Swedish project

Benjamin Brachi

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Contents

1 Complete protocol of the experiments

1.1 planting and setup

The list of the 203 accessions/genotypes used is presented in acc_list.txt. This list includes 200 re-sequenced Swedish accessions, Edi-0, Col-Fri and Col-Fri-FLC. Most Swedish accessions were planted in 8 replicates per block and Edi-0, Col-FRI and Col-FRI-FLC, 6043 Lov-1, 6974 Ull2-5, 7517 Var2-6, 8369 Rev-1, 8240 Kulturen-1, 8262 Bil-5, 8247 San-2, 6918 Fab-4 were planted in 16 replicates per block.

Each experiment is organized in a three complete randomized block design. Plantings followed the calendar presented in table 1.1.

1.2 Overview of the phenotypes collected and organisation.

To designate a particular round of experiment we'll use the year it was sown (not the year it was harvested).

Table 2 and 3 provide a the list of the phenotypes we have.

To be able to combine everything in one file, the easiest is probably to start from the initial randomizations, corrected for errors that were made during planting. Then we can add all the phenotypes in different columns. Some phenotypes will have many NAs, because only a subset of the plants were measured (/i.e./ microbiota, fitness).

2 Merging all phenotypes in one file and description

The script merging_phen_files_11202014.R was used in April 2014 to merge all phenotype files into one. I copied that script and updated the paths. This scripts uses the results from the treatment of each trait or set of traits fom the folders in "../all_phenotypes/"

Year	Experiment	Block	planting date	field installation date
2011	Adal	A	2011-08-08	2011-08-25
		B	2011-08-10	2011-08-25
		C	2011-08-12	2011-08-25
	Ramsta	A	2011-08-07	2011-08-24
		B	2011-08-09	2011-08-24
		C	2011-08-11	2011-08-24
	Ullstorp	A	2011-08-31	2011-09-17
		B	2011-09-02	2011-09-17
		C	2011-09-04	2011-09-17
	Ratckegarden	A	2011-09-01	2011-09-18
		B	2011-09-03	2011-09-18
		C	2011-09-05	2011-09-18
2012	Adal	A	2012-08-08	2012-08-25
		B	2012-08-10	2012-08-25
		C	2012-08-12	2012-08-25
	Ramsta	A	2012-08-07	2012-08-24
		B	2012-08-09	2012-08-24
		C	2012-08-11	2012-08-24
	Ullstorp	A	2012-08-31	2012-09-17
		B	2012-09-02	2012-09-17
		C	2012-09-04	2012-09-17
	Ratckegarden	A	2012-09-01	2012-09-18
		B	2012-09-03	2012-09-18
		C	2012-09-05	2012-09-18

Table 1: Calendar followed for the planting of the common garden experiments

Table 2: Table of the phenotypes we have collected (*or will collect* indicated in italic) in the common garden experiments from 2011.

