

N uptake maturity

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Contents

Necessary libraries	1
Read and check data, split by year	1
2021(Figure 3)	2
Graph	4
2022 (Figure 3)	6
Graph	8
2023 (Figure 3)	10
Graph	12
All pooled	14
Graph	17
Combine into 1 graph	19
Combine 0N into one table	20
Zero N	20

Necessary libraries

Read and check data, split by year

```
#read data
master = read_excel('C:/Users/zhang/Documents/GitHub/FallowRice_ContinuousRice_AgronomicPerformance/N uptake maturity')

master$NrateF <- as.factor(master$Nrate_kgha)

Nrate_trial <- master %>%
  #filter(Year != 2023) %>%
```

```

filter(Topdress!=1) %>%
filter(Stage=="Maturity") %>%
mutate(Year= as.factor(Year))

Nrate_trial_2021 <- master %>%
  filter(Year == 2021) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
  mutate(Year= as.factor(Year))

Nrate_trial_2022 <- master %>%
  filter(Year == 2022) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
  mutate(Year= as.factor(Year))

Nrate_trial_2023 <- master %>%
  filter(Year == 2023) %>%
  filter(Topdress!=1) %>%
  filter(Stage=="Maturity") %>%
  mutate(Year= as.factor(Year))

table(Nrate_trial_2021$Nrate_kgha)

```

```

##
##    0 115 155 185 225 260
##    6   6   6   6   6   6

```

2021(Figure 3)

```

model_2021 <- lmer(N_total_kgha ~ NrateF*Treatment+(1|Treatment:Blk)+(1:Blk), data=Nrate_trial_2021)

anova(model_2021)

```

```

## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF  F value    Pr(>F)
## NrateF          110725  22144.9      5     20 185.4816 4.843e-16 ***
## Treatment           629    628.6      1      4   5.2654  0.08343 .
## NrateF:Treatment     481     96.1      5     20   0.8050  0.55947
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

field_means_2021 = emmeans(model_2021,spec = 'Treatment',by = 'NrateF')
field_effects_2021 = contrast(field_means_2021, method = 'pairwise', adjust = "Tukey")

summary(field_effects_2021)

```

```

## NrateF = 0:
## contrast estimate   SE    df t.ratio p.value

```

```

## CR - FR      -25.68 11.8 12.6  -2.180  0.0489
##
## NrateF = 115:
## contrast estimate SE df t.ratio p.value
## CR - FR      -18.39 11.8 12.6  -1.561  0.1432
##
## NrateF = 155:
## contrast estimate SE df t.ratio p.value
## CR - FR      -22.26 11.8 12.6  -1.890  0.0820
##
## NrateF = 185:
## contrast estimate SE df t.ratio p.value
## CR - FR      -27.15 11.8 12.6  -2.305  0.0389
##
## NrateF = 225:
## contrast estimate SE df t.ratio p.value
## CR - FR      -18.78 11.8 12.6  -1.594  0.1356
##
## NrateF = 260:
## contrast estimate SE df t.ratio p.value
## CR - FR       -4.86 11.8 12.6  -0.413  0.6868
##
## Results are averaged over the levels of: Blk
## Degrees-of-freedom method: kenward-roger

```

```
cld(field_means_2021)
```

```

## NrateF = 0:
## Treatment emmean SE df lower.CL upper.CL .group
## CR          59.9 8.33 12.6    41.9    78 1
## FR          85.6 8.33 12.6    67.6   104 2
##
## NrateF = 115:
## Treatment emmean SE df lower.CL upper.CL .group
## CR         148.3 8.33 12.6   130.2   166 1
## FR         166.7 8.33 12.6   148.6   185 1
##
## NrateF = 155:
## Treatment emmean SE df lower.CL upper.CL .group
## CR         167.2 8.33 12.6   149.1   185 1
## FR         189.4 8.33 12.6   171.4   207 1
##
## NrateF = 185:
## Treatment emmean SE df lower.CL upper.CL .group
## CR         189.3 8.33 12.6   171.3   207 1
## FR         216.5 8.33 12.6   198.4   235 2
##
## NrateF = 225:
## Treatment emmean SE df lower.CL upper.CL .group
## CR         209.9 8.33 12.6   191.9   228 1
## FR         228.7 8.33 12.6   210.7   247 1
##
## NrateF = 260:
## Treatment emmean SE df lower.CL upper.CL .group

```

```
## CR          243.7 8.33 12.6    225.7      262  1
## FR          248.6 8.33 12.6    230.5      267  1
##
## Results are averaged over the levels of: Blk
## 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.
```

```
cld(emmeans(model_2021, ~ Treatment + NrateF), adjust = "Sidak")
```

```
## Treatment NrateF emmean SE df lower.CL upper.CL .group
## CR        0      59.9 8.33 12.6    31.0    88.9  1
## FR        0      85.6 8.33 12.6    56.6   114.6  1
## CR       115     148.3 8.33 12.6   119.3   177.2  2
## FR       115     166.7 8.33 12.6   137.7   195.6 234
## CR       155     167.2 8.33 12.6   138.2   196.1 23 5
## CR       185     189.3 8.33 12.6   160.4   218.3 34567
## FR       155     189.4 8.33 12.6   160.5   218.4 23456
## CR       225     209.9 8.33 12.6   181.0   238.9  4 678
## FR       185     216.5 8.33 12.6   187.5   245.5  5678
## FR       225     228.7 8.33 12.6   199.8   257.7  78
## CR       260     243.7 8.33 12.6   214.7   272.7  8
## FR       260     248.6 8.33 12.6   219.6   277.5  8
##
## Results are averaged over the levels of: Blk
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 12 estimates
## P value adjustment: sidak method for 66 tests
## 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.
```

```
cld_2021 <- cld(emmeans(model_2021, ~ Treatment + NrateF), adjust = "Sidak")
```

