

Mapping of QTL Conferring Resistance Against Phomopsis Stem Canker in Sunflower

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Introduction

Phomopsis stem canker (PSC)

- ❑ Causal organism: Two fungal species are known to cause PSC in the U.S.
 - *Phomopsis helianthi* (teleomorph *Diaporthe helianthi*), and
 - *Phomopsis gulyae* (teleomorph *Diaporthe gulyae*)
- ❑ *P. helianthi* is more prevalent than *P. gulyae* in the U.S. (Mathew et al. 2015)
- ❑ Yield loss due to PSC was reported as high as 50% in Europe
- ❑ Dramatic increase of PSC infestation in the Northern Great Plains since 2010
- ❑ Host resistance is governed by many minor genes with additive gene action
- ❑ PSC resistance sources have been reported in the USDA sunflower germplasm collection (Talukder et al. 2014)

Objective

Overall objective

- To improve PSC resistance in cultivated sunflower

Specific objectives

- To investigate the inheritance of PSC resistance in sunflower
- To identify genes/QTL associated with PSC resistance
- To identify SNP markers associated with PSC resistance genes/QTL
- To design PCR based primers for use in marker-assisted PSC resistance breeding

Materials & Methods

Plant Materials

- **Parents**

HA-R3 is highly tolerant to PSC

HA 89 is susceptible to PSC

- **Mapping population**

- 164 F₆-derived RILs developed through Single Seed Descent method from the cross between HA-R3 and HA 89

Materials & Methods

PSC Evaluation

- **Environments**

- 2016: Grandin, ND; Rothsay & Crookston, MN

- 2017: Glyndon, Rothsay & Crookston, MN

- 2018: Glyndon & Staples, MN

- **Field design**

- Randomized incomplete block with 3 replications

- **Field inoculation**

- Natural infestation

- **Disease incidence (DI) scoring**

- Percent plants showing PSC symptom

Materials & Methods

QTL Mapping

- **Genotyping**

Genotype-by-sequencing (GBS) technology was used for genotyping of 164 RILs

- **Linkage mapping**

- A genetic linkage map was developed comprised of 2,295 SNP markers on 17 linkage groups spanning 1,211.75 cM

- **QTL analysis**

- Best linear unbiased predictors (BLUPs) of PSC traits were obtained for combined and individual environments and used in composite interval mapping (CIM) program of WinQTL Cartographer

