Validation of Functional Polymorphisms Affecting Maize Plant Height by Unoccupied Aerial Systems (UASs) allows Novel Temporal Detection

Alper Adak, *Seth C. Murray, Clarissa Conrad, Yuanyuan Chen, Nithya Subramanian, Steven Anderson, Scott Wilde*
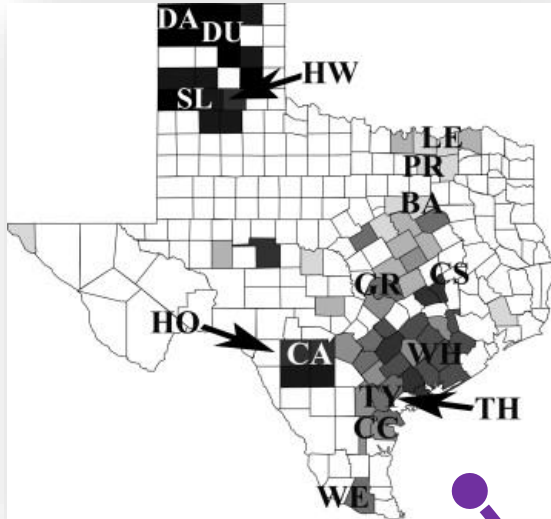
Department of Soil and Crop Sciences, Texas A&M University, College Station, Texas, United States of America
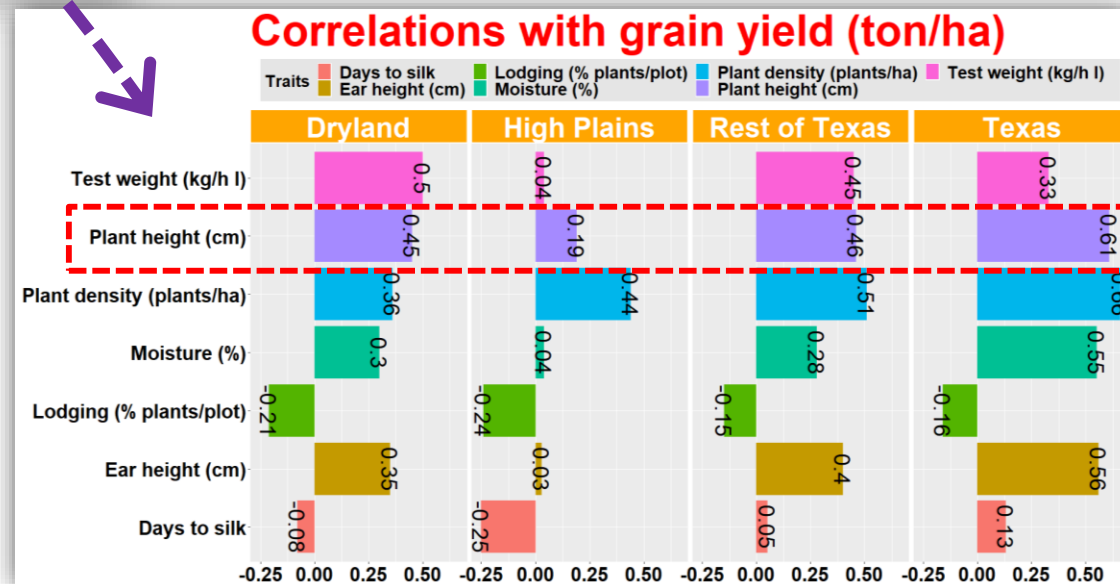
Background

Farfan, Ivan D. Barrero, et al. 2013. *Field crops research*, 149: 167-176.

Background

Figures were modified from Farfan, I.D.B, et al. 2015. *PLoS One*, 10(2).
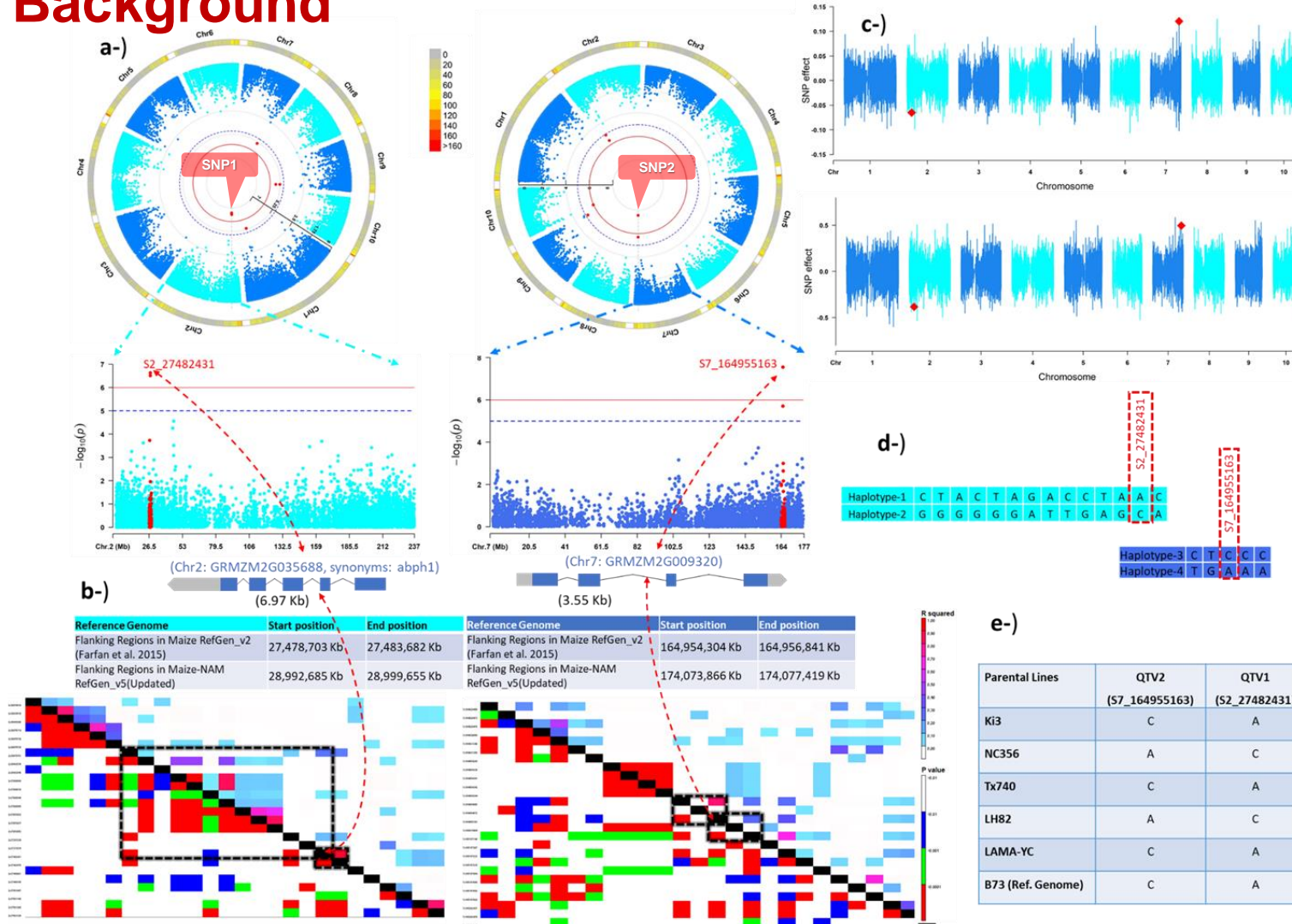
~60.000 SNPs were used in GWAS.

