Phenols for manuscript

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Contents

Necessary libraries

```
library(knitr)
library(rlang)
library(ggplot2)
theme_set(theme_bw())
library(emmeans)
library(multcomp)
library(PLS205)
library(lme4)
library(lmerTest)
library(multcompView)
library(car)
library(Rmisc)
library(dplyr) #https://r4ds.had.co.nz/ (Chapter 3, Chapter 5, look at filter and select)
# https://bookdown.org/ansellbr/WEHI_tidyR_course_book/
library(stringr)
library(data.table)
library(GGally)
library(formatR)
library(readxl)
library(mgcv)
library(openxlsx)
```

RES

```
RES <- read_excel("RES_25Jan2024.xlsx", sheet = 1)
RES <- mutate_if(RES, is.character, as.factor)
RES$Year <- as.factor(RES$Year)

#convert phenols from mg 100-1g OC to g kg-1 OC

RES$TotalP <- (RES$TotalP)*10
RES$TotalV <- (RES$TotalV)*10
RES$TotalC <- (RES$TotalC)*10
RES$TotalS <- (RES$TotalS)*10
RES$Total_phenols <- (RES$Total_phenols)*10


str(RES)
```

```
## tibble [12 x 9] (S3: tbl_df/tbl/data.frame)
##  $ Field        : Factor w/ 2 levels "CR","RF": 2 2 2 1 1 1 2 2 2 1 ...
##  $ Study        : Factor w/ 1 level "RES": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Blk          : Factor w/ 6 levels "RES 1","RES 2",..: 1 2 3 1 2 3 4 5 6 4 ...
##  $ Year         : Factor w/ 2 levels "2021","2022": 1 1 1 1 1 1 2 2 2 2 ...
##  $ TotalP       : num [1:12] 2.12 2 2.1 2.33 2.2 ...
##  $ TotalV       : num [1:12] 5 4.72 5.21 6.4 5.93 ...
##  $ TotalC       : num [1:12] 4.64 4.13 5.79 7.39 6.59 ...
##  $ TotalS       : num [1:12] 6.67 5.87 6.68 7.74 7.27 ...
##  $ Total_phenols: num [1:12] 18.4 16.7 19.8 23.9 22 ...
```

```
Total_P_RES <- lmer(TotalP ~ Field*Year+(1|Blk), data=RES)
Total_P_means_RES <- emmeans(Total_P_RES, spec ='Field')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
Total_P_effects_RES <- contrast(Total_P_means_RES, method = 'pairwise', adjust = "tukey")
anova(Total_P_RES)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq Mean Sq NumDF DenDF F value   Pr(>F)
## Field      0.00852 0.00852     1     4  0.7064 0.447960
## Year       0.44310 0.44310     1     4 36.7307 0.003742 **
## Field:Year 0.03708 0.03708     1     4  3.0741 0.154419
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(Total_P_means_RES)
```

```
##  Field emmean     SE   df lower.CL upper.CL .group
##  RF      1.89 0.0513 7.58     1.77     2.01  1
##  CR      1.94 0.0513 7.58     1.82     2.06  1
##
```

```
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
summary(Total_P_effects_RES)
```

```
##  contrast estimate     SE df t.ratio p.value
##  CR - RF    0.0533 0.0634  4   0.840  0.4480
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
Total_V_RES <- lmer(TotalV ~ Field*Year+(1|Blk), data=RES)
Total_V_means_RES <- emmeans(Total_V_RES, spec ='Field')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
Total_V_effects_RES <- contrast(Total_V_means_RES, method = 'pairwise', adjust = "tukey")
anova(Total_V_RES)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq Mean Sq NumDF DenDF F value  Pr(>F)
## Field      1.44138 1.44138     1     4  9.0905 0.03935 *
## Year       3.15026 3.15026     1     4 19.8681 0.01118 *
## Field:Year 0.38789 0.38789     1     4  2.4463 0.19285
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(Total_V_means_RES)
```

```
##  Field emmean    SE   df lower.CL upper.CL .group
##  RF      4.58 0.173 7.89     4.18     4.98  1
##  CR      5.28 0.173 7.89     4.88     5.68   2
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
summary(Total_V_effects_RES)
```

```
##  contrast estimate   SE df t.ratio p.value
##  CR - RF     0.693 0.23  4   3.015  0.0394
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```r
Total_C_RES <- lmer(TotalC ~ Field*Year+(1|Blk), data=RES)
```

```
## boundary (singular) fit: see help('isSingular')
```

```r
Total_C_means_RES <- emmeans(Total_C_RES, spec ='Field')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```r
Total_C_effects_RES <- contrast(Total_C_means_RES, method = 'pairwise', adjust = "tukey")
anova(Total_C_RES)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF DenDF F value   Pr(>F)
## Field      5.1635  5.1635     1     8 12.8822 0.007093 **
## Year       3.4450  3.4450     1     8  8.5948 0.018949 *
## Field:Year 0.8735  0.8735     1     8  2.1794 0.178113
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
cld(Total_C_means_RES)
```

```
##  Field emmean    SE df lower.CL upper.CL .group
##  RF      4.59 0.258  8     3.99     5.18  1
##  CR      5.90 0.258  8     5.30     6.49   2
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```r
summary(Total_C_effects_RES)
```

```
##  contrast estimate    SE df t.ratio p.value
##  CR - RF      1.31 0.366  4   3.589  0.0230
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```r
Total_S_RES <- lmer(TotalS ~ Field*Year+(1|Blk), data=RES)
Total_S_means_RES <- emmeans(Total_S_RES, spec ='Field')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```r
Total_S_effects_RES <- contrast(Total_S_means_RES, method = 'pairwise', adjust = "tukey")
anova(Total_S_RES)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
## Field      1.0606  1.0606     1     4  4.3546 0.1052
## Year       1.6718  1.6718     1     4  6.8643 0.0588 .
## Field:Year 0.3826  0.3826     1     4  1.5710 0.2783
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(Total_S_means_RES)
```

```
##  Field emmean    SE   df lower.CL upper.CL .group
##  RF      6.10 0.235 7.46     5.55     6.65  1
##  CR      6.69 0.235 7.46     6.14     7.24  1
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
summary(Total_S_effects_RES)
```

```
##  contrast estimate    SE df t.ratio p.value
##  CR - RF     0.595 0.285  4   2.087  0.1052
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
Total_phenols_RES <- lmer(Total_phenols ~ Field*Year+(1|Blk), data=RES)
Total_phenols_means_RES <- emmeans(Total_phenols_RES, spec ='Field')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
Total_phenols_effects_RES <- contrast(Total_phenols_means_RES, method = 'pairwise', adjust = "tukey")
anova(Total_phenols_RES)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF DenDF F value  Pr(>F)
## Field      21.114  21.114     1     4  7.8280 0.04892 *
## Year       37.700  37.700     1     4 13.9770 0.02015 *
## Field:Year  5.610   5.610     1     4  2.0799 0.22271
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(Total_phenols_means_RES)
```

```
##  Field emmean    SE   df lower.CL upper.CL .group
##  RF      17.2 0.685 7.99     15.6     18.7  1
```

```
##  CR      19.8 0.685 7.99     18.2     21.4   2
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
summary(Total_phenols_effects_RES)
```

```
##  contrast estimate    SE df t.ratio p.value
##  CR - RF      2.65 0.948  4   2.798  0.0489
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

Regional Survey

