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title: "Trends in growth, rwp and photosyn"
output: html_document
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```

Objective: To see if CO2 mesophyll resistance (rwp) is realted to total growth traits.

Data limiations: photosynthesis realted traits are from greenhouse and growth characteristics are from field.

Growth data files: Corv_2012_Growth_rep1.csv, Corv_2012_Growth_rep2.csv, Corv_2012_Growth_rep3.csv, GWAS_Clatskanis_july_2013_Height_Diameter.csv

Photosyn data files: datainput_2_27_2015.csv

Local Git directory: setwd("~/GitHub/poplar_GWAS_photosyn")

````{r, echo=FALSE, results='hide'}
setwd("~/Desktop/poplar_data")
library(dplyr)
library(ggvis)

dat1<-read.csv("datainput_2_27_2015.csv")
head(dat1)
names(dat1)

dat1$id<-toupper(dat1$id) #all letters upper case
dat1$id<-gsub("*.CSV", "", dat1$id) # replace .csv to blank
head(dat1)
str(dat1)

datClatHt<-read.csv("GWAS_Clatskanis_july_2013_Height_Diameter.csv")
datCor_1<-read.csv("Corv_2012_Growth_rep1.csv")
datCor_2<-read.csv("Corv_2012_Growth_rep2.csv")
datCor_3<-read.csv("Corv_2012_Growth_rep3.csv")

````

Field Traits
```
HBS3    Height to the bud scar of year 3 (2011 height)
HBS2    Height to the bud scar of year 2 (2010 height)
HHB     height to the highest branch                    columns F-M are mostly repeated, but
with 4 noted trees.     What are they for?
D20     diameter 20cm
D50     diameter 50cm - for stem taper
BA      Branch angle
SB      sylleptic branches from last year's growth (2011)
LENT    # lenticels in 5cm along trunk
Tephrina        0-4: 0=zero; 1=1-25%; 2=26-50%; 3=51-75%; 4=76-100%
Venturia        0-4: 0=zero; 1=1-25%; 2=26-50%; 3=51-75%; 4=76-100%
```

Data manipulation and Gm calculation
Note: can only caluclate Gm for samples that have rwp > 0.

````{r, echo=FALSE}
dat2<-dat1 %>% select(id, Asat=Asat_ALight, Duplicate, Jmax25, Rdlight25, Resistwp25,
Resistch25, gamma.25, Asat_ALight) %>% filter(Duplicate == "Unique" & Resistwp25 > 0) %>%
mutate(Gm = 1/Resistwp25)
````

**Relationship with Clatskanis Height Diameter data using replilcate 1 **

````{r, echo=FALSE}

```
##start with block replicate of 2 measured
datClatHt_1<-datClatHt %>%
    select(Block, id = Identity, HBS3, HBS2, D20, D50) %>%
    filter(Block == 1)
#join with dat2
datClatHt_1_join<-inner_join(dat2, datClatHt_1, by = "id")

#plots
datClatHt_1_join %>%
    ggvis(~Resistwp25, ~Asat) %>%
    layer_points() %>%
    scale_numeric("y", domain = c(0, 20), nice = FALSE, clamp = TRUE)

datClatHt_1_join %>%
    ggvis(~as.numeric(D50), ~Resistwp25) %>%
    layer_points()

datClatHt_1_join %>%
    ggvis(~as.numeric(D50), ~Gm) %>%
    layer_points() %>%
     scale_numeric("y", domain = c(0, 4), nice = FALSE, clamp = TRUE)

datClatHt_1_join %>%
    ggvis(~as.numeric(D20), ~Resistwp25) %>%
    layer_points()

datClatHt_1_join %>%
    ggvis(~as.numeric(HBS2), ~Resistwp25) %>%
    layer_points()

datClatHt_1_join %>%
    ggvis(~as.numeric(HBS3), ~Resistwp25) %>%
    layer_points()

D50<-as.numeric(datClatHt_1_join$D50)
D20<-as.numeric(datClatHt_1_join$D20)
rwp<-as.numeric(datClatHt_1_join$Resistwp25)
cor.test(rwp, D50, method = "pearson")
cor.test(rwp,D20, method = "pearson")
```

**Relationship with Clatskanis Height Diameter data using replilcate 2 **

```{r, echo=FALSE}

datClatHt_2<-datClatHt %>%
    select(Block, id = Identity, HBS3, HBS2, D20, D50) %>%
    filter(Block == 2)
#join with dat2
datClatHt_2_join<-inner_join(dat2, datClatHt_2, by = "id")

#plots
datClatHt_2_join %>%
    ggvis(~Resistwp25, ~Asat) %>%
    layer_points() %>%
    scale_numeric("y", domain = c(0, 20), nice = FALSE, clamp = TRUE)

datClatHt_2_join %>%
    ggvis(~as.numeric(D50), ~Resistwp25) %>%
    layer_points()

datClatHt_2_join %>%
    ggvis(~as.numeric(D50), ~Gm) %>%
    layer_points() %>%
     scale_numeric("y", domain = c(0, 4), nice = FALSE, clamp = TRUE)
```