Graph

```
Nrate_trial_2021_dataframe <- Nrate_trial_2021 %>%
  group_by(Treatment, Nrate_kgha) %>%
  mutate(N_total_kgha_se = sd(N_total_kgha)/sqrt(3)) %>%
  summarise(N_total_kgha = mean(N_total_kgha),
            N_total_kgha_se = mean(N_total_kgha_se))
```

```
## 'summarise()' has grouped output by 'Treatment'. You can override using the
## '.groups' argument.
```

```

Nuptake_graph_2021 <-
ggplot(Nrate_trial_2021, aes(x=Nrate_kgha, y=N_total_kgha, color=Treatment))+
  geom_point(size=1, alpha=0.4)+
  geom_point(data=Nrate_trial_2021_dataframe, size=2.5)+ #this is the mean values
  scale_shape_manual(values = c("circle"))+
  geom_smooth(aes(group = Treatment),method = lm, level = 0.95)+
  scale_color_manual(values=c("#0072B2", "#FF9900"), name = "Treatment", labels = c("Continuous Rice (CR",
  scale_x_continuous(name=expression("N rate (kg N ha"-1*)")), limits = c(-20, 320), breaks = seq(0,
  #scale_x_continuous(name=expression("N rate (kg N ha"-1*)")), limits = c(-20, 320), expand = c(0,
  scale_y_continuous(name=expression("N uptake (kg N ha"-1*)")), limits = c(0, 300), expand = c(0, 0
  #geom_errorbar(aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se), width=3, pos
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..rr.label..)),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(60, 90))+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..eq.label..)),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(70, 100))+
  theme(axis.text = element_text(size = 14), axis.title = element_text(size=16))+
  theme(legend.text = element_text(size = 16),legend.title = element_text(size = 18))+
  theme(plot.title = element_text(hjust = 0.5, size = 20, face = "bold"))+
  ggtitle(expression("2021"))
  #annotate(
  #"text",
  #x = c(0),
  #y = Nrate_trial_2021_dataframe %>%
  #  filter(Treatment == "FR", Nrate_kgha == 0) %>%
  #  mutate(N_total_kgha_plus_higher = N_total_kgha + 25) %>%
  #  pull(N_total_kgha_plus_higher),
  #label = "*",
  #size = 7,
  #vjust = 0
  #)

```

Nuptake_graph_2021

```

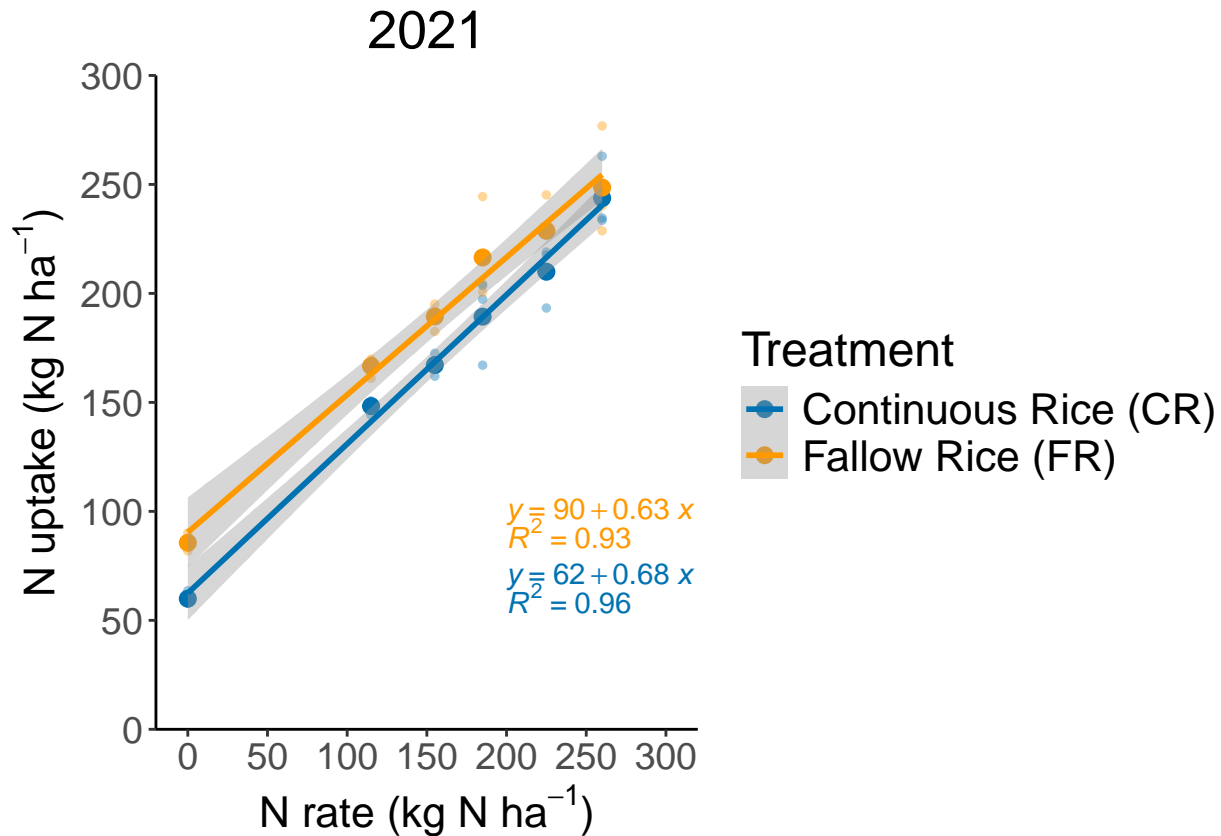
## Warning: The dot-dot notation ('..rr.label..') was deprecated in ggplot2 3.4.0.
## i Please use 'after_stat(rr.label)' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.