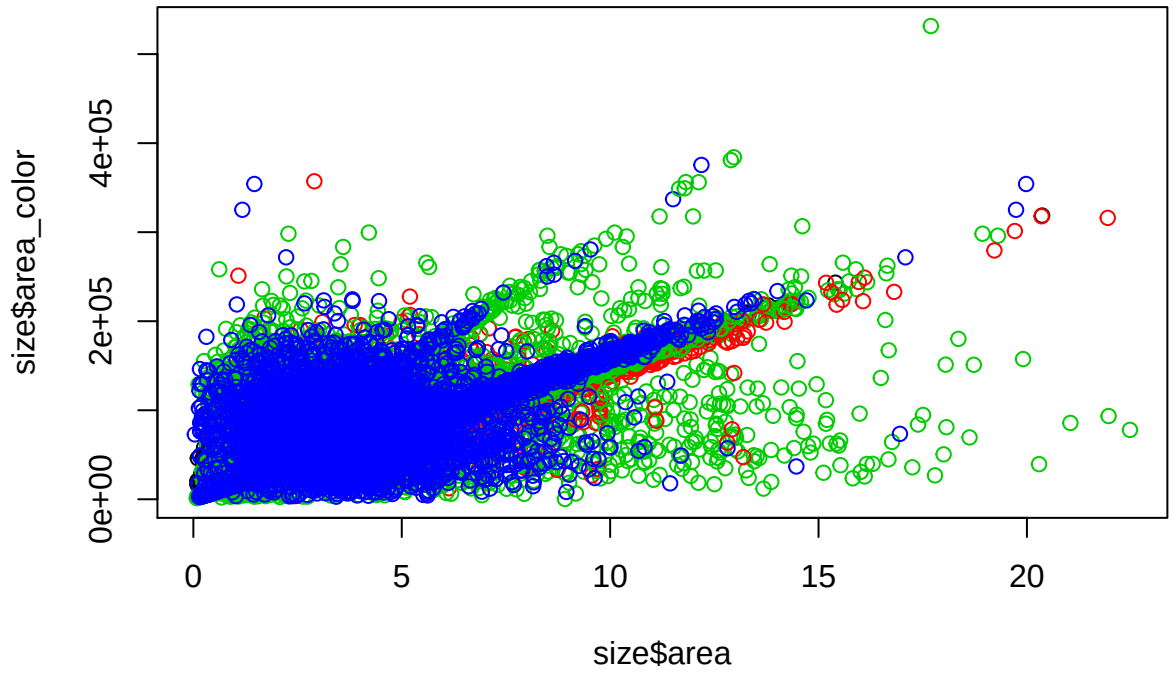
phenotype	ULL 2011	RAT 2011	RAM 2011	ADA 2011
flowering time before winter	X	X	X	X
flowering time in the spring				
herbivore damage in the fall		X		
rosette size	X	X		
overwinter survival	X	X	X	X
survival to seed set (Approx)	X	X	X	X
fecundity estimate	X	X	X	X
microbial community	*X*	*X*	*X*	*X*

Table 3: Table of the phenotypes we have collected (*or will collect* indicated in italic) in the common garden experiments from 2012.