346 hybrids generated by top cross between Tx-714 and 346 inbred lines originating in temperate, sub-tropical and tropical areas were used.
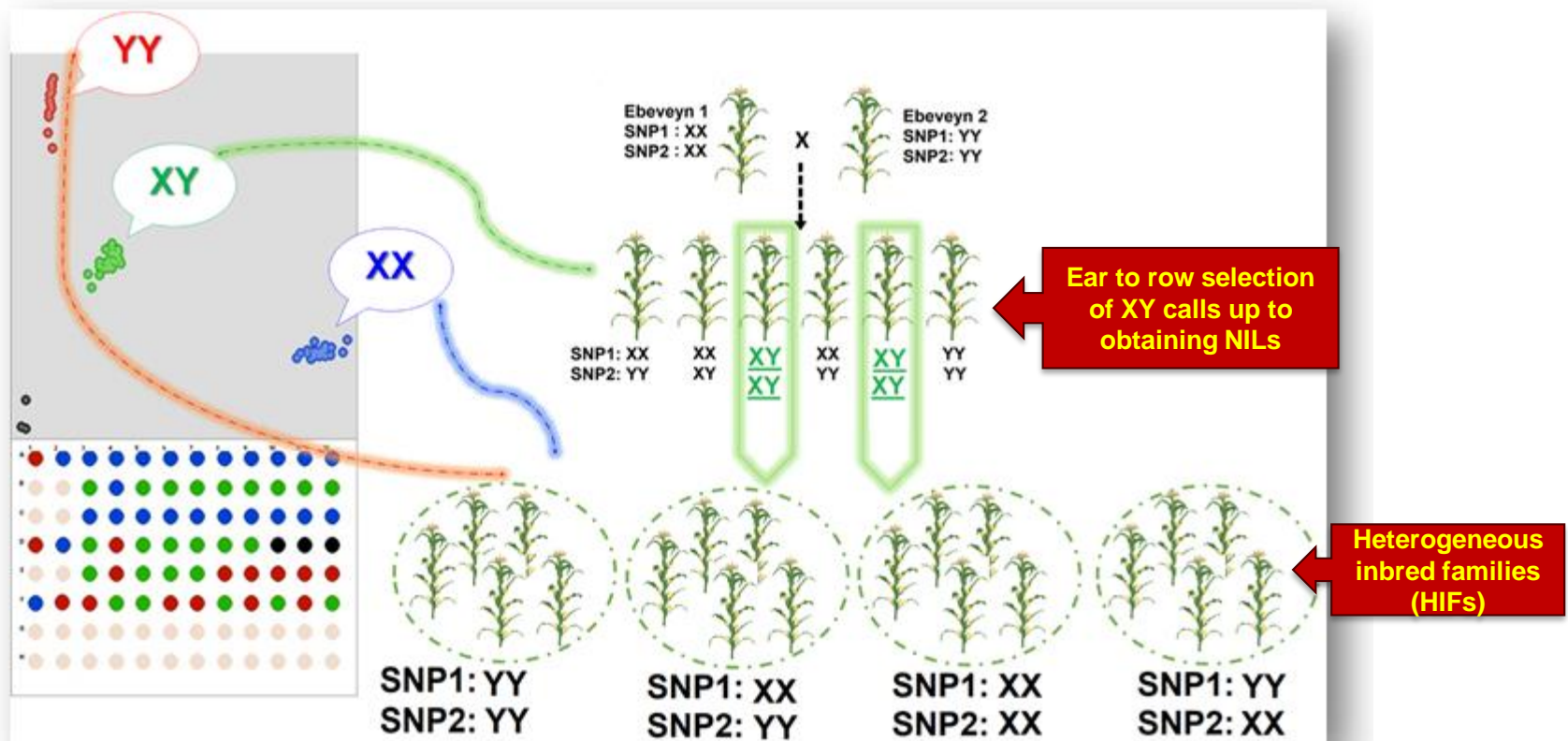
Objectivies

1 • Using PCR (KASP) based marker assisted selection to develop multiple HIFs by back-crossing four different linkage mapping populations.

2 • Validation of the precise plant height effects of two robust QTV-SNPs across the developed HIFs using temporal data by UASs.
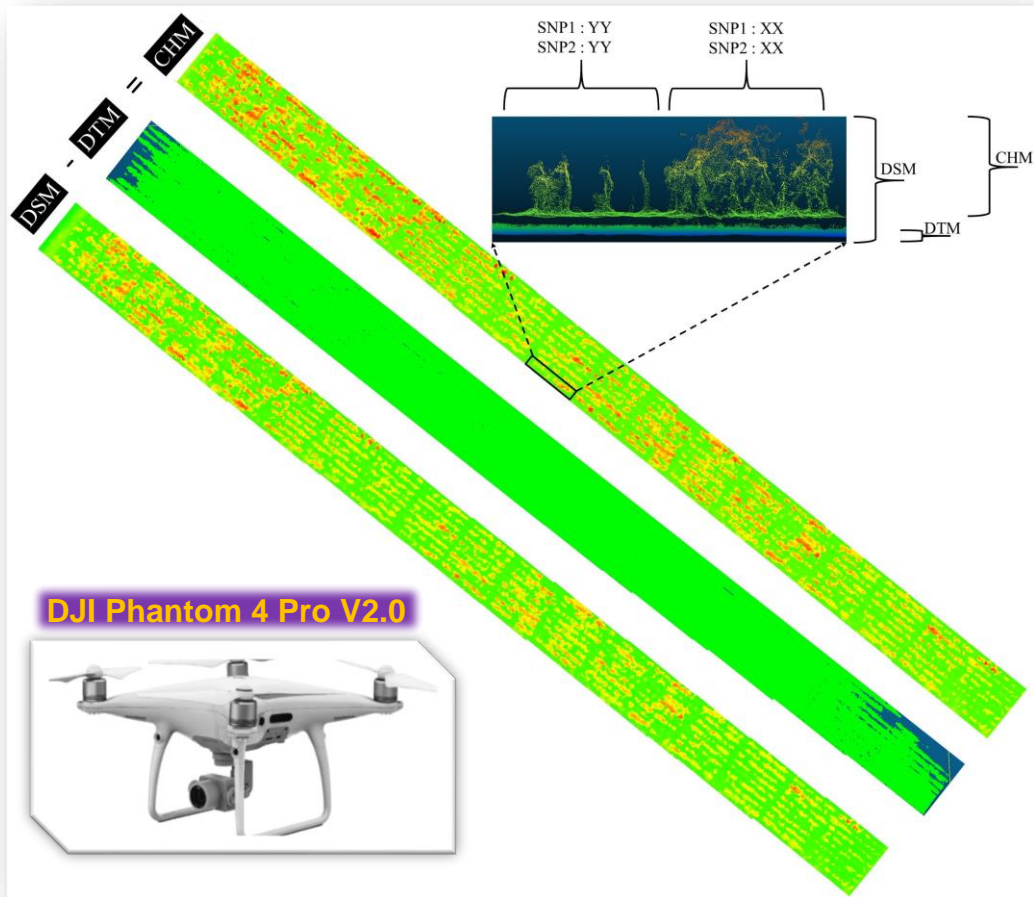
Materials and Methods

> Yuanyuan, Chen (2016) determined the linkage populations and designed KASP marker using these SNPs.

Materials and Methods
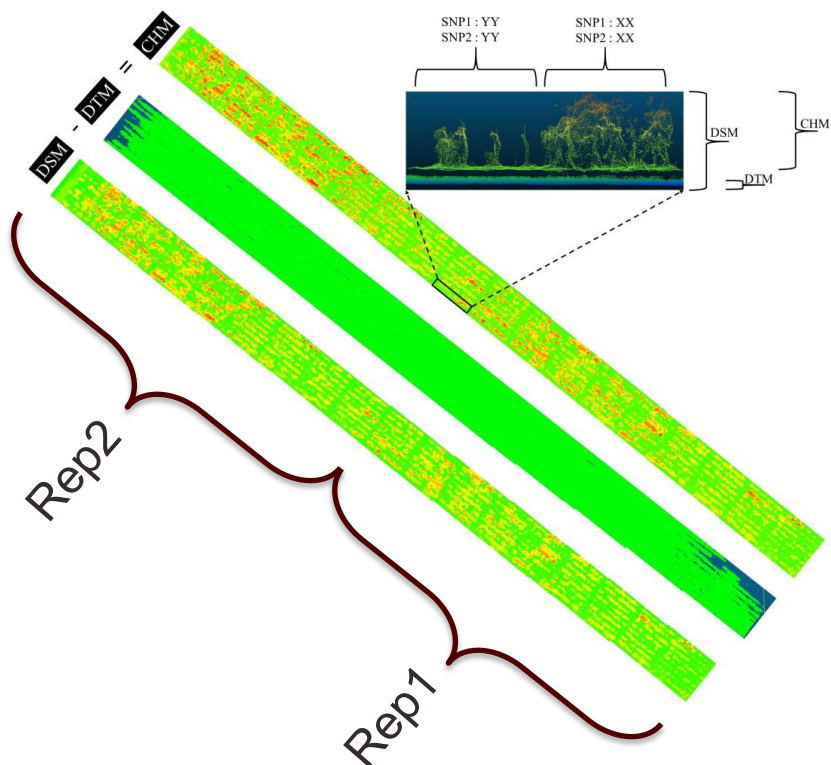
UAS data processing pipeline


DJI Phantom 4 Pro V2.0

UASs-Phenotyping,

➢ DJI Phantom 4 Pro V2.0 (25 meters altitude, ones/twice a week 72 DPI resolution with 90 percent overlap)

➢ Orthomosaics and point clouds were created using Agisoft Metashape software (Totally,11 flights were used.)

➢ Cloud Compare (version: 2.11.alpha) software was used to extract plot based plant height.