```

```

## 'geom_smooth()' using formula = 'y ~ x'

```



2022 (Figure 3)

```
model_2022 <- lmer(N_total_kgha ~ NrateF*Treatment+(1|Treatment:Blk)+(1:Blk), data=Nrate_trial_2022)
anova(model_2022)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## NrateF          95639  19127.8      5     20  63.1071 1.477e-11 ***
## Treatment         2385   2384.9      1      4   7.8683  0.04856 *
## NrateF:Treatment   1134    226.8      5     20   0.7482  0.59698
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
field_means_2022 = emmeans(model_2022, spec = 'Treatment', by = 'NrateF')
field_effects_2022 = contrast(field_means_2022, method = 'pairwise', adjust = "Tukey")
summary(field_effects_2022)
```

```
## NrateF = 0:
## contrast estimate SE df t.ratio p.value
## CR - FR      -31.6 16.9 16.9 -1.872  0.0786
```

```
##
## NrateF = 115:
## contrast estimate SE df t.ratio p.value
## CR - FR -23.4 16.9 16.9 -1.384 0.1842
##
## NrateF = 155:
## contrast estimate SE df t.ratio p.value
## CR - FR -43.1 16.9 16.9 -2.555 0.0205
##
## NrateF = 185:
## contrast estimate SE df t.ratio p.value
## CR - FR -43.4 16.9 16.9 -2.574 0.0198
##
## NrateF = 225:
## contrast estimate SE df t.ratio p.value
## CR - FR -28.8 16.9 16.9 -1.707 0.1061
##
## NrateF = 260:
## contrast estimate SE df t.ratio p.value
## CR - FR -11.1 16.9 16.9 -0.659 0.5188
##
## Results are averaged over the levels of: Blk
## Degrees-of-freedom method: kenward-roger
```

```
cld(field_means_2022)
```

```
## NrateF = 0:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 66.4 11.9 16.9 41.3 91.6 1
## FR 98.0 11.9 16.9 72.8 123.2 1
##
## NrateF = 115:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 142.4 11.9 16.9 117.2 167.6 1
## FR 165.8 11.9 16.9 140.6 190.9 1
##
## NrateF = 155:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 148.1 11.9 16.9 122.9 173.2 1
## FR 191.2 11.9 16.9 166.0 216.3 2
##
## NrateF = 185:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 176.8 11.9 16.9 151.6 201.9 1
## FR 220.2 11.9 16.9 195.0 245.3 2
##
## NrateF = 225:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 205.1 11.9 16.9 180.0 230.3 1
## FR 233.9 11.9 16.9 208.7 259.1 1
##
## NrateF = 260:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 235.6 11.9 16.9 210.4 260.7 1
```

```
## FR          246.7 11.9 16.9    221.5    271.8  1
##
## Results are averaged over the levels of: Blk
## 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.
```

```
cld(emmeans(model_2022, ~ Treatment + NrateF), adjust = "Sidak")
```

```
## Treatment NrateF emmean   SE   df lower.CL upper.CL .group
## CR         0      66.4 11.9 16.9    27.1    106    1
## FR         0      98.0 11.9 16.9    58.7    137   12
## CR        115     142.4 11.9 16.9   103.1    182   23
## CR        155     148.1 11.9 16.9   108.7    187   23
## FR        115     165.8 11.9 16.9   126.4    205   34
## CR        185     176.8 11.9 16.9   137.4    216  345
## FR        155     191.2 11.9 16.9   151.8    231 3456
## CR        225     205.1 11.9 16.9   165.8    244  456
## FR        185     220.2 11.9 16.9   180.8    260  456
## FR        225     233.9 11.9 16.9   194.6    273   56
## CR        260     235.6 11.9 16.9   196.2    275    6
## FR        260     246.7 11.9 16.9   207.3    286    6
##
## Results are averaged over the levels of: Blk
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 12 estimates
## P value adjustment: sidak method for 66 tests
## 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.
```

```
cld_2022 <- cld(emmeans(model_2022, ~ Treatment + NrateF), adjust = "Sidak")
```

Graph

```
Nrate_trial_2022_dataframe <- Nrate_trial_2022 %>%
  group_by(Treatment, Nrate_kgha) %>%
  mutate(N_total_kgha_se = sd(N_total_kgha)/sqrt(3)) %>%
  summarise(N_total_kgha = mean(N_total_kgha),
            N_total_kgha_se = mean(N_total_kgha_se))
```

```
## 'summarise()' has grouped output by 'Treatment'. You can override using the
## '.groups' argument.
```