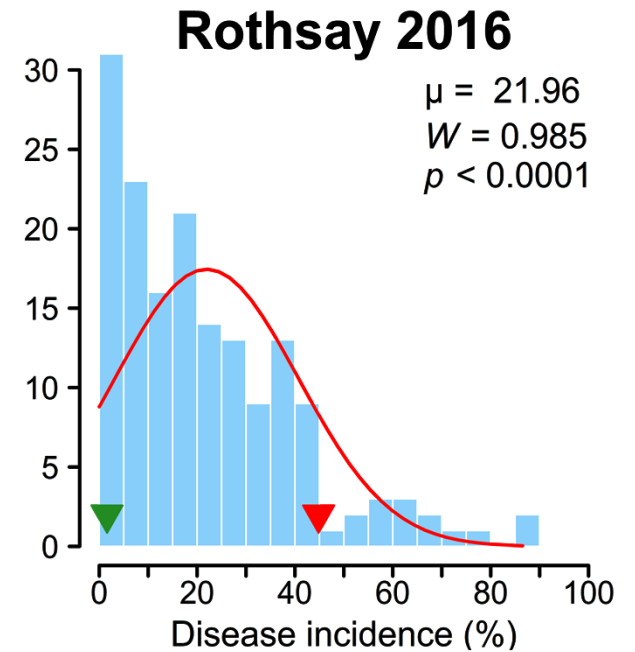
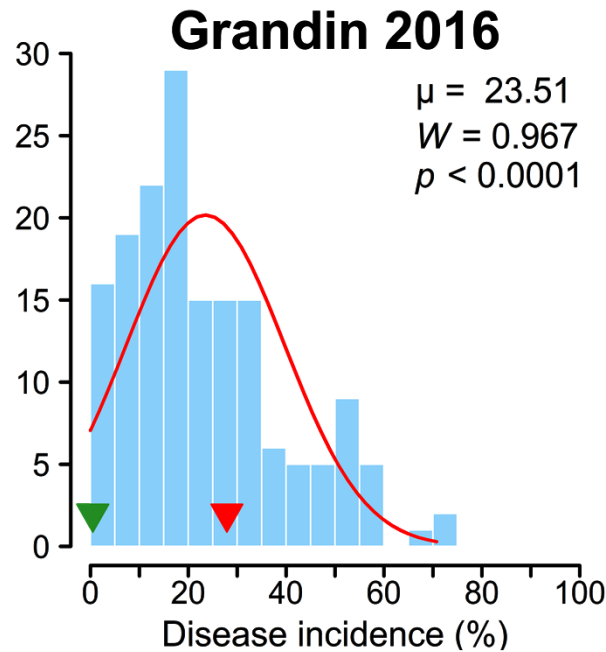
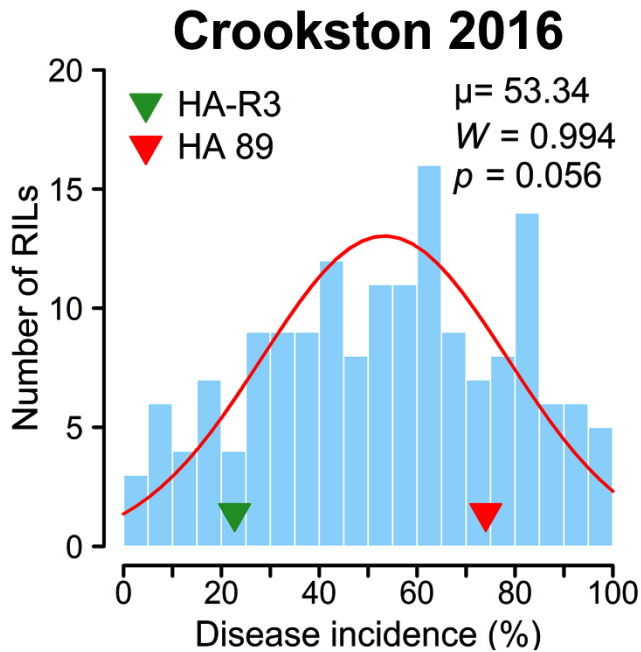
Results

Table 1. Analysis of variance of PSC disease incidence (DI) for HA-R3/HA 89 RIL population evaluated in eight environments

