

# Supplementary information

## *Data plots & R script*

### **DA McGranahan**

*School of Natural Resource Sciences, Range Science; North Dakota State University, Fargo, ND*

### **BN Poling**

*School of Natural Resource Sciences, Range Science; North Dakota State University, Fargo, ND*

# Annual crops

## Raw data

In the following graphs, different colors indicate the mean and standard error of undusted (orange) and dusted plants (blue). Open blue points indicate measurements 1-2 hours prior to dust application; closed points represent measurements taken 1-2 hours after dust application.

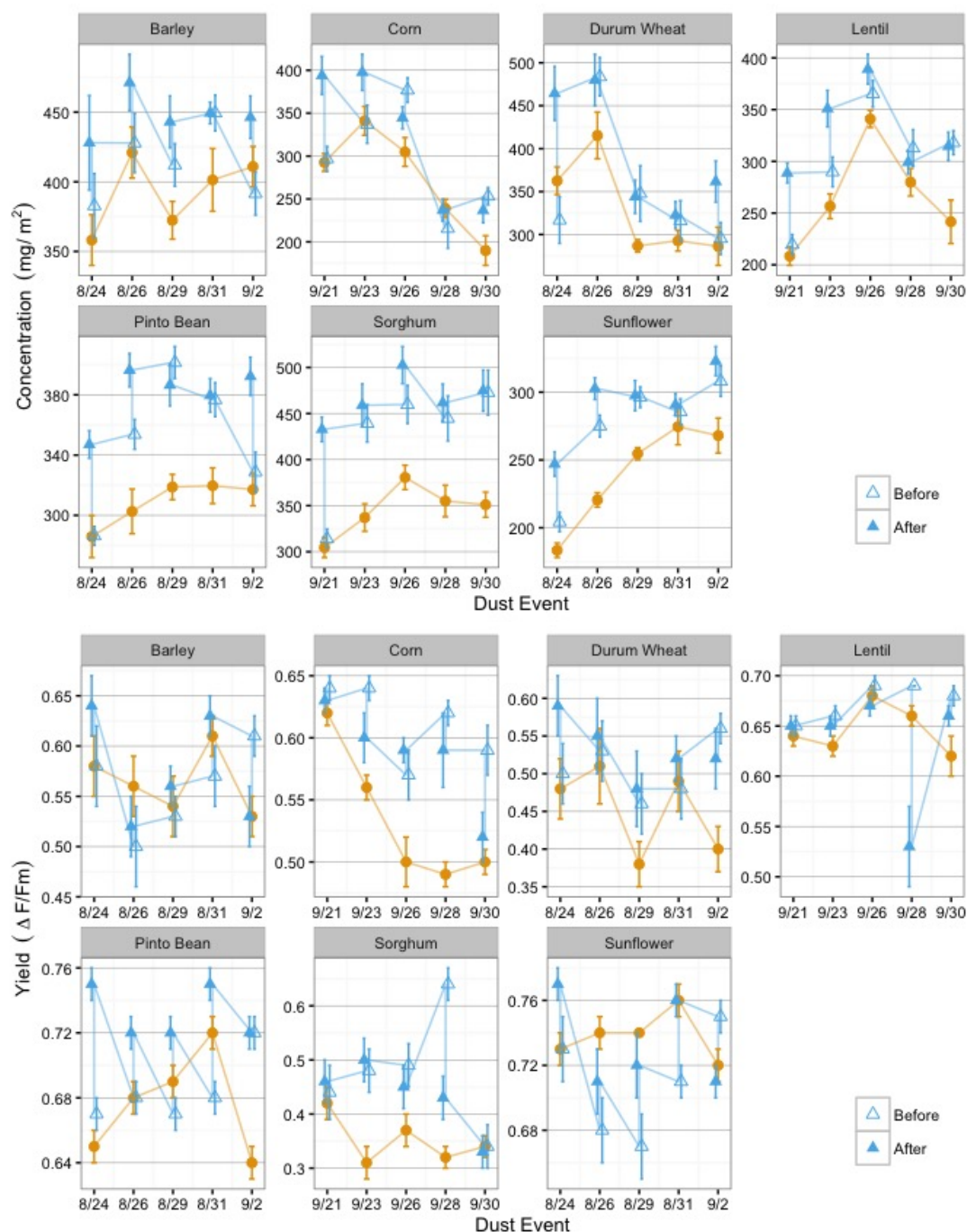


Figure 1: **TOP:** Chlorophyll concentration; **BOTTOM:** Photosynthetic yield (synonymous with quantum yield in further analysis and main manuscript).

