

# Supplementary information

*Raw data plots, diagnostic statistics, and R script*

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# 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.

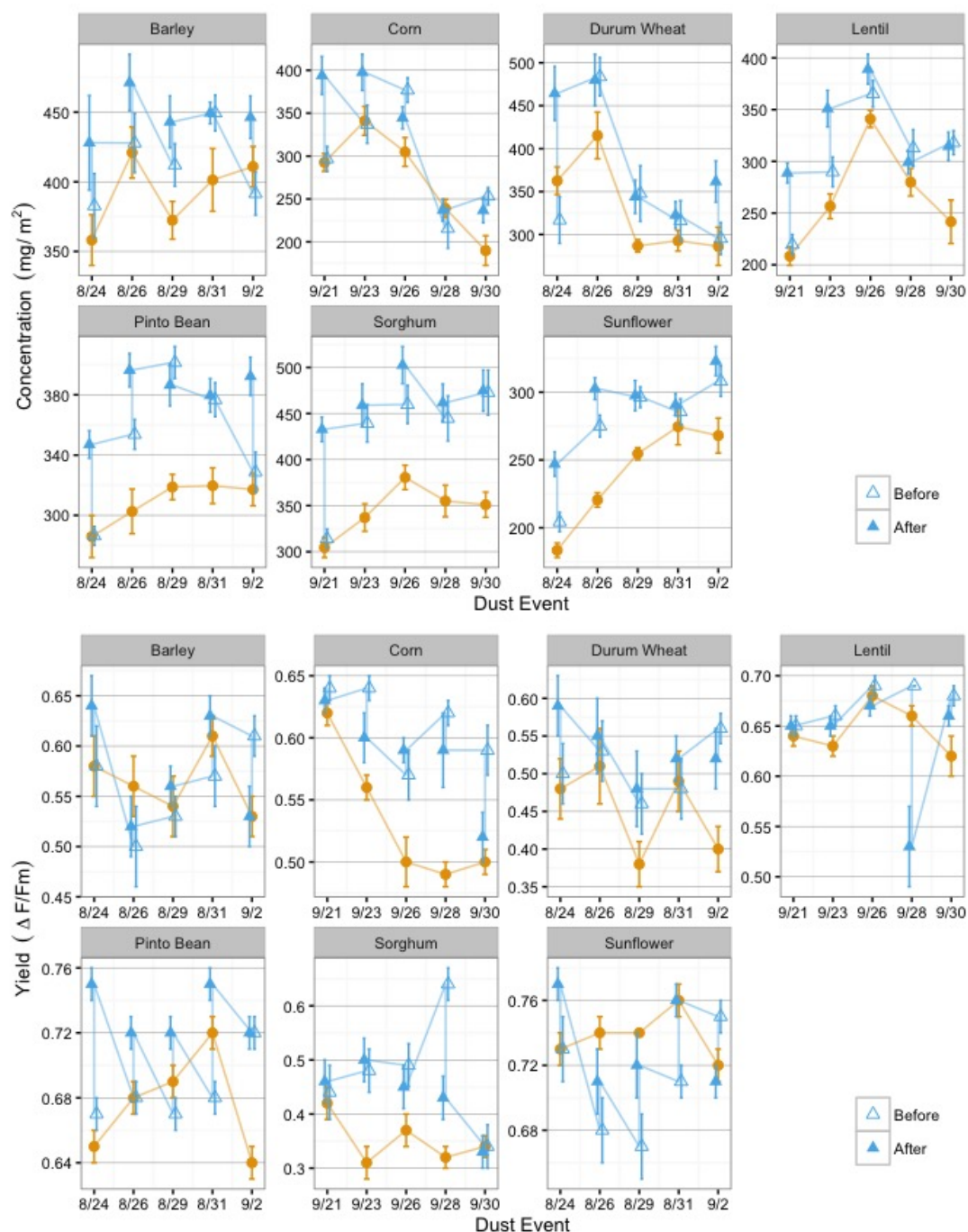


Figure 1: **TOP:** Chlorophyll concentration; **BOTTOM:** Photosynthetic yield.