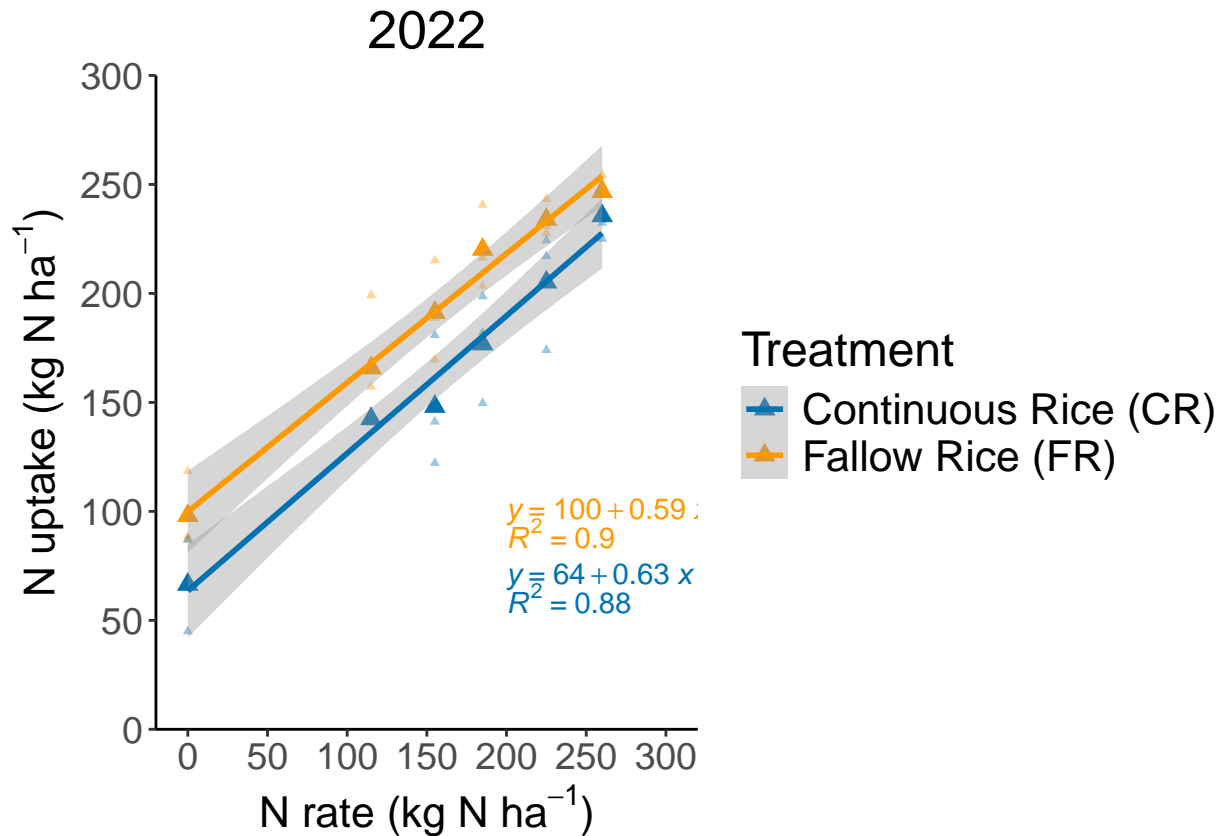
```

Nuptake_graph_2022 <-
ggplot(Nrate_trial_2022, aes(x=Nrate_kgha, y=N_total_kgha, color=Treatment))+
  geom_point(size=1, alpha=0.4, shape="triangle")+
  geom_point(data=Nrate_trial_2022_dataframe, size=2.5, shape="triangle")+ #this is the mean values
  #scale_shape_manual(values = c("triangle"))+
  geom_smooth(aes(group = Treatment),method = lm, level = 0.95)+
  scale_color_manual(values=c("#0072B2", "#FF9900"), name = "Treatment", labels = c("Continuous Rice (CR",
  scale_x_continuous(name=expression("N rate (kg N ha"-1*)")), limits = c(-20, 320), breaks = seq(0,
  #scale_x_continuous(name=expression("N rate (kg N ha"-1*)")), limits = c(-20, 320), expand = c(0,
  scale_y_continuous(name=expression("N uptake (kg N ha"-1*)")), limits = c(0, 300), expand = c(0, 0
  #geom_errorbar(aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se), width=3, pos
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..rr.label..)),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(60, 90))+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..eq.label..)),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(70, 100))+
  theme(axis.text = element_text(size = 14), axis.title = element_text(size=16))+
  theme(legend.text = element_text(size = 16),legend.title = element_text(size = 18))+
  theme(plot.title = element_text(hjust = 0.5, size = 20, face = "bold"))+
  ggtitle(expression("2022"))

Nuptake_graph_2022

```

```
## 'geom_smooth()' using formula = 'y ~ x'
```



2023 (Figure 3)

```
model_2023 <- lmer(N_total_kgha ~ NrateF*Treatment+(1|Treatment:Blk)+(1:Blk), data=Nrate_trial_2023)
anova(model_2023)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## NrateF          48865   9772.9      5     20 21.3442 2.157e-07 ***
## Treatment         8664    8663.5      1      4 18.9213  0.01216 *
## NrateF:Treatment   1517     303.3      5     20  0.6625  0.65603
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
field_means_2023 = emmeans(model_2023,spec = 'Treatment',by = 'NrateF')
field_effects_2023 = contrast(field_means_2023, method = 'pairwise', adjust = "Tukey")
summary(field_effects_2023)
```

```
## NrateF = 0:
## contrast estimate SE df t.ratio p.value
## CR - FR       -37.5 17.9 23.7 -2.090  0.0475
```

```
##
## NrateF = 90:
## contrast estimate SE df t.ratio p.value
## CR - FR -56.2 17.9 23.7 -3.136 0.0045
##
## NrateF = 120:
## contrast estimate SE df t.ratio p.value
## CR - FR -39.6 17.9 23.7 -2.207 0.0373
##
## NrateF = 150:
## contrast estimate SE df t.ratio p.value
## CR - FR -40.2 17.9 23.7 -2.244 0.0345
##
## NrateF = 180:
## contrast estimate SE df t.ratio p.value
## CR - FR -14.5 17.9 23.7 -0.808 0.4271
##
## NrateF = 210:
## contrast estimate SE df t.ratio p.value
## CR - FR -25.6 17.9 23.7 -1.427 0.1665
##
## Results are averaged over the levels of: Blk
## Degrees-of-freedom method: kenward-roger
```

```
cld(field_means_2023)
```

```
## NrateF = 0:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 56.1 12.7 23.7 29.9 82.3 1
## FR 93.6 12.7 23.7 67.4 119.7 2
##
## NrateF = 90:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 84.5 12.7 23.7 58.3 110.7 1
## FR 140.7 12.7 23.7 114.5 166.9 2
##
## NrateF = 120:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 113.6 12.7 23.7 87.4 139.8 1
## FR 153.1 12.7 23.7 127.0 179.3 2
##
## NrateF = 150:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 136.8 12.7 23.7 110.6 163.0 1
## FR 177.0 12.7 23.7 150.9 203.2 2
##
## NrateF = 180:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 156.3 12.7 23.7 130.1 182.5 1
## FR 170.8 12.7 23.7 144.6 197.0 1
##
## NrateF = 210:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 175.0 12.7 23.7 148.8 201.2 1
```

```
## FR          200.6 12.7 23.7    174.4    226.7  1
##
## Results are averaged over the levels of: Blk
## 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.
```

```
cld(emmeans(model_2023, ~ Treatment + NrateF), adjust = "Sidak")
```

```
## Treatment NrateF emmean SE df lower.CL upper.CL .group
## CR        0      56.1 12.7 23.7    16.1    96.2  1
## CR        90      84.5 12.7 23.7    44.4   124.5 12
## FR        0      93.6 12.7 23.7    53.5   133.6 123
## CR       120     113.6 12.7 23.7    73.5   153.6 1234
## CR       150     136.8 12.7 23.7    96.8   176.9 2345
## FR       90     140.7 12.7 23.7   100.6   180.8 2345
## FR       120     153.1 12.7 23.7   113.1   193.2 2345
## CR       180     156.3 12.7 23.7   116.2   196.4  345
## FR       180     170.8 12.7 23.7   130.7   210.8   45
## CR       210     175.0 12.7 23.7   134.9   215.0   45
## FR       150     177.0 12.7 23.7   137.0   217.1   45
## FR       210     200.6 12.7 23.7   160.5   240.6    5
##
## Results are averaged over the levels of: Blk
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 12 estimates
## P value adjustment: sidak method for 66 tests
## 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.
```

```
cld_2023 <- cld(emmeans(model_2023, ~ Treatment + NrateF), adjust = "Sidak")
```