```
Growers <- read_excel("Regional_survey_25Jan2024.xlsx", sheet = 1)
Growers <- mutate_if(Growers, is.character, as.factor)
Growers$Year <- as.factor(Growers$Year)


Growers$TotalP <- (Growers$TotalP)*10
Growers$TotalV <- (Growers$TotalV)*10
Growers$TotalC <- (Growers$TotalC)*10
Growers$TotalS <- (Growers$TotalS)*10
Growers$Total_phenols <- (Growers$Total_phenols)*10

str(Growers)
```

```
## tibble [18 x 11] (S3: tbl_df/tbl/data.frame)
##  $ Field        : Factor w/ 2 levels "CR","RF": 2 2 2 2 1 1 1 1 1 1 ...
##  $ Study        : Factor w/ 1 level "Grower": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Site         : num [1:18] 3 1 4 2 3 4 2 1 7 5 ...
##  $ TotalP       : num [1:18] 1.62 1.4 1.77 2.02 1.82 ...
##  $ TotalV       : num [1:18] 3.87 3.13 4.08 4.95 4.43 ...
##  $ TotalC       : num [1:18] 3.02 1.61 3.28 3.53 6.48 ...
##  $ TotalS       : num [1:18] 4.35 4.02 5.63 6.66 6.09 ...
##  $ Total_phenols: num [1:18] 12.9 10.2 14.8 17.2 18.8 ...
##  $ Year         : Factor w/ 2 levels "2021","2022": 1 1 1 1 1 1 1 1 2 2 ...
##  $ Lat          : num [1:18] 39 38.9 38.8 39.5 39 ...
##  $ Long         : num [1:18] -122 -122 -122 -122 -122 ...
```

