

DPFLI USMP

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10/14/2019

Methods

Data collection

Dependent variables:

- compaction depth (penetrometer read 300 psi)
- infiltration rate (for 32 fl oz water)
- weed density (all species, 1-3 scale)
- weed abundance (top 2 most abundant species, 0-10 scale)
- root weight (wet, 5 radishes)
- root length (each radish)

Data organization (+ any quality control...)

```
Usmp <- read.csv("~/Box Sync/DPFLI/data/USMPdata2019.csv")
head(Usmp)
```

```
##  SAMPL_TIME COL ROW      TIL  MIX PND INFIL_OZ.SEC TOTRAD_oz RADL_CM
## 1      Early  A   1 Tractor null   5          NA      NA      NA
## 2      Early  A   1 Tractor null   6          NA      NA      NA
## 3      Early  A   1 Tractor null   7          NA      NA      NA
## 4      Early  A   1 Tractor null  10          NA      NA      NA
## 5      Early  A   2 Tractor pere   9          NA      NA      NA
## 6      Early  A   2 Tractor pere   7          NA      NA      NA
##   Wd_Abn Wd_Dn
## 1      7    4
## 2      7    4
## 3      7    4
## 4      7    4
## 5      6    4
## 6      6    4
```

```
# Average subsamples
```

```
Usmp <- group_by(.data = Usmp,
                  SAMPL_TIME, TIL, MIX, COL, ROW)
Usmp <- summarise(.data = Usmp,
                  PND = mean(PND),
                  INFL = mean(INFIL_OZ.SEC),
                  TOTRAD = mean(TOTRAD_oz),
                  RADL = mean(RADL_CM),
                  WEEDAB = mean(Wd_Abn),
                  WEEDEN = mean(Wd_Dn))
```

Statistical tests (both planned and run)

Hoping that ROW and COL are not significant, since they just indicate replication.

- compaction depth ~ tillage * date + cover + row + column
- infiltration (wdsp only) ~ tillage * date + cover + row + column
- weed abundance ~ tillage * date + cover + row + column
- weed density ~ tillage * date + cover + row + column
- root weight (comp only) ~ tillage * date + cover + row + column
- root length (comp only) ~ tillage * date + cover + row + column

```
# tillage ANOVA stat result
```

```
summary(aov(PND ~ TIL * SAMPL_TIME + MIX + ROW * COL,