phenotype	ULL 2012	RAT 2012	RAM 2012	ADA 2012
flowering time before winter	X	X	X	X
flowering time in the spring	X	X	X	X
herbivore damage in the fall				
rosette size	X	X	X	X
overwinter survival	X	X	X	X
survival to seed set (Approx)	X	X	X	X
fecundity estimate	*X*	*X*	*X*	*X*
microbial community	*X*	*X*	*X*	*X*

```
read_chunk("./scripts/merging_phen_files.R")
```

```
##reading the randomization file.

acc=read.table("./data/acc_list.txt", sep="\t", h=T)


##reading orginal data files for each phenotype

##rosette data (for bothe years):
size=read.table("../all_phenotypes/size/rosette_size.txt", sep="\t", h=T)
size$experiment=toupper(size$experiment)
size$combi=paste(size$experiment, size$tray, size$row, size$col, sep="_")
color=read.table("../all_phenotypes/color/color_rosettes.txt", sep="\t", h=T)
color$exp=toupper(color$exp)
color$combi=paste(color$exp, color$tray, color$row, color$col, sep="_")

##I need to keep only one time point per year per experiment in this file.
size=size[(size$date=="20111119" & size$experiment=="ULL")==F,]
size=size[(size$date=="20121120" & size$experiment=="RAT")==F,]
color=color[(color$date=="20111119" & color$exp=="ULL")==F,]
color=color[(color$date=="20121120" & color$exp=="RAT")==F,]

##compare the area column from the color and size data
size$area_color=color$area[match(size$combi, color$combi)]
plot(size$area, size$area_color, col=as.factor(size$experiment))
```




```
##Here the area in pixel number (in color) and the area in cm^2 (size) doesn't have a correlation of one

##the stockiness is not in the size data.
size$stockiness=(4*pi*size$area/(size$perimeter^2))
```

```
################################################
#######   2011 experiments   ###################
################################################

##read the survival data

surv=read.table("../all_phenotypes/survival/survival_2011.txt", h=T, sep="\t")
surv$id=acc$lines[match(surv$line, acc$tubes)]
surv$name=acc$name[match(surv$line, acc$tubes)]

##clean up surv (typos).

surv$spring[surv$spring==11]=1
surv$spring[surv$spring==10]=NA
surv$spring[surv$spring=="?"]=NA
surv$spring[surv$spring=="-"]=NA
surv=droplevels(surv)

##subset size and color to keep only the 2011 data

size2011=size[size$year==2011,]
color2011=color[color$year==2011,]

##read the herbivory data scored in RAT

herb=read.table("../all_phenotypes/herbivory/rat.snail.2011.csv", sep=",", h=T)[,1:5]

##read the last fecundity dataset for 2011

fecundity=read.table("../all_phenotypes/fecundity/fecundity_2011.txt", sep="\t", h=T)
##swopping rows and cols for fecundity to be consistent with the other datasets
#x=colnames(fecundity)[c(1:3, 5, 4, 6:ncol(fecundity))]
#colnames(fecundity)=x

##now merge all this, based on surv.

surv$combi=paste(surv$exp, surv$tray, surv$row, surv$column, sep="_")
fecundity$combi=paste(fecundity$exp, fecundity$tray, fecundity$row, fecundity$col, sep="_")
herb$combi=paste("RAT", herb$tray, herb$row, herb$column, sep="_")

##now built the data table.

data2011=surv

##having the planting date in the data would be nice.

dates=data.frame(expand.grid(c("ADA", "RAM", "ULL", "RAT"), c("A", "B", "C")))
dates=dates[order(dates[,1]),]
colnames(dates)=c("exp", "block")
dates$planting=as.Date(c("2011-08-08","2011-08-10", "2011-08-12", "2011-08-07", "2011-08-09", "2011-08-
dates$comb=paste(dates$exp, dates$block, sep="_")
comb=paste(data2011$exp,data2011$block, sep="_")
data2011$planting_date=dates$planting[match(comb, dates$comb)]
```

```
##match in the phenotypes from size2011
data2011$rosette_date=size2011[match(data2011$combi, size2011$combi),"date"]
data2011$area=size2011[match(data2011$combi, size2011$combi),"area"]
data2011$perimeter=size2011[match(data2011$combi, size2011$combi),"perimeter"]
data2011$max_diameter=size2011[match(data2011$combi, size2011$combi),"max_diameter"]
data2011$sdR=size2011[match(data2011$combi, size2011$combi),"sdR"]
data2011$circle_area=size2011[match(data2011$combi, size2011$combi),"circle_area"]
data2011$stockiness=size2011[match(data2011$combi, size2011$combi),"stockiness"]
##match in the color phenotype
data2011$color=color2011[match(data2011$combi, color2011$combi),"color"]
##match in the herbivory scores
data2011$herbivory=herb[match(data2011$combi, herb$combi),"slug"]
##match in the fecundity estimates
data2011$fecundity=fecundity$fecundity[match(data2011$combi, fecundity$combi)]
##make the rosette_date a working date column.
x=data2011$rosette_date