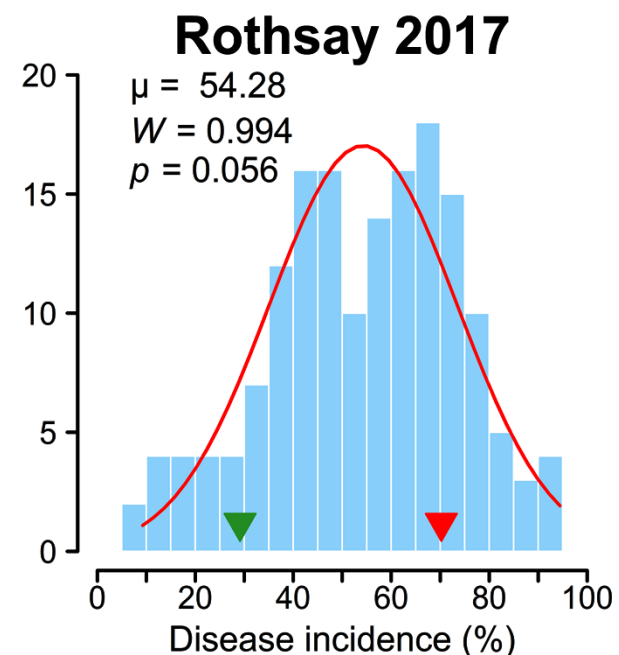
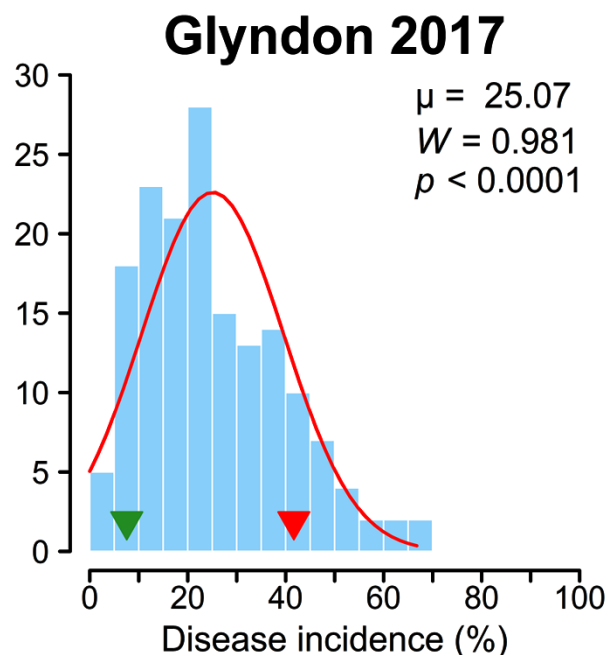
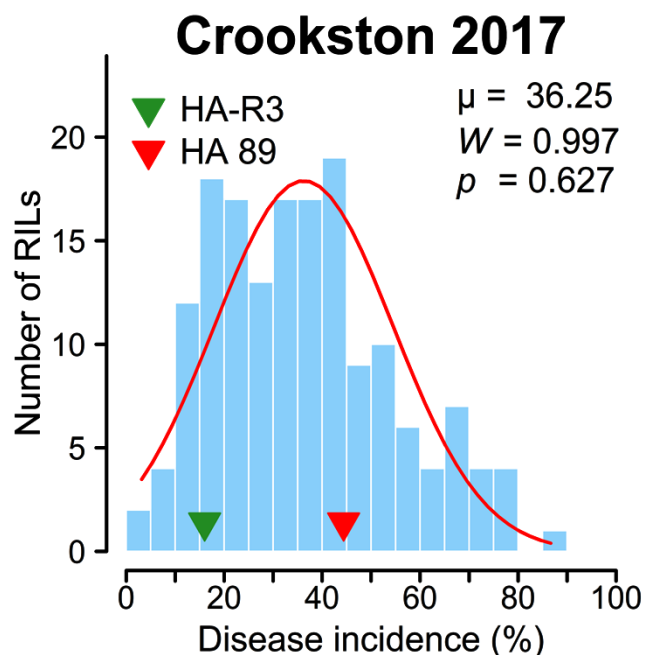
Component	df	Variance estimate	Confidence limit (0.05)		F/Z value	Pr > F/Z
			lower	upper		
Env	7	-	-	-	53.77	<.0001
Rep (Env)	23	$\sigma^2_r = 10.52$	5.45	28.16	2.49	0.0065
Genotype	163	$\sigma^2_g = 89.38$	68.74	121.00	6.79	<.0001
Genotype x Env	1137	$\sigma^2_{ge} = 126.25$	110.47	145.69	14.18	<.0001
Error	2599	$\sigma^2_e = 238.05$	225.62	251.54		

Analysis was performed using PROC MIXED of SAS version 9.4. All factors were treated as random effects except environment

