## Diallel Research Report One Jinliang Yang October 13th, 2014

One purpose of this manual is to document research progress and to facilitate communication. I try to make this **pvpDiallel** project completely reproducible with the help of some R packages. The dependencies in this project are managed by **Packrat**. It enables the collaborator to run it immediately after cloning this repo without installing anything. Because some of the work is time consuming, I tend to turn off these code chunks that need heavy computational power. But you could still find the source codes or their paths in this report. This document itself was generated in **Rstudio** using **rmarkdown** with the **tufte\_handout** output format.

```
# set up the project and global environment
library(knitr)
opts_knit$set(root.dir = normalizePath("../"))
```

## Phenotypic data

The phenotypic data *per se*, GCA and SCA was reformatted from Sofiane's files and transformed them to a data matrix. The following chunk of code could not be re-ran because data from external folders were loaded. The original phenotypic data could be found here /group/jrigrp2/DiallelSofiane/GeneticValues/ on farm.

```
### data per se, GCA and SCA
source("munge/1.raw_pheno/1.A.1_format_pheno.R")
source("munge/1.raw_pheno/1.A.2_format_gca_sca.R")

plot the phentoypic data per se
source("profiling/1.pheno/1.A.1_pheno_plot.R")
```

From Figure 1, the phenotypic values of seven traits were bell-shape distributed. After normality tests using shapiro.test, the p-value for the first trait **ASI** was a little bit above 0.05 and all the others are >>0.05. These normality test p-values are: 0.052, 0.187, 0.196, 0.87, 0.591, 0.823, 0.482. Generally, we do not have evidences to reject the normal distribution of these phenotypes. And, the trait values may not need to be transformed.

#### Levels of heterosis of the seven traits

As reported by Flint-Garcia *et al* <sup>1</sup> and observed by my previous studies, the levels of heterosis are varied. The variation of the levels

<sup>&</sup>lt;sup>1</sup> Flint-Garcia SA, Buckler ES, Tiffin P, Ersoz E, Springer NM (2009) Heterosis Is Prevalent for Multiple Traits in Diverse Maize Germplasm. PLoS ONE 4(10): e7433. doi:10.1371/journal. pone.0007433

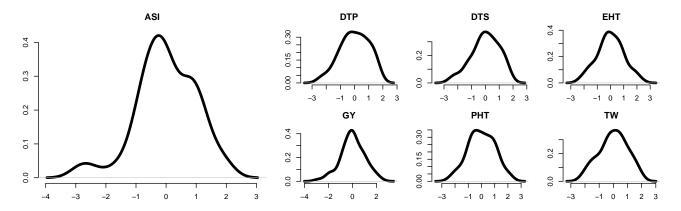


Figure 1: phenotypic data distribution

of heterosis was also observed in the current study using both pMPH and pBPH. Interestingly, ASI showed a negative heterosis; DTS, DTP and TW exhibited almost no heterosis; PHT and EHT exhibited moderate levels of heterosis; and GY exhibited very strong heterosis.

source("profiling/1.pheno/1.A.2\_pheno\_loh\_plot.R")

#### percentage of mid-parental heterosis

# 0 က 2 pMPH 0 ASI DTS DTP TW PHT **EHT** GY phenotypic traits

### percentage of better parental heterosis

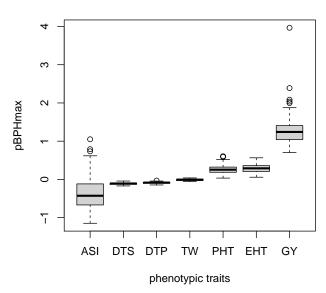


Figure 2: Variation of the levels of heterosis

## Correlation of the seven phenotypic traits

```
source("profiling/1.pheno/1.A.3_pheno_cor_plot.R")
### get the pheno per se
myp1 <- get_pheno(trait = trait, pheno = "valHyb")</pre>
```

```
pairs(myp1[, 2:8], text.panel = diag, upper.panel = panel.smooth,
    lower.panel = panel.cor, gap = 0, main = "",
    pch = 19, col = "grey", lwd = 2)
```