UAS data processing pipeline

Rep2

Rep1

SNP1 : YY
SNP2 : YY

SNP1 : XX
SNP2 : XX

DSM - DTM = CHM

DSM

DTM

CHM

Accuracy assessment
(UASs vs ruler measurement)

Means

Medians

UAS-PHT

R = 0.995

R = 0.831

R = 0.825

Population 1
Population 2
Population 3
Population 4

Flight Dates

Sowing date

Plant height
125
100
75
50
25
0

2019

- ➢ 144 HIFs were grown based on RCDB design with two replications

- ➢ HIFs were advanced by four linkage mapping populations **(Recurrent parent x donor parents: LAMA x LH82, Ki3 x NC356, NC356 x Ki3, Tx740 x NC356)**
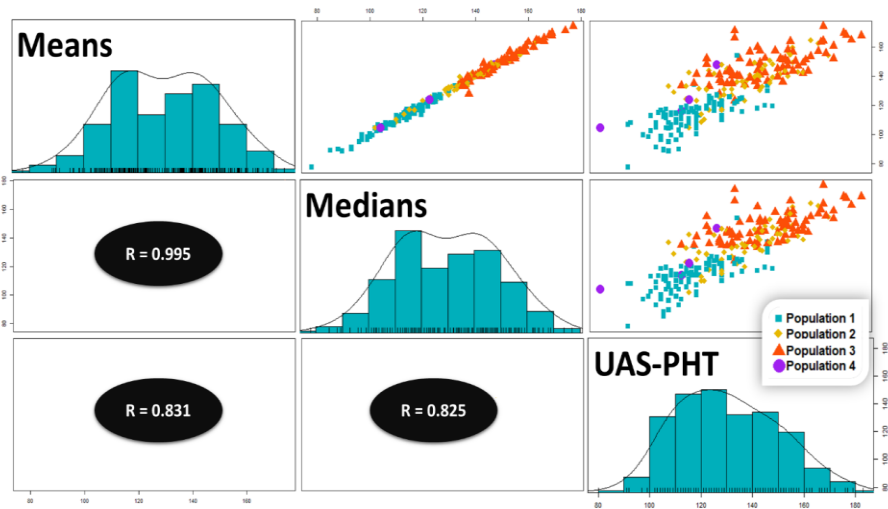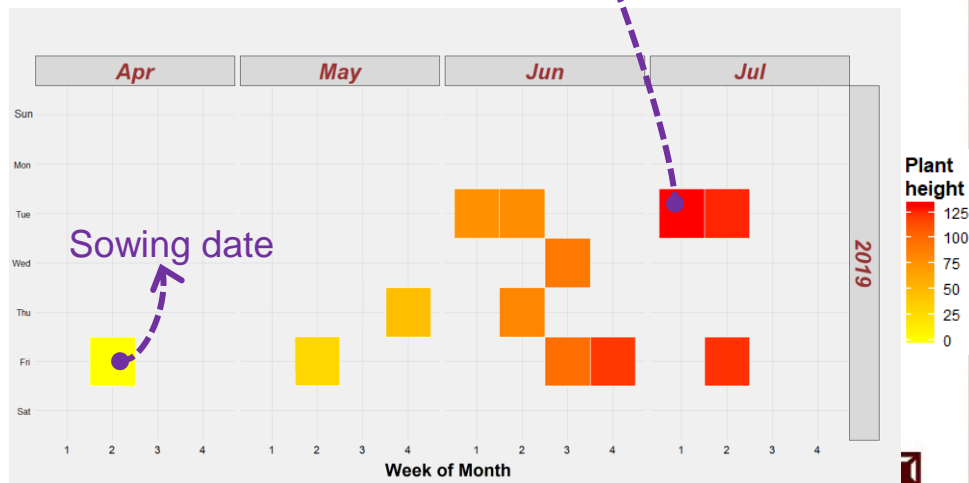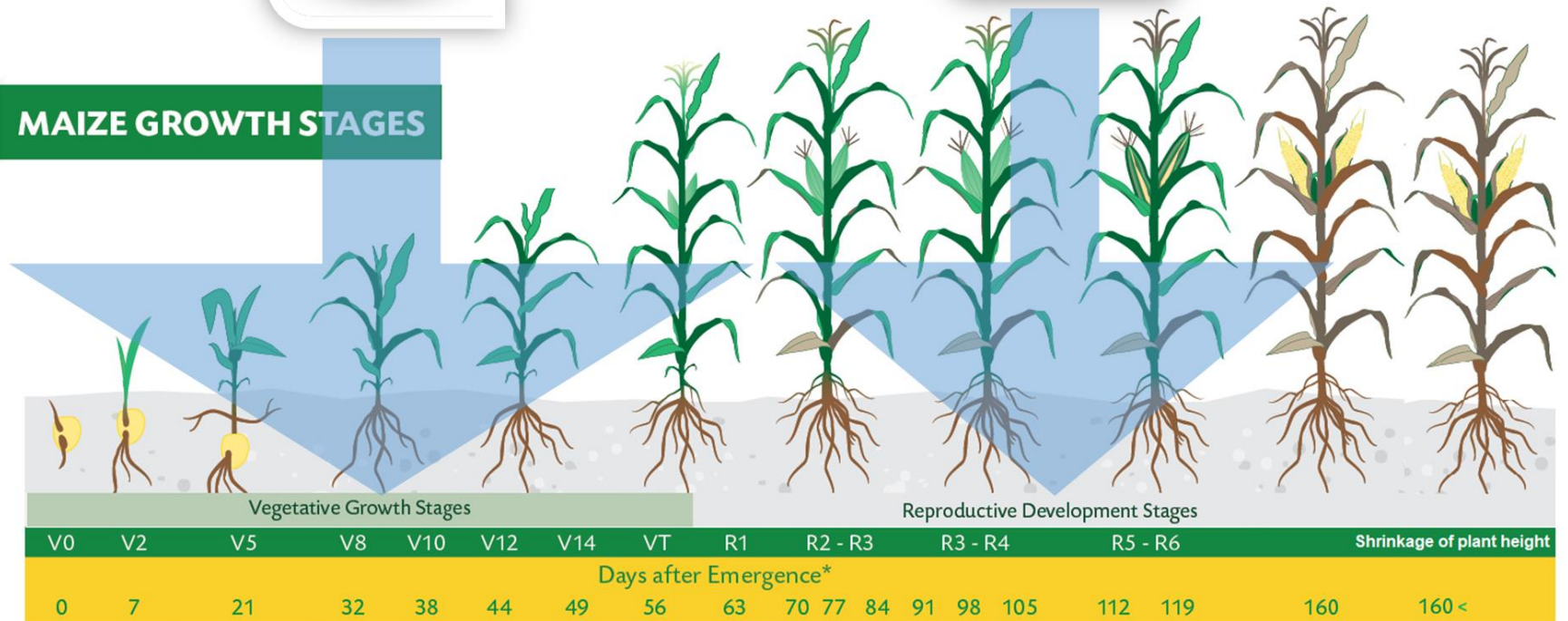
First 7 flights cover the first 70 days.

Following 4 flights cover 100 days after planting.

MAIZE GROWTH STAGES

Vegetative Growth Stages								Reproductive Development Stages								
V0	V2	V5	V8	V10	V12	V14	VT	R1	R2 - R3		R3 - R4			R5 - R6		Shrinkage of plant height
Days after Emergence*																
0	7	21	32	38	44	49	56	63	70	77	84	91	98	105	112	119	160	160 <

* The number of days varies between different growth classes and environments.

Photo credit : http://www.pannar.com

Statistical models;

Pop	SNP1	SNP2
1	XX	XX
1	XX	YY
1	XX	XX
1	XX	YY

or

Pop	SNP1	SNP2
1	YY	XX
1	YY	YY
1	YY	XX
1	YY	YY

$$Y: \mu + \boldsymbol{\sigma^2_{SNPs}} + \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$

Ruler measurements

| Pop	SNP1	SNP2
1	XX	XX
1	XX	YY
1	XX	XX
1	XX	YY
2	XX	XX
2	XX	YY
2	XX	XX
2	XX	YY
3	XX	XX
3	XX	YY
3	XX	XX
3	XX	YY

$$Y: \mu + \sigma^2_{Pop} + \boldsymbol{\sigma^2_{SNPs}} + \left[\boldsymbol{\sigma^2_{Pop} * \sigma^2_{SNPs}}\right] + \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$

Ruler measurements and UASs data

$$Y: \mu + \sigma^2_{Pop} + \sigma^2_{SNP1} + \sigma^2_{SNP2} + \left[\sigma^2_{Pop} * \sigma^2_{SNP1}\right] + \left[\sigma^2_{Pop} * \sigma^2_{SNP2}\right] + \left[\boldsymbol{\sigma^2_{SNP1} * \sigma^2_{SNP2}}\right]$$
$$+ \left[\boldsymbol{\sigma^2_{Pop} * \sigma^2_{SNP1} * \sigma^2_{SNP2}}\right] + \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$