Graph

```
Nrate_trial_2023_dataframe <- Nrate_trial_2023 %>%
  group_by(Treatment, Nrate_kgha) %>%
  mutate(N_total_kgha_se = sd(N_total_kgha)/sqrt(3)) %>%
  summarise(N_total_kgha = mean(N_total_kgha),
            N_total_kgha_se = mean(N_total_kgha_se))
```

```
## 'summarise()' has grouped output by 'Treatment'. You can override using the
## '.groups' argument.
```

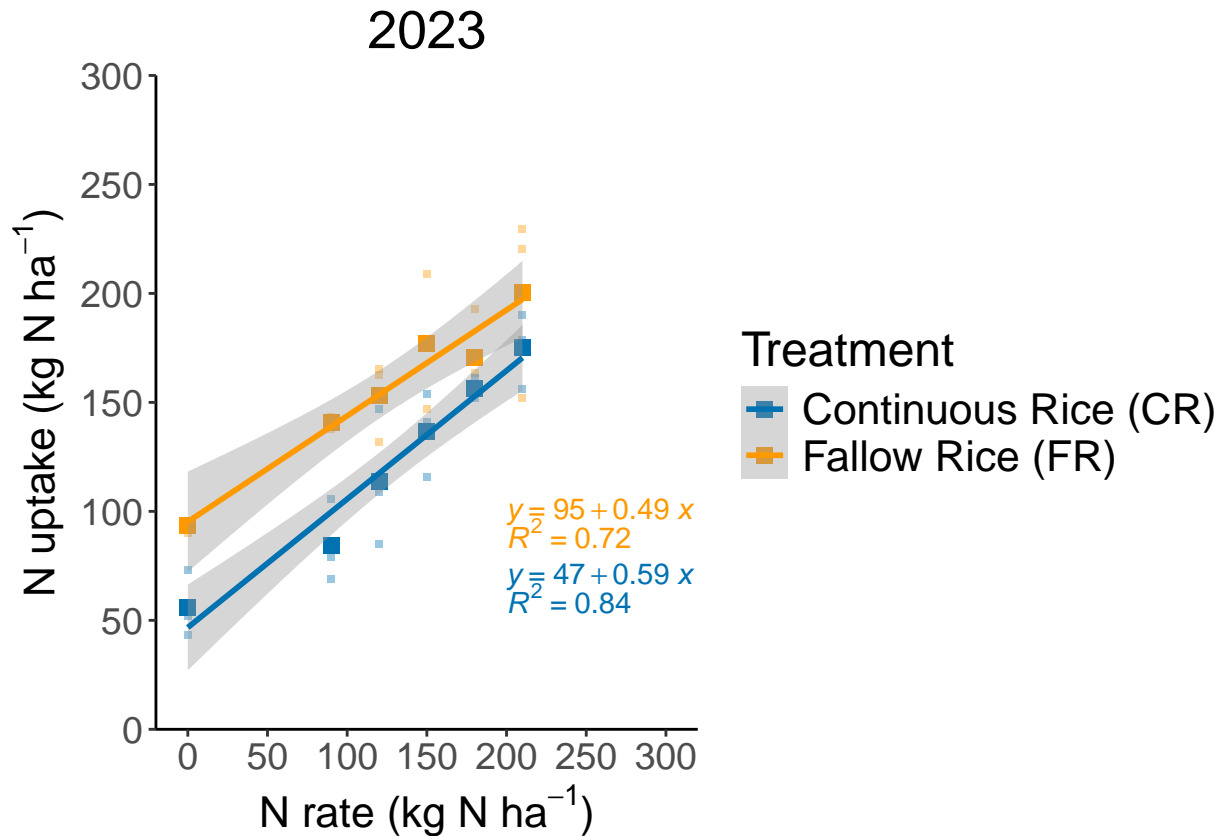
```

Nuptake_graph_2023 <-
ggplot(Nrate_trial_2023, aes(x=Nrate_kgha, y=N_total_kgha, color=Treatment))+
  geom_point(size=1, alpha=0.4, shape="square")+
  geom_point(data=Nrate_trial_2023_dataframe, size=2.5, shape="square")+ #this is the mean values
  #scale_shape_manual(values = c("square"))+
  geom_smooth(aes(group = Treatment),method = lm, level = 0.95)+
  scale_color_manual(values=c("#0072B2", "#FF9900"), name = "Treatment", labels = c("Continuous Rice (CR",
  scale_x_continuous(name=expression("N rate (kg N ha"-1*)")), limits = c(-20, 320), breaks = seq(0,
  #scale_x_continuous(name=expression("N rate (kg N ha"-1*)")), limits = c(-20, 320), expand = c(0,
  scale_y_continuous(name=expression("N uptake (kg N ha"-1*)")), limits = c(0, 300), expand = c(0, 0
  #geom_errorbar(aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se), width=3, pos
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..rr.label..)),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(60, 90))+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..eq.label..)),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(70, 100))+
  theme(axis.text = element_text(size = 14), axis.title = element_text(size=16))+
  theme(legend.text = element_text(size = 16),legend.title = element_text(size = 18))+
  theme(plot.title = element_text(hjust = 0.5, size = 20, face = "bold"))+
  ggtitle(expression("2023"))