            data = Usmp))
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## TIL           2  176.36    88.18   74.258 < 2e-16 ***
## SAMPL_TIME    1    2.63     2.63    2.211   0.1426
## MIX           3    6.95     2.32    1.952   0.1317
## ROW           1    4.38     4.38    3.689   0.0599 .
## COL           3   34.70    11.57    9.742 2.86e-05 ***
## TIL:SAMPL_TIME 2    5.13     2.57    2.161   0.1247
## ROW:COL       3    8.13     2.71    2.283   0.0889 .
## Residuals    56   66.50     1.19
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# weed ANOVA stat result
```

```
summary(aov(WCEDAB ~ TIL * SAMPL_TIME + MIX + ROW * COL,
            data = Usmp))
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## TIL           2    5.78     2.89    2.057   0.13741
## SAMPL_TIME    1    0.00     0.00    0.000   1.00000
## MIX           3  115.78    38.59   27.477 4.67e-11 ***
## ROW           1   16.33    16.33   11.629   0.00121 **
## COL           3   29.17     9.72    6.922   0.00048 ***
## TIL:SAMPL_TIME 2    0.00     0.00    0.000   1.00000
## ROW:COL       3    7.40     2.47    1.756   0.16611
## Residuals    56   78.65     1.40
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(aov(PND ~ TIL * SAMPL_TIME + MIX + ROW * COL,
            data = Usmp))
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## TIL           2  176.36    88.18   74.258 < 2e-16 ***
## SAMPL_TIME    1    2.63     2.63    2.211   0.1426
## MIX           3    6.95     2.32    1.952   0.1317
## ROW           1    4.38     4.38    3.689   0.0599 .
## COL           3   34.70    11.57    9.742 2.86e-05 ***
## TIL:SAMPL_TIME 2    5.13     2.57    2.161   0.1247
## ROW:COL       3    8.13     2.71    2.283   0.0889 .
## Residuals    56   66.50     1.19
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Results

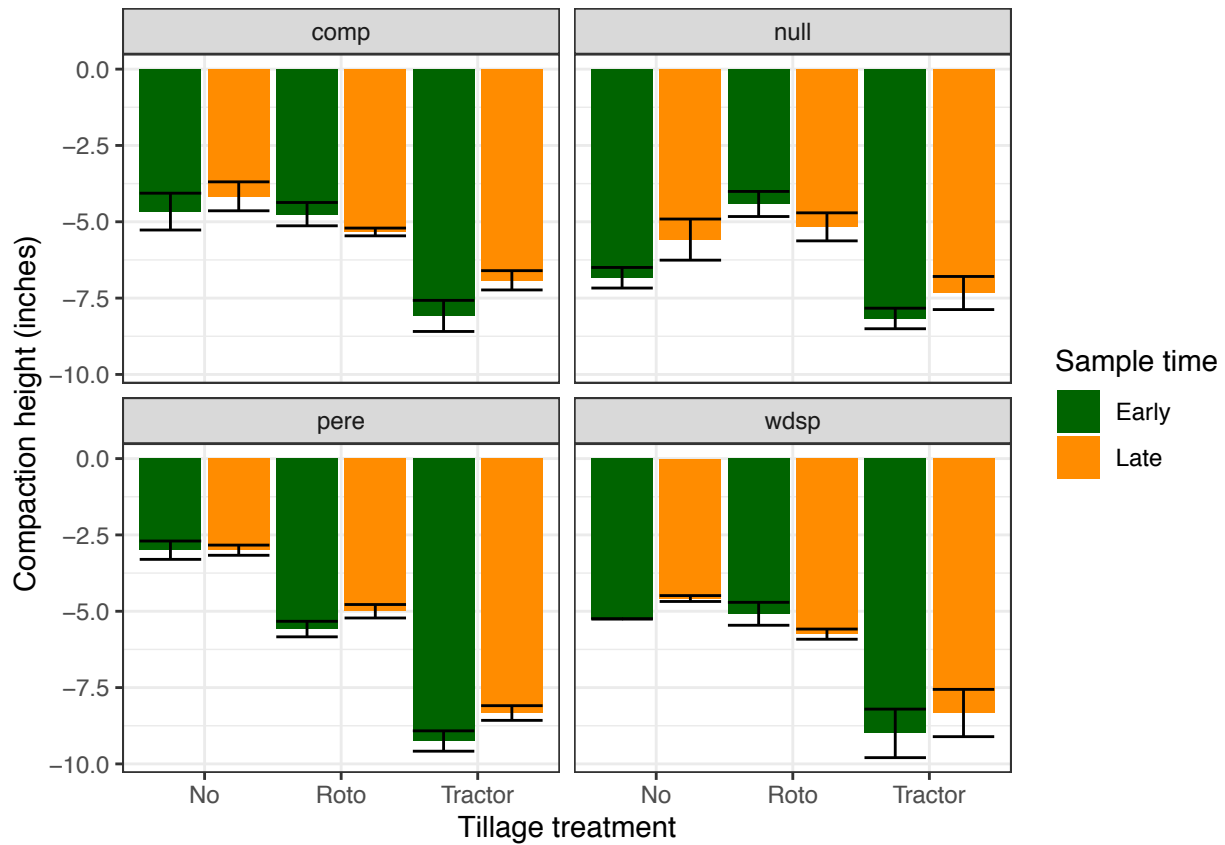
There seem to be some statistical effects of the rows/columns (presumably artificial since there are so few-letters A-D, #1-3), but (I think reasonably) ignoring those:

- COMPACTION was (most) significantly affected by TILLAGE

