Mapping QTLs for plant height variation in RIL population derived from cross between Harry x Wesley semi-dwarf wheat lines.

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Background

- Plant height not only determines plant architecture but also effects grain yield.
- Plant height is a complex dynamic process controlled by a network of genes and environmental factors.
- Height variation in lines containing different set of *Rht* genes have been extensively studied.
- However, height variation in progenies derived from semi-dwarf lines containing same set of *Rht* gene have not been studied.

Objectives

- Determine the genetic variability of plant height in RIL population derived from semi-dwarf wheat lines containing *Rht-B1* gene.
- Identify QTLs/genes responsible for plant height variation in RIL population of semi-dwarf wheat lines.
- Assess QTL main effects, epistasis and their interaction with environment

Materials and Methods

Plant Material

- 204 RILs (F_6:F_{10}) obtained from the cross 'Harry x Wesley'.
- 3 checks: Two parents and Freeman
- Harry: Adapted to rained systems
- Wesley: Drought sensitive cultivar
- Both are carriers of *Rht-B1* dwarfing gene.
- Evaluated : Under high to low rainfall sites (Lincoln, Mead, Grant, Sidney and Clay Center)

Experimental design

- Augmented Randomized Incomplete Block Design.
- 12 incomplete blocks, 17 lines plus 3 checks randomized per incomplete block.

Genotyping

- Genotyping by sequencing method (Elshire *et al*. 2011).
- TASSEL GBS pipeline was used to call SNPs.

Statistical analysis

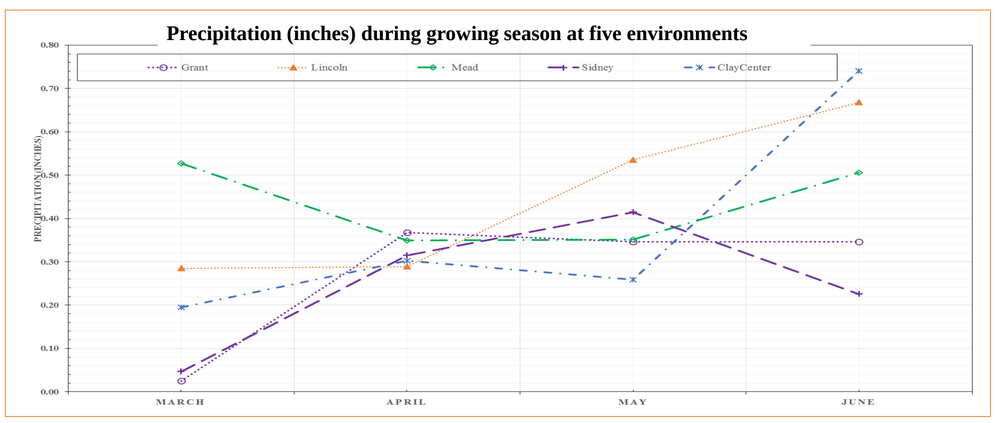
- ANOVA
- BLUPs

Map Construction

- The BIN tool in QTL IciMapping version 4.0
- Remove high missing rate markers (>30%) and redundant markers
- Genetic linkage map constructed:
  - 440 unique makers spanned 1822 cM in length.
  - The average interval length was 4.14 cM.

QTL mapping

- QTL analysis was performed using IciMapping version 4.0
  - QTL main effects (ICIM-ADD)
  - Digenetic QTL epistasis (ICIM-EPI)
  - QTL × environment interactions (MET)