y=as.Date(paste(substring(x, 1, 4),substring(x, 5, 6), substring(x, 7,8), sep="-"))
data2011$rosette_date=y
##reorder the columns a little
data2011=data2011[,c("exp", "block", "tray", "row", "column", "line", "id", "name", "planting_date", "e
##save it!
saveRDS(data2011, file="./data/data2011.rds")
write.table(data2011, "./data/data2011.txt", col.names=T, row.names=F, quote=F, sep="\t")


##################################################
#######   2012 experiments   ####################
##################################################

##read the survival data
surv=read.table("../all_phenotypes/survival/survival_2012.txt", h=T, sep="\t")
surv$id=acc$lines[match(surv$line, acc$tubes)]
surv$name=acc$name[match(surv$line, acc$tubes)]

##put it in better shape
surv$combi=paste(surv$exp, surv$tray, surv$row, surv$column, sep="_")
surv$block[surv$tray<=27]="A"
surv$block[surv$tray>=28 & surv$tray<=54]="B"
surv$block[surv$tray>=55]="C"

##subset size to keep only data for the 2012 experiments
size2012=size[size$year==2012,]
color2012=color[color$year==2012,]

##read some flowering time data, from the North (FTN) and the South (FTS)
FTS=read.table("../all_phenotypes/FT/FT_2012_South_dates.txt", sep="\t", h=T)
FTN=read.table("../all_phenotypes/FT/FT_2012_North_dates.txt", sep="\t", h=T)

##read the 2012 fecundity estimates
fecundity=read.table("../all_phenotypes/fecundity/fecundity_2012.txt", sep="\t", h=T)
##swopping rows and cols for fecundity.
x=colnames(fecundity)
#[c(1:3, 5, 4, 6:ncol(fecundity))]
```

```
#colnames(fecundity)=x
fecundity$combi=paste(fecundity$exp, fecundity$tray, fecundity$row, fecundity$col, sep="_")

##combine all data based on surv.

data2012=surv

##clean up the surv column

data2012$survival_03162013[data2012$survival_03162013==11]=1
data2012$survival_03162013[data2012$survival_03162013==","]=NA
data2012=droplevels(data2012)

##add the fall flowering and survival column from the phenotyping Rod did on the images.

for(e in c("ADA", "RAM", "ULL", "RAT")){
if(e=="ADA"){fbw=cbind(e, read.table(paste("../all_phenotypes/fbw_2012/fbw_2012_", e, ".txt", sep=""), s
}
fbw$combi=paste(fbw$e, fbw$tray, fbw$row, fbw$column, sep="_")


##clean it up

fbw[fbw$ft_fall=="9","ft_fall"]=0
fbw[fbw$ft_fall=="no photo","ft_fall"]=NA

##use this flowering before winter as a fall column. It's the same as what was done in 2011 but photos w
data2012$fall=fbw[match(data2012$combi, fbw$combi),"ft_fall"]

##add planting date

dates=data.frame(expand.grid(c("ADA", "RAM", "ULL", "RAT"), c("A", "B", "C")))
dates=dates[order(dates[,1]),]
colnames(dates)=c("exp", "block")
dates$planting=as.Date(c("2012-08-08","2012-08-10", "2012-08-12", "2012-08-07", "2012-08-09", "2012-08-
dates$comb=paste(dates$exp, dates$block, sep="_")
comb=paste(data2012$exp,data2012$block, sep="_")
data2012$planting_date=dates$planting[match(comb, dates$comb)]

##add the rosette data
data2012$rosette_date=size2012[match(data2012$combi, size2012$combi),"date"]
data2012$area=size2012[match(data2012$combi, size2012$combi),"area"]
data2012$perimeter=size2012[match(data2012$combi, size2012$combi),"perimeter"]
data2012$max_diameter=size2012[match(data2012$combi, size2012$combi),"max_diameter"]
data2012$sdR=size2012[match(data2012$combi, size2012$combi),"sdR"]
data2012$circle_area=size2012[match(data2012$combi, size2012$combi),"circle_area"]
data2012$stockiness=size2012[match(data2012$combi, size2012$combi),"stockiness"]
##add the color data
data2012$color=color2012[match(data2012$combi, color2012$combi),"color"]
##add the fecundity data
data2012$fecundity=fecundity$fit[match(data2012$combi, fecundity$combi)]

##add flowering time in the spring data (not available for 2011)
```

```
colnames(FTS)[5]="col"
FT=rbind(FTN, FTS)

FT$combi=paste(FT$exp, FT$tray,FT$row, FT$col, sep="_")
data2012$flowering_date=FT[match(data2012$combi, FT$combi),"flowering_date"]
data2012$FT=FT[match(data2012$combi, FT$combi),"FT"]

##make the rosette_date a working date column.

x=data2012$rosette_date
y=as.Date(paste(substring(x, 1, 4),substring(x, 5, 6), substring(x, 7,8), sep="-"))
data2012$rosette_date=y

##reorder col

data2012=data2012[,c("exp", "block", "tray", "row", "column", "line", "id", "name", "planting_date", "e

colnames(data2012)[match("survival_03162013", colnames(data2012))]="spring"

##save it:
saveRDS(data2012, file="./data/data2012.rds")
write.table(data2012, "./data/data2012.txt", col.names=T, row.names=F, quote=F, sep="\t")
```