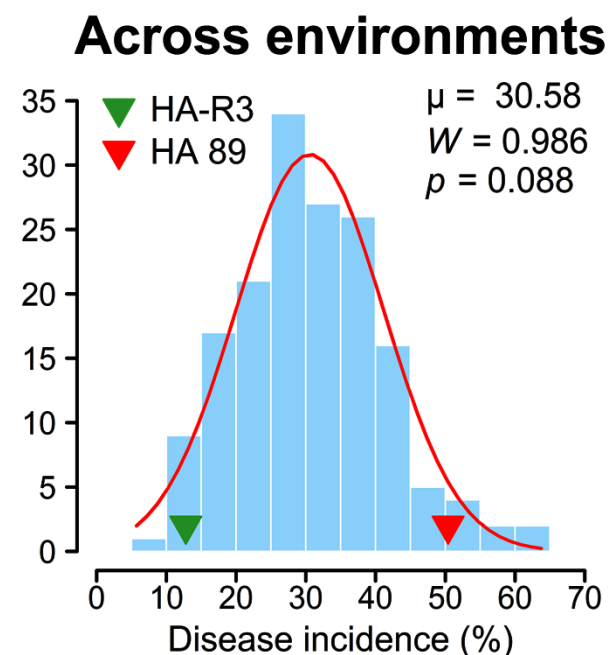
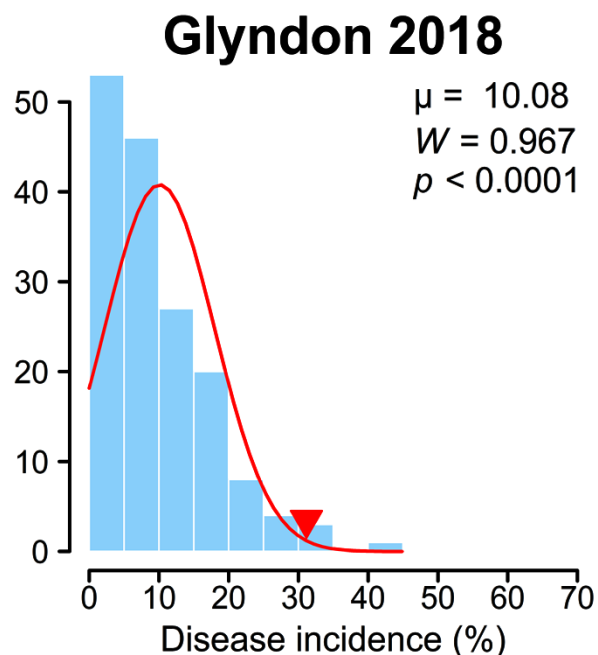
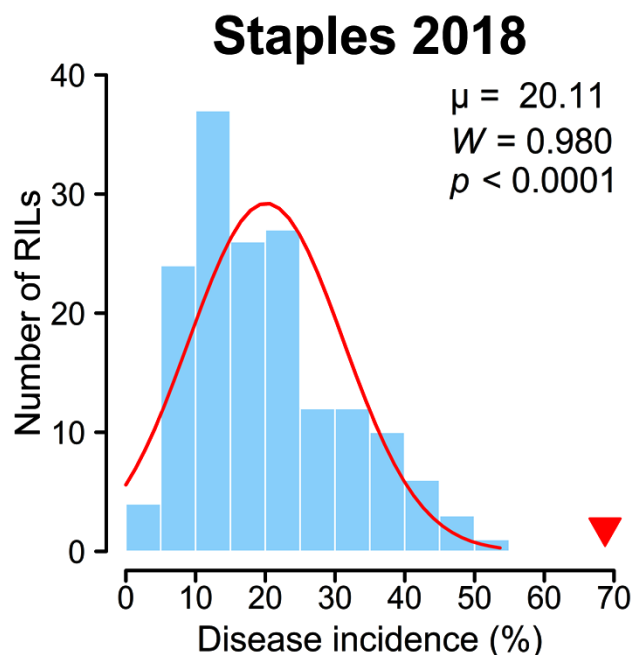
Results