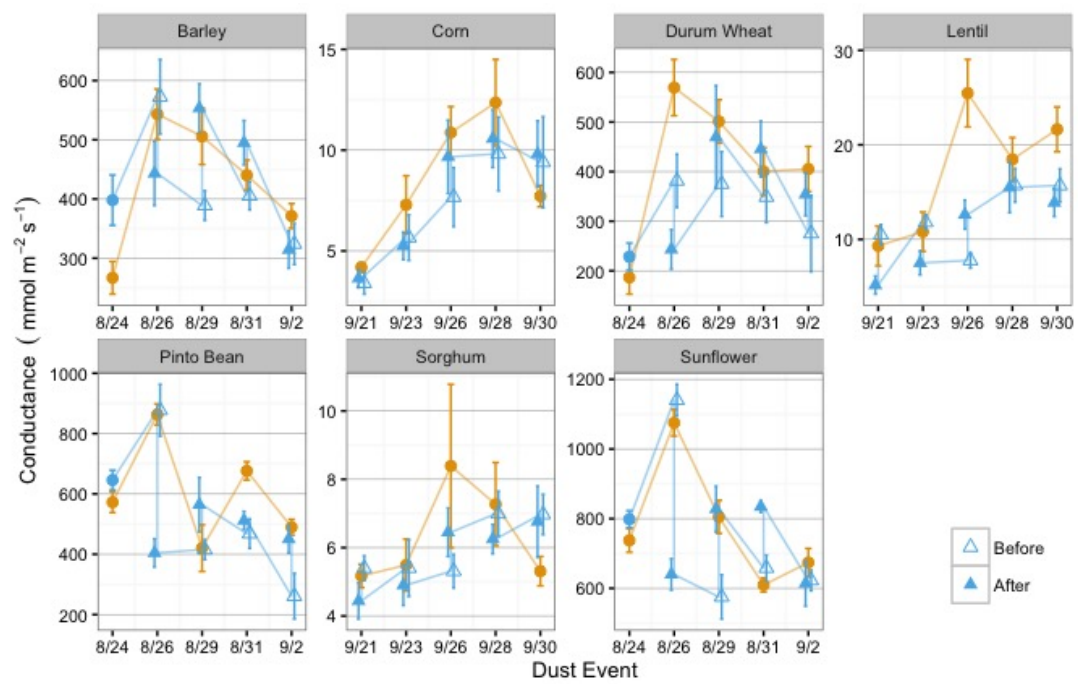


Figure 2: Stomatal conductance

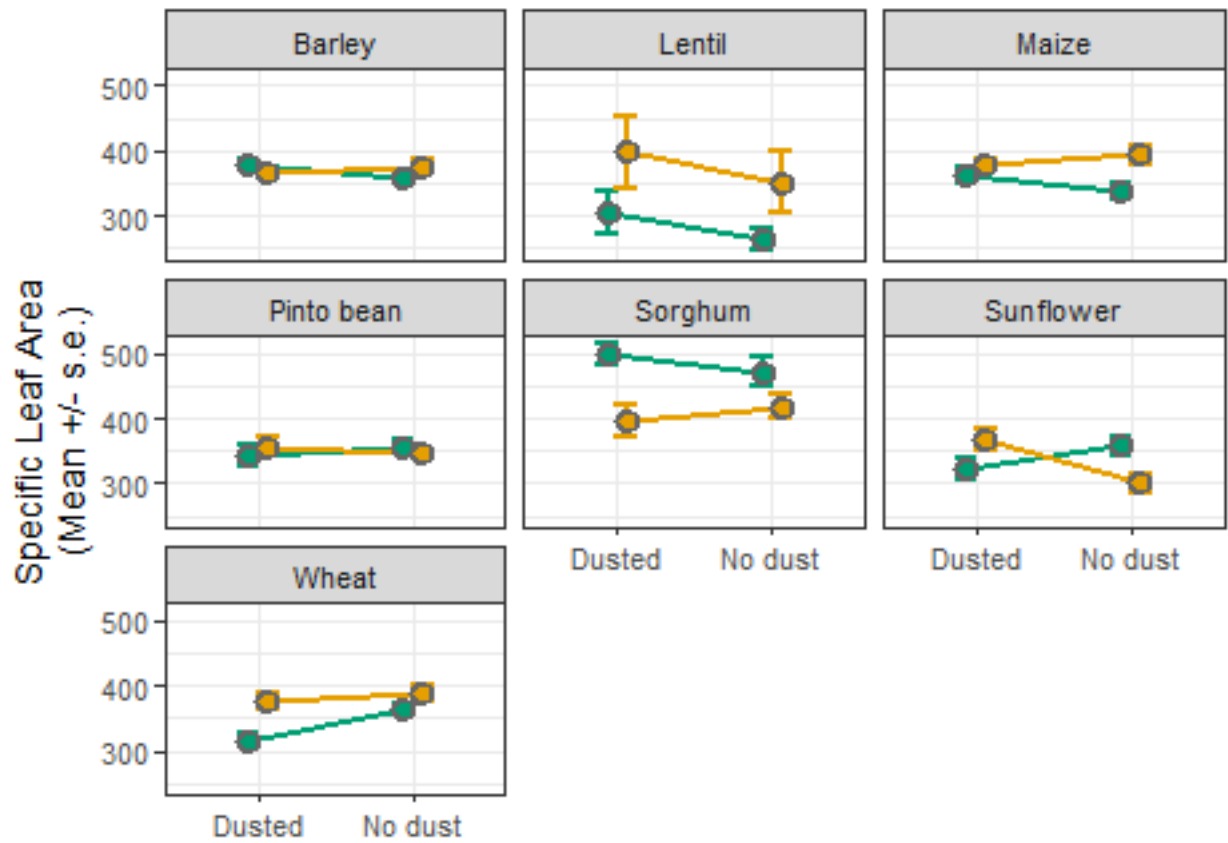


Figure 3: Raw data for specific leaf area by species. Colors differentiate randomly-assigned blocks.

	npar	AIC	BIC	logLik	deviance	Chisq	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.