This results in two files, one for each year. There are named data_2011.txt (or .R for the binary version) and data_2012.txt (or .R for the binary version).

The column names for each files are summarized below.

2.1 columns in data2011

- exp: name of the experiment
- block: experimental block within the experiment
- tray: tray within the experiments row: coordinate 1 of position of the plants on a tray (varies from 1 to 11)
- column: coordinate 2 of position of the plants on a tray (varies from 1 to 6)
- line: number from 1 to 203 designating the accessions planted
- id: accession id of the accession as refered to in the call_method_75 of the 250 KSNPs data.
- name: actual name of the accession (might be messed up by encoding, use ids!!)
- planting_date: the planting date. All plants of the same block within the same experiment have the same date.
- errors: errors during planting (only use lines with ".")
- fall: score of survival,flowering, and pathogene infections the survival code
- spring: score of survival,flowering, and pathogene infections the survival code
- sampled: TRUE if the sample has been sample for microbial community analysis in the spring.Otherwise FALSE.
- rosette_date: Date at which the photographe that was use to make rosette measurements was taken.
- area: rosette area on the photograph in cm2
- perimeter: rosette perimiter (cm)
- max_diameter: maximum diameter of the plant.
- sdR: standard deviation of the plants radius
- circle_area: area of a circle of diameter "max_diameter"
- stockiness: measure of plant stockiness: $(4pi$area)/(perimeter)ˆ2
- color: a measure of color variation from green to purple. lower values are greener.

- herbivory: herbivore damage score from 0 to 3, 0: no damage, 3: extensive damage.
- fecundity: area of occupied by the mature plant stems (number of pixels of the image that are the plant, not the area of the bounding box) as a proportion of the total number of pixel on the image.

2.2 columns for data2012 (only columns that are different):

- epi: sampled by Fernando and Manu for RNASeq.
- PC_sampled: TRUE if the sample has been sample for microbial community analysis in the spring.Otherwise FALSE.
- flowering_date: the date at which the plant was scored as flowered (if reading from the text file, in R, as.Date() will turn it to a date format.
- FT: time from planting to the date the plant was scored as flowered.

2.3 Add some derived phenotype columons and clean up

This next chunck of script does some cleaning up, and compute derive phenotypes such as ow, sss, fitness (composite of fecundity and sss).

```
read_chunk("./scripts/deriv_phen.R")
```

Table 4: Number of data points for each value of ows and sss in the 2011 experiments

ows	sss	Freq
0	0	1860
1	0	1588
NA	0	1011
0	1	166
1	1	11305
NA	1	33
0	NA	1
1	NA	3276
NA	NA	2144

Table 5: Number of data points for each value of ows and sss in the 2012 experiments