Ruler measurements and UASs data

Pop	SNP1	SNP2
1	XX	XX
1	XX	YY
1	YY	XX
1	YY	YY
2	XX	XX
2	XX	YY
2	YY	XX
2	YY	YY

A&M

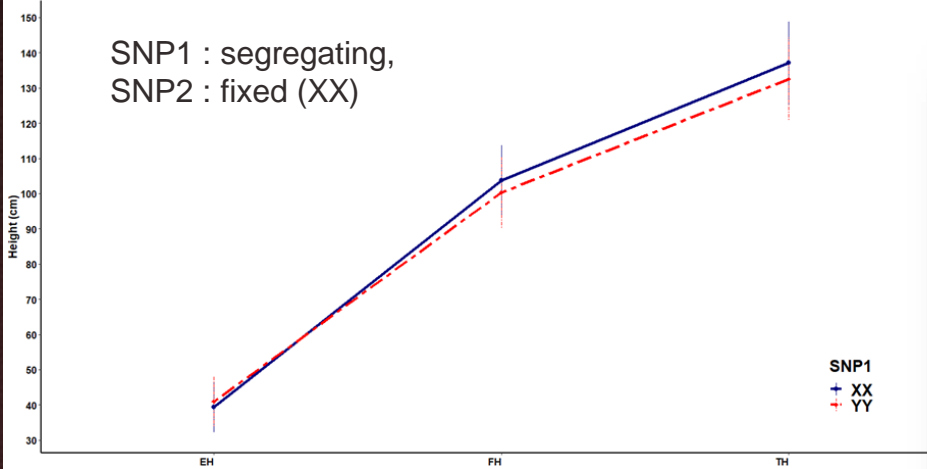# Results of Eq. [1] for ruler measurement
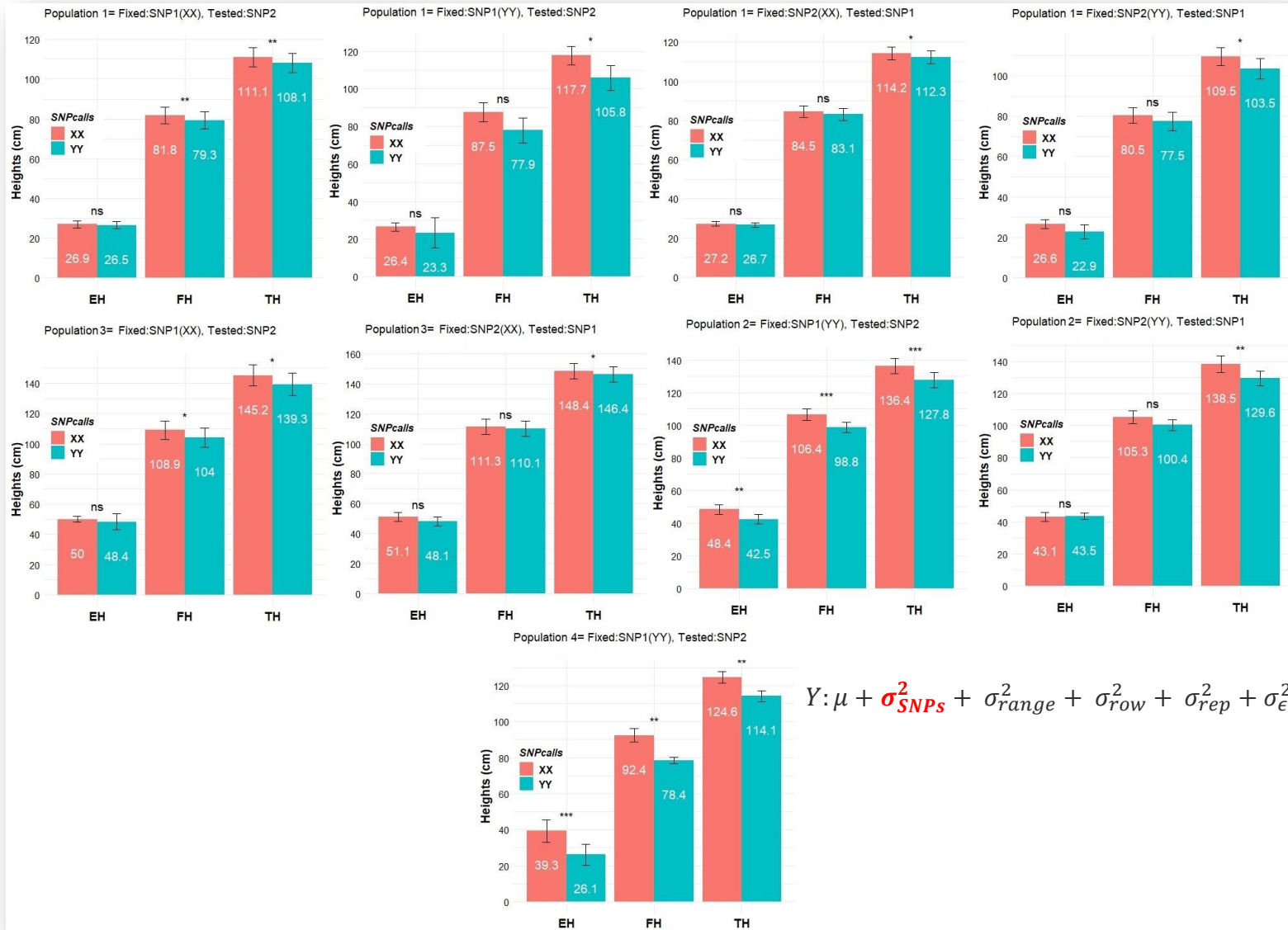
$$Y : \mu + \boldsymbol{\sigma^2_{SNPs}} + \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$

Results of Eq. [2] for ruler measurement

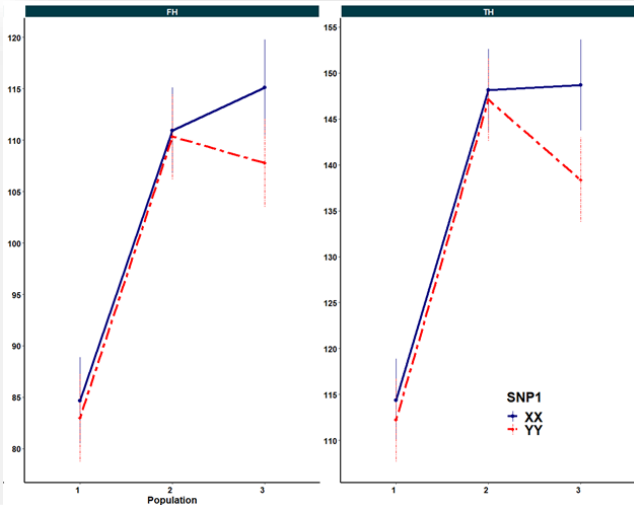$$Y: \mu + \sigma^2_{Pop} + \boldsymbol{\sigma^2_{SNPs}} + \left[\sigma^2_{Pop} * \sigma^2_{SNPs}\right] + \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$

SNP1 : segregating,
SNP2 : fixed (XX)

$$Y: \mu + \sigma^2_{Pop} + \boldsymbol{\sigma^2_{SNPs}} + \left[\sigma^2_{Pop} * \sigma^2_{SNPs}\right] + \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$

SNP1 : fixed (XX),
SNP2 : segregating
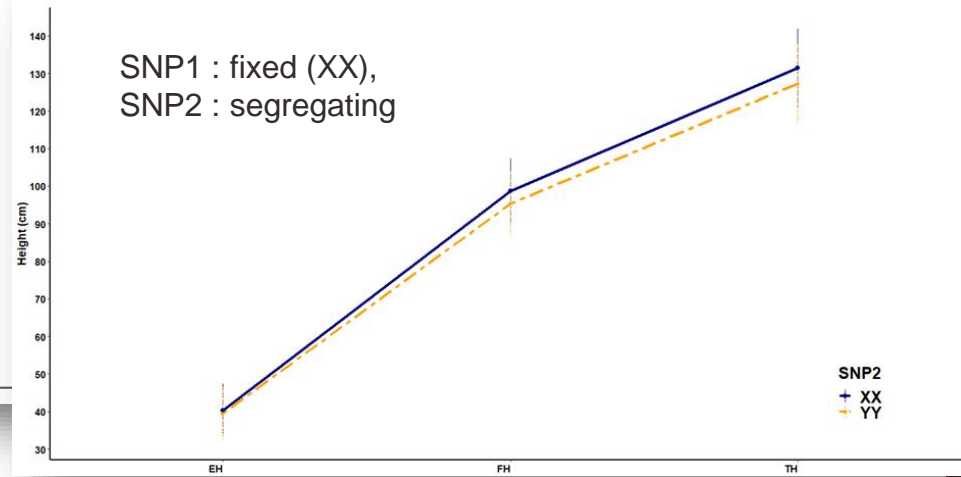
$$Y: \mu + \sigma^2_{Pop} + \sigma^2_{SNPs} + \left[\boldsymbol{\sigma^2_{Pop} * \sigma^2_{SNPs}}\right] + \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$

$$Y: \mu + \sigma^2_{Pop} + \sigma^2_{SNPs} + \left[\boldsymbol{\sigma^2_{Pop} * \sigma^2_{SNPs}}\right] + \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$