```
Total_P_Growers <- lmer(TotalP ~ Field*Year+(1|Site), data=Growers)
Total_P_means_Growers <- emmeans(Total_P_Growers, spec ='Field')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
Total_P_effects_Growers <- contrast(Total_P_means_Growers, method = 'pairwise', adjust = "tukey")
anova(Total_P_Growers)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq Mean Sq NumDF DenDF F value   Pr(>F)
## Field      0.44961 0.44961     1     7 12.8844 0.008863 **
## Year       0.04444 0.04444     1     7  1.2735 0.296301
## Field:Year 0.03220 0.03220     1     7  0.9227 0.368754
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(Total_P_means_Growers)
```

```
##  Field emmean    SE   df lower.CL upper.CL .group
##  RF      1.80 0.131 8.77     1.50     2.10  1
##  CR      2.12 0.131 8.77     1.82     2.41   2
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
summary(Total_P_effects_Growers)
```

```
##  contrast estimate     SE df t.ratio p.value
##  CR - RF     0.318 0.0886  7   3.589  0.0089
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
Total_V_Growers <- lmer(TotalV ~ Field*Year+(1|Site), data=Growers)
Total_V_means_Growers <- emmeans(Total_V_Growers, spec ='Field')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
Total_V_effects_Growers <- contrast(Total_V_means_Growers, method = 'pairwise', adjust = "tukey")
anova(Total_V_Growers)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF DenDF F value   Pr(>F)
## Field      5.8331  5.8331     1     7 12.4968 0.009533 **
## Year       1.4030  1.4030     1     7  3.0057 0.126568
## Field:Year 0.0293  0.0293     1     7  0.0628 0.809272
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(Total_V_means_Growers)
```

```
##  Field emmean    SE  df lower.CL upper.CL .group
##  RF      4.61 0.403 9.6     3.71     5.51  1
##  CR      5.75 0.403 9.6     4.85     6.66   2
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
summary(Total_V_effects_Growers)
```

```
##  contrast estimate    SE df t.ratio p.value
##  CR - RF      1.15 0.324  7   3.535  0.0095
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
Total_C_Growers <- lmer(TotalC ~ Field*Year+(1|Site), data=Growers)
Total_C_means_Growers <- emmeans(Total_C_Growers, spec ='Field')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
Total_C_effects_Growers <- contrast(Total_C_means_Growers, method = 'pairwise', adjust = "tukey")
anova(Total_C_Growers)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq Mean Sq NumDF DenDF F value   Pr(>F)
## Field      24.7896 24.7896     1     7 16.2315 0.005003 **
## Year        3.2279  3.2279     1     7  2.1135 0.189320
## Field:Year  7.4047  7.4047     1     7  4.8484 0.063552 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(Total_C_means_Growers)
```

```
##  Field emmean    SE   df lower.CL upper.CL .group
##  RF      4.28 0.606 10.9     2.94     5.61  1
##  CR      6.64 0.606 10.9     5.30     7.97   2
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
summary(Total_C_effects_Growers)
```

```
##  contrast estimate    SE df t.ratio p.value
##  CR - RF      2.36 0.586  7   4.029  0.0050
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
Total_S_Growers <- lmer(TotalS ~ Field*Year+(1|Site), data=Growers)
Total_S_means_Growers <- emmeans(Total_S_Growers, spec ='Field')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
Total_S_effects_Growers <- contrast(Total_S_means_Growers, method = 'pairwise', adjust = "tukey")
anova(Total_S_Growers)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq Mean Sq NumDF DenDF F value   Pr(>F)
## Field      12.2354 12.2354     1     7 14.7325 0.006389 **
## Year        3.8270  3.8270     1     7  4.6081 0.068955 .
## Field:Year  0.1097  0.1097     1     7  0.1321 0.726970
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(Total_S_means_Growers)
```