ows	sss	Freq
0	0	245
1	0	1174
NA	0	0
0	1	20
1	1	10263
NA	1	0
0	NA	0
1	NA	4437
NA	NA	5245

```
##    sss
```

```
## ows     1
##   0   166
##   1 11305

##    sss
## ows     1
##   0    20
##   1 10263

##       exp block tray row column  line   id name planting_date errors fall
## 27    ULL     A    1   5      3 empty <NA> <NA>    2011-08-31      .    1
## 1906  ULL     B   29  10      4 empty <NA> <NA>    2011-09-02      .    1
## 2671  ULL     B   41   6      1 empty <NA> <NA>    2011-09-02      .    1
## 2710  ULL     B   42   1      4 empty <NA> <NA>    2011-09-02      .    1
## 3519  ULL     B   54   4      3 empty <NA> <NA>    2011-09-02      .    1
## 5638  RAT     A    5   5      4 empty <NA> <NA>    2011-09-01      .    1
## 5922  RAT     A    9   8      6 empty <NA> <NA>    2011-09-01      .    1
## 7335  RAT     B   31   2      3 empty <NA> <NA>    2011-09-03      .    1
## 10946 RAM     A    4  10      2 empty <NA> <NA>    2011-08-07      .    2
## 12366 RAM     A   26   4      6 empty <NA> <NA>    2011-08-07      .    1
## 14744 RAM     C   62   5      2 empty <NA> <NA>    2011-08-11      .    1
## 15417 RAM     C   72   7      3 empty <NA> <NA>    2011-08-11      .    2
## 16322 ADA     A    5   4      2 empty <NA> <NA>    2011-08-08      .    1
## 19018 ADA     B   46   2      4 empty <NA> <NA>    2011-08-10      .    2
## 19826 ADA     C   58   5      2 empty <NA> <NA>    2011-08-12      .    1
## 20825 ADA     C   73   6      5 empty <NA> <NA>    2011-08-12      .    2
## 21075 ADA     C   77   4      3 empty <NA> <NA>    2011-08-12      .    1
## 21343 ADA     C   81   5      1 empty <NA> <NA>    2011-08-12      .    1
##       spring sampled rosette_date       area perimeter max_diameter
## 27         1   FALSE   2011-11-01  0.1644465   2.26089    0.6358726
## 1906       1   FALSE   2011-11-01 10.7207054  18.87364    4.4923238
## 2671       1   FALSE         <NA>         NA        NA           NA
## 2710       1   FALSE   2011-11-01  4.9950378  14.00717    3.0131634
## 3519       1   FALSE   2011-11-01  8.5278268  19.42155    4.0276701
## 5638       1   FALSE         <NA>         NA        NA           NA
## 5922       1   FALSE   2011-11-01  7.3085737  16.06244    3.9042611
## 7335       1   FALSE   2011-11-01  6.3106981  16.61579    3.6469942
## 10946      3   FALSE         <NA>         NA        NA           NA
## 12366      1   FALSE         <NA>         NA        NA           NA
## 14744      1   FALSE         <NA>         NA        NA           NA
## 15417      0   FALSE         <NA>         NA        NA           NA
## 16322      0   FALSE         <NA>         NA        NA           NA
## 19018      0   FALSE         <NA>         NA        NA           NA
## 19826      0   FALSE         <NA>         NA        NA           NA
## 20825      0   FALSE         <NA>         NA        NA           NA
## 21075      1   FALSE         <NA>         NA        NA           NA
## 21343      1    TRUE         <NA>         NA        NA           NA
##             sdR circle_area stockiness         color herbivory
## 27    0.1597015   0.3175632  0.4042737  0.0387945875        NA
## 1906  1.3388041  15.8500993  0.3782004  0.0227967715        NA
## 2671         NA          NA         NA  0.0001529256        NA
## 2710  0.8995149   7.1307505  0.3199249 -0.0070943860        NA
## 3519  1.1267250  12.7408282  0.2841061 -0.0044856454        NA
## 5638         NA          NA         NA -0.0208655204         1
```

```
## 5922  1.1088705  11.9720243  0.3559751 -0.0375922040         2
## 7335  1.0108851  10.4462406  0.2872404 -0.0109174673         2
## 10946        NA          NA         NA             NA        NA
## 12366        NA          NA         NA             NA        NA
## 14744        NA          NA         NA             NA        NA
## 15417        NA          NA         NA             NA        NA
## 16322        NA          NA         NA             NA        NA
## 19018        NA          NA         NA             NA        NA
## 19826        NA          NA         NA             NA        NA
## 20825        NA          NA         NA             NA        NA
## 21075        NA          NA         NA             NA        NA
## 21343        NA          NA         NA             NA        NA
##          fecundity ows sss
## 27    0.0001391575   1   1
## 1906  0.0019261142   1   1
## 2671  0.0086442599   1   1
## 2710  0.0036855498   1   1
## 3519  0.0121254426   1   1
## 5638  0.0212770067   1   1
## 5922  0.0102497566   1   1
## 7335  0.0116773049   1   1
## 10946           NA   0   0
## 12366           NA   1   0
## 14744 0.0003396863   1   1
## 15417           NA   0   0
## 16322           NA   0   0
## 19018           NA   0   0
## 19826           NA   0   0
## 20825           NA   0   0
## 21075 0.0033375336   1   1
## 21343           NA   1  NA
```