```
Usmpg <- group_by(.data = Usmp,
                  SAMPL_TIME, TIL, MIX)
Usmpgsum <- summarise(.data = Usmpg,
                      PND.se = -sd(PND) / length(sqrt(PND)),
                      PND = -mean(PND),
                      INFL.se = sd(INFL) / length(sqrt(INFL)),
                      INFL = mean(INFL),
                      TOTRAD.se = sd(TOTRAD) / length(sqrt(TOTRAD)),
                      TOTRAD = mean(TOTRAD),
                      RADL.se = sd(RADL) / length(sqrt(RADL)),
                      RADL = mean(RADL),
                      WEEDAB.se = sd(WEEDAB) / length(sqrt(WEEDAB)),
                      WEEDAB = mean(WEEDAB),
                      WEEDEN.se = sd(WEEDEN) / length(sqrt(WEEDEN)),
                      WEEDEN = mean(WEEDEN))
```

Figure 1: Compaction by tillage, cover crop mix, sample date

```
# Version A
ggplot(data = Usmpgsum,
       aes(x = TIL, y = PND, fill = SAMPL_TIME)) +
  geom_bar(stat = "identity",
          position = position_dodge(width = 1)) +
  geom_errorbar(aes(ymax = PND + PND.se,
                   ymin = PND - PND.se),
               position = position_dodge(width = 1)) +
  facet_wrap( ~MIX) +
  theme_bw() +
  scale_fill_manual(values=c("dark green", "dark orange")) +
  xlab("Tillage treatment") +
  ylab("Compaction height (inches)") +
  labs(fill = "Sample time")
```



