

Amount of feed substrate and moisture content

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Introduction

Compare amount of feed (DM) and moisture content on day 0, *i.e.* at the start of the experiment.

Load packages

```
library(plyr)
library(ggplot2)
library(sciplot)
library(reshape2)
library(nlme)
library(emmeans)
library(knitr)
```

Input files

```
diet.df <- read.delim("./input_data/Schreven_Ch4_diet_specs.txt", header = T)
```

1. Input data

```
# factors and variables
diet.df$Rep <- as.factor(diet.df$Rep)
diet.df$ContainerID <- as.factor(diet.df$ContainerID)
diet.df$Batch <- as.factor(diet.df$Batch)
diet.df$pMoist0 <- 100 * diet.df$pMoist0

# melt dataframe
diet.m <- reshape2::melt(diet.df[, -7])
```

```
## Using ContainerID, Diet, Treatment, Batch, Rep as id variables
```

```
# subsets per diet
diet.cf <- subset(diet.m, Diet == "CF")
diet.cm <- subset(diet.m, Diet == "CM")
```

2. LMM

Linear mixed model regression, with random intercept for batch.

```
# chicken feed, amount of feed
m.cf.feed <- lme(value ~ Treatment, random = ~1|Batch,
                 data = subset(diet.cf, variable == "total_gDM"))
anova(m.cf.feed)
```

```
##           numDF denDF  F-value p-value
## (Intercept)      1    11 6168.648  <.0001
## Treatment        3    11  520.632  <.0001
```

```
CLD(emmeans(m.cf.feed, ~ Treatment), Letters = letters, method = "tukey")
```

```
## Treatment emmean    SE df lower.CL upper.CL .group
## S/E       18.1 0.251  1    14.9    21.3    a
## Si/E       19.9 0.251  1    16.7    23.1    b
## Si/Es      20.0 0.251  1    16.8    23.2   bc
## Ss/E       20.1 0.251  1    16.9    23.3    c
##
## Degrees-of-freedom method: containment
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 4 estimates
## significance level used: alpha = 0.05
```

```
# chicken feed, moisture content
m.cf.water <- lme(value ~ Treatment, random = ~1|Batch,
                 data = subset(diet.cf, variable == "pMoist0"))
anova(m.cf.water)
```

```
##          numDF denDF    F-value p-value
## (Intercept)      1    11 26537.090 <.0001
## Treatment        3    11  1476.705 <.0001
```

```
CLD(emmeans(m.cf.water, ~ Treatment), Letters = letters, method = "tukey")
```

```
## Treatment emmean      SE df lower.CL upper.CL .group
## Ss/E      68.1 0.426  1    62.6    73.5    a
## Si/E      68.4 0.426  1    63.0    73.8    b
## Si/Es     69.2 0.426  1    63.8    74.7    c
## S/E       71.3 0.426  1    65.9    76.7    d
##
## Degrees-of-freedom method: containment
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 4 estimates
## significance level used: alpha = 0.05
```

```
# chicken manure, amount of feed
m.cm.feed <- lme(value ~ Treatment, random = ~1|Batch,
                 data = subset(diet.cm, variable == "total_gDM"))
anova(m.cm.feed)
```

```
##          numDF denDF    F-value p-value
## (Intercept)      1    18 3270.187 <.0001
## Treatment        3    18   7.401  0.002
```

```
CLD(emmeans(m.cm.feed, ~ Treatment), Letters = letters, method = "tukey")
```

```
## Treatment emmean      SE df lower.CL upper.CL .group
## S/E       20.6 0.443  2    18.7    22.5    a
## Si/Es     21.9 0.443  2    20.0    23.8    b
## Ss/E      22.0 0.443  2    20.1    24.0    b
## Si/E      22.1 0.443  2    20.2    24.0    b
##
## Degrees-of-freedom method: containment
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 4 estimates
## significance level used: alpha = 0.05
```

```
# chicken manure, moisture content
m.cm.water <- lme(value ~ Treatment, random = ~1|Batch,
                  data = subset(diet.cm, variable == "pMoist0"))
anova(m.cm.water)
```

```
##          numDF denDF    F-value p-value
## (Intercept)      1    18 22761.37 <.0001
## Treatment        3    18   8.31  0.0011
```

```
CLD(emmeans(m.cm.water, ~ Treatment), Letters = letters, method = "tukey")
```

```
## Treatment emmean SE df lower.CL upper.CL .group
## Si/Es 65.8 0.476 2 63.7 67.8 a
## Ss/E 65.9 0.476 2 63.9 68.0 a
## Si/E 65.9 0.476 2 63.9 68.0 a
## S/E 67.1 0.476 2 65.0 69.1 b
##
## Degrees-of-freedom method: containment
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 4 estimates
## significance level used: alpha = 0.05
```

3. Collect EMM

Supplementary Table S1 in the manuscript.

```
# chicken feed
cf.fd.emm <- CLD(emmeans(m.cf.feed, ~ Treatment), Letters = letters, method = "tukey")
cf.fd.emm$Diet <- "CF"
cf.fd.emm$variable <- "total_gDM"
cf.wat.emm <- CLD(emmeans(m.cf.water, ~ Treatment), Letters = letters, method = "tukey")
cf.wat.emm$Diet <- "CF"
cf.wat.emm$variable <- "pMoist0"

# chicken manure
cm.fd.emm <- CLD(emmeans(m.cm.feed, ~ Treatment), Letters = letters, method = "tukey")
cm.fd.emm$Diet <- "CM"
cm.fd.emm$variable <- "total_gDM"
cm.wat.emm <- CLD(emmeans(m.cm.water, ~ Treatment), Letters = letters, method = "tukey")
cm.wat.emm$Diet <- "CM"
cm.wat.emm$variable <- "pMoist0"

# combine
diets.emm <- rbind(cf.fd.emm, cm.fd.emm, cf.wat.emm, cm.wat.emm)
kable(diets.emm[,c(9,8,1:3,7)])
```

	variable	Diet	Treatment	emmean	SE	.group
1	total_gDM	CF	S/E	18.09090	0.2513605	a
2	total_gDM	CF	Si/E	19.92275	0.2513605	b
3	total_gDM	CF	Si/Es	19.99442	0.2513605	bc
4	total_gDM	CF	Ss/E	20.11902	0.2513605	c
11	total_gDM	CM	S/E	20.58322	0.4430521	a
31	total_gDM	CM	Si/Es	21.93965	0.4430521	b
41	total_gDM	CM	Ss/E	22.04648	0.4430521	b
21	total_gDM	CM	Si/E	22.07958	0.4430521	b
42	pMoist0	CF	Ss/E	68.06505	0.4263175	a
22	pMoist0	CF	Si/E	68.37659	0.4263175	b
32	pMoist0	CF	Si/Es	69.24918	0.4263175	c
12	pMoist0	CF	S/E	71.28429	0.4263175	d
33	pMoist0	CM	Si/Es	65.75114	0.4759467	a
43	pMoist0	CM	Ss/E	65.91207	0.4759467	a
23	pMoist0	CM	Si/E	65.94862	0.4759467	a
13	pMoist0	CM	S/E	67.08853	0.4759467	b

```
# Export table  
write.csv(diets.emm[,c(9,8,1:3,7)], "./tables/Supplementary_Table_S1.csv")
```