```
##       exp block tray row column  line   id name planting_date errors fall
## 27    ULL     A    1   5      3 empty <NA> <NA>    2011-08-31      .    1
## 1906  ULL     B   29  10      4 empty <NA> <NA>    2011-09-02      .    1
## 2671  ULL     B   41   6      1 empty <NA> <NA>    2011-09-02      .    1
## 2710  ULL     B   42   1      4 empty <NA> <NA>    2011-09-02      .    1
## 3519  ULL     B   54   4      3 empty <NA> <NA>    2011-09-02      .    1
## 5638  RAT     A    5   5      4 empty <NA> <NA>    2011-09-01      .    1
## 5922  RAT     A    9   8      6 empty <NA> <NA>    2011-09-01      .    1
## 7335  RAT     B   31   2      3 empty <NA> <NA>    2011-09-03      .    1
## 10946 RAM     A    4  10      2 empty <NA> <NA>    2011-08-07      .    2
## 12366 RAM     A   26   4      6 empty <NA> <NA>    2011-08-07      .    1
## 14744 RAM     C   62   5      2 empty <NA> <NA>    2011-08-11      .    1
## 15417 RAM     C   72   7      3 empty <NA> <NA>    2011-08-11      .    2
## 16322 ADA     A    5   4      2 empty <NA> <NA>    2011-08-08      .    1
## 19018 ADA     B   46   2      4 empty <NA> <NA>    2011-08-10      .    2
## 19826 ADA     C   58   5      2 empty <NA> <NA>    2011-08-12      .    1
## 20825 ADA     C   73   6      5 empty <NA> <NA>    2011-08-12      .    2
## 21075 ADA     C   77   4      3 empty <NA> <NA>    2011-08-12      .    1
## 21343 ADA     C   81   5      1 empty <NA> <NA>    2011-08-12      .    1
##       spring sampled rosette_date       area perimeter max_diameter
## 27         1   FALSE   2011-11-01  0.1644465   2.26089    0.6358726
## 1906       1   FALSE   2011-11-01 10.7207054  18.87364    4.4923238
```

```
## 2671       1   FALSE         <NA>         NA        NA           NA
## 2710       1   FALSE   2011-11-01  4.9950378  14.00717    3.0131634
## 3519       1   FALSE   2011-11-01  8.5278268  19.42155    4.0276701
## 5638       1   FALSE         <NA>         NA        NA           NA
## 5922       1   FALSE   2011-11-01  7.3085737  16.06244    3.9042611
## 7335       1   FALSE   2011-11-01  6.3106981  16.61579    3.6469942
## 10946      3   FALSE         <NA>         NA        NA           NA
## 12366      1   FALSE         <NA>         NA        NA           NA
## 14744      1   FALSE         <NA>         NA        NA           NA
## 15417      0   FALSE         <NA>         NA        NA           NA
## 16322      0   FALSE         <NA>         NA        NA           NA
## 19018      0   FALSE         <NA>         NA        NA           NA
## 19826      0   FALSE         <NA>         NA        NA           NA
## 20825      0   FALSE         <NA>         NA        NA           NA
## 21075      1   FALSE         <NA>         NA        NA           NA
## 21343      1    TRUE         <NA>         NA        NA           NA
##             sdR circle_area stockiness         color herbivory
## 27    0.1597015   0.3175632  0.4042737  0.0387945875        NA
## 1906  1.3388041  15.8500993  0.3782004  0.0227967715        NA
## 2671         NA          NA         NA  0.0001529256        NA
## 2710  0.8995149   7.1307505  0.3199249 -0.0070943860        NA
## 3519  1.1267250  12.7408282  0.2841061 -0.0044856454        NA
## 5638         NA          NA         NA -0.0208655204         1
## 5922  1.1088705  11.9720243  0.3559751 -0.0375922040         2
## 7335  1.0108851  10.4462406  0.2872404 -0.0109174673         2
## 10946        NA          NA         NA            NA        NA
## 12366        NA          NA         NA            NA        NA
## 14744        NA          NA         NA            NA        NA
## 15417        NA          NA         NA            NA        NA
## 16322        NA          NA         NA            NA        NA
## 19018        NA          NA         NA            NA        NA
## 19826        NA          NA         NA            NA        NA
## 20825        NA          NA         NA            NA        NA
## 21075        NA          NA         NA            NA        NA
## 21343        NA          NA         NA            NA        NA
##          fecundity ows sss
## 27    0.0001391575   1   1
## 1906  0.0019261142   1   1
## 2671  0.0086442599   1   1
## 2710  0.0036855498   1   1
## 3519  0.0121254426   1   1
## 5638  0.0212770067   1   1
## 5922  0.0102497566   1   1
## 7335  0.0116773049   1   1
## 10946           NA   0   0
## 12366           NA   1   0
## 14744 0.0003396863   1   1
## 15417           NA   0   0
## 16322           NA   0   0
## 19018           NA   0   0
## 19826           NA   0   0
## 20825           NA   0   0
## 21075 0.0033375336   1   1
## 21343           NA   1  NA
```

```
##
##  ADA  RAM  RAT  ULL
##    0    0 3424 4709
```

```
##
##  ADA  RAM  RAT  ULL
## 3958 4901 3851 3705
```