```
# Version B
ggplot(data = Usmpgsum,
  aes(x = MIX, y = PND, fill = SAMPL_TIME)) +
  geom_bar(stat = "identity",
    position = position_dodge(width = 1)) +
  geom_errorbar(aes(ymax = PND + PND.se,
    ymin = PND - PND.se,
    position = position_dodge(width = 1)) +
  facet_wrap( ~TIL) +
  theme_bw() +
  scale_fill_manual(values=c("dark green","dark orange")) +
  xlab("Cover crop mix") +
  ylab("Compaction height (inches)") +
  labs(fill = "Sample time")
```

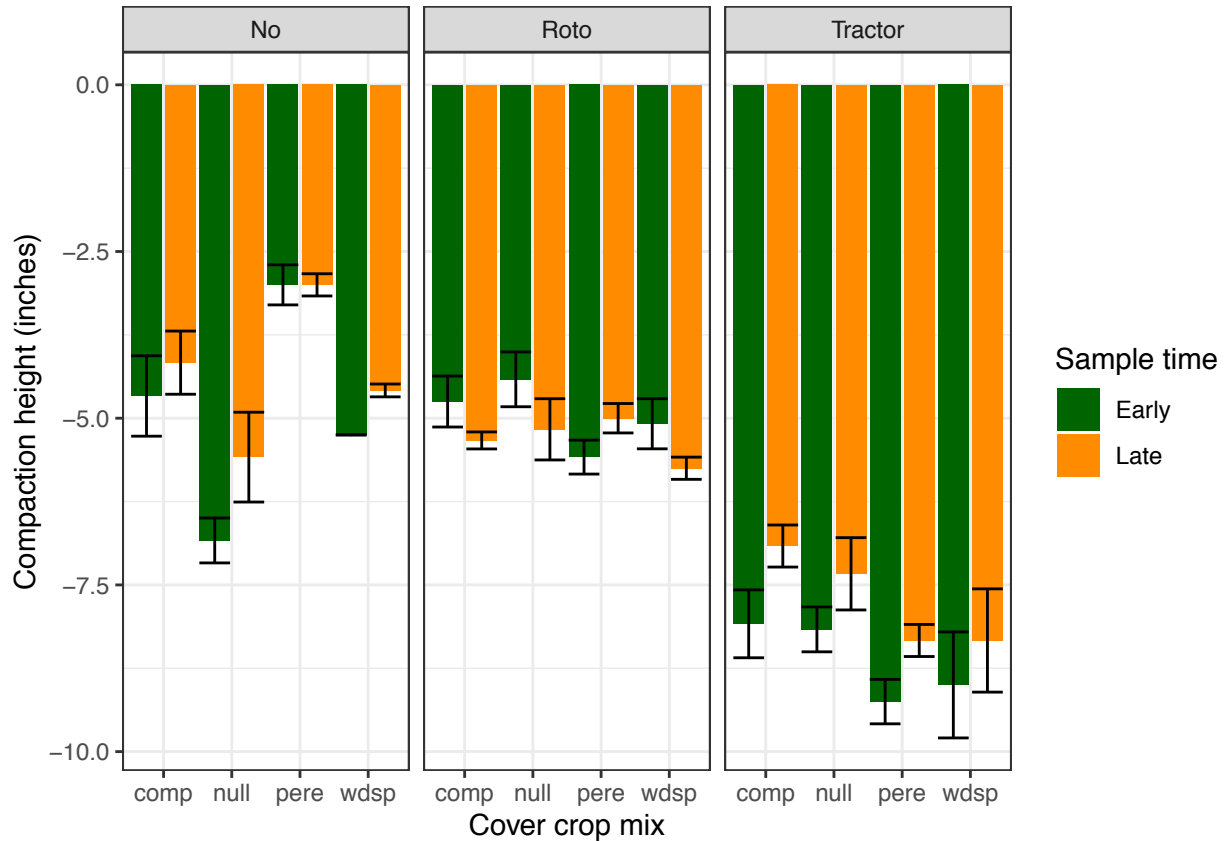


Figure 2: Infiltration by tillage

(For *weed suppression* treatment only, due to data completeness, assuming it is representative of other treatments for infiltration.

I do think this is justified because the statistics show that cover crop mix did not significantly affect compaction results.)

- INFILTRATION was significantly affected by both TILLAGE and SAMPLE DATE

```
Usmp_wdsp <- subset(Usmp, subset=MIX=="wdsp")
```

```
summary(aov(INFL ~ TIL * SAMPL_TIME + ROW + COL,
  data = Usmp_wdsp))
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## TIL           2  1.2558   0.6279   10.285 0.00473 **
## SAMPL_TIME    1  0.8320   0.8320   13.629 0.00498 **
## ROW           1  0.0919   0.0919    1.505 0.25105
## COL           2  0.0101   0.0050    0.082 0.92159
## TIL:SAMPL_TIME 2  0.3170   0.1585    2.596 0.12876
## Residuals     9  0.5495   0.0611
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Usmpg_wdsp <- group_by(.data = Usmp_wdsp,
  SAMPL_TIME, TIL)
```

```
Usmpgsum_wdsp <- summarise(.data = Usmpg_wdsp,
```

```

PND.se = sd(PND) / length(sqrt(PND)),
PND = mean(PND),
INFL.se = sd(INFL) / length(sqrt(INFL)),
INFL = mean(INFL),
TOTRAD.se = sd(TOTRAD) / length(sqrt(TOTRAD)),
TOTRAD = mean(TOTRAD),
RADL.se = sd(RADL) / length(sqrt(RADL)),
RADL = mean(RADL),
WEEDAB.se = sd(WEEDAB) / length(sqrt(WEEDAB)),
WEEDAB = mean(WEEDAB),
WEEDEN.se = sd(WEEDEN) / length(sqrt(WEEDEN)),
WEEDEN = mean(WEEDEN)

```