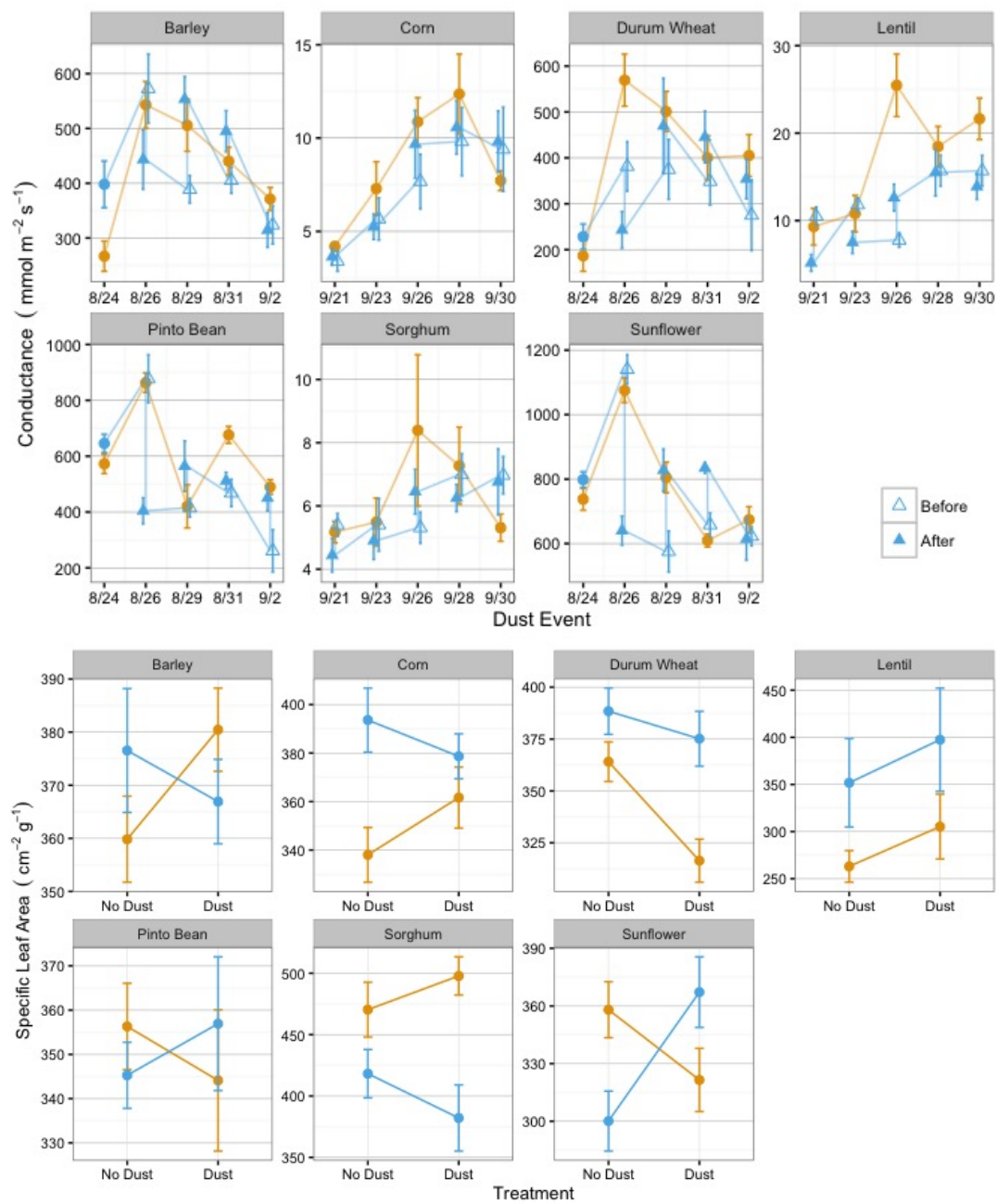


Figure 2: **TOP:** Stomatal conductance; **BOTTOM:** Specific leaf area.