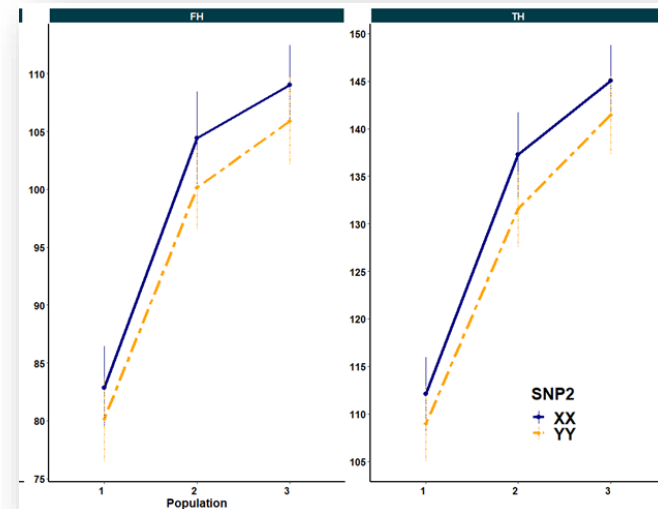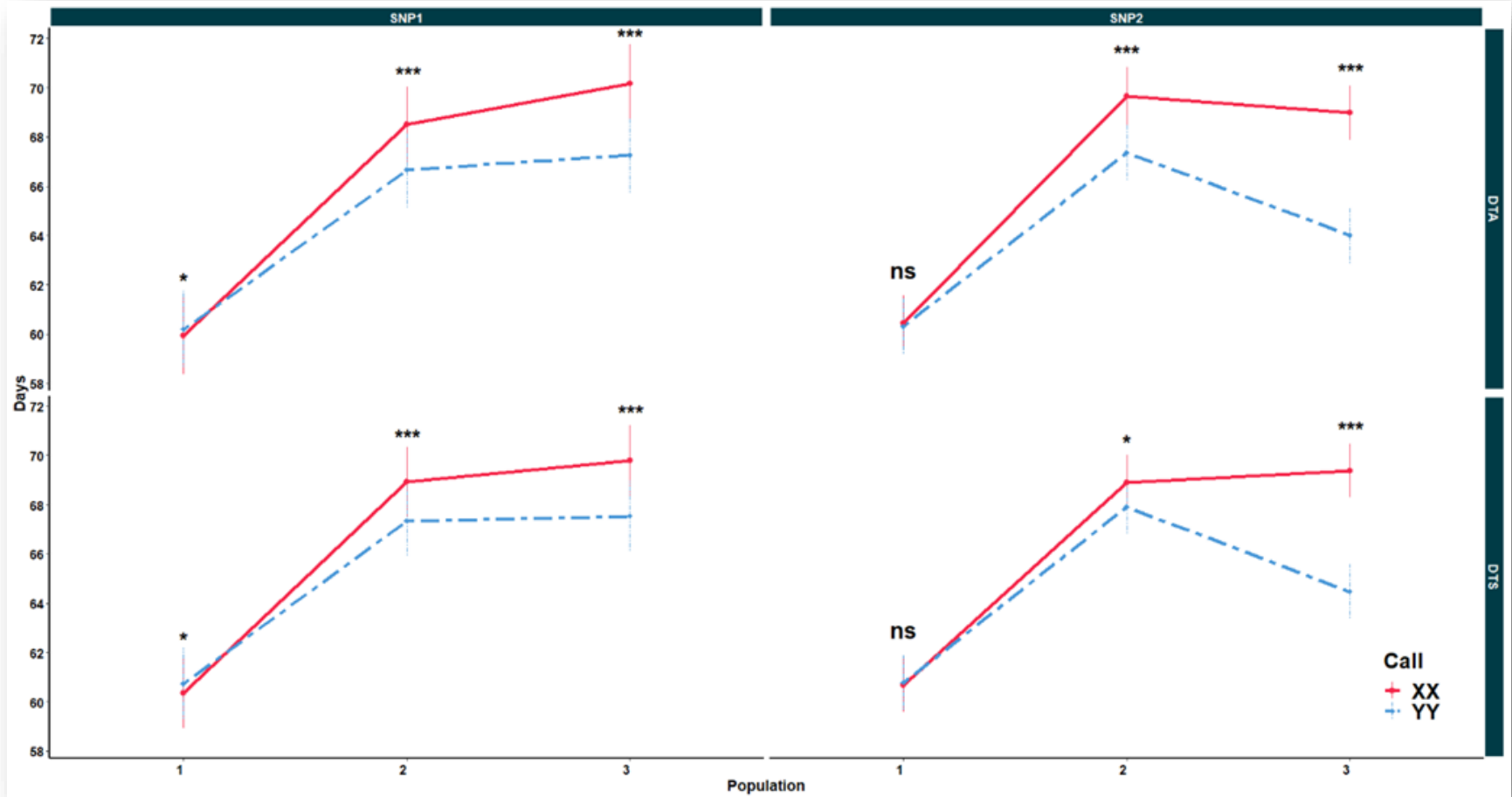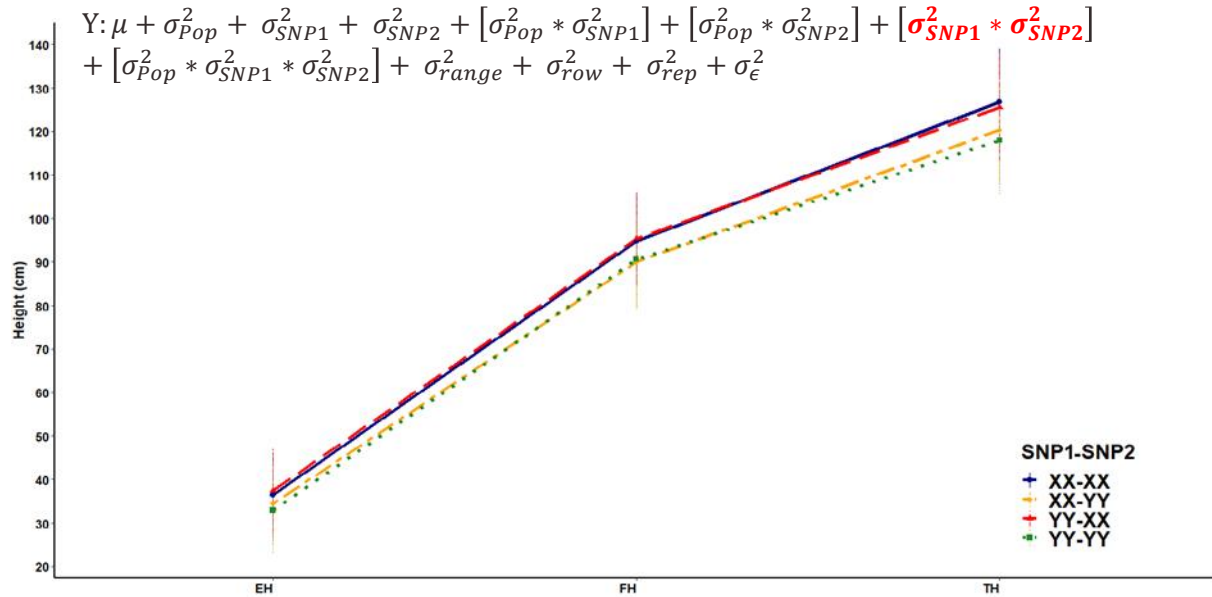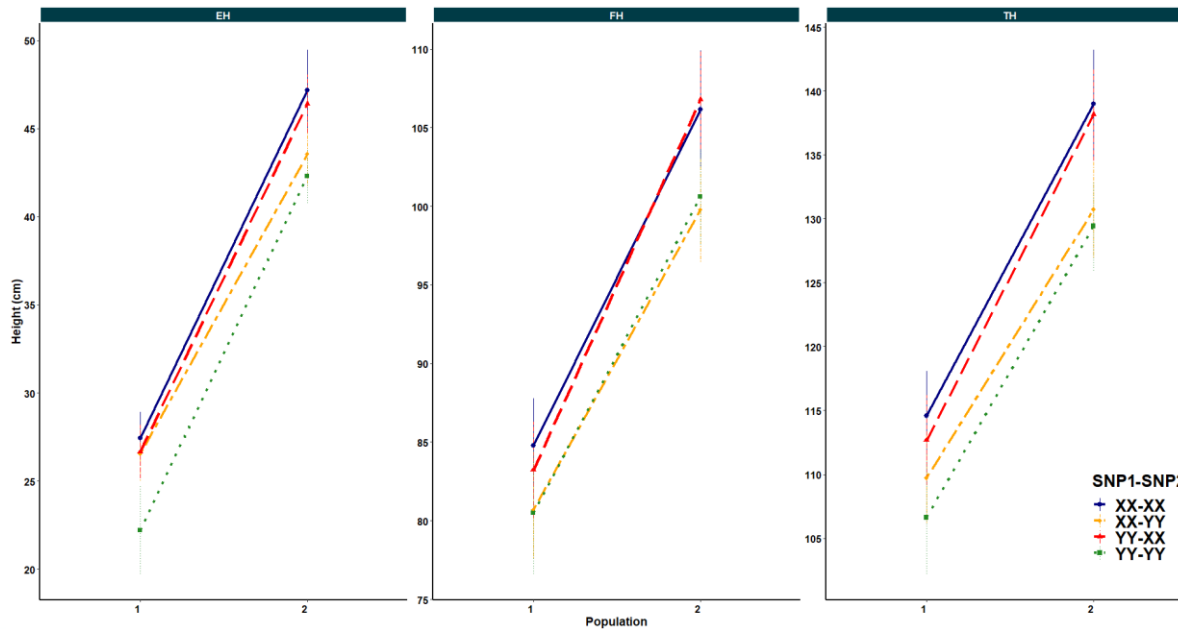# Results of Eq. [2] when DTA and DTS were response.