```

Nuptake_graph_2023

```
## 'geom_smooth()' using formula = 'y ~ x'
```



All pooled

```
model_all <- lmer(N_total_kgha ~ NrateF*Treatment+(1|Treatment:Blk)+(1:Blk), data=Nrate_trial)
anova(model_all)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##               Sum Sq Mean Sq NumDF  DenDF  F value    Pr(>F)
## NrateF         269628  26962.8     10  66.373  104.4336 < 2.2e-16 ***
## Treatment         8147   8147.3      1  16.396   31.5566 3.519e-05 ***
## NrateF:Treatment   3177    317.7     10  66.373    1.2305  0.2885
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
field_means_all = emmeans(model_all,spec = 'Treatment',by = 'NrateF')
field_effects_all = contrast(field_means_all, method = 'pairwise', adjust = "Tukey")
summary(field_effects_all)
```

```
## NrateF = 0:
## contrast estimate    SE    df t.ratio p.value
## CR - FR      -31.57  8.52  70.8  -3.704  0.0004
```

```

##
## NrateF = 90:
## contrast estimate SE df t.ratio p.value
## CR - FR -54.97 14.67 80.8 -3.747 0.0003
##
## NrateF = 115:
## contrast estimate SE df t.ratio p.value
## CR - FR -21.49 10.41 76.2 -2.065 0.0423
##
## NrateF = 120:
## contrast estimate SE df t.ratio p.value
## CR - FR -38.31 14.67 80.8 -2.612 0.0107
##
## NrateF = 150:
## contrast estimate SE df t.ratio p.value
## CR - FR -38.98 14.67 80.8 -2.658 0.0095
##
## NrateF = 155:
## contrast estimate SE df t.ratio p.value
## CR - FR -33.30 10.41 76.2 -3.200 0.0020
##
## NrateF = 180:
## contrast estimate SE df t.ratio p.value
## CR - FR -13.25 14.67 80.8 -0.903 0.3692
##
## NrateF = 185:
## contrast estimate SE df t.ratio p.value
## CR - FR -35.90 10.41 76.2 -3.450 0.0009
##
## NrateF = 210:
## contrast estimate SE df t.ratio p.value
## CR - FR -24.35 14.67 80.8 -1.660 0.1008
##
## NrateF = 225:
## contrast estimate SE df t.ratio p.value
## CR - FR -24.41 10.41 76.2 -2.345 0.0216
##
## NrateF = 260:
## contrast estimate SE df t.ratio p.value
## CR - FR -8.61 10.41 76.2 -0.827 0.4108
##
## Results are averaged over the levels of: Blk
## Degrees-of-freedom method: kenward-roger

```

```
cld(field_means_all)
```

```

## NrateF = 0:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 60.8 6.03 70.8 48.8 72.8 1
## FR 92.4 6.03 70.8 80.4 104.4 2
##
## NrateF = 90:
## Treatment emmean SE df lower.CL upper.CL .group
## CR 85.5 10.37 80.8 64.8 106.1 1

```

```

## FR          140.4 10.37 80.8    119.8    161.1    2
##
## NrateF = 115:
## Treatment emmean    SE    df lower.CL upper.CL .group
## CR          144.9  7.36 76.2    130.2    159.5    1
## FR          166.3  7.36 76.2    151.7    181.0    2
##
## NrateF = 120:
## Treatment emmean    SE    df lower.CL upper.CL .group
## CR          114.6 10.37 80.8     93.9    135.2    1
## FR          152.9 10.37 80.8    132.2    173.5    2
##
## NrateF = 150:
## Treatment emmean    SE    df lower.CL upper.CL .group
## CR          137.8 10.37 80.8    117.2    158.5    1
## FR          176.8 10.37 80.8    156.2    197.4    2
##
## NrateF = 155:
## Treatment emmean    SE    df lower.CL upper.CL .group
## CR          157.1  7.36 76.2    142.5    171.8    1
## FR          190.4  7.36 76.2    175.8    205.1    2
##
## NrateF = 180:
## Treatment emmean    SE    df lower.CL upper.CL .group
## CR          157.3 10.37 80.8    136.6    177.9    1
## FR          170.5 10.37 80.8    149.9    191.2    1
##
## NrateF = 185:
## Treatment emmean    SE    df lower.CL upper.CL .group
## CR          182.6  7.36 76.2    167.9    197.2    1
## FR          218.5  7.36 76.2    203.8    233.1    2
##
## NrateF = 210:
## Treatment emmean    SE    df lower.CL upper.CL .group
## CR          176.0 10.37 80.8    155.3    196.6    1
## FR          200.3 10.37 80.8    179.7    221.0    1
##
## NrateF = 225:
## Treatment emmean    SE    df lower.CL upper.CL .group
## CR          207.0  7.36 76.2    192.4    221.7    1
## FR          231.4  7.36 76.2    216.8    246.1    2
##
## NrateF = 260:
## Treatment emmean    SE    df lower.CL upper.CL .group
## CR          239.1  7.36 76.2    224.5    253.8    1
## FR          247.7  7.36 76.2    233.1    262.4    1
##
## Results are averaged over the levels of: Blk
## 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.