```
##  Field emmean    SE   df lower.CL upper.CL .group
##  RF      6.53 0.641 8.77     5.08     7.99  1
##  CR      8.19 0.641 8.77     6.74     9.65   2
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
summary(Total_S_effects_Growers)
```

```
##  contrast estimate    SE df t.ratio p.value
##  CR - RF      1.66 0.432  7   3.838  0.0064
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

```
Total_phenols_Growers <- lmer(Total_phenols ~ Field*Year+(1|Site), data=Growers)
Total_phenols_means_Growers <- emmeans(Total_phenols_Growers, spec ='Field')
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
Total_phenols_effects_Growers <- contrast(Total_phenols_means_Growers, method = 'pairwise', adjust = "tu
anova(Total_phenols_Growers)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq Mean Sq NumDF DenDF F value   Pr(>F)
## Field      133.692 133.692     1     7 16.5548 0.004757 **
## Year        25.938  25.938     1     7  3.2118 0.116212
## Field:Year   7.299   7.299     1     7  0.9039 0.373413
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(Total_phenols_means_Growers)
```

```
##  Field emmean   SE   df lower.CL upper.CL .group
##  RF      17.2 1.72 9.45     13.3     21.1  1
##  CR      22.7 1.72 9.45     18.8     26.6   2
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
summary(Total_phenols_effects_Growers)
```

```
##  contrast estimate   SE df t.ratio p.value
##  CR - RF      5.48 1.35  7   4.069  0.0048
##
## Results are averaged over the levels of: Year
## Degrees-of-freedom method: kenward-roger
```

Import graphing data

```
manuscript_graphing <- read_excel("Phenols_graphing_manuscript_25Jan2024.xlsx", sheet = 1)

RES_graphing <- manuscript_graphing %>% filter(Study == "RES")
str(RES_graphing)
```

```
## tibble [10 x 5] (S3: tbl_df/tbl/data.frame)
##  $ Type                  : chr [1:10] "Total_phenols" "Total_phenols" "TotalP" "TotalP" ...
##  $ Field                 : chr [1:10] "CR" "RF" "CR" "RF" ...
##  $ Study                 : chr [1:10] "RES" "RES" "RES" "RES" ...
##  $ Phenols_level_mg_100gOC: num [1:10] 1.981 1.716 0.194 0.189 0.528 ...
##  $ Phenols_level         : num [1:10] 19.81 17.16 1.94 1.89 5.28 ...
```