$$Y: \mu + \sigma^2_{Pop} + \sigma^2_{SNPs} + [\sigma^2_{Pop} * \sigma^2_{SNPs}] + \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$
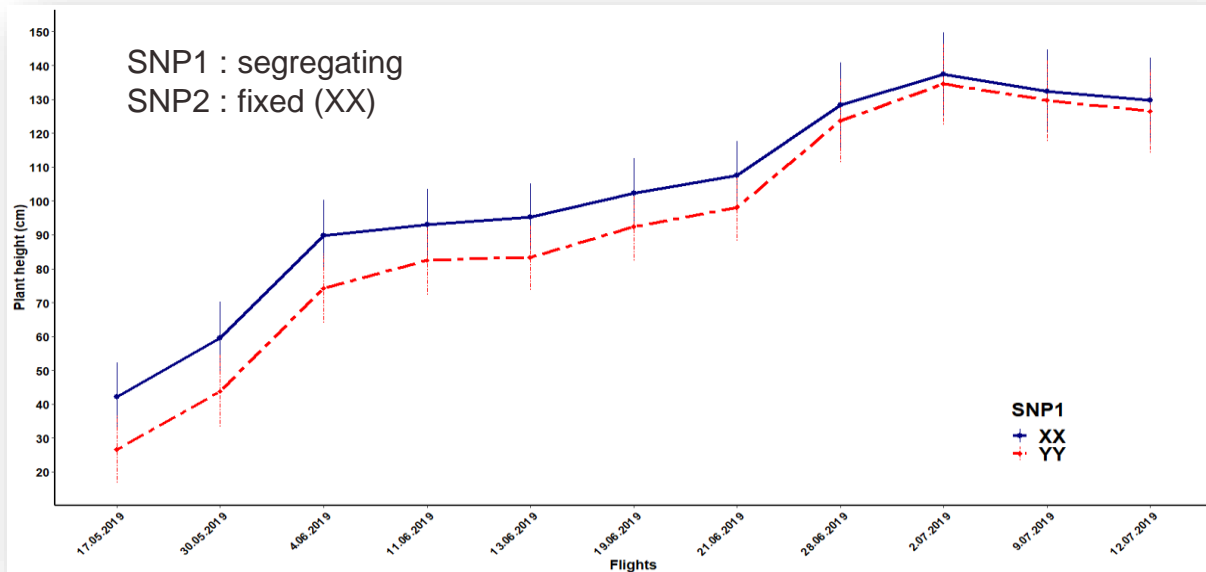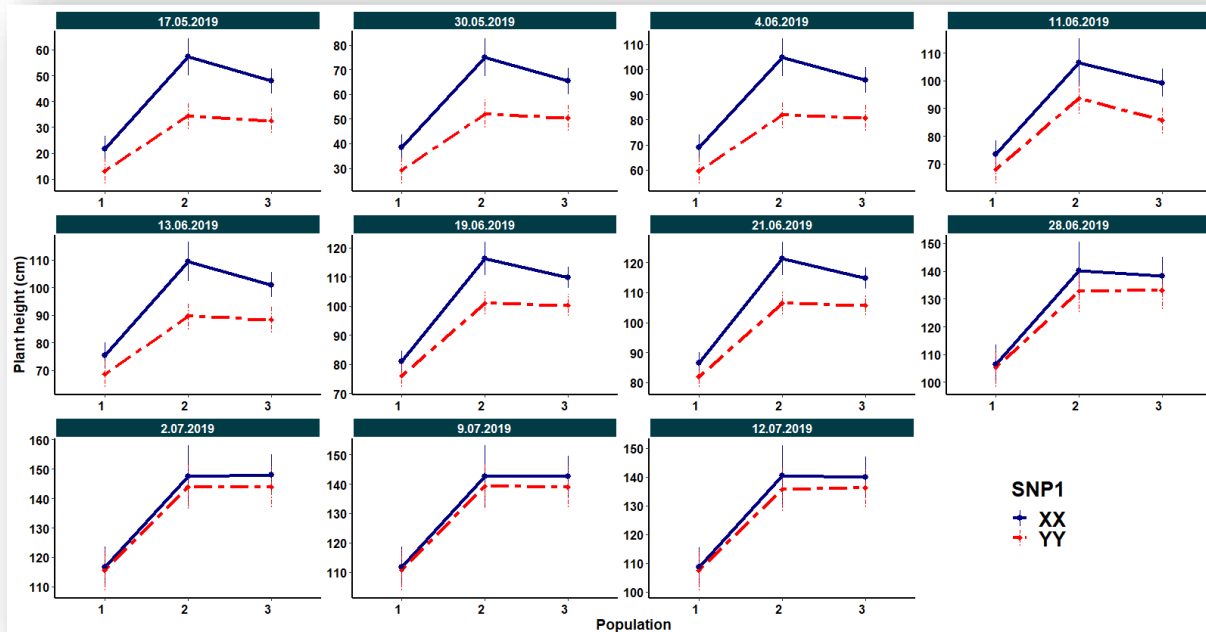
Results of Eq. [3] for ruler measurement

$$Y: \mu + \sigma^2_{Pop} + \sigma^2_{SNP1} + \sigma^2_{SNP2} + [\sigma^2_{Pop} * \sigma^2_{SNP1}] + [\sigma^2_{Pop} * \sigma^2_{SNP2}] + \mathbf{[\sigma^2_{SNP1} * \sigma^2_{SNP2}]}$$
$$+ [\sigma^2_{Pop} * \sigma^2_{SNP1} * \sigma^2_{SNP2}] + \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$

$$Y: \mu + \sigma^2_{Pop} + \sigma^2_{SNP1} + \sigma^2_{SNP2} + [\sigma^2_{Pop} * \sigma^2_{SNP1}] + [\sigma^2_{Pop} * \sigma^2_{SNP2}] + [\sigma^2_{SNP1} * \sigma^2_{SNP2}]$$
$$+ \mathbf{[\sigma^2_{Pop} * \sigma^2_{SNP1} * \sigma^2_{SNP2}]} + \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$
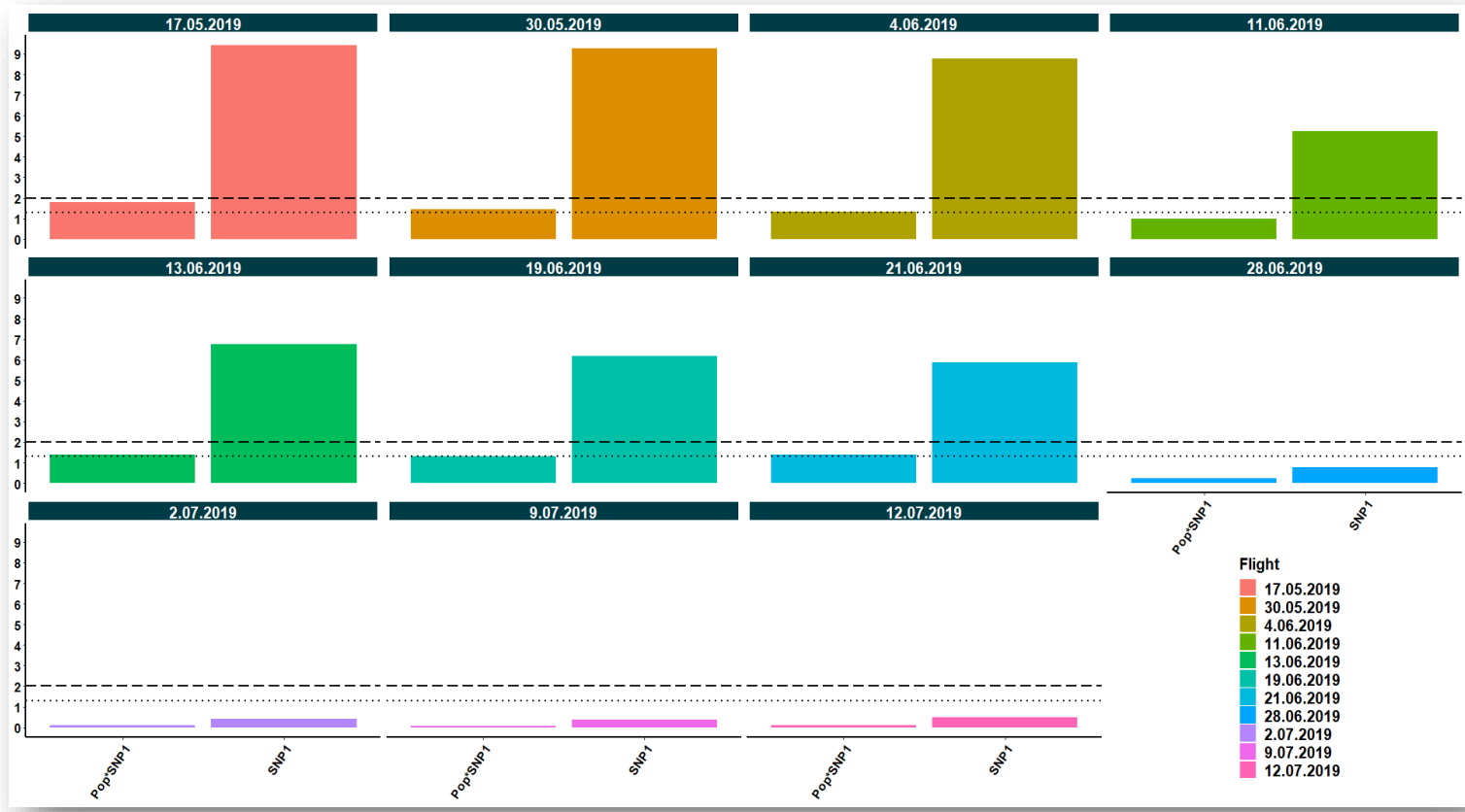
Results of Eq. [2] for UASs data

SNP1 : segregating
SNP2 : fixed (XX)

$$Y: \mu + \sigma^2_{Pop} + \boldsymbol{\sigma^2_{SNPs}}$$
$$+ \left[\sigma^2_{Pop} * \sigma^2_{SNPs}\right]$$
$$+ \sigma^2_{range} + \sigma^2_{row}$$
$$+ \sigma^2_{rep} + \sigma^2_{\epsilon}$$

$$Y: \mu + \sigma^2_{Pop} + \sigma^2_{SNPs}$$
$$+ \left[\boldsymbol{\sigma^2_{Pop} * \sigma^2_{SNPs}}\right]$$
$$+ \sigma^2_{range} + \sigma^2_{row}$$
$$+ \sigma^2_{rep} + \sigma^2_{\epsilon}$$