```



```
cld(emmeans(model_all, ~ Treatment + NrateF),adjust = "Sidak")
```

```
## Treatment NrateF emmean SE df lower.CL upper.CL .group
## CR 0 60.8 6.03 70.8 41.8 79.9 1
## CR 90 85.5 10.37 80.8 52.9 118.1 123
## FR 0 92.4 6.03 70.8 73.4 111.4 12 4
## CR 120 114.6 10.37 80.8 82.0 147.2 2345
## CR 150 137.8 10.37 80.8 105.2 170.4 4567
## FR 90 140.4 10.37 80.8 107.8 173.1 3 567
## CR 115 144.9 7.36 76.2 121.7 168.0 56
## FR 120 152.9 10.37 80.8 120.3 185.5 5678
## CR 155 157.1 7.36 76.2 133.9 180.3 5678
## CR 180 157.3 10.37 80.8 124.7 189.9 5678
## FR 115 166.3 7.36 76.2 143.2 189.5 678
## FR 180 170.5 10.37 80.8 137.9 203.1 56789
## CR 210 176.0 10.37 80.8 143.4 208.6 6789
## FR 150 176.8 10.37 80.8 144.2 209.4 6789
## CR 185 182.6 7.36 76.2 159.4 205.7 789
## FR 155 190.4 7.36 76.2 167.2 213.6 89
## FR 210 200.3 10.37 80.8 167.7 232.9 890A
## CR 225 207.0 7.36 76.2 183.9 230.2 90
## FR 185 218.5 7.36 76.2 195.3 241.6 90A
## FR 225 231.4 7.36 76.2 208.3 254.6 0A
## CR 260 239.1 7.36 76.2 215.9 262.3 0A
## FR 260 247.7 7.36 76.2 224.6 270.9 A
##
## Results are averaged over the levels of: Blk
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 22 estimates
## P value adjustment: sidak method for 231 tests
## 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.
```

```
cld_all <- cld(emmeans(model_all, ~ Treatment + NrateF),adjust = "Sidak")
```

Graph

```
all_Nuptake_graph <-
ggplot(Nrate_trial, aes(x=Nrate_kgha, y=N_total_kgha, color=Treatment, shape=Year))+
  geom_point(size=2.5)+
  geom_smooth(aes(group = Treatment), method = lm, level = 0.95)+
  scale_color_manual(values=c("#0072B2", "#FF9900"), name = "Treatment", labels = c("Continuous rice (CR)", "Fallow (F)"))+
  scale_x_continuous(name=expression("N rate (kg N ha"^-1)*"), limits = c(-20, 320), expand = c(0, 0.05), labels = c("N rate (kg N ha"^-1)*"), position = "bottom")+
  scale_y_continuous(name=expression("N uptake (kg N ha"^-1)*"), limits = c(0, 300), expand = c(0, 0.05), labels = c("N uptake (kg N ha"^-1)*"), position = "bottom")+
  #geom_errorbar(aes(ymin=N_total_kgha-N_total_kgha_se, ymax=N_total_kgha+N_total_kgha_se), width=3, position = "bottom")+
  #geom_vline(xintercept = c(41, 50, 78, 84, 121, 136), linetype = "dashed", color = "black") +
  theme_classic()+
  stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha, color=Treatment, group = Treatment,
```

```

    label = paste(..rr.label..),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(60, 90))+
stat_regline_equation(aes(x=Nrate_kgha, y=N_total_kgha,color=Treatment,group = Treatment,
    label = paste(..eq.label..),
    show.legend = FALSE,
    label.x = 200,
    label.y = c(70, 100))+
theme(axis.text = element_text(size = 14), axis.title = element_text(size=16))+
theme(legend.text = element_text(size = 12),legend.title = element_text(size = 14))+
theme(plot.title = element_text(hjust = 0.5, size = 20, face = "bold"))+
ggtitle(expression("Total N uptake: All"))+
theme(legend.position = "bottom")

all_Nuptake_graph

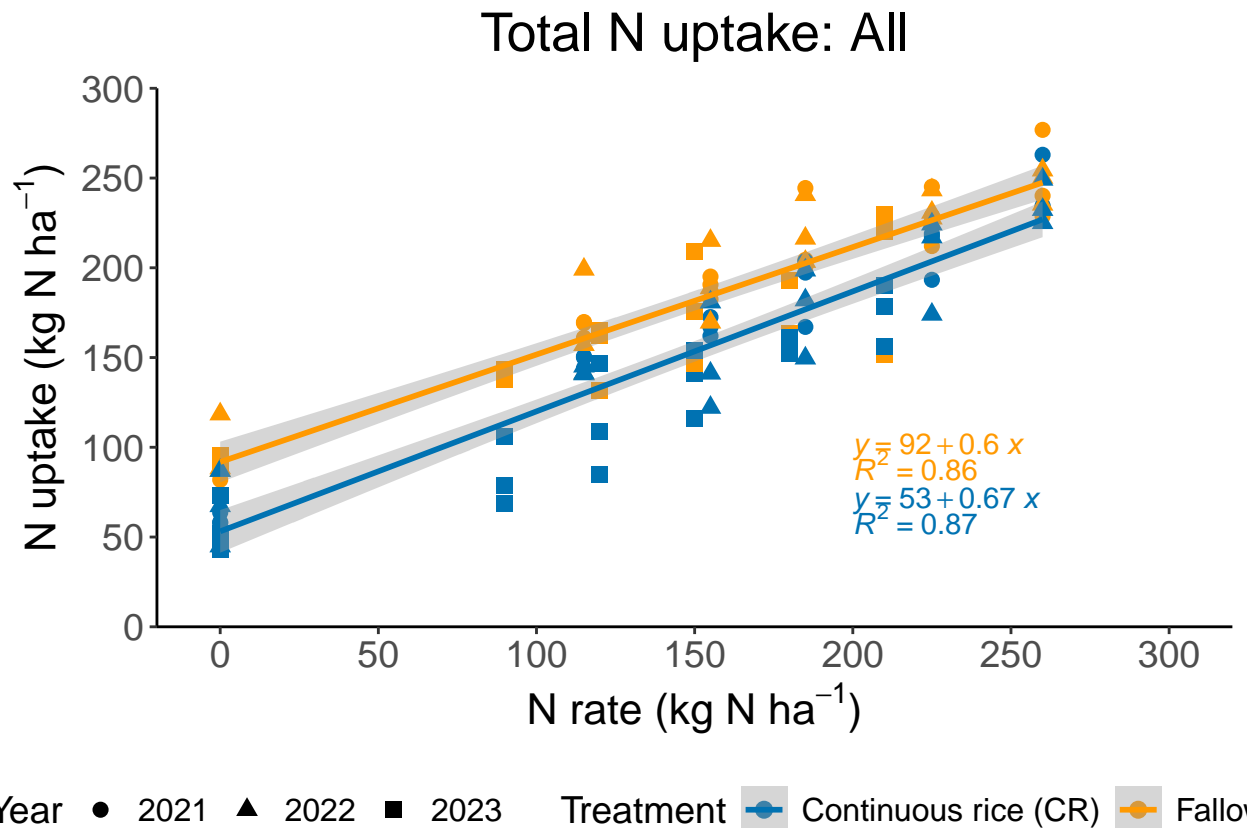
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```