```
datClatHt_2_join %>%
    ggvis(~as.numeric(D50), ~Asat) %>%
    layer_points() %>%
    scale_numeric("y", domain = c(0, 20), nice = FALSE, clamp = TRUE)

datClatHt_2_join %>%
    ggvis(~as.numeric(D20), ~Resistwp25) %>%
    layer_points()

datClatHt_2_join %>%
    ggvis(~as.numeric(D20), ~Asat) %>%
    layer_points() %>%
    scale_numeric("y", domain = c(0, 20), nice = FALSE, clamp = TRUE)

datClatHt_2_join %>%
    ggvis(~as.numeric(HBS2), ~Resistwp25) %>%
    layer_points()

datClatHt_2_join %>%
    ggvis(~as.numeric(HBS2), ~Asat) %>%
    layer_points() %>%
    scale_numeric("y", domain = c(0, 20), nice = FALSE, clamp = TRUE)

datClatHt_2_join %>%
    ggvis(~as.numeric(HBS3), ~Resistwp25) %>%
    layer_points() %>%
    scale_numeric("y", domain = c(0, 20), nice = FALSE, clamp = TRUE)

datClatHt_2_join %>%
    ggvis(~as.numeric(HBS3), ~Asat) %>%
    layer_points() %>%
    scale_numeric("y", domain = c(0, 20), nice = FALSE, clamp = TRUE)


D50<-as.numeric(datClatHt_2_join$D50)
D20<-as.numeric(datClatHt_2_join$D20)
rwp<-as.numeric(datClatHt_2_join$Resistwp25)
cor.test(rwp, D50, method = "pearson")
cor.test(rwp,D20, method = "pearson")

```
```

**correlegrams**
**Clatskanis Height Diameter data using replilcate 2**
```{r, fig.width=10, fig.height=7}
library(corrgram)

#convert some columns to numeric

datClatHt_2_join<-datClatHt_2_join %>% select(-Duplicate, -id, -Block)
datClatHt_2_join[, c(8:11)] <- sapply(datClatHt_2_join[, c(8:11)], as.numeric)

corrgram(datClatHt_2_join, order=TRUE, lower.panel=panel.shade,
  upper.panel=panel.pie, text.panel=panel.txt,
  main="Clatsk_rep2")
```



**correlegrams**
**Clatskanis Height Diameter data using replilcate 1**
```{r, fig.width=10, fig.height=7}
library(corrgram)

#convert some columns to numeric
```

```
datClatHt_1_join<-datClatHt_1_join %>% select(-Duplicate, -id, -Block)
datClatHt_1_join[, c(8:11)] <- sapply(datClatHt_1_join[, c(8:11)], as.numeric)

corrgram(datClatHt_1_join, order=TRUE, lower.panel=panel.shade,
  upper.panel=panel.pie, text.panel=panel.txt,
  main="Clatsk_rep1")
```

**correlegrams**
**Corvalis replilcate 1**
```{r, fig.width=10, fig.height=7}

datCor_1<-datCor_1 %>% select(id=Geno, Height=Corv_R1_Height_2012, DBH=Corv_R1_DBH_2012,
SylBr=SylBr_2012)
datCor_1_join<-inner_join(dat2, datCor_1, by = "id")
datCor_1_join<-datCor_1_join %>% select(-Duplicate)
datCor_1_join[, c(9:11)] <- sapply(datCor_1_join[, c(9:11)], as.numeric)

corrgram(datCor_1_join, order=TRUE, lower.panel=panel.shade,
  upper.panel=panel.pie, text.panel=panel.txt,
  main="Corvalis_rep1")

```

**correlegrams**
**Corvalis replilcate 2**

```{r, fig.width=10, fig.height=7}

datCor_2<-datCor_2 %>% select(id=Geno, Height=Corv_R2_Height_2012, DBH=Corv_R3_DBH_2012,
SylBr=SylBr_2012)
datCor_2_join<-inner_join(dat2, datCor_2, by = "id")
datCor_2_join<-datCor_2_join %>% select(-Duplicate)
datCor_2_join[, c(9:11)] <- sapply(datCor_2_join[, c(9:11)], as.numeric)

corrgram(datCor_2_join, order=TRUE, lower.panel=panel.shade,
  upper.panel=panel.pie, text.panel=panel.txt,
  main="Corvalis_rep2")

```

**correlegrams**
**Corvalis replilcate 3**

```{r, fig.width=10, fig.height=7}

datCor_3<-datCor_3 %>% select(id=Geno, Height=Corv_R3_Height_2012, DBH=Corv_R3_DBH_2012,
SylBr=SylBr_2012)
datCor_3_join<-inner_join(dat2, datCor_3, by = "id")
datCor_3_join<-datCor_3_join %>% select(-Duplicate)
datCor_3_join[, c(9:11)] <- sapply(datCor_3_join[, c(9:11)], as.numeric)

corrgram(datCor_3_join, order=TRUE, lower.panel=panel.shade,
  upper.panel=panel.pie, text.panel=panel.txt,
  main="Corvalis_rep3")

```