$-\log_{10}(0.05)$ = pointed line

$-\log_{10}(0.01)$ = dashed line

SNP1 : fixed (XX)
SNP2 : segregating
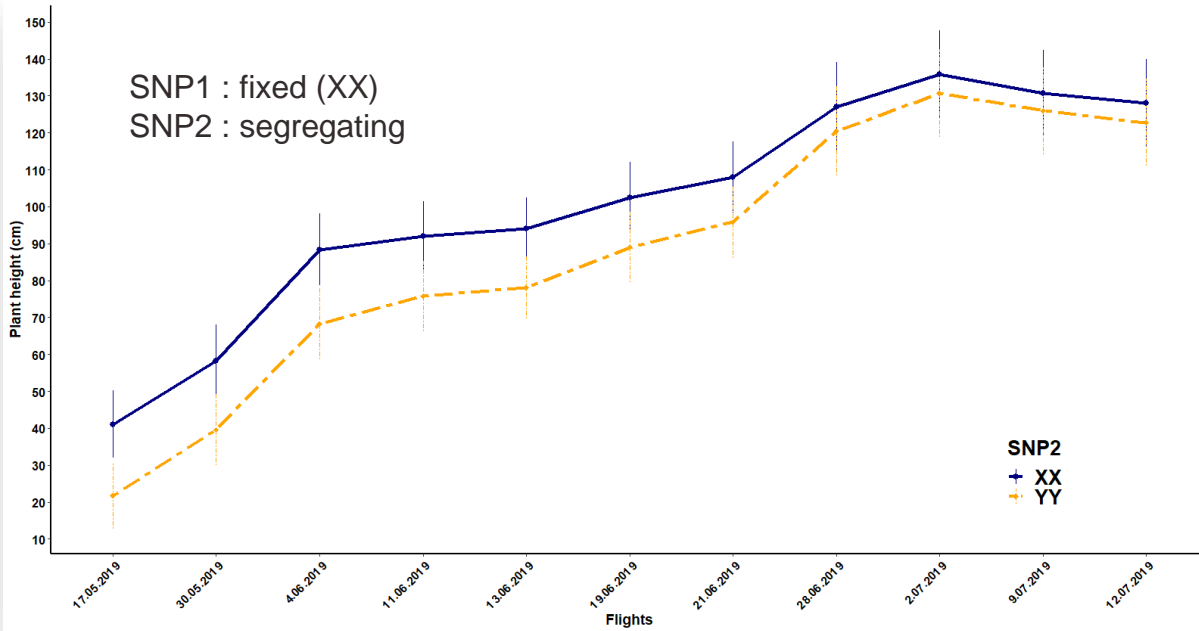
$$Y: \mu + \sigma^2_{Pop} + \boldsymbol{\sigma^2_{SNPs}}$$
$$+ \left[\sigma^2_{Pop} * \sigma^2_{SNPs}\right]$$
$$+ \sigma^2_{range} + \sigma^2_{row}$$
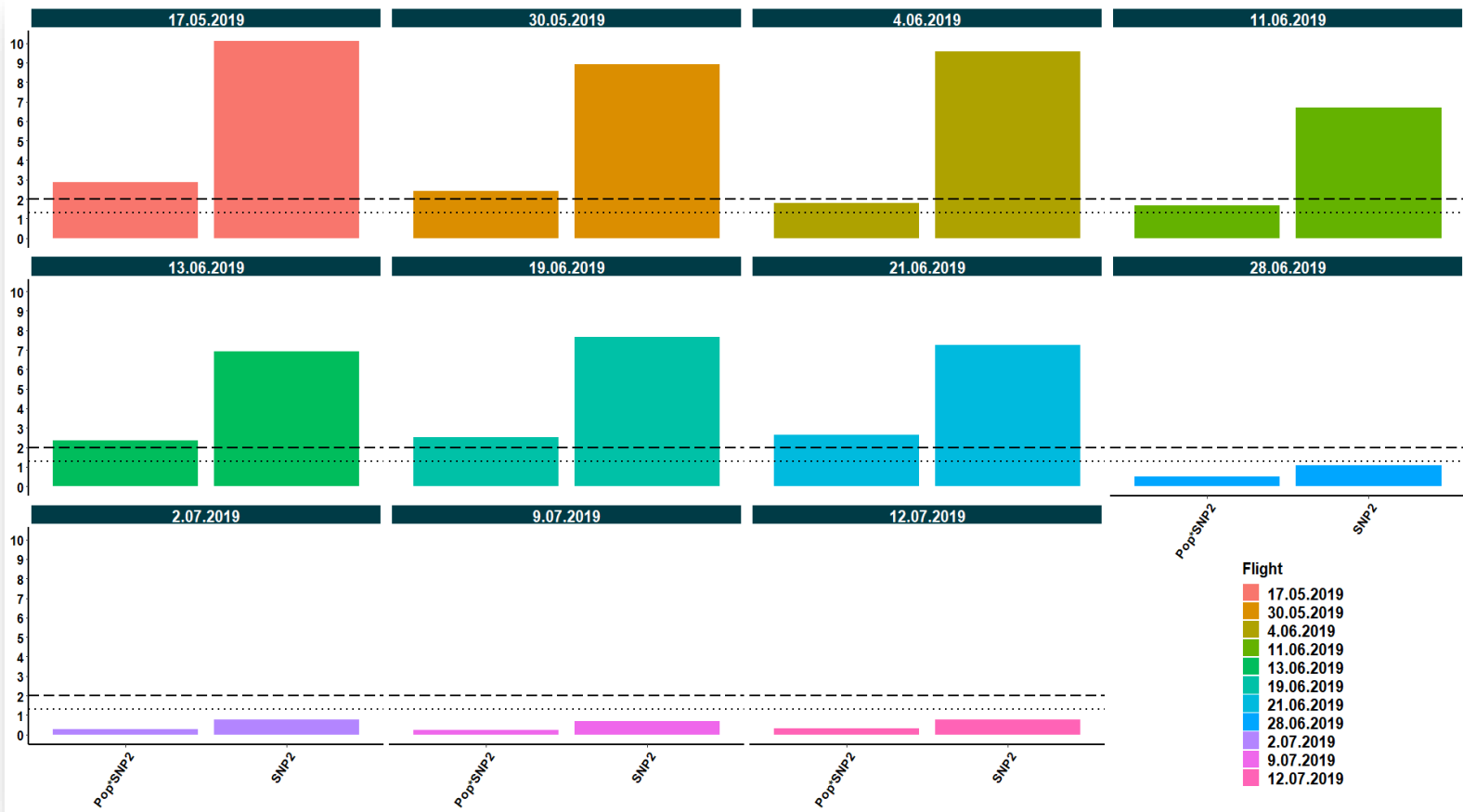$$+ \sigma^2_{rep} + \sigma^2_{\epsilon}$$
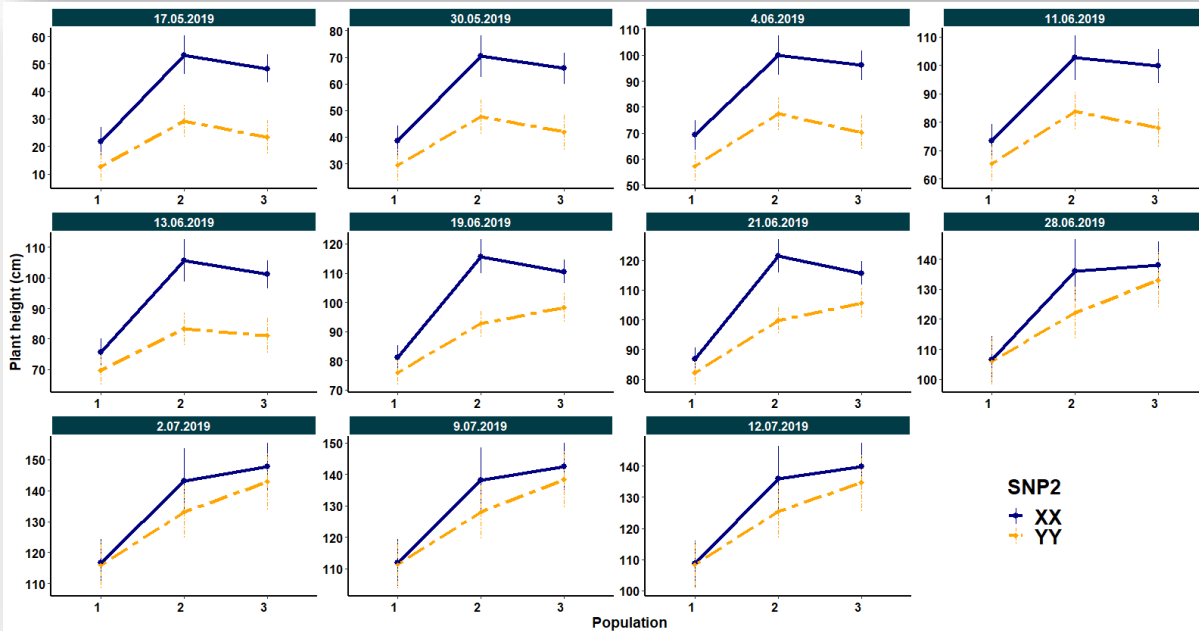
$$Y: \mu + \sigma^2_{Pop} + \sigma^2_{SNPs}$$
$$+ \left[\boldsymbol{\sigma^2_{Pop} * \sigma^2_{SNPs}}\right]$$
$$+ \sigma^2_{range} + \sigma^2_{row}$$
$$+ \sigma^2_{rep} + \sigma^2_{\epsilon}$$