```

## Warning: The following aesthetics were dropped during statistical transformation: shape.
## i This can happen when ggplot fails to infer the correct grouping structure in
##   the data.
## i Did you forget to specify a 'group' aesthetic or to convert a numerical
##   variable into a factor?
## The following aesthetics were dropped during statistical transformation: shape.
## i This can happen when ggplot fails to infer the correct grouping structure in
##   the data.
## i Did you forget to specify a 'group' aesthetic or to convert a numerical
##   variable into a factor?
## The following aesthetics were dropped during statistical transformation: shape.
## i This can happen when ggplot fails to infer the correct grouping structure in
##   the data.
## i Did you forget to specify a 'group' aesthetic or to convert a numerical
##   variable into a factor?

```



Combine into 1 graph

```
N_uptake_maturity <- ggarrange(Nuptake_graph_2021 + theme(legend.position = "none"),
  Nuptake_graph_2022 + theme(legend.position = "none"),
  Nuptake_graph_2023 + theme(legend.position = "none"),
  #all_Nuptake_graph,
  nrow = 1,
  ncol = 3,
  common.legend = TRUE,
  #legend.grob = get_legend(all_Nuptake_graph),
  legend = "bottom")
```

```
## 'geom_smooth()' using formula = 'y ~ x'
## 'geom_smooth()' using formula = 'y ~ x'
## 'geom_smooth()' using formula = 'y ~ x'
## 'geom_smooth()' using formula = 'y ~ x'
```

```
ggsave(filename = "N_uptake_maturity.jpg", # Include the file extension here
  plot = N_uptake_maturity, # Specify the plot
  path = "C:/Users/zhang/Documents/GitHub/FallowRice_ContinuousRice_AgronomicPerformance/Figures",
  dpi = 400,
  height = 20, width = 50, units = "cm")
```

Combine 0N into one table

```
all_means <- rbind(as.data.frame(field_means_2021) %>% mutate(Year = 2021),
  as.data.frame(field_means_2022) %>% mutate(Year = 2022),
  as.data.frame(field_means_2023) %>% mutate(Year = 2023),
  as.data.frame(field_means_all) %>% mutate(Year = "Avg")
  ) %>% arrange(Year) %>% filter(NrateF == "0") %>%
  mutate(Nuptake = round(emmean, 1))

write_xlsx(all_means, "C:/Users/zhang/Documents/GitHub/FallowRice_ContinuousRice_AgronomicPerformance/N
```

Zero N

```
zero_N <- Nrate_trial %>% filter(Nrate_kgha == 0)

model_zero <- lmer(N_total_kgha ~ Treatment*Year+(1|Blk), data=zero_N)

anova(model_zero)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##               Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Treatment      4485.8   4485.8     1     6  26.2948 0.002162 **
## Year            290.0    145.0     2     6   0.8500 0.473116
## Treatment:Year  104.1     52.1     2     6   0.3052 0.747757
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
zero_means_average = emmeans(model_zero, spec = 'Treatment', by = "Year")
zero_effects_average = contrast(zero_means_average, method = 'pairwise', adjust = "Tukey")
summary(zero_effects_average)
```

```
## Year = 2021:
## contrast estimate SE df t.ratio p.value
## CR - FR      -25.7 10.7  6  -2.408  0.0527
##
## Year = 2022:
## contrast estimate SE df t.ratio p.value
## CR - FR      -31.6 10.7  6  -2.961  0.0252
##
## Year = 2023:
## contrast estimate SE df t.ratio p.value
## CR - FR      -37.5 10.7  6  -3.513  0.0126
##
## Degrees-of-freedom method: kenward-roger
```