

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

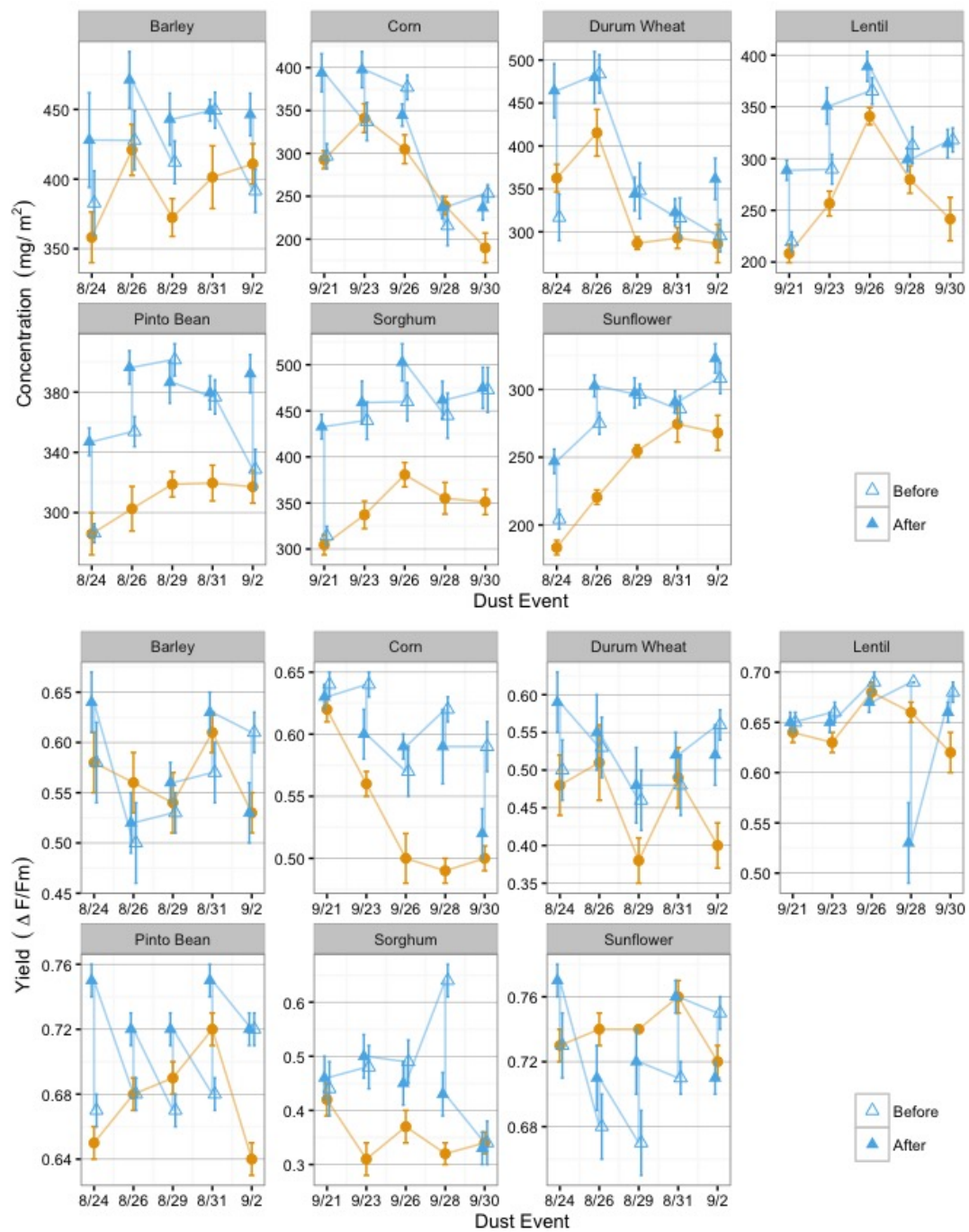


Figure 1: **TOP:** Chlorophyll concentration; **BOTTOM:** Photosynthetic yield.

