Supplementary Materials: Emerging Fusarium Mycotoxins Fusaproliferin, Beauvericin, Enniatins, and Moniliformin in Serbian Maize

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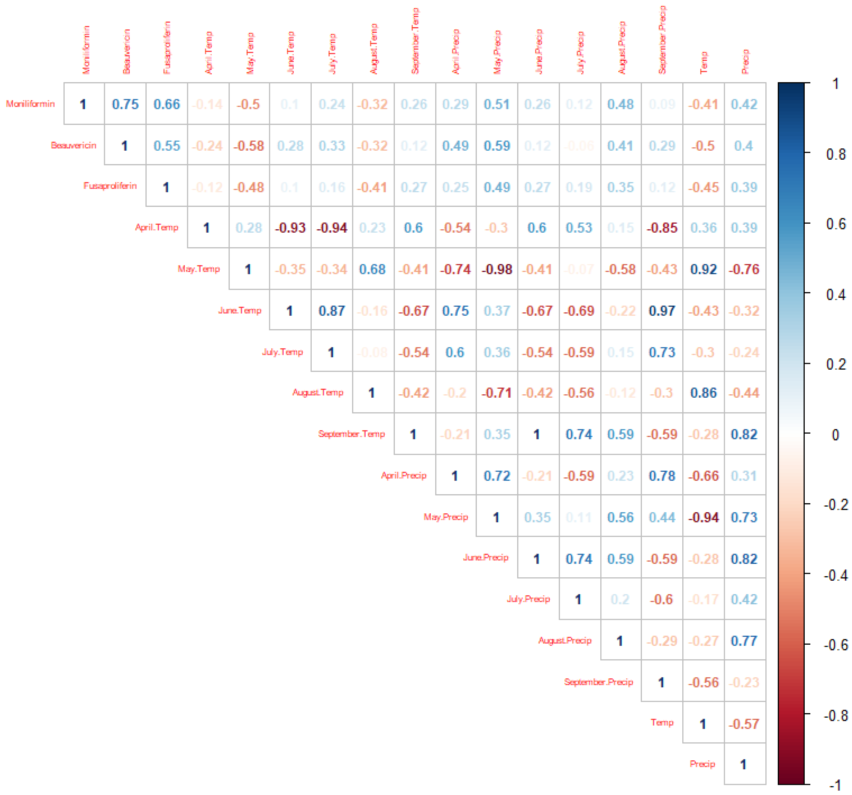
Normality test:

```
[1] "Moniliformin"

        Shapiro-Wilk normality test

data:  df[[i]]

W = 0.71536, p-value = 3.833e-15

[1] "Beauvericin"

        Shapiro-Wilk normality test

data:  df[[i]]

W = 0.45344, p-value < 2.2e-16

[1] "Fusaproliferin"

        Shapiro-Wilk normality test

data:  df[[i]]

W = 0.12177, p-value < 2.2e-16

[1] "April.Temp"

        Shapiro-Wilk normality test

data:  df[[i]]

W = 0.83133, p-value = 2.184e-11

[1] "May.Temp"

        Shapiro-Wilk normality test

data:  df[[i]]

W = 0.81032, p-value = 3.536e-12

[1] "June.Temp"
```

```
	Shapiro-Wilk normality test
data:  df[[i]]
W = 0.78115, p-value = 3.503e-13
[1] "July.Temp"
	Shapiro-Wilk normality test
data:  df[[i]]
W = 0.87256, p-value = 1.279e-09
[1] "August.Temp"
	Shapiro-Wilk normality test
data:  df[[i]]
W = 0.67654, p-value = 3.76e-16
[1] "September.Temp"
	Shapiro-Wilk normality test
data:  df[[i]]
W = 0.81324, p-value = 4.517e-12
[1] "April.Precip"
	Shapiro-Wilk normality test
data:  df[[i]]
W = 0.77426, p-value = 2.096e-13
[1] "May.Precip"
	Shapiro-Wilk normality test
data:  df[[i]]
W = 0.76691, p-value = 1.224e-13
[1] "June.Precip"
	Shapiro-Wilk normality test
data:  df[[i]]
W = 0.7955, p-value = 1.062e-12
```

```
[1] "July.Precip"

        Shapiro-Wilk normality test

data:  df[[i]]

W = 0.76561, p-value = 1.115e-13

[1] "August.Precip"

        Shapiro-Wilk normality test

data:  df[[i]]

W = 0.85182, p-value = 1.504e-10

[1] "September.Precip"

        Shapiro-Wilk normality test

data:  df[[i]]

W = 0.84275, p-value = 6.272e-11

[1] "Temp"

        Shapiro-Wilk normality test

data:  df[[i]]

W = 0.78317, p-value = 4.082e-13

[1] "Precip"

        Shapiro-Wilk normality test

data:  df[[i]]

W = 0.86504, p-value = 5.74e-10
```

