45"),
        col=c("white", "white", "gray95", "gray95" ),
        main = "Total legh of scutellum")
stripchart(Lanquin$Scut, vertical=TRUE, add=TRUE,
           method="stack", col='black', pch=19, at = 2)
stripchart(Capitata$Scut, vertical=TRUE, add=TRUE,
           method="stack", col='dodgerblue3', pch=19, at = 1)
stripchart(Macullipennis$Scut, vertical=TRUE, add=TRUE,
           method="stack", col='lightgoldenrod', pch=19, at = 2)
legend("topright", legend = c("Lanquin", "T. dimdiata capitata",
                              "T. dimdiata maculipennis"),
       col = c('black', 'dodgerblue3', 'lightgoldenrod'),
       cex = 0.5, pch = 19, bty = "n")

```

### Total length of scutellum