3 Compute heritabilities and blups per accession

```
read_chunk("./scripts/heritability.R")
```

This is slow, because of the bootstrapping. Set to not run.

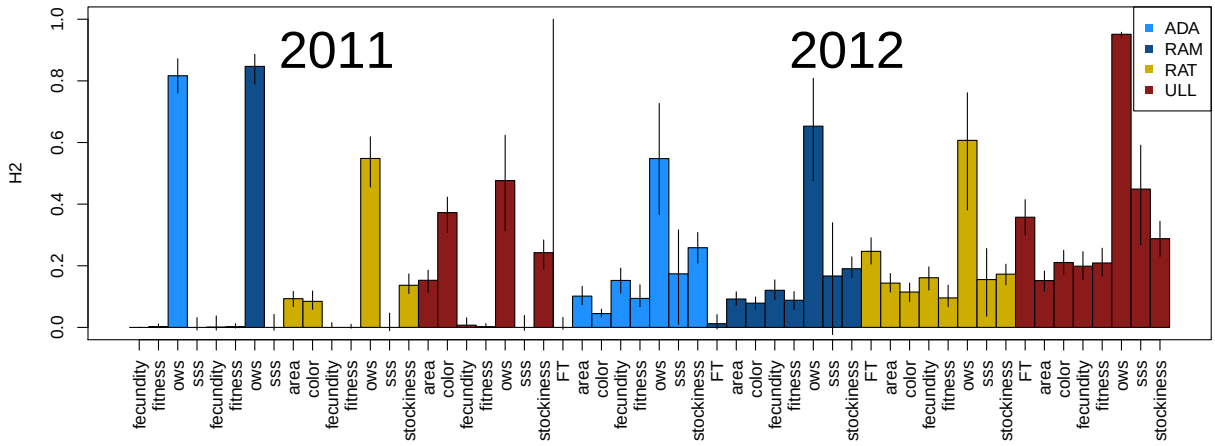


Figure 1: Heritability of traits in the common garden experiments.