Spearman Correlation



	Moniliformin	Beauvericin	Fusaproliferin	April.Temp	May.Temp	June.Temp	July.Temp	August.Temp	September.Temp	April.Precip	May.Precip	June.Precip	July.Precip	August.Precip	September.Precip	Temp	Precip
Moniliformin	1	0.75	0.66	-0.14	-0.5	0.1	0.24	-0.32	0.26	0.29	0.51	0.26	0.12	0.48	0.09	-0.41	0.42
Beauvericin		1	0.55	-0.24	-0.58	0.28	0.33	-0.32	0.12	0.49	0.59	0.12	-0.06	0.41	0.29	-0.5	0.4
Fusaproliferin			1	-0.12	-0.48	0.1	0.16	-0.41	0.27	0.25	0.49	0.27	0.19	0.35	0.12	-0.45	0.39
April.Temp				1	0.28	-0.93	-0.94	0.23	0.6	-0.54	-0.3	0.6	0.53	0.15	-0.85	0.36	0.39
May.Temp					1	-0.35	-0.34	0.68	-0.41	-0.74	-0.98	-0.41	-0.07	-0.58	-0.43	0.92	-0.76
June.Temp						1	0.87	-0.16	-0.67	0.75	0.37	-0.67	-0.69	-0.22	0.97	-0.43	-0.32
July.Temp							1	-0.08	-0.54	0.6	0.36	-0.54	-0.59	0.15	0.73	-0.3	-0.24
August.Temp								1	-0.42	-0.2	-0.71	-0.42	-0.56	-0.12	-0.3	0.86	-0.44
September.Temp									1	-0.21	0.35	1	0.74	0.59	-0.59	-0.28	0.82
April.Precip										1	0.72	-0.21	-0.59	0.23	0.78	-0.66	0.31
May.Precip											1	0.35	0.11	0.56	0.44	-0.94	0.73
June.Precip												1	0.74	0.59	-0.59	-0.28	0.82
July.Precip													1	0.2	-0.6	-0.17	0.42
August.Precip														1	-0.29	-0.27	0.77
September.Precip															1	-0.56	-0.23
Temp																1	-0.57
Precip																	1

Figure S1. Spearman Correlation Results (*r*).