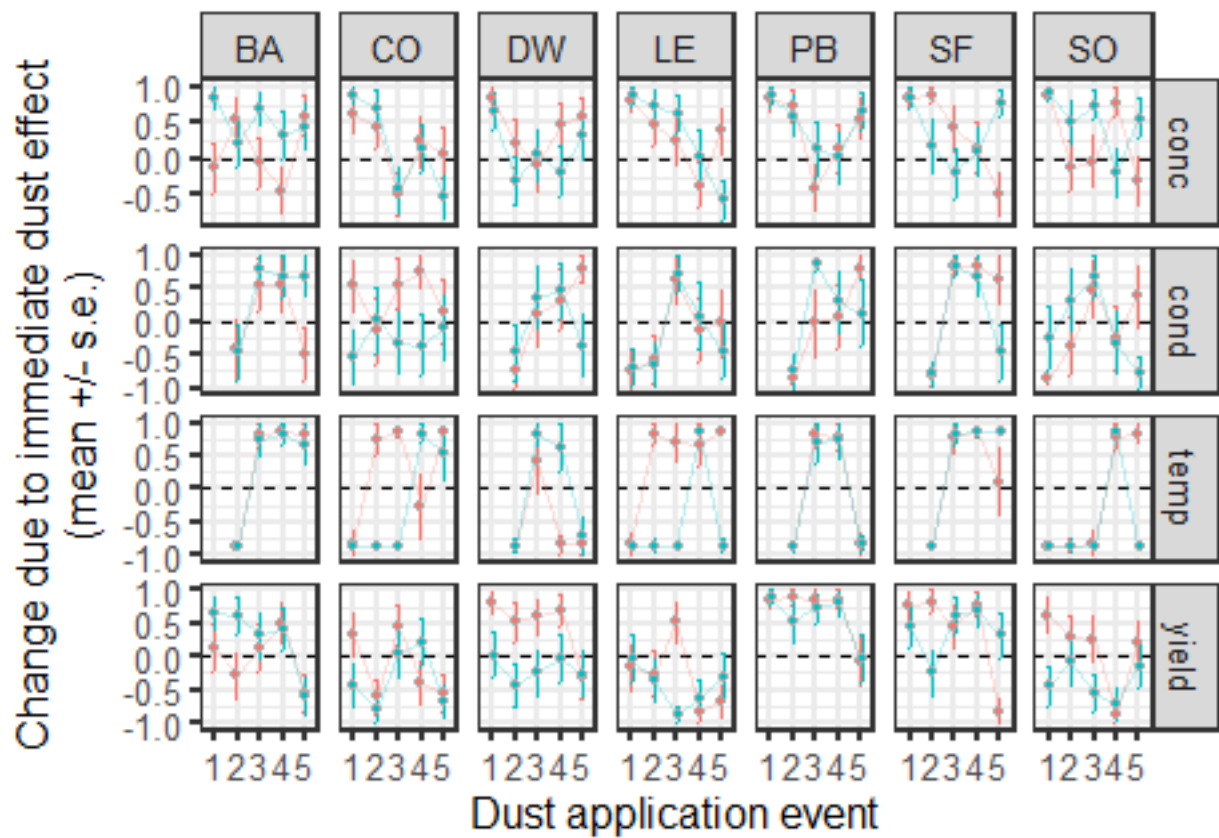


Figure 4: Immediate changes (after dusting values - pre-dusting values) in three physiological responses among 7 annual crop species over 5 dust application events that occurred 3 days apart. Colors indicate two blocks on different greenhouse benches.