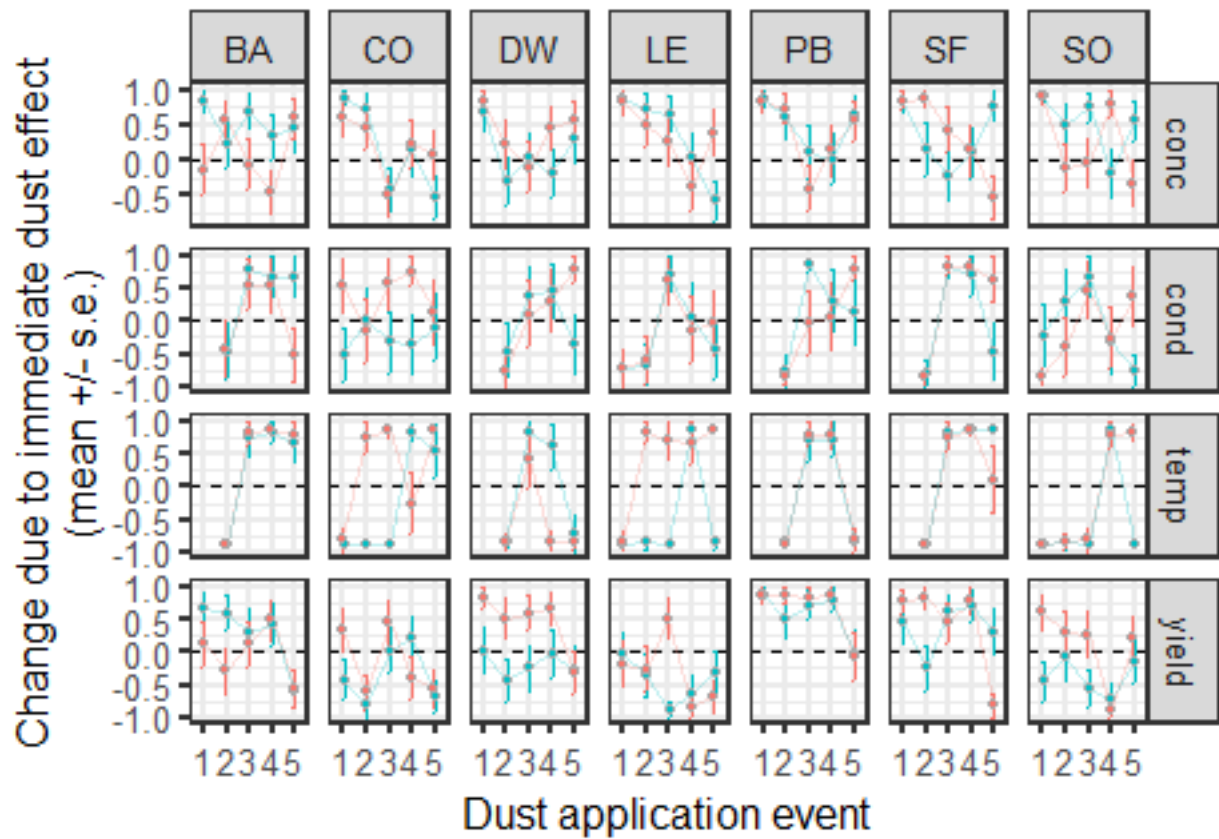


Figure 3: Immediate changes (after dusting values - pre-dusting values) in three physiological responses among 7 annual crop species over 5 dust application events that occurred 3 days apart. Colors indicate two blocks on different greenhouse benches.

### Short-term responses

	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
diff0	2	4292.0	4302.8	-2144.0	4288.0			
diff1	6	4228.8	4261.2	-2108.4	4216.8	71.2	4	0.000

Table 1: Immediate physiological responses to dusting vary among response measurements.