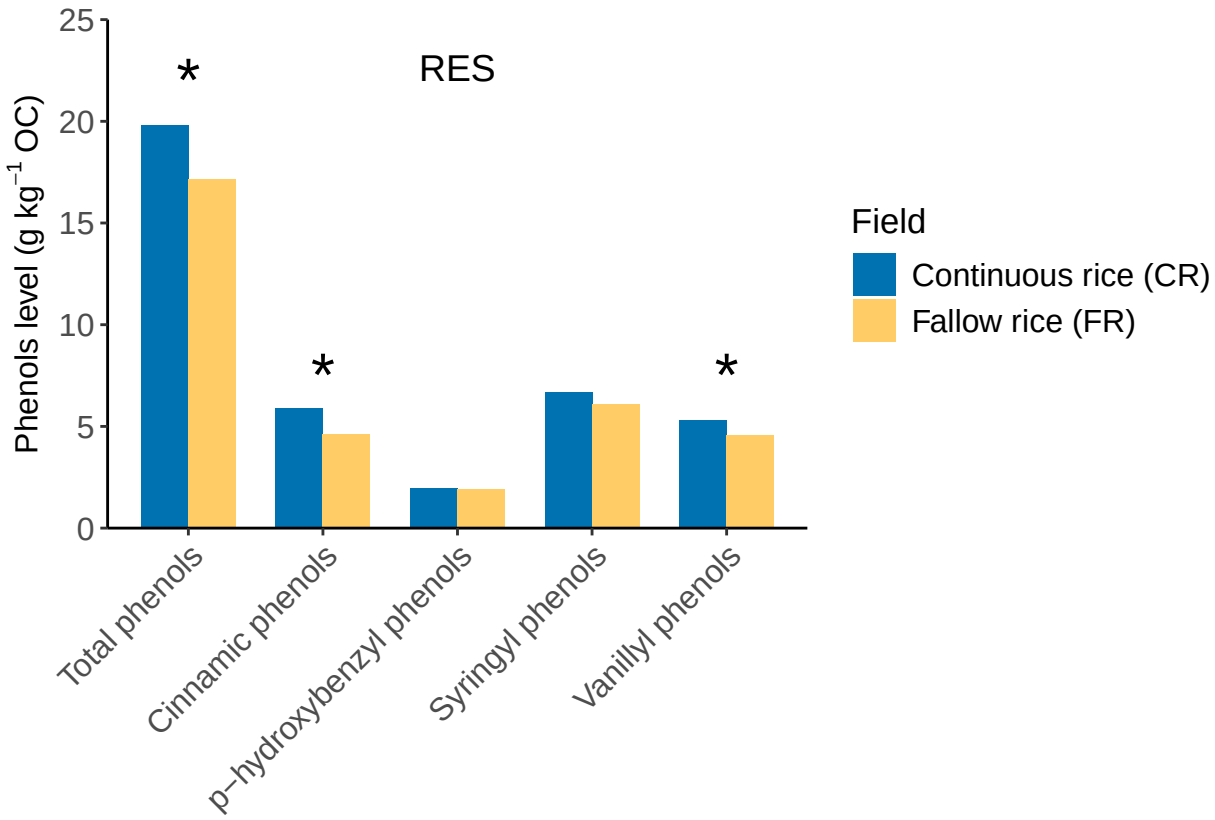
```r
Growers_Graphing <- manuscript_graphing %>% filter(Study == "Grower")
str(Growers_Graphing)
```

```
## tibble [10 x 5] (S3: tbl_df/tbl/data.frame)
##  $ Type                   : chr [1:10] "Total_phenols" "Total_phenols" "TotalP" "TotalP" ...
##  $ Field                  : chr [1:10] "CR" "RF" "CR" "RF" ...
##  $ Study                  : chr [1:10] "Grower" "Grower" "Grower" "Grower" ...
##  $ Phenols_level_mg_100gOC: num [1:10] 2.295 1.761 0.214 0.181 0.583 ...
##  $ Phenols_level          : num [1:10] 22.95 17.61 2.14 1.81 5.83 ...
```

Graphing RES

```r
RES_phenols_graph <-
ggplot(RES_graphing, aes(x = Type, y = Phenols_level, fill = Field)) +
  geom_bar(stat = "identity", position = "dodge", width = 0.7) +
  labs(x = "Type", y = "Phenols_level", fill = "Field") +
  scale_fill_manual(values = c("#0072B2","#FFCC66"),labels = c("Continuous rice (CR)", "Fallow rice (FR
  scale_y_continuous(name=expression("Phenols level (g kg"^{-1}*" OC)"), limits = c(0,25), expand = c(0
  scale_x_discrete(name="", labels = c("Total phenols", "Cinnamic phenols", "p-hydroxybenzyl phenols",
  theme_classic() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1, size= 12))+
  theme(axis.text.y = element_text(size= 12),axis.title = element_text(size=12))+
  theme(legend.text = element_text(size = 12),legend.title = element_text(size = 13))+
    annotate(
  "text",
  x = c(1,2,5),  # X-axis positions for annotations
  y = c(21,6.5,6.5),  # Y-axis positions for annotations
  label = "*",
  size = 8,
  vjust = 0  # Adjust vertical position of asterisks
)+
  annotate(
  "text",
  x = c(3),  # X-axis positions for annotations
  y = c(22),  # Y-axis positions for annotations
  label = "RES",
  size = 5,
  vjust = 0
)

RES_phenols_graph
```