## Perennial Grasses

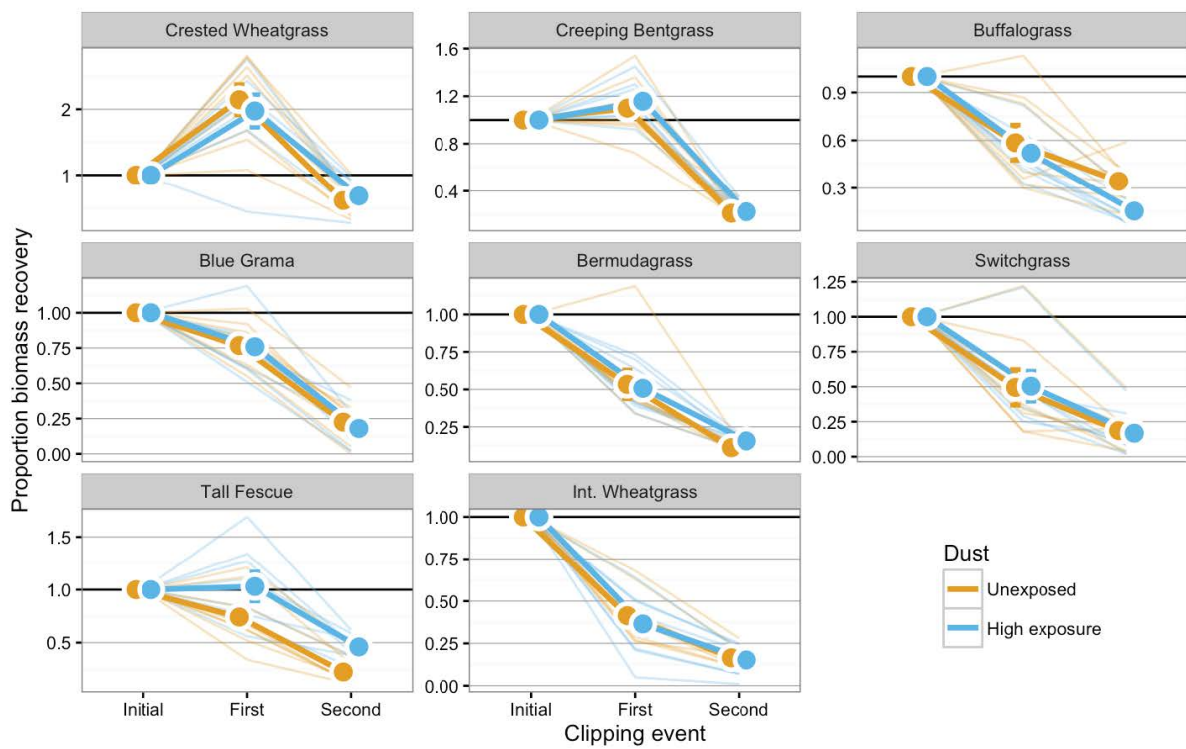


Figure 5: Biomass recovery for eight perennial grasses following two rounds of clipping under dusted and undusted conditions.

## R script

Data available in attached R environment `DustEffectsData.Rdata`



```
# # # 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)
# Overall differences
st_ov <-
  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'))
#
# # 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)) ~ spp + t_c + (1|block:pot),
                    data=SLA2, REML=FALSE)
sla.int <- lme4::lmer(scale(log(SLA)) ~ spp * t_c + (1|block:pot),
                    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),

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                                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) ~ spp + t_c + (1|block:date:pot),
                                data=Por, REML=FALSE)
conduct.int <- lme4::lmer(scale(lcond) ~ 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) ~ spp + t_c + (1|block:date:pot),
                                data=Temp, REML=FALSE)
temp.int <- lme4::lmer(scale(temp) ~ 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) ~ spp + t_c + (1|block:date:pot),
                                data=CCM, REML=FALSE)
conc.int <- lme4::lmer(scale(lconc) ~ 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)~ spp + t_c + (1|block:date:pot),
                                data=OS1, REML=FALSE)
yield.int <- lme4::lmer(scale(yield) ~ 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)
# Stomatal conductance

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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 <- AICcmavg::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 <- AICcmavg::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 <- AICcmavg::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(