## Perennial Grasses

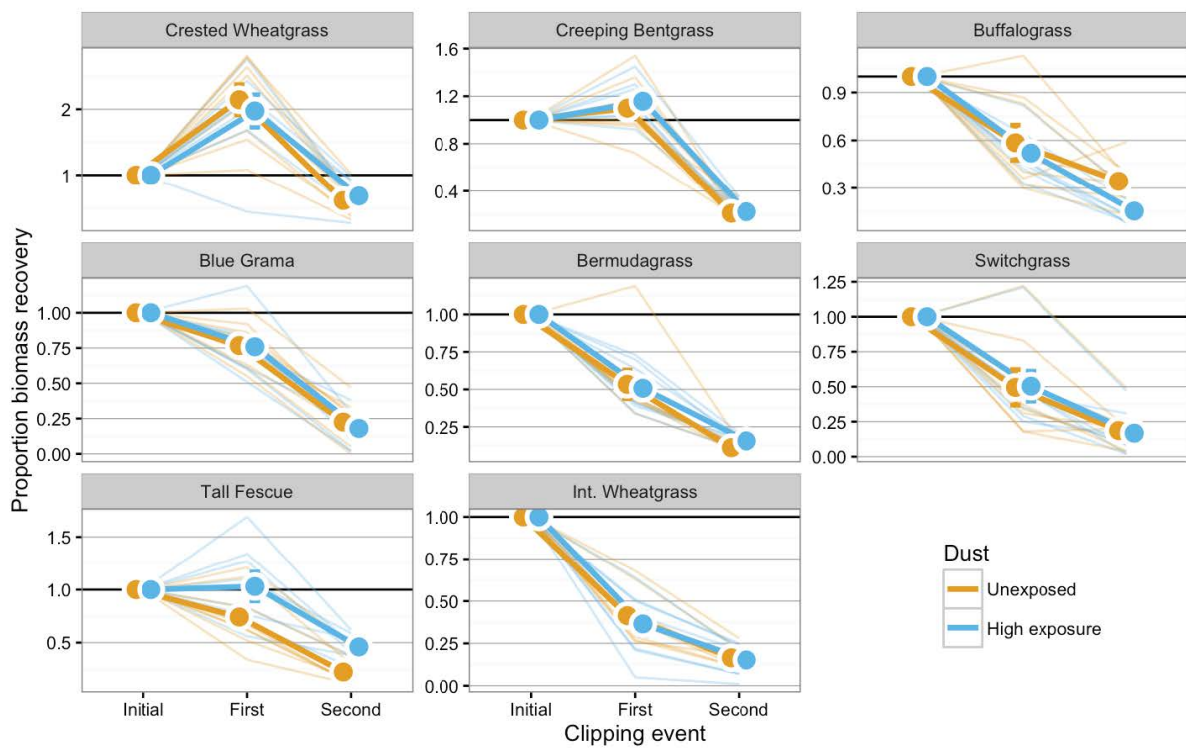


Figure 4: Biomass recovery for eight perennial grasses following two rounds of clipping under dusted and undusted conditions.

## R script

```
#  
# Annual crops  
#  
#  
# Short-term responses  
#  
#  
# Regression modelling  
#  
# Model fitting  
#  
# Responses by species  
#  
# Chlorophyll concentration  
conc0 <- lme4::lmer(diff ~ 0 + (1|block:round:pot), REML = F,  
                  data = filter(diff_dat, response == "conc"))  
conc1 <- lme4::lmer(diff ~ 0 + spp + (1|block:round:pot), REML = F,  
                  data = filter(diff_dat, response == "conc"))  
  
conc_diff_CI <- as.data.frame(confint(conc1)) %>%  
  rownames_to_column("term") %>%  
  slice(-(1:2)) %>%  
  bind_cols(tibble(  
    estimate = lme4::fixef(conc1),  
    response = "Chlorophyll\nconcentration") )  
# Stomatal conductance  
cond0 <- lme4::lmer(diff ~ 0 + (1|block:round:pot), REML = F,  
                  data = filter(diff_dat, response == "cond"))  
cond1 <- lme4::lmer(diff ~ 0 + spp + (1|block:round:pot), REML = F,  
                  data = filter(diff_dat, response == "cond"))  
  
cond_diff_CI <- as.data.frame(confint(cond1)) %>%  
  rownames_to_column("term") %>%  
  slice(-(1:2)) %>%  
  bind_cols(tibble(  
    estimate = lme4::fixef(cond1),  
    response = "Stomatal\nconductance") )  
# Photosynthetic yield  
yield0 <- lme4::lmer(diff ~ 0 + (1|block:round:pot), REML = F,  
                  data = filter(diff_dat, response == "yield"))  
yield1 <- lme4::lmer(diff ~ 0 + spp + (1|block:round:pot), REML = F,  
                  data = filter(diff_dat, response == "yield"))  
  
yield_diff_CI <- as.data.frame(confint(yield1)) %>%  
  rownames_to_column("term") %>%  
  slice(-(1:2)) %>%  
  bind_cols(tibble(  
    estimate = lme4::fixef(yield1),
```

```

        response = "Photosynthetic\nyield") )

# Leaf temperature
temp0 <- lme4::lmer(diff ~ 0 + (1|block:round:pot), REML = F,
                  data = filter(diff_dat, response == "temp"))
temp1 <- lme4::lmer(diff ~ 0 + spp + (1|block:round:pot), REML = F,
                  data = filter(diff_dat, response == "temp"))

temp_diff_CI <- as.data.frame(confint(temp1)) %>%
  rownames_to_column("term") %>%
  slice(-(1:2)) %>%
  bind_cols(tibble(
    estimate = lme4::fixef(temp1),
    response = "Leaf\ntemperature") )

#
# Overall responses
#
diff0 <- lme4::lmer(diff ~ 0 + (1|block:round:spp:pot),
                  data= diff_dat, REML = F)
diff1 <- lme4::lmer(diff ~ 0 + response + (1|block:round:spp:pot),
                  data= diff_dat, REML = F)
dmc <- anova(diff0, diff1)

# Plotting
#
# Species-level differences

bind_rows(cond_diff_CI,
          conc_diff_CI,
          yield_diff_CI,
          temp_diff_CI) %>%
  setNames(c("term", "ciL", "ciU",
            "estimate", "response")) %>%
  mutate_at(vars(ciL:estimate), ~ round(., 5)) %>%
  mutate(term = factor(term,
                      levels=c("sppBA", "sppDW",
                                "sppCO", "sppSO",
                                "sppLE", "sppPB",
                                "sppSF"),
                      labels=c("Barley (C3)",
                                "Wheat (C3)",
                                "Maize (C4)",
                                "Sorghum (C4)",
                                "Lentil",
                                "Pinto bean",
                                "Sunflower"))) ) %>%

ggplot() +
  coord_flip() + theme_bw(14) +
  geom_hline(yintercept = 0, lty=2) +
  geom_errorbar(aes(x=response,
                   ymin=ciL, ymax=ciU),
               width=0.25,
               size=1,