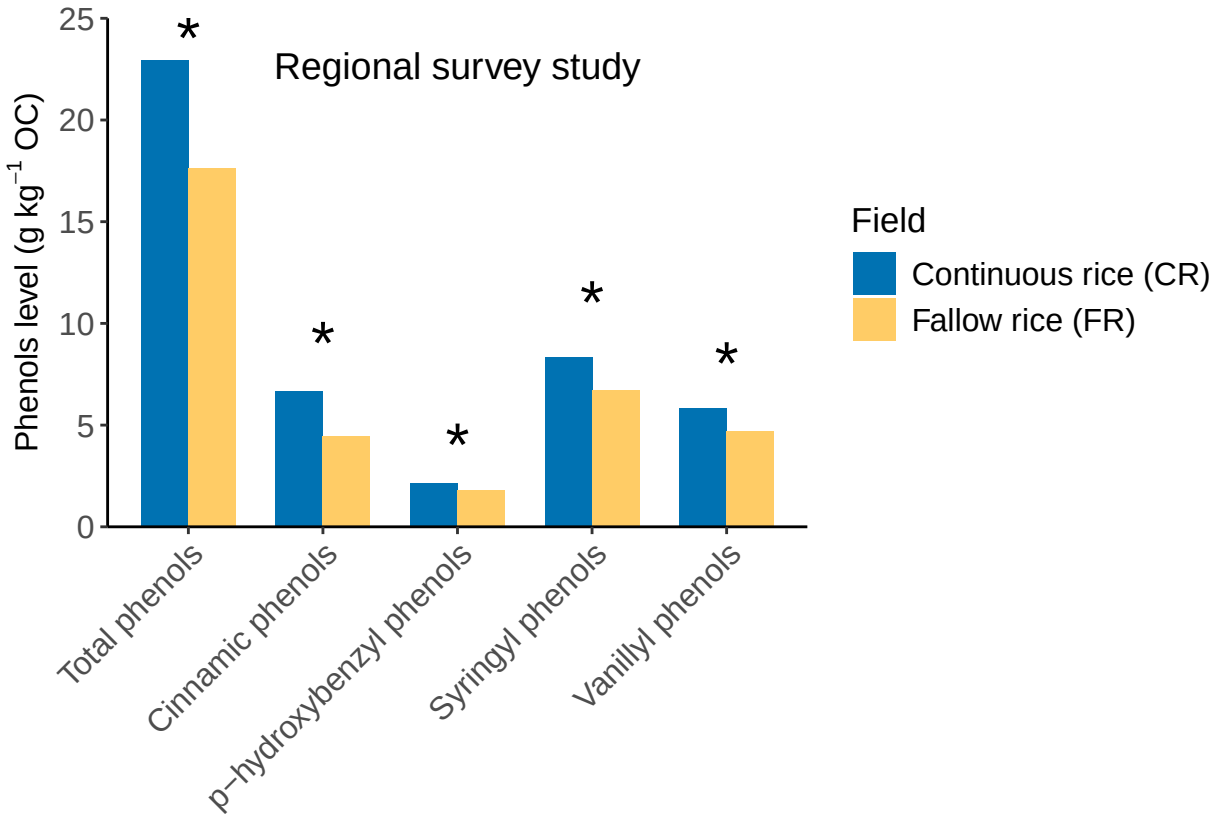

```
ggsave(RES_phenols_graph, filename = "RES_phenols_graph_22Jan2024.png", height = 15, width = 20, units =
```

Graphing growers' fields

```
Grower_phenols_graph<-
ggplot(Growers_Graphing, aes(x = Type, y = Phenols_level, fill = Field)) +
  geom_bar(stat = "identity", position = "dodge", width = 0.7) +
  labs(x = "Type", y = "Phenols_level", fill = "Field") +
  scale_fill_manual(values = c("#0072B2","#FFCC66"),labels = c("Continuous rice (CR)", "Fallow rice (FR
  scale_y_continuous(name=expression("Phenols level (g kg"^{-1}*" OC)"), limits = c(0,25), expand = c(0
  scale_x_discrete(name="", labels = c("Total phenols", "Cinnamic phenols", "p-hydroxybenzyl phenols",
  theme_classic() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1, size= 12))+
  theme(axis.text.y = element_text(size= 12),axis.title = element_text(size=12))+
  theme(legend.text = element_text(size = 12),legend.title = element_text(size = 13))+
    annotate(
  "text",
  x = c(1,2,3,4,5),  # X-axis positions for annotations
  y = c(23,8,3,10,7),  # Y-axis positions for annotations
  label = "*",
  size = 8,
  vjust = 0  # Adjust vertical position of asterisks
)+
```

```
  annotate(
  "text",
  x = c(3),  # X-axis positions for annotations
  y = c(22),  # Y-axis positions for annotations
  label = "Regional survey study",
  size = 5,
  vjust = 0
)

Grower_phenols_graph
```




```
ggsave(Grower_phenols_graph, filename = "Growers_phenols_graph_22Jan2024.png", height = 15, width = 20,
```