```

ggplot(data = Usmpgsum_wdsp,
  aes(x = TIL, y = INFL, fill = SAMPL_TIME)) +
  geom_bar(stat = "identity",
    position = position_dodge(width = 1)) +
  geom_errorbar(aes(ymax = INFL + INFL.se,
    ymin = INFL - INFL.se),
    position = position_dodge(width = 1)) +
  theme_bw() +
  scale_fill_manual(values=c("light blue","dark blue")) +
  xlab("Tillage treatment") +
  ylab("Infiltration rate (fl oz / sec)") +
  labs(fill = "Sample time")

```

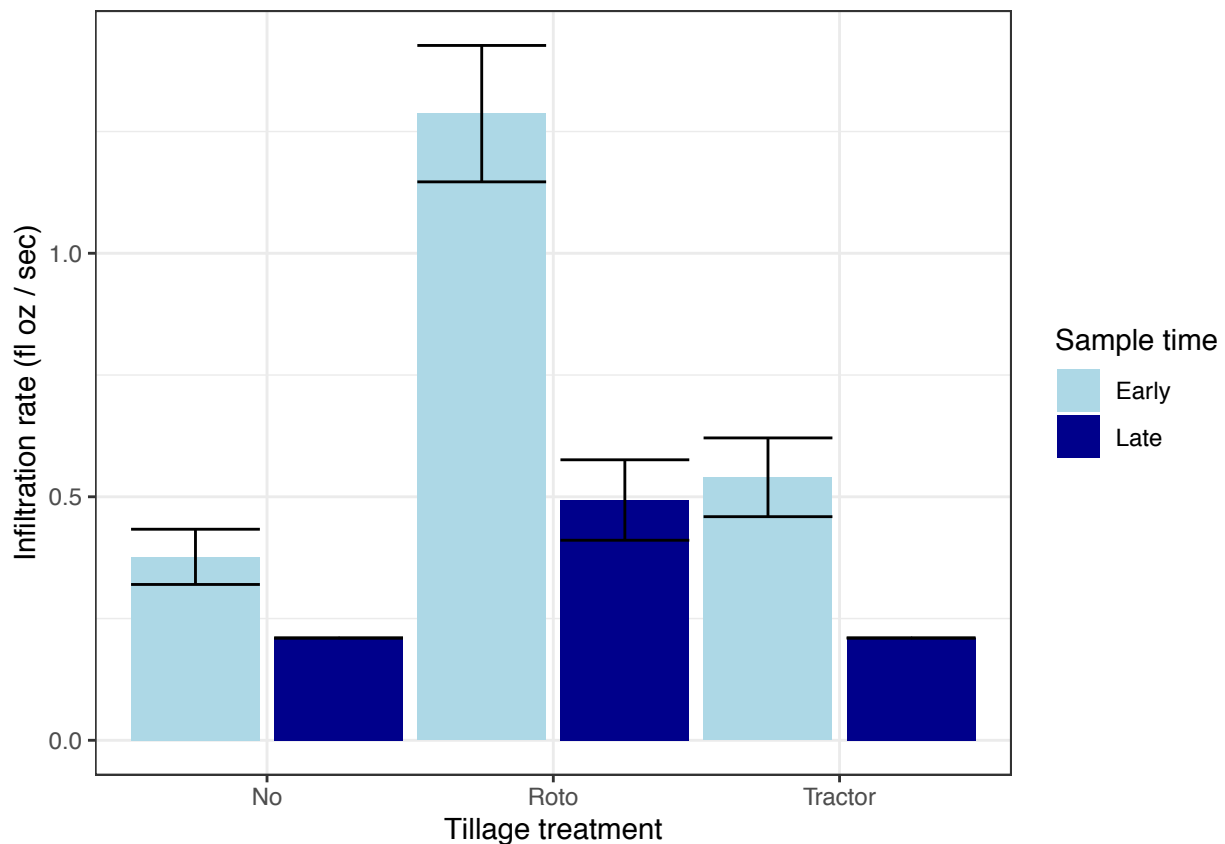
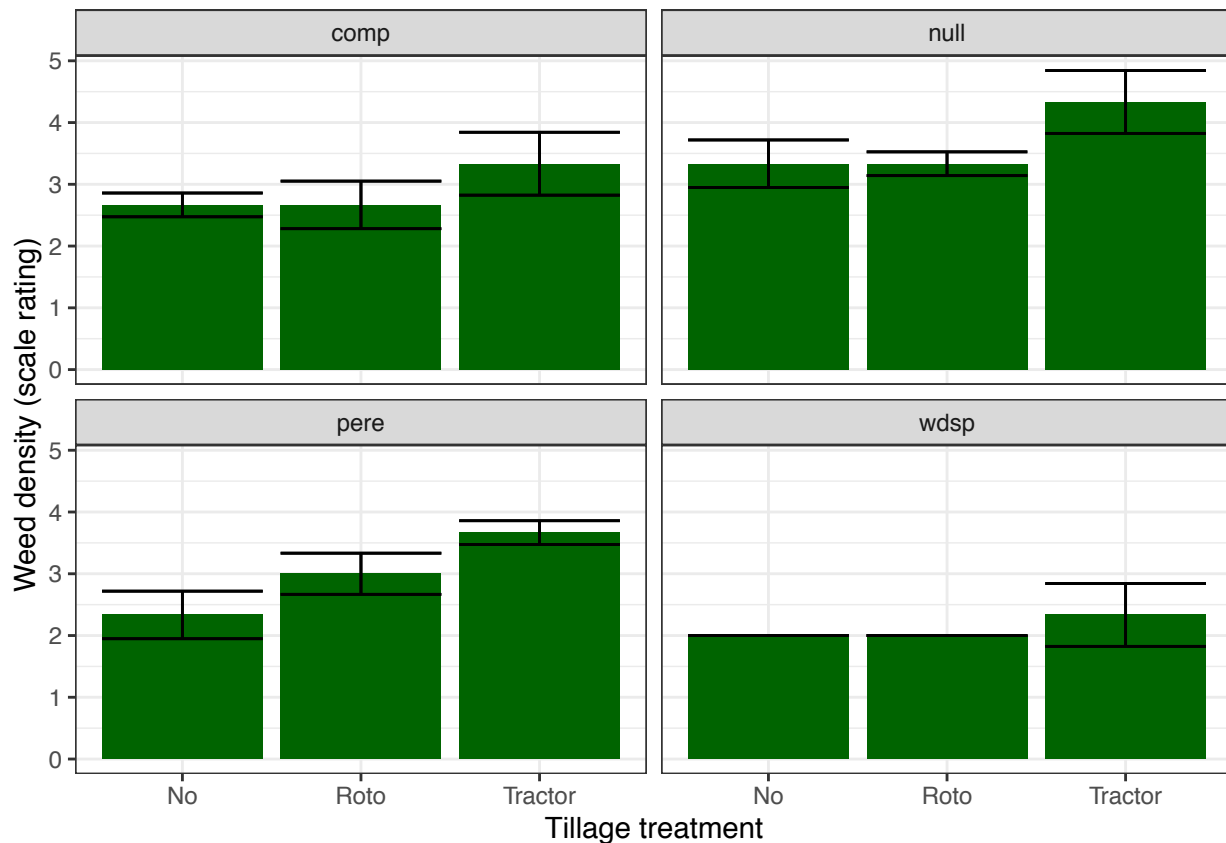


Figure 3a:

- WEED DENSITY was (most) significantly affected by TILLAGE