```

```

        color=cbPal5[3]) +
geom_point(aes(x=response, y=estimate),
            size=3,
            pch=21,
            stroke = 1,
            color="black",
            fill = cbPal5[3]) +
labs(y="Dust effect",
     title = "Responses by species (immediate)") +
ylim(c(-1.1,1.1)) +
facet_wrap(~ term, nrow = 2) +
theme(panel.grid.major.y = element_blank(),
      axis.title.y = element_blank(),
      axis.text.y = element_text(color="black"))
# Overall differences
as.data.frame(confint(diff1)) %>%
  rownames_to_column("term") %>%
  slice(-(1:2)) %>%
  bind_cols(tibble(
    estimate = lme4::fixef(diff1)) ) %>%
  setNames(c("term", "ciL", "ciU", "estimate"))%>%
mutate(term = recode(term,
  responseconc = "Chlorophyll\nconcentration",
  responsecond = 'Stomatal\nconductance',
  responseyield = 'Photosynthetic\nyield',
  responsetemp = 'Leaf\ntemperature')) %>%

ggplot() +
  coord_flip() + theme_bw(14) +
geom_hline(yintercept = 0, lty=2) +
  geom_errorbar(aes(x=term,
    ymin=ciL, ymax=ciU),
    width=0.25,
    size=1.5,
    color=cbPal5[3]) +
geom_point(aes(x=term, y=estimate),
            size=4,
            pch=21,
            stroke = 1.5,
            color="black",
            fill = cbPal5[3]) +
labs(y="Dust effect",
     title = "Overall responses") +
theme(panel.grid.major.y = element_blank(),
      axis.title.y = element_blank(),
      axis.text.y = element_text(color="black"))
# For long-term analysis
SLA2 <- SLA.dat[(1:672),c(1:3,8)] %>%
  mutate(lsla=log(SLA)) %>%
  filter(lsla>=4.5) %>%
  group_by(block, spp, t_c) %>%
  mutate(pot = seq(1,n(), 1)) %>%