Results



Results

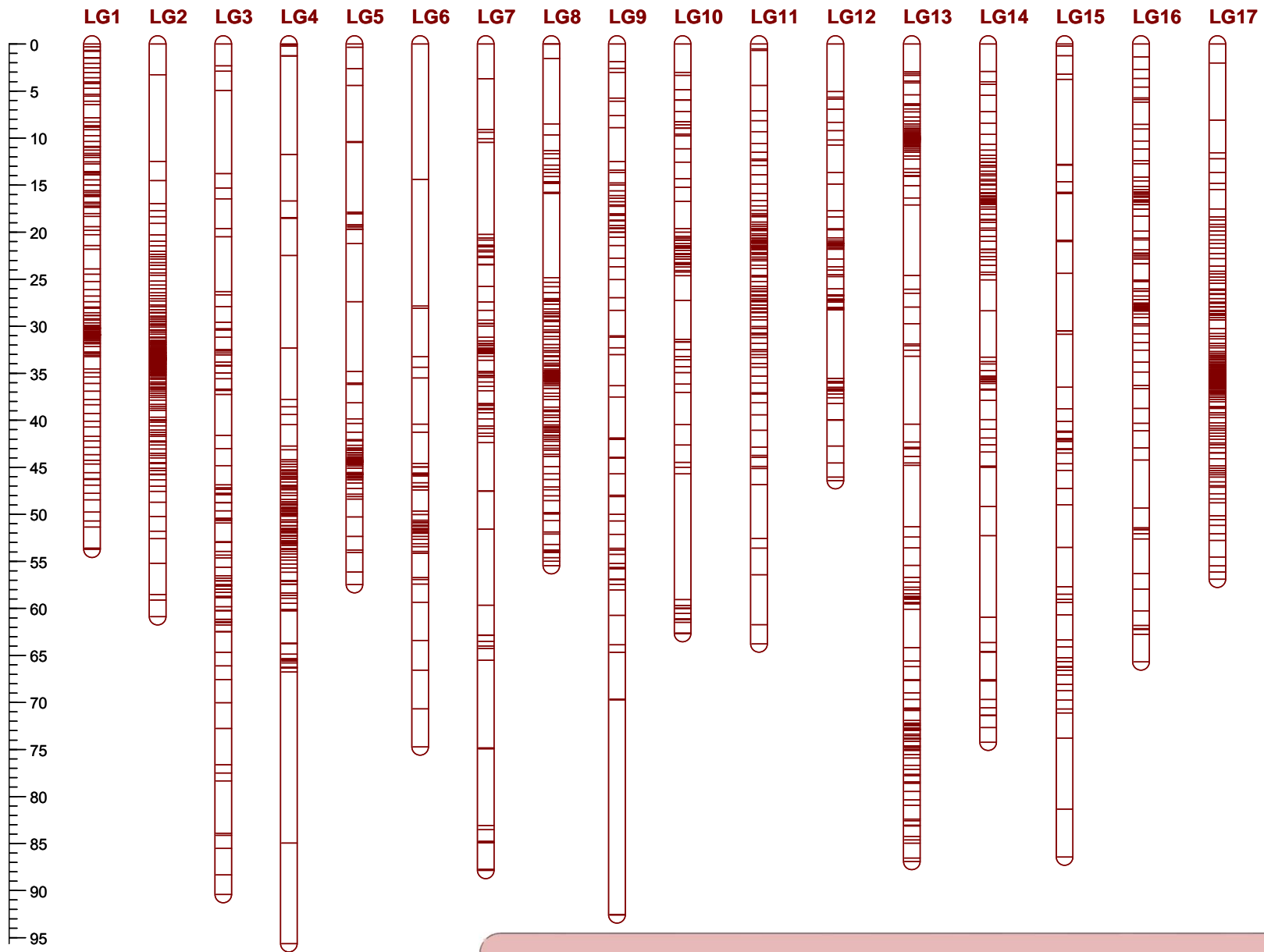


Correlations of PSC DI scores among different environments

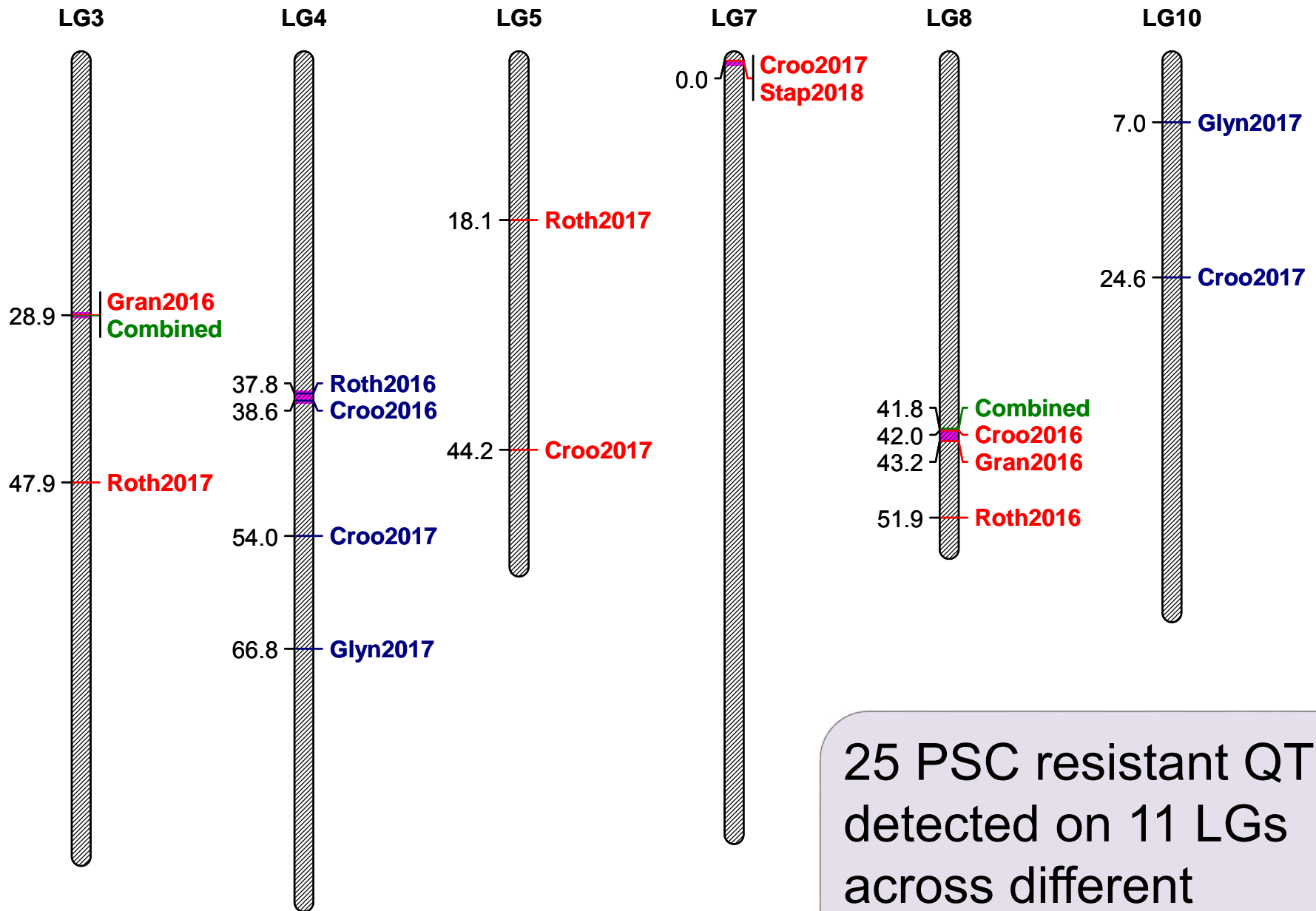
Crookston $\mu = 53.3$	2016	
$r = 0.43^{***}$	Rothsay $\mu = 22.0$	
$r = 0.30^{***}$	$r = 0.53^{***}$	Grandin $\mu = 23.5$

$r = -0.066$	$r = 0.15$	$r = 0.32^{***}$	Rothsay. $\mu = 54.3$	2017	
$r = 0.22^{**}$	$r = 0.41^{***}$	$r = 0.50^{***}$	$r = 0.48^{***}$	Crookston. $\mu = 36.2$	
$r = 0.13$	$r = 0.40^{***}$	$r = 0.50^{***}$	$r = 0.41^{***}$	$r = 0.56^{***}$	Glyndon $\mu = 25.1$