$-\log_{10}(0.05)$ = pointed line

$-\log_{10}(0.01)$ = dashed line
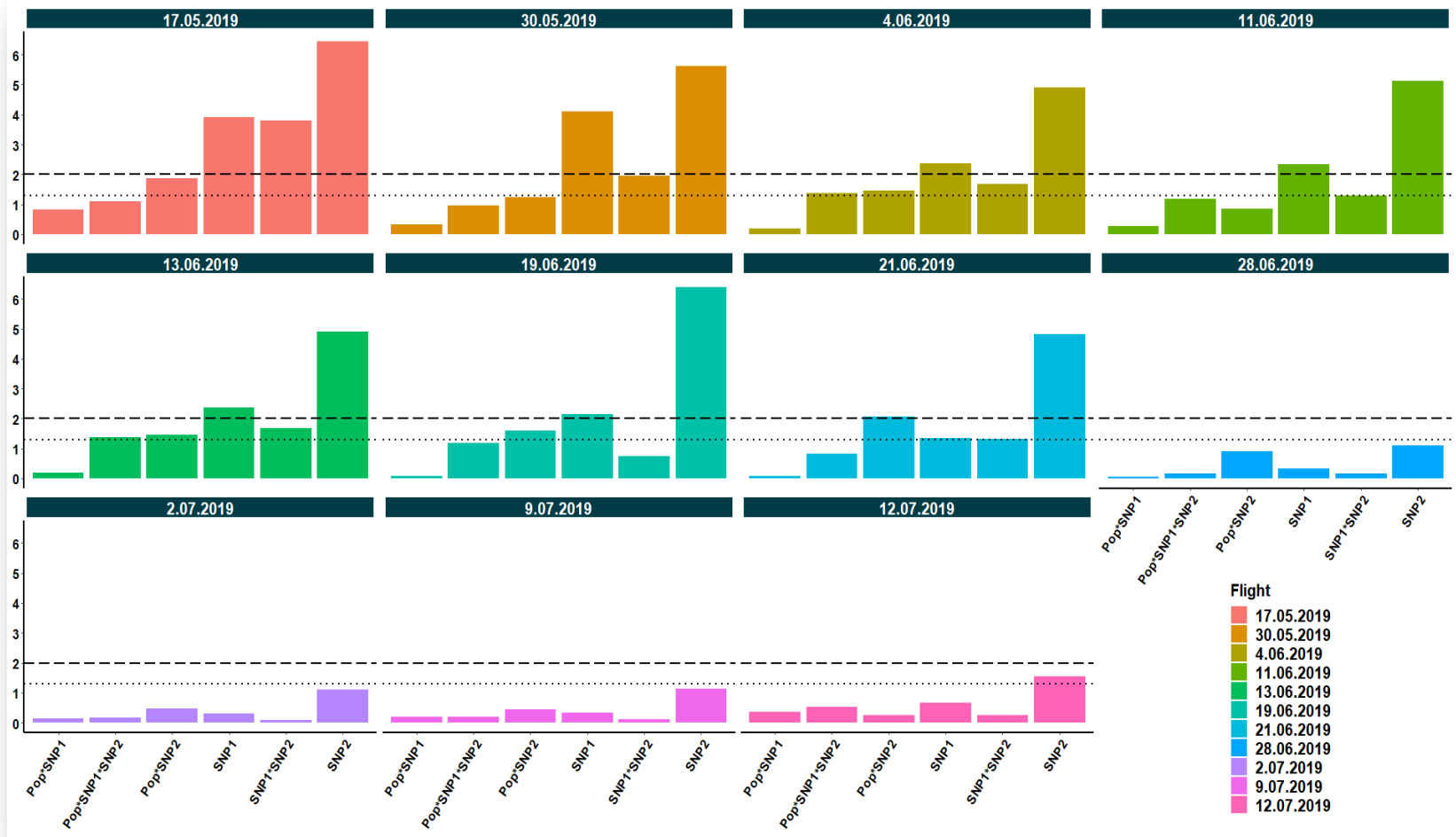
Results of Eq. [3] for UASs data

SNP1 : segregating
SNP2 : segregating

$$Y: \mu + \sigma^2_{Pop} + \sigma^2_{SNP1} + \sigma^2_{SNP2}$$
$$+ \left[\sigma^2_{Pop} * \sigma^2_{SNP1}\right]$$
$$+ \left[\sigma^2_{Pop} * \sigma^2_{SNP2}\right]$$
$$+ \left[\boldsymbol{\sigma^2_{SNP1} * \sigma^2_{SNP2}}\right]$$
$$+ \left[\sigma^2_{Pop} * \sigma^2_{SNP1} * \sigma^2_{SNP2}\right]$$
$$+ \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$
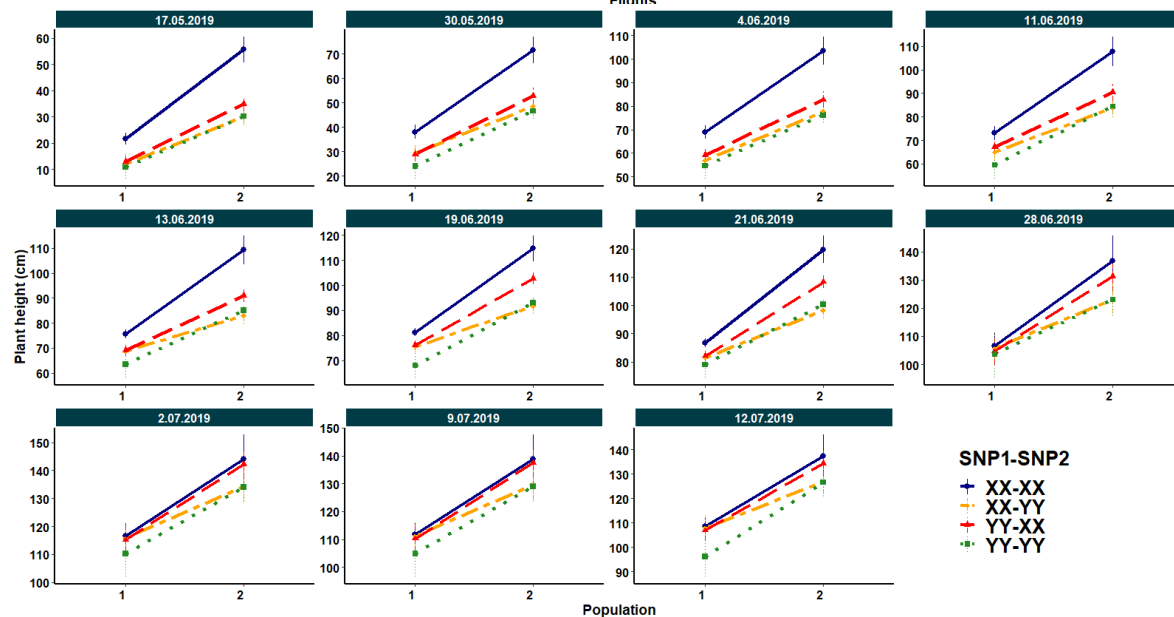
$$Y: \mu + \sigma^2_{Pop} + \sigma^2_{SNP1} + \sigma^2_{SNP2}$$
$$+ \left[\sigma^2_{Pop} * \sigma^2_{SNP1}\right]$$
$$+ \left[\sigma^2_{Pop} * \sigma^2_{SNP2}\right]$$
$$+ \left[\sigma^2_{SNP1} * \sigma^2_{SNP2}\right]$$
$$+ \left[\boldsymbol{\sigma^2_{Pop} * \sigma^2_{SNP1} * \sigma^2_{SNP2}}\right]$$
$$+ \sigma^2_{range} + \sigma^2_{row} + \sigma^2_{rep} + \sigma^2_{\epsilon}$$

$-\log_{10}(0.05)$ = pointed line

$-\log_{10}(0.01)$ = dashed line

Conclusion

❑   Effects of both SNPs varied from 10 to 25 cm in early growing stages but these differences narrowed to 3 cm as populations reached the termination of growing period.

❑   Interactions between SNP1-SNP2 and SNPs-population have also lost towards the end of growing period (Especially after vegetative growth period)

❑   Allelic effect sizes of quantitative traits can be dynamic in temporal growth resulting in informative phenotypic variability is being overlooked following traditional phenotyping methods.
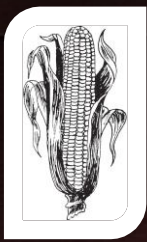
Texas A&M University
Quantitative Genetics and Maize Breeding

Dr. Seth C. Murray

Dr. Steven Anderson

MSc. Holly Lane

Grad. Shakirah Nakasagga

Grad. Nathalia Penna Cruzato

Grad. Colby Ratcliff

R.A. David Rooney

Dr. Nithya Subramanian

Dr. Scott Wilde

Dr. Yuanyuan Chen

R.A. Regan Lindsey

TEXAS A&M
AGRILIFE