```
# Version A
ggplot(data = Usmpgsum,
       aes(x = TIL, y = WEEDEN)) +
  geom_bar(stat = "identity",
          position = position_dodge(width = 1),
          fill = "dark green") +
  geom_errorbar(aes(ymax = WEEDEN + WEEDEN.se,
                  ymin = WEEDEN - WEEDEN.se),
              position = position_dodge(width = 1)) +
  facet_wrap( ~MIX) +
  theme_bw() +
  xlab("Tillage treatment") +
  ylab("Weed density (scale rating)")
```



```
# Version B
ggplot(data = Usmpgsum,
       aes(x = MIX, y = WEEDEN)) +
  geom_bar(stat = "identity",
          position = position_dodge(width = 1),
          fill = "dark green") +
  geom_errorbar(aes(ymax = WEEDEN + WEEDEN.se,
                  ymin = WEEDEN - WEEDEN.se),
              position = position_dodge(width = 1)) +
  facet_wrap( ~TIL) +
```

```
theme_bw() +
xlab("Cover crop mix") +
ylab("Weed density (scale rating)")
```

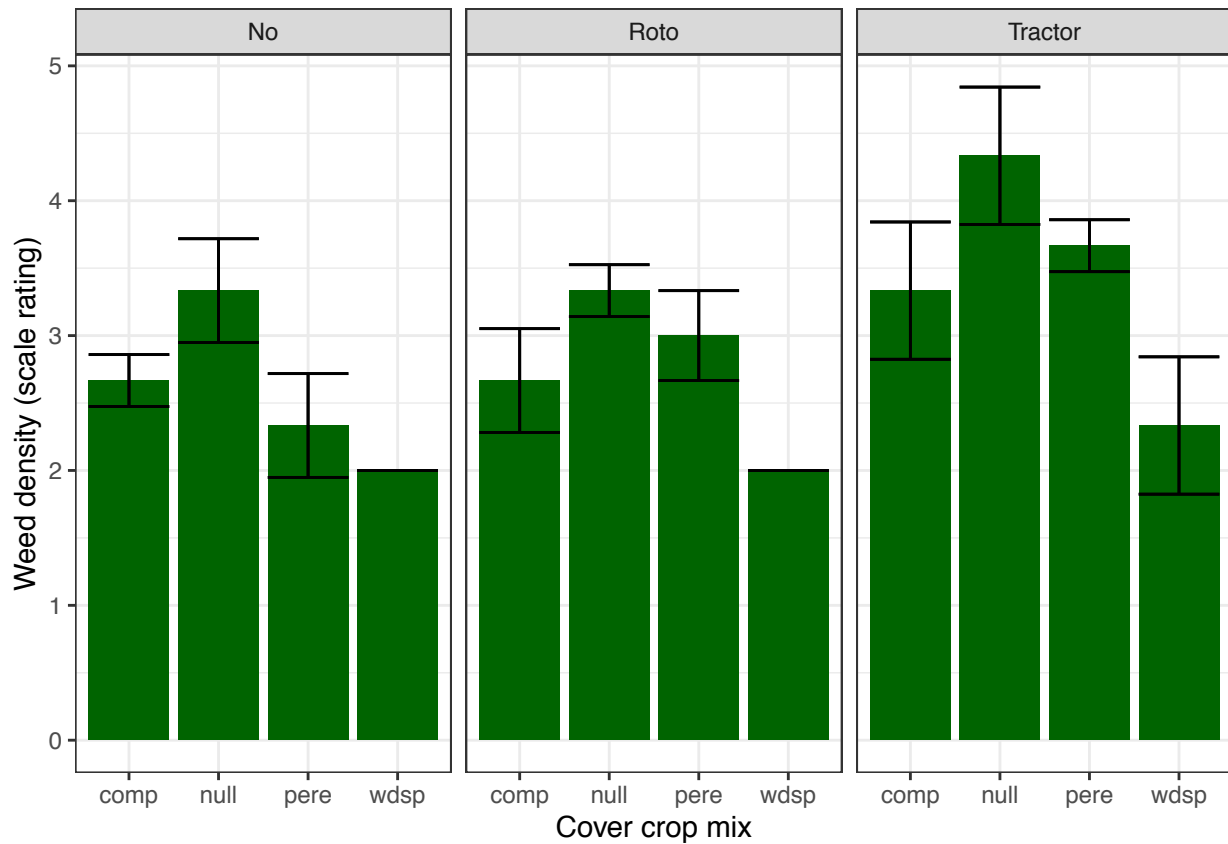
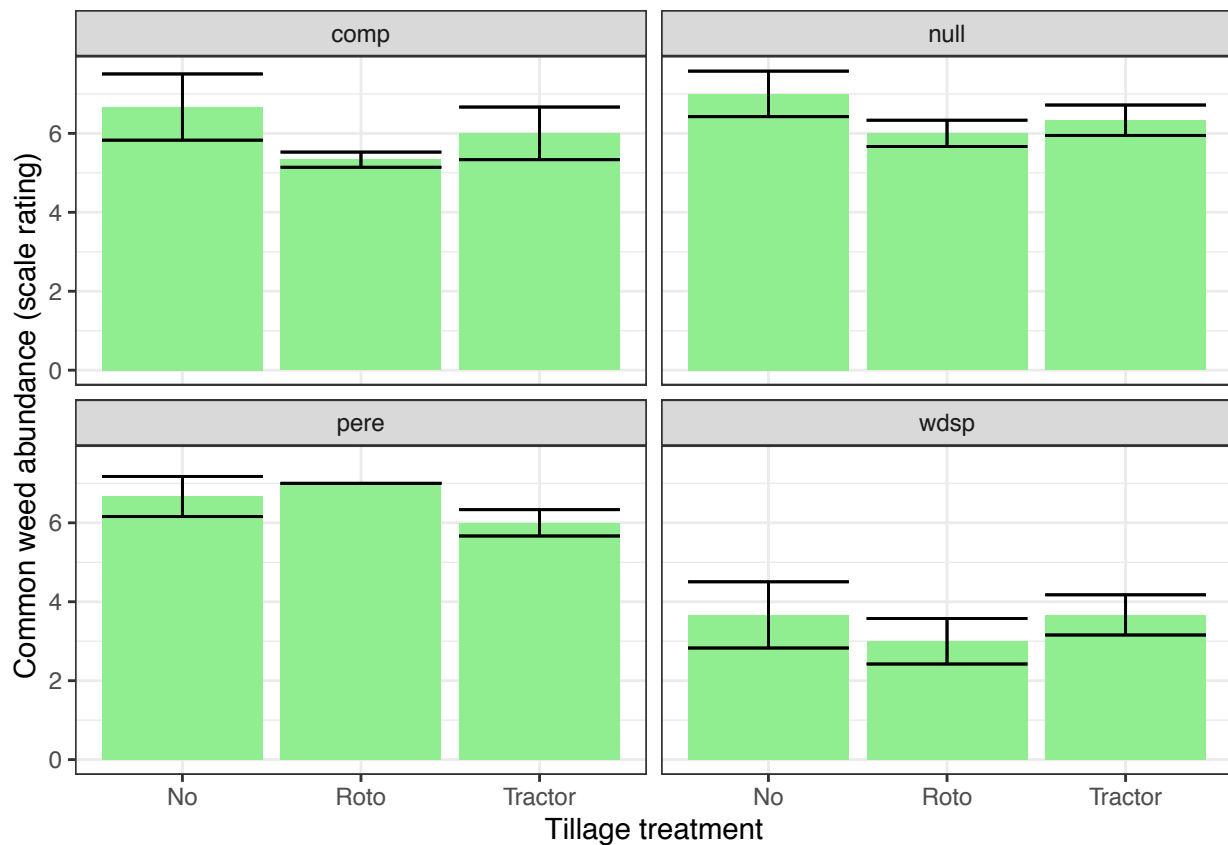


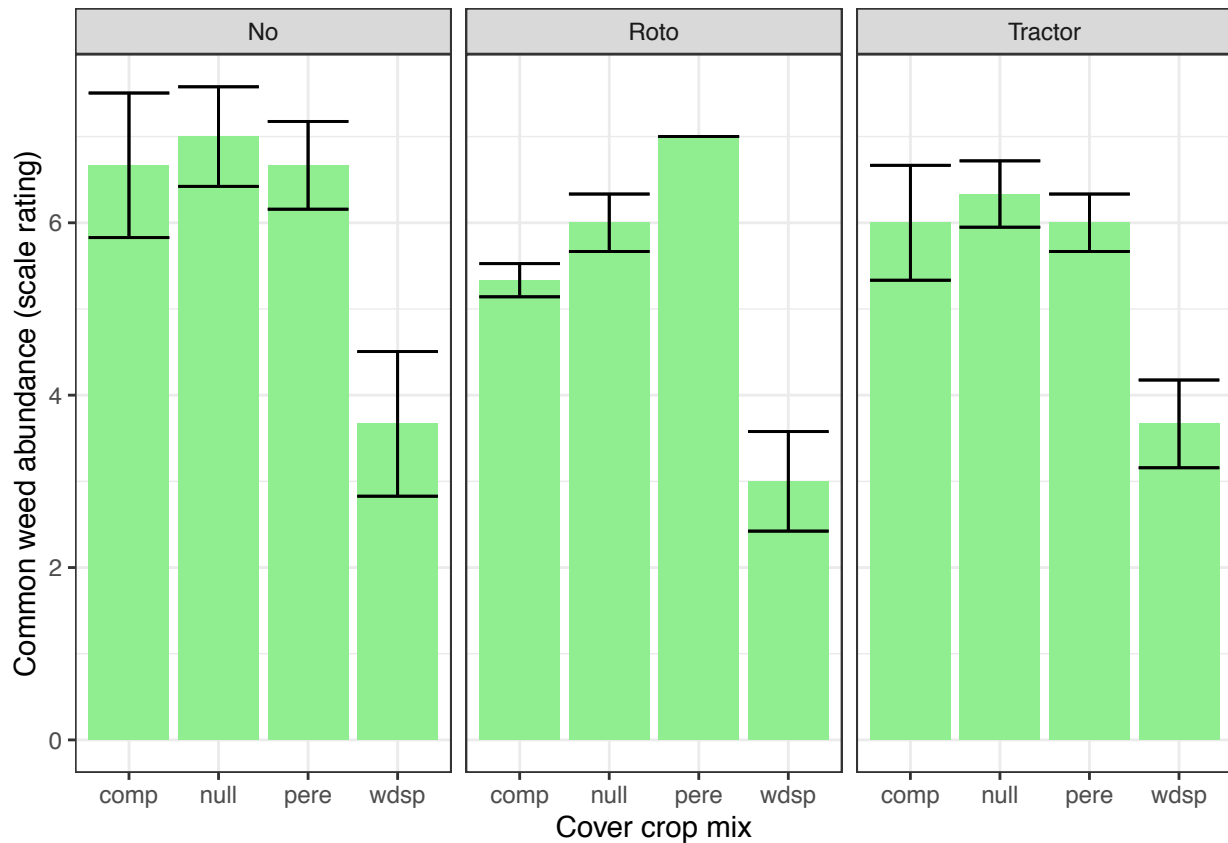
Figure 3b:

- WEED ABUNDANCE was (most) significantly affected by COVER CROP MIX