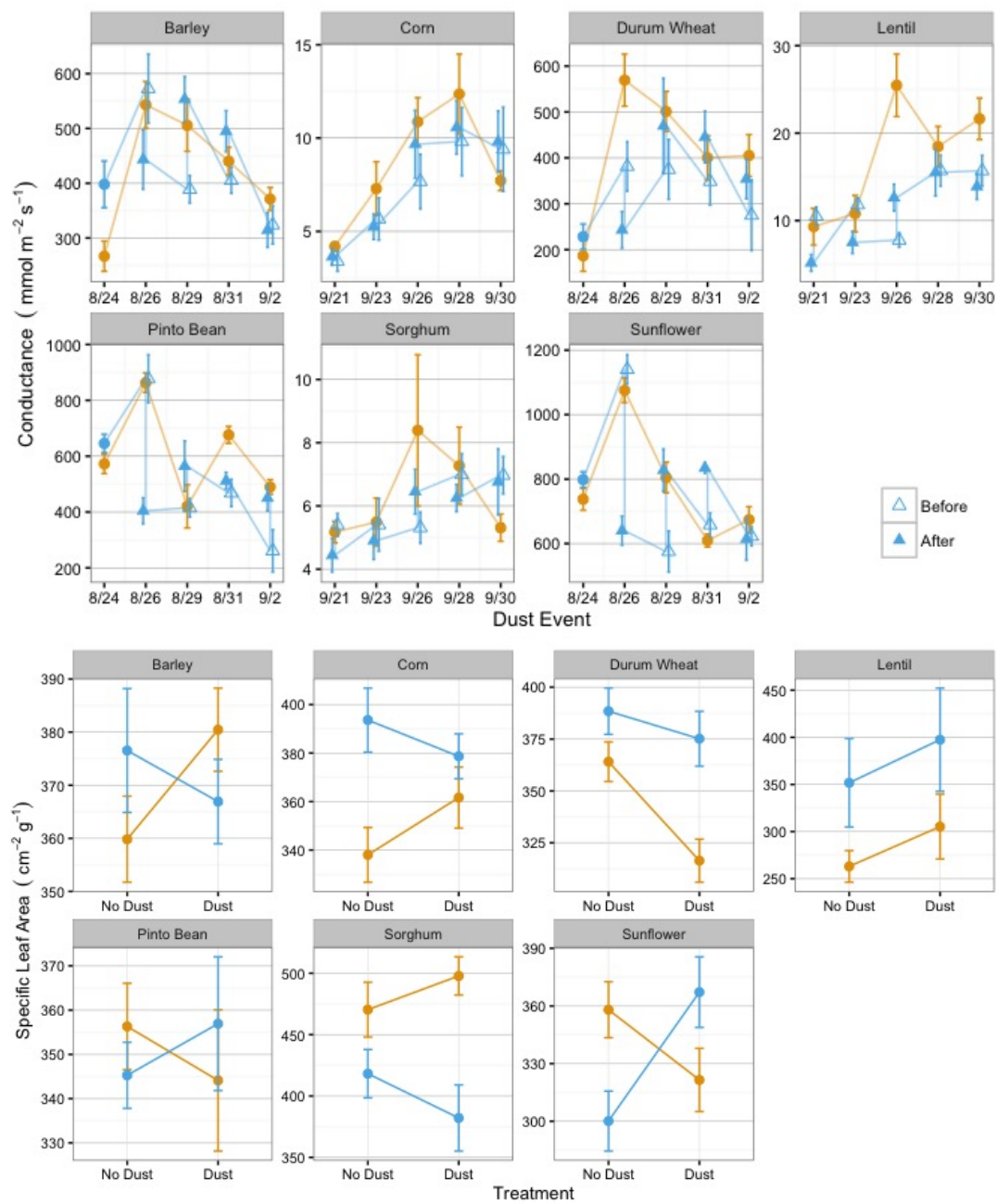


Figure 2: **TOP:** Stomatal conductance; **BOTTOM:** Specific leaf area.