Kruskal-Wallis rank sum test

```
>kruskal.test(analysis_data2$Moniliformin~analysis_data2$Region)

        Kruskal-Wallis rank sum test

data:  analysis_data2$Moniliformin by analysis_data2$Region

Kruskal-Wallis chi-squared = 5.4866, df = 1, p-value = 0.01916

>kruskal.test(analysis_data2$Moniliformin~analysis_data2$Year)

        Kruskal-Wallis rank sum test

data:  analysis_data2$Moniliformin by analysis_data2$Year

Kruskal-Wallis chi-squared = 33.225, df = 2, p-value = 6.101e-08

>kruskal.test(analysis_data2$Moniliformin~analysis_data2$Temp)

        Kruskal-Wallis rank sum test

data:  analysis_data2$Moniliformin by analysis_data2$Temp

Kruskal-Wallis chi-squared = 45.42, df = 5, p-value = 1.192e-08
```

```
>kruskal.test(analysis_data2$Moniliformin~analysis_data2$Precip)

        Kruskal-Wallis rank sum test

data:  analysis_data2$Moniliformin by analysis_data2$Precip

Kruskal-Wallis chi-squared = 45.42, df = 5, p-value = 1.192e-08

>kruskal.test(analysis_data2$Fusaproliferin~analysis_data2$Region)

        Kruskal-Wallis rank sum test

data:  analysis_data2$Fusaproliferin by analysis_data2$Region

Kruskal-Wallis chi-squared = 1.6736, df = 1, p-value = 0.1958

>kruskal.test(analysis_data2$Fusaproliferin~analysis_data2$Year)

        Kruskal-Wallis rank sum test

data:  analysis_data2$Fusaproliferin by analysis_data2$Year

Kruskal-Wallis chi-squared = 35.254, df = 2, p-value = 2.211e-08

>kruskal.test(analysis_data2$Fusaproliferin~analysis_data2$Temp)

        Kruskal-Wallis rank sum test

data:  analysis_data2$Fusaproliferin by analysis_data2$Temp

Kruskal-Wallis chi-squared = 38.228, df = 5, p-value = 3.396e-07

>kruskal.test(analysis_data2$Fusaproliferin~analysis_data2$Precip)

        Kruskal-Wallis rank sum test

data:  analysis_data2$Fusaproliferin by analysis_data2$Precip

Kruskal-Wallis chi-squared = 38.228, df = 5, p-value = 3.396e-07

>kruskal.test(analysis_data2$Beauvericin~analysis_data2$Region)

        Kruskal-Wallis rank sum test

data:  analysis_data2$Beauvericin by analysis_data2$Region

Kruskal-Wallis chi-squared = 14.166, df = 1, p-value = 0.0001673

>kruskal.test(analysis_data2$Beauvericin~analysis_data2$Year)

        Kruskal-Wallis rank sum test

data:  analysis_data2$Beauvericin by analysis_data2$Year
```

```
Kruskal-Wallis chi-squared = 42.572, df = 2, p-value = 5.697e-10
>kruskal.test(analysis_data2$Beauvericin~analysis_data2$Temp)
          Kruskal-Wallis rank sum test
data:  analysis_data2$Beauvericin by analysis_data2$Temp
Kruskal-Wallis chi-squared = 53.931, df = 5, p-value = 2.165e-10
>kruskal.test(analysis_data2$Beauvericin~analysis_data2$Precip)
          Kruskal-Wallis rank sum test
data:  analysis_data2$Beauvericin by analysis_data2$Precip
Kruskal-Wallis chi-squared = 53.931, df = 5, p-value = 2.165e-10
```

Stepwise regression with backward steps

```
> full.model <- lm(Moniliformin ~., data = df)
> # Stepwise regression model
>step.model<- stepAIC(full.model, direction = "backward", trace = FALSE)
>summary(step.model)
Call:
lm(formula = Moniliformin ~ Beauvericin + May.Temp + June.Temp +
July.Temp + August.Temp, data = df)
Residuals:
Min      1Q  Median      3Q     Max
-438.96 -108.10  -88.63   66.95 1413.07
Coefficients:
         Estimate Std. Error t value Pr(>|t|)
(Intercept) -4152.033   2374.424  -1.749  0.08264 .
Beauvericin     3.109      1.366   2.276  0.02445 *
May.Temp      148.220     63.831   2.322  0.02174 *
June.Temp    -282.054    137.055  -2.058  0.04153 *
```

```
July.Temp     529.457    126.171   4.196 4.91e-05 ***
August.Temp  -183.888     62.182  -2.957  0.00367 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
Residual standard error: 300.8 on 134 degrees of freedom
Multiple R-squared:  0.2555,        Adjusted R-squared:  0.2278
F-statistic: 9.199 on 5 and 134 DF,  p-value: 1.512e-07
> full.model <- lm(Fusaproliferin ~., data = df)
> # Stepwise regression model
>step.model<- stepAIC(full.model, direction = "backward", trace = FALSE)
>summary(step.model)
Call:
lm(formula = Fusaproliferin ~ 1, data = df)
Residuals:
Min     1Q Median     3Q    Max
  -522   -522   -522   -243  38088
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    522.4      278.4   1.877   0.0627 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
Residual standard error: 3294 on 139 degrees of freedom
>full.model<- lm(Beauvericin ~., data = df)
> # Stepwise regression model
>step.model<- stepAIC(full.model, direction = "backward", trace = FALSE)
>summary(step.model)
Call:
```

```
lm(formula = Beauvericin ~ Moniliformin + May.Temp, data = df)

Residuals:

Min      1Q  Median      3Q     Max

-23.204  -8.008  -5.297   1.140 116.738

Coefficients:

             Estimate Std. Error t value Pr(>|t|)

(Intercept)  53.171322  19.505027   2.726  0.00725 **

Moniliformin  0.011551   0.004858   2.378  0.01879 *

May.Temp     -2.685720   1.067909  -2.515  0.01306 *

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Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 18.58 on 137 degrees of freedom

Multiple R-squared:  0.1139,	Adjusted R-squared:  0.101

F-statistic: 8.806 on 2 and 137 DF,  p-value: 0.0002525
```