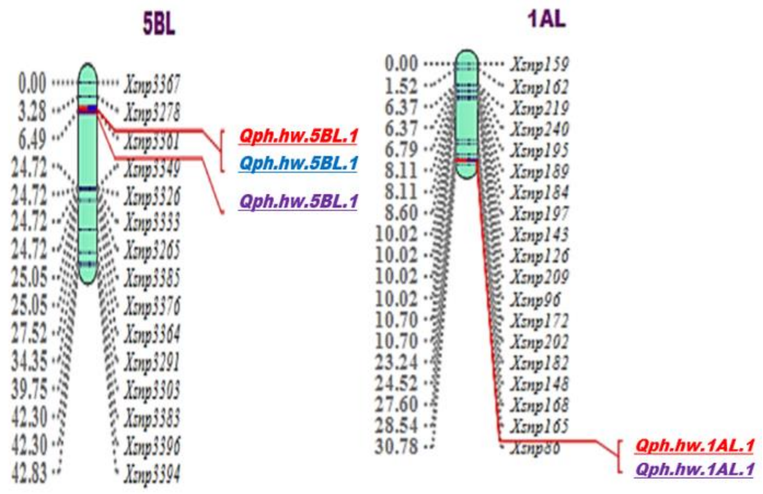
Results and Discussion

Phenotypic summary of Plant height (cm) evaluated at five environments

Environments	Parents		RILs				
	Harry	Wesley	Mean	Min	Max	SD[ł]	CV[ǂ]
Lincoln	102	96.23	104.05	88.00	120.00	7.34	7.21
Mead	104	97.25	104.85	85.00	130.00	7.84	7.48
ClayCenter	96	70.20	83.58	68.58	105.06	6.05	7.25
Grant	86	72.20	87.62	74.20	105	7.54	8.62
Sidney	96	81.60	91.92	70	104	8.19	8.90

QTLs affecting height on chromosome 1AL and 5BL at three environments

-----Mead -----Lincoln -----Clay Centre



QTLs associated with height in five environments

QTL	Location	(cM)	Marker interval	LOD Score	PVE (%)	Add
Qph.hw.3B.1	Sidney	280	*Xsnp1806-Xsnp1400*	3.95	9.91	-1.97
Qph.hw.1AL.1	Claycenter	30	*Xsnp165-Xsnp86*	4.05	9.16	1.69
Qph.hw.5BL.1	Claycenter	5	*Xsnp3278-Xsnp3361*	3.28	7.24	-1.49
Qph.hw.3B.1	Grant	292	*Xsnp1737-Xsnp1400*	3.95	12.89	-2.22
Qph.hw.5BL.1	Lincoln	5	*Xsnp3278-Xsnp3361*	3.97	10.89	-1.93
Qph.hw.1AL.1	Mead	30	*Xsnp165-Xsnp86*	3.43	6.74	1.73
Qph.hw.5BL.1	Mead	5	*Xsnp3361-Xsnp3349*	6.75	13.68	-2.45
Qph.hw.7A.1	Mead	66	*Xsnp4401-Xsnp4359*	3.08	5.76	-1.59

Highly significant digenetic epistatic QTLs for plant height

QTL x environment interactions affecting plant height

References

Elshire et al. (2011) *PLoS One* **6**, e19379.

Zhang et al. (2008) *J Genet Genomic* **35**, 119-127.

Meng et al. (2015) *The Crop Journal* **3**, 269-283..

- Performance for plant height differed in all environments.
- Transgressive segregation was observed in both directions.
- ANOVA (over and within environment) reveals significant differences in:
  - Genotypes, environments, and genotype x environments
- Heritability estimate of pooled data was 86.7%.

Pooled analysis of variance for Plant height (cm) in five environments

Source	Df	Mean Square	F Value	Pr>F
Checks	2	3412	33.82	<0.001
Lines	203	44.96	12.01	<0.001
iblock(Environment)	66	18.46	1.75	0.0034
Environment	5	1674.20	263.58	<0.001
Checks x Environment	10	100.88	9.55	<0.001
Lines x Environment	1030	17.87	1.69	<0.001
Residual	132	10.57		

- 4 distinct QTLs were detected on 1AL, 3B, 5BL and 7A.
- QTL *Qph.hw.5BL.1* detected in 3 environments (High rainfall).
- QTL *Qph.hw.3B.1* in two (Low rainfall).
- Phenotypic variance explained ranged from 5.76 to 12.89%.
- QTLs *Qph.hw.1AL.1*, *Qph.hw.5BL.1* and *Qph.hw.3B.1* are new and identified first time in semi-dwarf wheat lines.
- *Qph.hw.1AL.1* and *Qph.hw.5BL.1* are likely possible candidate genes for plant height manipulation.

- 10 pairs of significant digenetic interactions were identified across five environments.
- Interactions across chromosomes occurred mostly in the A and B genome.
- Various authors previously found digenetic interactions for wheat plant height in between A and B genome.

- Significant QTL x environment interactions was evident.
- Few QTLs appeared to be environment-specific.
- Phenotypic variance explained by QTL x environment interaction was small ranged from 2.76 to 0.02%.

Conclusions

- Presence of genetic variability in plant height in progeny of cross between semi-dwarf parents.
- Identified QTLs may be utilized to modify the plant height in specific crosses. Taller semi-dwarfs under drought and shorter semi-dwarfs under rainfall are desirable.

Future work

- Evaluation of the lines under low and high rainfall environments to detect the presence of identified QTLs .
- Comparative analysis of the identified QTLs.