

SUPPLEMENTARY MATERIAL

**Microplastics in the Gastrointestinal Tract and Gills of Fish (*Dormitator latifrons*)
from Monterrico Multiple Use Natural Reserve, Guatemala**

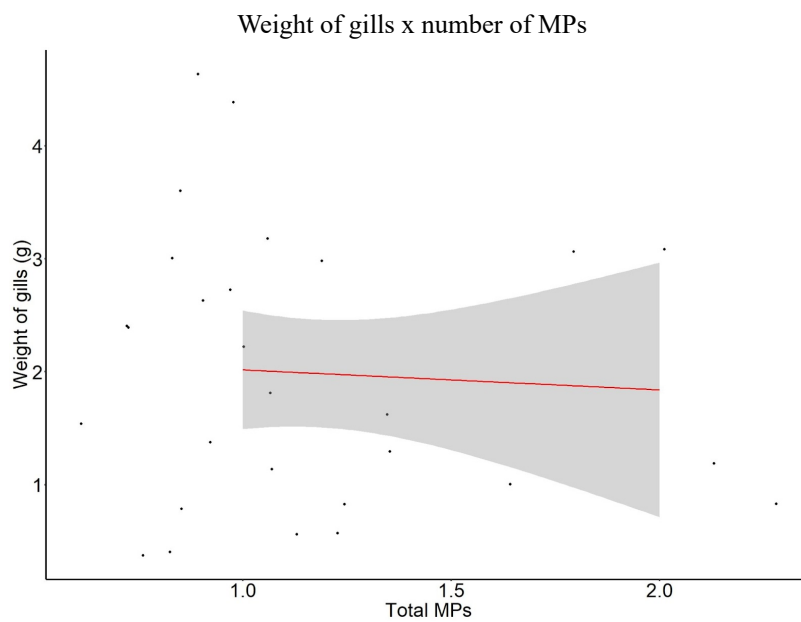
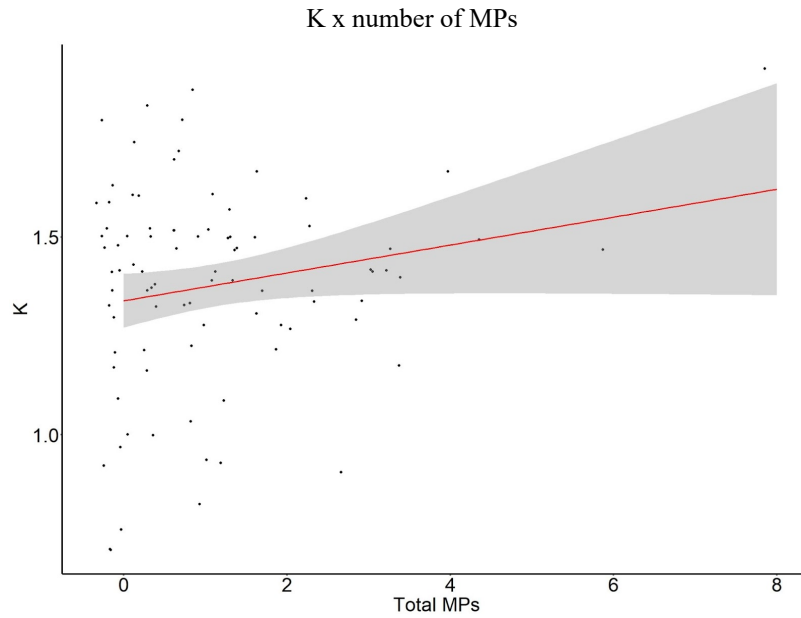


Table 1. Summary of results of microplastics in fish (*Dormitator latifrons*) from Monterrico Multiple Use Natural Reserve. N =89.

Parameter	GIT	Gill	Both organs
Fish with MPs	51	25	66
MPs found	98	33	122
% Frequency	57.3	28.1	74.15
Average (MP/individual)	1.10	0.37	1.37
Average Abundance	1.92	1.32	1.84

Note: Average abundance: number of microplastics by individual in which MPs were recorded; GIT: Gastrointestinal tract

CÓDIGO R STUDIO PARA EL ANÁLISIS DE DATOS “BASE DE DATOS PECES”

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```
library(readxl)

setwd("c://Users/Carlos Mazariegos/Desktop/Bessie/") #CAMBIAR LA RUTA EN LA COMPUTADORA
DONDE SE CORRERÁN LOS ANÁLISIS

bes<- read_excel("Base de datos peces MPS.xlsx", sheet = "Color_GIT")

library(ggplot2)

library(tidyr)

library(dplyr)