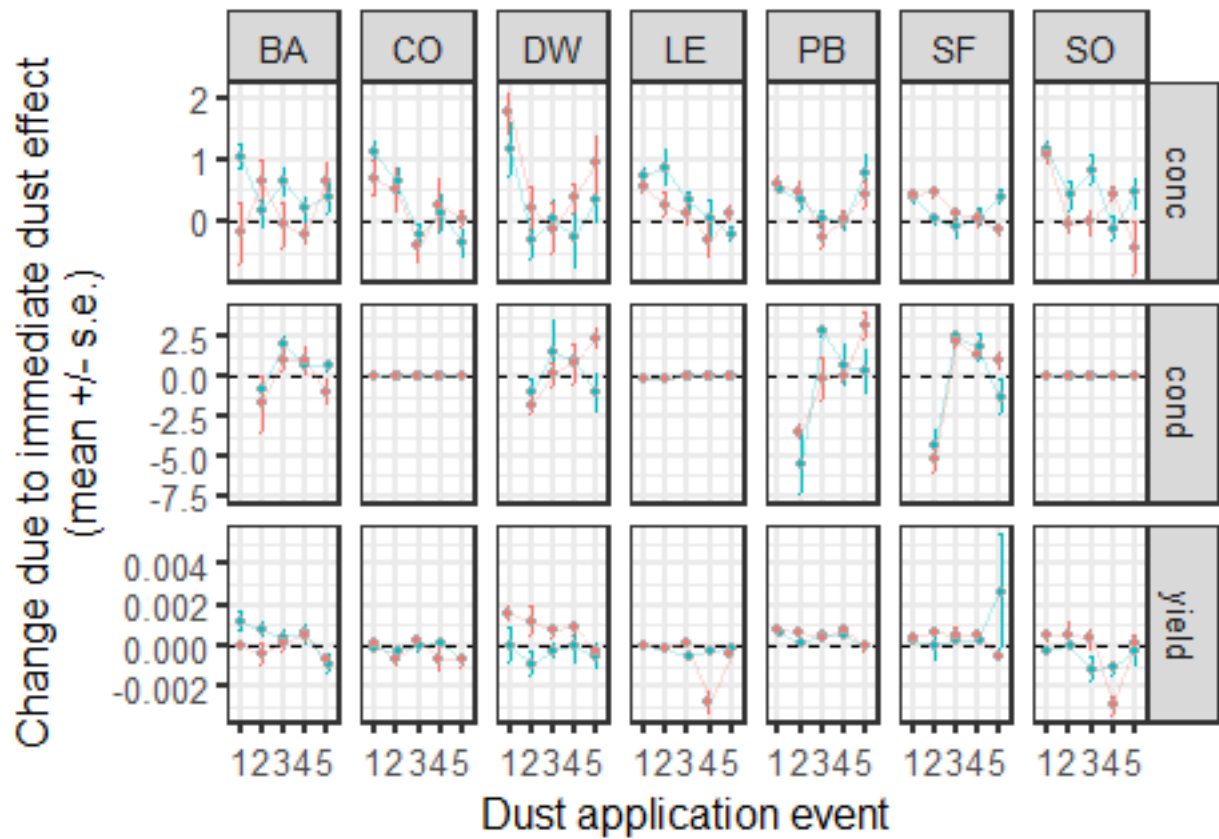


Figure 3: Immediate changes (after dusting values - pre-dusting values) in three physiological responses among 7 annual crop species over 5 dust application events that occurred 3 days apart. Colors indicate two blocks on different greenhouse benches.

Short-term responses

	Df	AIC	BIC	logLik	deviance	Chisq	Chi Df	Pr(>Chisq)
diff0	2	3817.2	3827.6	-1906.6	3813.2			
diff1	5	3783.2	3809.3	-1886.6	3773.2	39.9	3	0.000