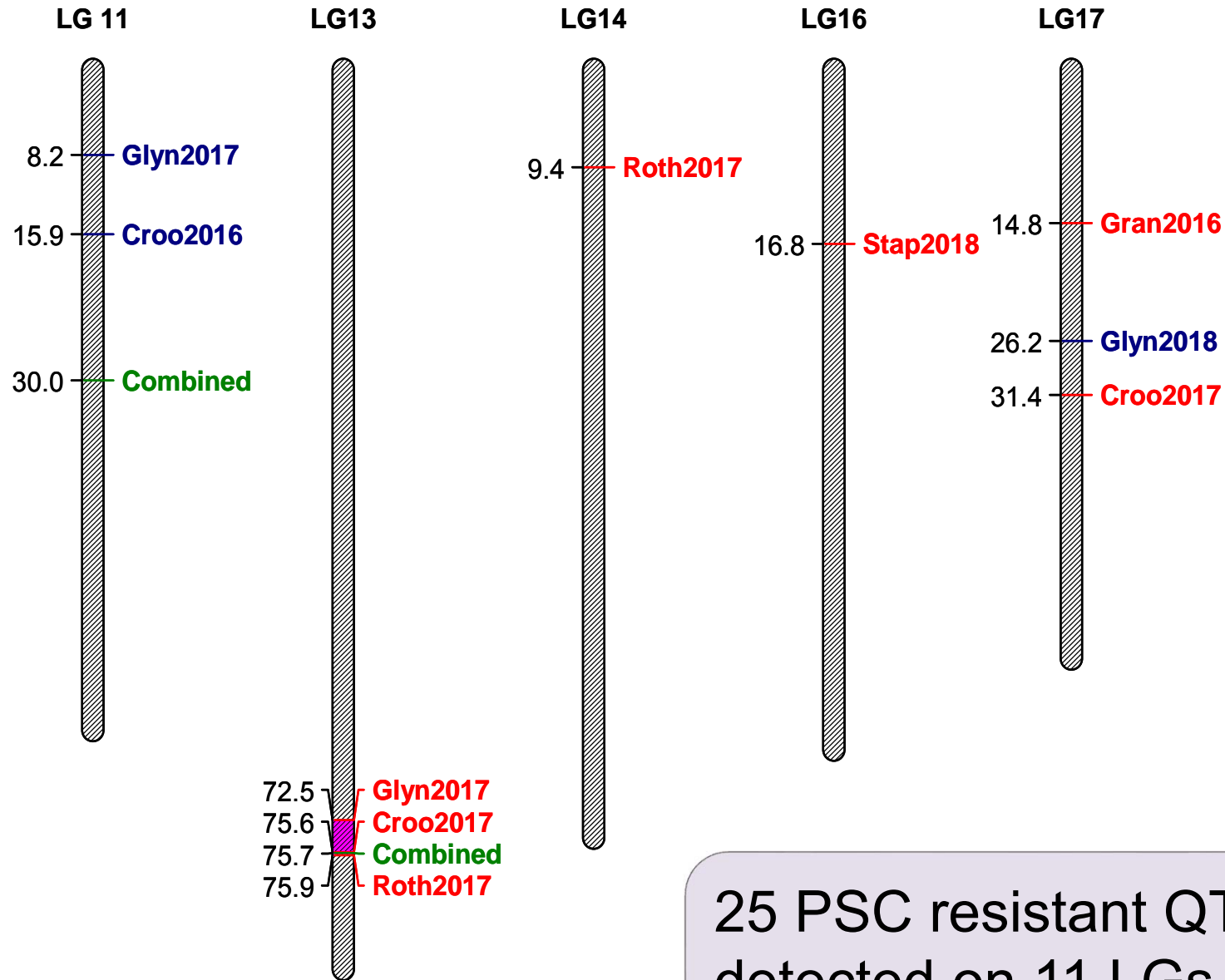
$r = 0.21^{**}$	$r = 0.40^{***}$	$r = 0.65^{***}$	$r = 0.15$	$r = 0.39^{***}$	$r = 0.45^{***}$	Staples $\mu = 20.1$	2018	
$r = 0.11$	$r = 0.29^{***}$	$r = 0.50^{***}$	$r = 0.29^{***}$	$r = 0.34^{***}$	$r = 0.48^{***}$	$r = 0.34^{***}$	Glyndon. $\mu = 10.1$	



Linkage map of HA-R3 x HA 89 RIL population developed using 2,295 SNP markers



25 PSC resistant QTL detected on 11 LGs across different environments



25 PSC resistant QTL detected on 11 LGs across different environments

Future Plan

Design of PCR based primers for SNPs flanking important QTL to use in marker-assisted PSC resistance sunflower breeding

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