```



```

    ungroup
Por <- filter(sc1, response == "cond") %>%
  mutate(lcond=log(value + 1)) %>%
  group_by(block, spp, t_c) %>%
  mutate(pot = seq(1,n(), 1)) %>%
  ungroup
Temp <- filter(sc1, response == "temp") %>%
  rename(temp = value) %>%
  group_by(block, spp, t_c) %>%
  mutate(pot = seq(1,n(), 1)) %>%
  ungroup
CCM <- ccm %>%
  mutate(lconc=log(value + 1)) %>%
  filter(lconc>=4) %>%
  group_by(block, spp, t_c) %>%
  mutate(pot = seq(1,n(), 1)) %>%
  ungroup
OS1 <- filter(os1, value <= 0.999) %>%
  rename(yield = value) %>%
  group_by(block, spp, t_c) %>%
  mutate(pot = seq(1,n(), 1)) %>%
  ungroup

#
# Long-term responses
#
# Mixed-effect model fitting
# Specific leaf area
sla.null <- lme4::lmer(scale(log(SLA)) ~ 1 + (1|block:pot),
  data=SLA2, REML=FALSE)
sla.spp <- lme4::lmer(scale(log(SLA)) ~ spp + (1|block:pot),
  data=SLA2, REML=FALSE)
sla.treat <- lme4::lmer(scale(log(SLA)) ~ t_c + (1|block),
  data=SLA2, REML=FALSE)
sla.add <- lme4::lmer(scale(log(SLA)) ~ 0 + spp + t_c + (1|block:pot),
  data=SLA2, REML=FALSE)
sla.int <- lme4::lmer(scale(log(SLA)) ~ 0 + spp * t_c + (1|block:pot),
  data=SLA2, REML=FALSE)
# Somatal conductance
conduct.null <- lme4::lmer(scale(lcond) ~ 1 + (1|block:date:pot),
  data=Por, REML=FALSE)
conduct.spp <- lme4::lmer(scale(lcond) ~ spp + (1|block:date:pot),
  data=Por, REML=FALSE)
conduct.treat <- lme4::lmer(scale(lcond) ~ t_c + (1|block:date:pot),
  data=Por, REML=FALSE)
conduct.add <- lme4::lmer(scale(lcond) ~ 0 + spp + t_c + (1|block:date:pot),
  data=Por, REML=FALSE)
conduct.int <- lme4::lmer(scale(lcond) ~ 0 + spp * t_c + (1|block:date:pot),
  data=Por, REML=FALSE)
# Leaf temperature
temp.null <- lme4::lmer(scale(temp) ~ 1 + (1|block:date:pot),
  data=Temp, REML=FALSE)

```

```

temp.spp <- lme4::lmer(scale(temp) ~ spp + (1|block:date:pot),
                      data=Temp, REML=FALSE)
temp.treat <- lme4::lmer(scale(temp) ~ t_c + (1|block:date:pot),
                        data=Temp, REML=FALSE)
temp.add <- lme4::lmer(scale(temp) ~ 0 + spp + t_c + (1|block:date:pot),
                      data=Temp, REML=FALSE)
temp.int <- lme4::lmer(scale(temp) ~ 0 + spp * t_c + (1|block:date:pot),
                      data=Temp, REML=FALSE)

# Chlorophyll content
conc.null <- lme4::lmer(scale(lconc) ~ 1 + (1|block:date),
                       data=CCM, REML=FALSE)
conc.spp <- lme4::lmer(scale(lconc) ~ spp + (1|block:date:pot),
                      data=CCM, REML=FALSE)
conc.treat <- lme4::lmer(scale(lconc) ~ t_c + (1|block:date:pot),
                        data=CCM, REML=FALSE)
conc.add <- lme4::lmer(scale(lconc) ~ 0 + spp + t_c + (1|block:date:pot),
                      data=CCM, REML=FALSE)
conc.int <- lme4::lmer(scale(lconc) ~ 0 + spp*t_c + (1|block:date:pot),
                      data=CCM, REML=FALSE)

# Quantum yield
yield.null <- lme4::lmer(scale(yield)~ 1 + (1|block:date:pot),
                        data=OS1, REML=FALSE)
yield.spp <- lme4::lmer(scale(yield)~ spp + (1|block:date:pot),
                      data=OS1, REML=FALSE)
yield.treat <- lme4::lmer(scale(yield)~ t_c + (1|block:date:pot),
                        data=OS1, REML=FALSE)
yield.add <- lme4::lmer(scale(yield)~ 0 + spp + t_c + (1|block:date:pot),
                      data=OS1, REML=FALSE)
yield.int <- lme4::lmer(scale(yield) ~ 0 + spp*t_c + (1|block:date:pot),
                      data=OS1, REML=FALSE)

# AICc-based model selection
# Specific leaf area
sla.mod.names <- c("sla.null", "sla.spp",
                  "sla.treat", "sla.add",
                  "sla.int")
sla.mods <- lst( )

for(i in 1:length(sla.mod.names)) {
  sla.mods[[i]] <- get(sla.mod.names[i]) }
sla_aic_tab <- AICcmavg::aictab(cand.set = sla.mods,
                              modnames = sla.mod.names)

# Stomatal conductance
conduct.mod.names <- c("conduct.null", "conduct.spp",
                     "conduct.treat", "conduct.add",
                     "conduct.int")
conduct.mods <- lst( )

for(i in 1:length(conduct.mod.names)) {
  conduct.mods[[i]] <- get(conduct.mod.names[i]) }
cond_aic_tab <- AICcmavg::aictab(cand.set = conduct.mods,
                                modnames = conduct.mod.names)