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

Perennial Grasses

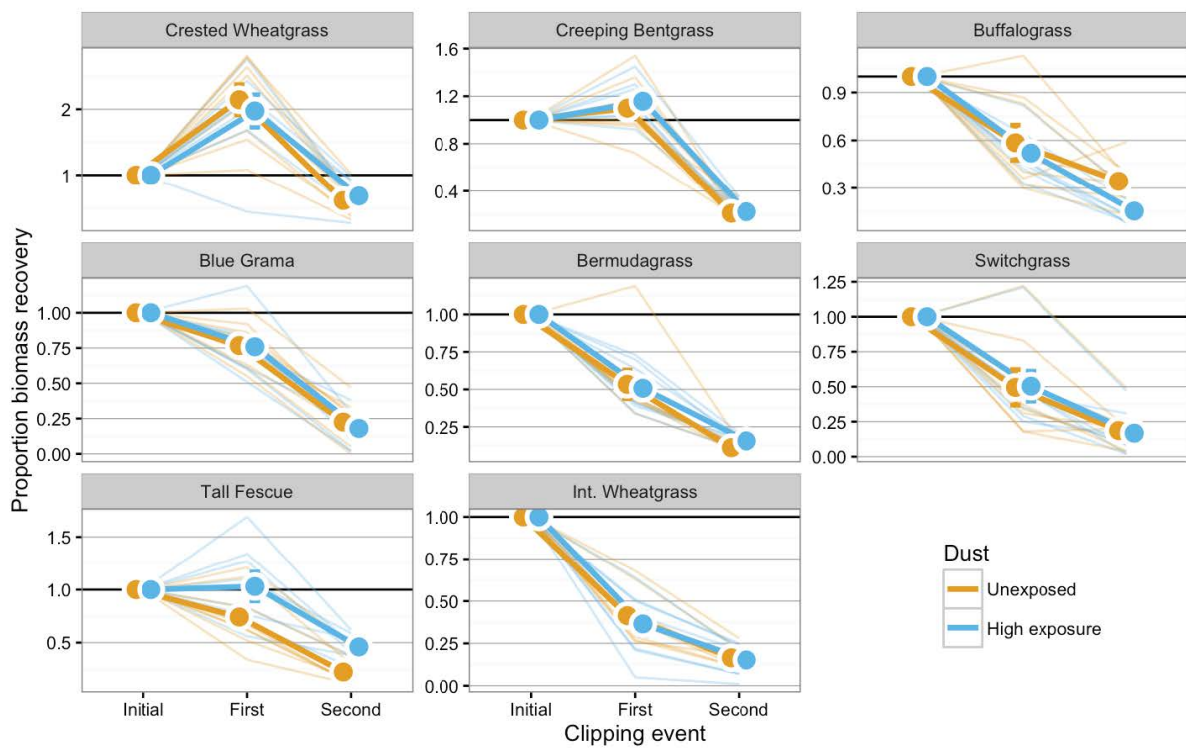


Figure 4: Biomass recovery for eight perennial grasses following two rounds of clipping under dusted and undusted conditions.

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") )
diffCIs <- bind_rows(cond_diff_CI,
                    conc_diff_CI,
                    yield_diff_CI)
colnames(diffCIs) <- c("term", "ciL", "ciU", "estimate", "response")
#
# Overall responses
#
diff0 <- lme4::lmer(diff ~ 0 + (1|block:round:spp),
                  data= diff_dat, REML = F)
diff1 <- lme4::lmer(diff ~ 0 + response + (1|block:round:spp),
                  data= diff_dat, REML = F)
dmc <- anova(diff0, diff1)

diff_CI <- as.data.frame(confint(diff1)) %>%
  rownames_to_column("term") %>%
  slice(-(1:2)) %>%
  bind_cols(tibble(
    estimate = lme4::fixef(diff1)) )
colnames(diff_CI) <- c("term", "ciL", "ciU", "estimate")
#
# Long-term responses
#
# Mixed-effect model fitting
# Specific leaf area
sla.null <- lme4::lmer(scale(log(SLA)) ~ 1 + (1|block),
                    data=SLA2, REML=FALSE)
sla.spp <- lme4::lmer(scale(log(SLA)) ~ spp + (1|block),
                    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),
                    data=SLA2, REML=FALSE)
sla.int <- lme4::lmer(scale(log(SLA)) ~ 0 + spp * t_c + (1|block),
                    data=SLA2, REML=FALSE)
# Stomatal 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)
# Chlorophyll content
conc.null <- lme4::lmer(scale(lconc) ~ 1 + (1|block:date:pot),
                    data=CCM2, REML=FALSE)
conc.spp <- lme4::lmer(scale(lconc) ~ spp + (1|block:date:pot),
                    data=CCM2, REML=FALSE)

```

```

conc.treat <- lme4::lmer(scale(lconc) ~ t_c + (1|block:date:pot),
                        data=CCM2, REML=FALSE)
conc.add <- lme4::lmer(scale(lconc) ~ 0 + spp + t_c + (1|block:date:pot),
                      data=CCM2, REML=FALSE)
conc.int <- lme4::lmer(scale(lconc) ~ 0 + spp*t_c + (1|block:date),
                      data=CCM2, 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 <- AICcmodavg::aictab(cand.set = sla.mods,
                                modnames = sla.mod.names)

# 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 <- AICcmodavg::aictab(cand.set = conduct.mods,
                                modnames = conduct.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 <- AICcmoavg::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") )
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)
colnames(sppCIs) <- c("term", "ciL", "ciU", "estimate", "response")

sppCIs <- sppCIs %>%
  mutate(term = factor(term,
    levels=c("t_cT", "sppDW:t_cT",
      "sppC0:t_cT", "sppS0: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" ) )
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)
colnames(cropCIs) <- c("term", "ciL", "ciU", "estimate", "response")

cropCIs <-
  sla.av.params %>% mutate(response = "Specific\nleaf area") %>%
  bind_rows(cropCIs)
#
# 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),
                     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 <- AICcmmodavg::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) )

```