```
# Version A
ggplot(data = Usmpgsum,
       aes(x = TIL, y = WEEDAB)) +
  geom_bar(stat = "identity",
          position = position_dodge(width = 1),
          fill = "light green") +
  geom_errorbar(aes(ymin = WEEDAB - WEEDAB.se,
                  ymax = WEEDAB + WEEDAB.se),
               position = position_dodge(width = 1)) +
  facet_wrap( ~MIX) +
  theme_bw() +
  xlab("Tillage treatment") +
  ylab("Common weed abundance (scale rating)")
```

```
# Version B
ggplot(data = Usmpgsum,
  aes(x = MIX, y = WEEDAB)) +
  geom_bar(stat = "identity",
    position = position_dodge(width = 1),
    fill = "light green") +
  geom_errorbar(aes(ymax = WEEDAB + WEEDAB.se,
    ymin = WEEDAB - WEEDAB.se),
    position = position_dodge(width = 1)) +
  facet_wrap( ~TIL) +
  theme_bw() +
  xlab("Cover crop mix") +
  ylab("Common weed abundance (scale rating)")
```



Figures S1, S2 (Not-significant results)

Only for *Compaction* cover crop mixture and *Late* sampling time.

```
Usmp_comp <- subset(Usmp, subset=MIX=="comp" & SAMPL_TIME=="Late")
```

```
# Weight
```

```
summary(aov(TOTRAD ~ TIL, data = Usmp_comp))
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## TIL         2  34.67   17.33     1.5  0.296
## Residuals    6  69.33   11.56
```

```
# Length
```

```
summary(aov(RADL ~ TIL, data = Usmp_comp))
```

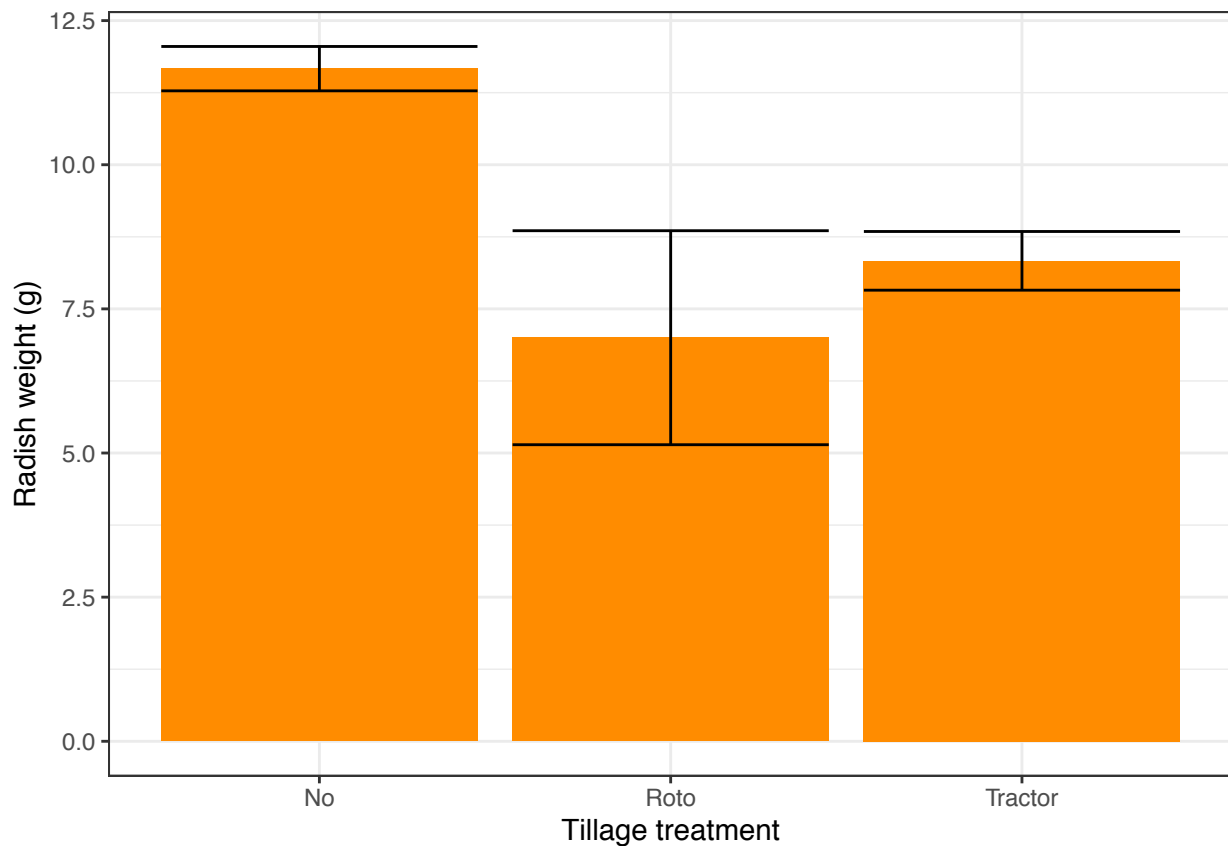
```
##           Df Sum Sq Mean Sq F value Pr(>F)
## TIL         2  14.80    7.400    1.045  0.418
## Residuals    5  35.42    7.084
## 1 observation deleted due to missingness
```

```
Usmpg_comp <- group_by(.data = Usmp_comp, TIL)
```

```
Usmpgsum_comp <- summarise(.data = Usmpg_comp,
  PND.se = sd(PND) / length(sqrt(PND)),
  PND = mean(PND),
  INFL.se = sd(INFL) / length(sqrt(INFL)),
  INFL = mean(INFL),
  TOTRAD.se = sd(TOTRAD) / length(sqrt(TOTRAD)),
```

```
TOTRAD = mean(TOTRAD),
RADL.se = sd(RADL) / length(sqrt(RADL)),
RADL = mean(RADL))
```

```
# S1: Weight
ggplot(Usmpgsum_comp, aes(x=TIL, y=TOTRAD)) +
  geom_bar(stat="identity", fill="dark orange") +
  geom_errorbar(aes(ymax=TOTRAD+TOTRAD.se,
                    ymin=TOTRAD-TOTRAD.se)) +
  theme_bw() +
  xlab("Tillage treatment") +
  ylab("Radish weight (g)")
```



```
# S2: Length
ggplot(Usmpgsum_comp, aes(x=TIL, y=RADL)) +
  geom_bar(stat="identity", fill="yellow") +
  geom_errorbar(aes(ymax=RADL+RADL.se,
                    ymin=RADL-RADL.se)) +
  theme_bw() +
  xlab("Tillage treatment") +
  ylab("Radish root length (inches)")
```

```
## Warning: Removed 1 rows containing missing values (position_stack).
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