```

```

# Leaf temeprature
temp.mod.names <- c("temp.null", "temp.spp",
                   "temp.treat", "temp.add",
                   "temp.int")

temp.mods <- lst( )

for(i in 1:length(temp.mod.names)) {
  temp.mods[[i]] <- get(temp.mod.names[i]) }
temp_aic_tab <- AICcmodavg::aictab(cand.set = temp.mods,
                                  modnames = temp.mod.names)

# Chlorophyll
conc.mod.names <- c("conc.null", "conc.spp",
                   "conc.treat", "conc.add",
                   "conc.int")

conc.mods <- lst( )

for(i in 1:length(conc.mod.names)) {
  conc.mods[[i]] <- get(conc.mod.names[i]) }
conc_aic_tab <- AICcmodavg::aictab(cand.set = conc.mods,
                                  modnames = conc.mod.names)

# Photosynthetic yield
yield.mod.names <- c("yield.null", "yield.spp",
                   "yield.treat", "yield.add",
                   "yield.int")

yield.mods <- lst( )

for(i in 1:length(yield.mod.names)) {
  yield.mods[[i]] <- get(yield.mod.names[i]) }
yld_aic_tab <- AICcmodavg::aictab(cand.set = yield.mods,
                                  modnames = yield.mod.names)

#
# Estimating regression coefficients & 95% CIs
#
# By crop species
cond_CI <- as.data.frame(confint(conduct.int)) %>%
  rownames_to_column("term") %>%
  slice(-(1:9)) %>%
  bind_cols(tibble(
    estimate = lme4::fixef(conduct.int)[8:14],
    response = "Stomatal\nconductance" ) )
temp_CI <- as.data.frame(confint(temp.int)) %>%
  rownames_to_column("term") %>%
  slice(-(1:9)) %>%
  bind_cols(tibble(
    estimate = lme4::fixef(temp.int)[8:14],
    response = "Leaf\ntemperature" ) )
conc_CI <- as.data.frame(confint(conc.int)) %>%
  rownames_to_column("term") %>%
  slice(-(1:9)) %>%

```

```

        bind_cols(tibble(estimate = lme4::fixef(conc.int)[8:14],
                        response = "Chlorophyll\ncontent"))
yield_CI <- as.data.frame(confint(yield.int)) %>%
  rownames_to_column("term") %>%
  slice(-(1:9)) %>%
  bind_cols(tibble(estimate = lme4::fixef(yield.int)[8:14],
                  response = "Photosynthetic\nyield"))
sla_CI <- as.data.frame(confint(sla.int)) %>%
  rownames_to_column("term") %>%
  slice(-(1:9)) %>%
  bind_cols(tibble(estimate = lme4::fixef(sla.int)[8:14],
                  response = "Specific\nleaf area"))

sppCIs <- bind_rows( cond_CI,
                    conc_CI,
                    yield_CI,
                    sla_CI,
                    temp_CI) %>%
  setNames(c("term", "ciL", "ciU",
            "estimate", "response")) %>%
  mutate(term = factor(term,
    levels=c("t_cT", "sppDW:t_cT",
             "sppCO:t_cT", "sppSO:t_cT",
             "sppLE:t_cT", "sppPB:t_cT",
             "sppSF:t_cT"),
    labels=c("Barley (C3)", "Wheat (C3)",
             "Maize (C4)", "Sorghum (C4)",
             "Lentil", "Pinto bean",
             "Sunflower"))) )

#
# Overall dust effects
#
# Specific leaf area (using model averaging)

sla.mod.names.top <- c("sla.spp", "sla.add")
sla.mods.top <- lst( )
for(i in 1:length(sla.mod.names.top)) {
  sla.mods.top[[i]] <- get(sla.mod.names.top[i]) }

sla.terms <- c("sppBA", "sppDW", "sppPB",
              "sppSF", "sppCO", "sppLE",
              "sppSO", "t_cT" )
sla.av.params <- as_tibble(array(NA, c(length(sla.terms), 4)))
colnames(sla.av.params) <- c("term", "ciL", "ciU", "estimate")
for(i in 1:length(sla.terms)) {
  sla.av <- AICcmodavg::modavg(parm = paste(sla.terms[i]),
                              cand.set = sla.mods.top,
                              modnames = sla.mod.names.top)
  sla.av.params[i, 1] <- sla.terms[i]
  sla.av.params[i, 4] <- round(sla.av$Mod.avg.beta, 2)
  sla.av.params[i, 2] <- round(sla.av$Lower.CL, 3)