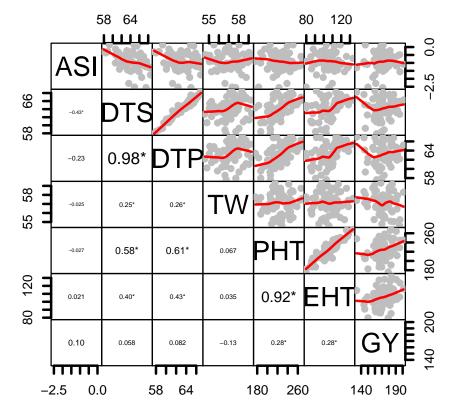


Figure 3: Correlation plot of the seven

In the Figure 3, correlations of trait per se were plotted with the above codes. For the Figure 4 and Figure 5, similar codes were used but not shown in this report.

As shown in Figure 3, DTS vs. DTP and PHT vs. EHT were highly positively correlated. These positive correlations were also hold for pBPH and pMPH. While, the trait values per se of ASI negatively correlated with DTS. However, the negative correlation become not statistically significant for pBPH and pMPH of the pairs of the traits. With the correlation of these traits, we expect to find some shared trait-associated variants after GWAS.

general combining ability of the traits

```
library(xtable)
source("profiling/1.pheno/1.B.1_GCA_table.R")
options(xtable.comment = FALSE)
```

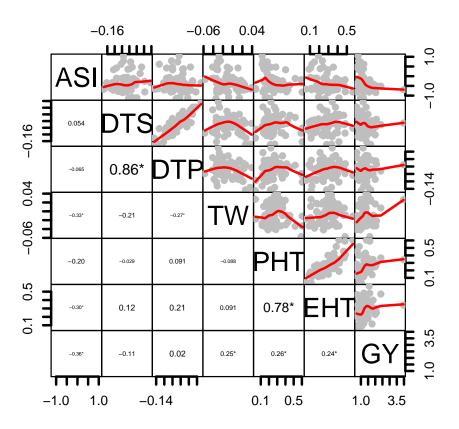


Figure 4: Correlation plot of pBPHmax

options(xtable.booktabs = TRUE) xtable(GCA, caption = "General combining abilities of the seven traits")

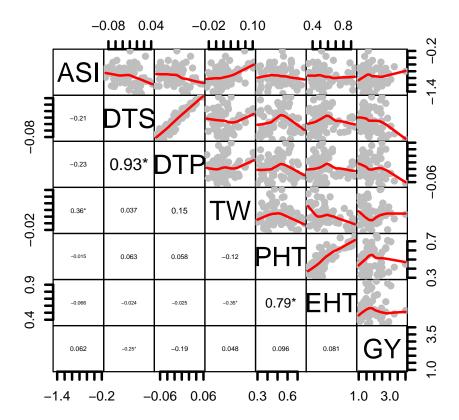


Figure 5: Correlation plot of pMPH

	ASI	DTP	DTS	EHT	GY	PHT	TW
B <sub>73</sub>	-0.19	0.31	0.51	9.43	7.42	10.90	-0.01
LH1	-0.54	1.50	2.02	-13.30	-11.39	-15.63	0.61
LH123HT	0.26	1.56	1.31	9.98	0.27	19.32	0.09
LH82	0.18	-1.79	-1.97	-12.80	6.38	-27.23	-0.06
MO17	-0.37	0.77	1.15	7.33	5.02	4.60	-0.64
PH207	-0.39	-2.01	-1.63	-6.71	<i>-</i> 7.59	-10.76	-0.74
PHG35	0.45	-0.41	-0.87	-1.17	-7.76	-2.80	-0.59
PHG39	0.13	1.46	1.34	5.81	9.04	12.98	1.35
PHG47	0.34	-0.89	-1.22	-6.02	9.55	-5.37	-1.28
PHG84	-0.09	2.62	2.71	0.82	-1.00	8.86	0.63
PHJ40	0.42	-3.42	-3.85	-4.51	-7.08	-15.71	0.80

Table 1: General combining abilities of the seven traits