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        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"))

# Combine CIs
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",
      "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.av <- AICcmoavg::modavg(parm = paste('t_cT'),
  cand.set = sla.mods.top,
  modnames = sla.mod.names.top)
sla_dust_CI <- tibble( term = 't_cT',
  `2.5 %` = round(sla.av$Lower.CL, 3),
  `97.5 %` = round(sla.av$Upper.CL, 3),
  estimate = round(sla.av$Mod.avg.beta, 2),
  response = "Specific\nleaf area")

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```

# Other responses from additive models alone
conduct_dust_CI <- as.data.frame(confint(conduct.add)) %>%
  rownames_to_column("term") %>%
  filter(term == "t_cT") %>%
  as_tibble() %>%
  mutate(estimate = lme4::fixef(conduct.add)
         [length(lme4::fixef(conduct.add))] ,
         response = "Stomatal\nconductance")
temp_dust_CI <- as.data.frame(confint(temp.add)) %>%
  rownames_to_column("term") %>%
  filter(term == "t_cT") %>%
  as_tibble() %>%
  mutate(estimate = lme4::fixef(temp.add)
         [length(lme4::fixef(temp.add))] ,
         response = "Leaf\ntemperature")
conc_dust_CI <- as.data.frame(confint(conc.add)) %>%
  rownames_to_column("term") %>%
  filter(term == "t_cT") %>%
  as_tibble() %>%
  mutate(estimate = lme4::fixef(conc.add)
         [length(lme4::fixef(conc.add))] ,
         response = "Chlorophyll\ncontent")
yield_dust_CI <- as.data.frame(confint(yield.add)) %>%
  rownames_to_column("term") %>%
  filter(term == "t_cT") %>%
  as_tibble() %>%
  mutate(estimate = lme4::fixef(yield.add)
         [length(lme4::fixef(yield.add))] ,
         response = "Photosynthetic\nyield")

# Combine CIs
cropCIs <- bind_rows(conduct_dust_CI,
                     conc_dust_CI,
                     yield_dust_CI,
                     temp_dust_CI,
                     sla_dust_CI) %>%
  rename(lwr = `2.5 %`, upr = `97.5 %`)

#
# 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) )

```