```

```

sla.av.params[i,3] <- round(sla.av$Upper.CL, 3) }

conduct.add.CI <- as.data.frame(confint(conduct.add)) %>%
  rownames_to_column("term") %>%
  slice(-(1:2)) %>%
  bind_cols(tibble(
    estimate = lme4::fixef(conduct.add),
    response = "Stomatal\nconductance" ) )
temp.add.CI <- as.data.frame(confint(temp.add)) %>%
  rownames_to_column("term") %>%
  slice(-(1:2)) %>%
  bind_cols(tibble(
    estimate = lme4::fixef(temp.add),
    response = "Leaf\ntemperature" ) )
conc.add.CI <- as.data.frame(confint(conc.add)) %>%
  rownames_to_column("term") %>%
  slice(-(1:2)) %>%
  bind_cols(tibble(estimate = lme4::fixef(conc.add),
    response = "Chlorophyll\ncontent"))
yield.add.CI <- as.data.frame(confint(yield.add)) %>%
  rownames_to_column("term") %>%
  slice(-(1:2)) %>%
  bind_cols(tibble(estimate = lme4::fixef(yield.add),
    response = "Photosynthetic\nyield"))

cropCIs <- bind_rows(conduct.add.CI,
  conc.add.CI,
  yield.add.CI,
  temp.add.CI) %>%
  setNames(c("term", "ciL", "ciU",
    "estimate", "response"))

cropCIs <-
  sla.av.params %>% mutate(response = "Specific\nleaf area") %>%
  bind_rows(cropCIs)
sppCIs %>%
ggplot() +
coord_flip() + theme_bw(14) +
geom_hline(yintercept = 0, lty=2) +
  geom_errorbar(aes(x=response,
    ymin=ciL, ymax=ciU),
    width=0.25,
    size=1,
    color=cbPal5[3]) +
  geom_point(aes(x=response, y=estimate),
    size=3,
    pch=21,
    stroke = 1,
    color="black",
    fill = cbPal5[3]) +

```

```

labs(y="Dust effect",
      title = "Responses by species (long-term)") +
ylim(c(-1.6,1.1)) +
facet_wrap(~ term, nrow = 2) +
theme(panel.grid.major.y = element_blank(),
      axis.title.y = element_blank(),
      axis.text.y = element_text(color="black"))
cropCIs %>%
  filter(term == "t_cT") %>%
ggplot() +
  coord_flip() + theme_bw(14) +
geom_hline(yintercept = 0, lty=2) +
  geom_errorbar(aes(x=response,
                    ymin=ciL, ymax=ciU,
                    width=0.25, size=1.5, color=cbPal5[3])) +
  geom_point(aes(x=response, y=estimate),
             size=4.5, pch=21, stroke = 1.5,
             color="black", fill = cbPal5[3]) +
labs(y="Dust effect",
      title = "Overall responses") +
theme(panel.grid.major.y = element_blank(),
      axis.title.y = element_blank(),
      axis.text.y = element_text(color="black"))

# cowplot::plot_grid(spp_gg, ov_gg,
#                    nrow = 2,
#                    rel_heights = c(2/3, 1/3))
#
# Perennial grasses
#
# Model fitting
gr_null <- lme4::lmer(recovery~ 1 + (1|block:event:pot),
                    data=recovery.dat, REML = F)
gr_trt <- lme4::lmer(recovery ~ trt + (1|block:event:pot),
                   data=recovery.dat, REML = F)
gr_spp <- lme4::lmer(recovery ~ 0 + species*trt + (1|block:event:pot),
                   data=recovery.dat, REML = F)

gr_photo <- lme4::lmer(recovery~ 0 + photo*trt + (1|block:event:pot),
                     data=recovery.dat, REML = F)
# AICc-based model selection
rcv.mod.names <- c("gr_null", "gr_trt",
                  "gr_spp", "gr_photo")
rcv.mods <- lst( )

for(i in 1:length(rcv.mod.names)) {
  rcv.mods[[i]] <- get(rcv.mod.names[i]) }
grass_aic_tab <- AICcmodavg::aictab(cand.set = rcv.mods,
                                   modnames = rcv.mod.names)
# Parameter extraction
gr_params <- bind_cols(

```

```
confint(gr_spp) %>%  
  as.data.frame %>%  
  rownames_to_column("term") %>%  
  slice(-c(1:2)),  
enframe(lme4::fixef(gr_spp)) %>%  
  select(value) )
```