#MPS en tracto por forma y color

temp <-

  theme_classic() + theme(axis.text = element_text(size = 30, color = "black"),

    axis.title = element_text(size = 30),

    axis.line = element_line(linewidth = 1.2),

    axis.ticks = element_line(linewidth = 1.2),

    legend.text = element_text(size = 30),

    legend.title = element_text(size = 30))

ggplot(bes, aes(x = Forma, y = order(Percentage), fill = Color)) + geom_bar(stat = "identity",

  position = "stack",

  color = "black",

  width = 0.6) +

  scale_fill_manual(values = c("black", "#377eb8", "darkgreen", "grey", "#e41a1c",

    "skyblue", "beige", "yellow")) + temp +

  scale_y_continuous(expand = expansion(mult = c(0,0.1))) +

  labs(x = "Shape", y = "Total MPs", fill = "Color")
```

```
#MPS por forma
```

```
bes2<- read_excel("Base de datos peces MPS.xlsx", sheet = "Forma_GIT")
```

```
ggplot(bes2, aes(x = reorder(Shape, -N), y = N)) + geom_col(width = 0.6, fill = "black") + temp +  
  scale_y_continuous(expand = expansion(mult = c(0,0.1))) +  
  labs(x = "Shape", y = "Total MPs", fill = "Color")
```

```
#MPS en branquias por forma y color
```

```
bes3<- read_excel("Base de datos peces MPS.xlsx", sheet = "Color_B")
```

```
ggplot(bes3, aes(x = Shape, y = order(Percentage), fill = Color)) + geom_bar(stat = "identity",  
  position = "stack",  
  color = "black",  
  width = 0.6) +  
  scale_fill_manual(values = c("black", "#377eb8", "darkgreen", "grey", "#e41a1c",  
  "skyblue", "beige", "yellow")) + temp +  
  scale_y_continuous(expand = expansion(mult = c(0,0.1))) +  
  labs(x = "Shape", y = "Total MPs", fill = "Color")
```

```
#MPS por forma en branquias
```

```
bes4<- read_excel("Base de datos peces MPS.xlsx", sheet = "Forma_B")
```

```
ggplot(bes4, aes(x = reorder(Shape, -N), y = N)) + geom_col(width = 0.6, fill = "black") + temp +  
  scale_y_continuous(expand = expansion(mult = c(0,0.1))) +  
  labs(x = "Shape", y = "Total MPs", fill = "Color")
```

```
#MPS y su relación con variables biométricas
```

```
bes5<- read_excel("Base de datos peces MPS.xlsx", sheet = "Bio_MPS")
```

```
modelo_peso<- lm(bes5$CF~bes5$Total_MPs, bes5)
```

```
summary(modelo_peso)
```

```
cor.test(y = bes5$CF, x = bes5$Total_MPs, method = "kendall")
```

```
ggplot(bes5, aes(y = round(bes5$CF, 1), x = Total_MPs)) +
```

```
  geom_jitter() + # puntos reales
```

```
  geom_smooth(method = "lm", se = TRUE, color = "red") +
```

```
  theme_minimal() +
```

```
  labs(x = "Total MPs",
```

```
        y = "K") + temp
```

```
#MPS en branquias y su relación con el peso húmedo de ellas
```

```
branq<- read_excel("Base de datos peces MPS.xlsx", sheet = "Bio2_MPS")
```

```
cor.test(y = branq$`Peso húmedo de branquias (g)`, x = branq$MPs_Bran, method = "kendall")
```

```
modelo_bran<- lm(branq$`Peso húmedo de branquias (g)`~branq$MPs_Bran, branq)
```

```
summary(modelo_bran)
```

```
ggplot(branq, aes(y = branq$`Peso húmedo de branquias (g)`, x = round(MPs_Bran, 0))) +
```

```
  geom_jitter() + # puntos reales
```

```
  geom_smooth(method = "lm", se = TRUE, color = "red") +
```

```
  theme_minimal() +
```

```
  labs(x = "Total MPs",
```

y = "Weight of gills (g)" + temp

#COMPARANDO LOS DOS VALORES DE MICROPLASTICOS

#PRUEBA DE NORMALIDAD

bes6<- read_excel("Base de datos peces MPS.xlsx", sheet = "Comparación")

shapiro.test(bes6\$MPS_GIT) #no se ajusta a la distribución normal

shapiro.test(bes6\$MPS_Bran) #no se ajusta a la distribución normal

#Prueba de Mann-Whitney

wilcox.test(bes6\$MPS_GIT, bes6\$MPS_Bran)