Inheritance of Phomopsis Stem Canker Resistance in Sunflower

Zahirul Talukder[1], William Underwood[2], Gerald Seiler[2], Guojia Ma[3], Lili Qi[2]

[1]Department of Plant Sciences, NDSU, Fargo, ND

[2]USDA-ARS Northern Crop Science Laboratory, Fargo, ND

[3]Department of Plant Pathology, NDSU, Fargo, ND

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INTRODUCTION

Phomopsis stem canker (PSC) caused by *Phomopsis helianthi* Munt.-Cvet. (telemorph *Diporthe helianthi*)

- First observed in former Yugoslavia in late 1970's
- Yield loss as high as 50% in Europe
- PSC is becoming wider in global distribution
- Increasingly become damaging to the U.S. sunflower since 2010
- Resistance to PSC is polygenic with additive gene action
- PSC tolerance have been reported in USDA sunflower germplasm collection

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GOAL OF THE PROJECT

Overall objective

- To improve Phomopsis resistance in cultivated sunflower

Specific objectives

- Investigate the inheritance of PSC resistance in sunflower
- Identify genes/QTL associated with PSC resistance
- Identify molecular markers associated with PSC resistance genes/QTL
- Design PCR based primers for use in marker-assisted PSC resistance breeding

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MATERIALS & METHODS

Plant Materials

- Parents

  HA-R3 is highly tolerant to PSC

  HA 89 is susceptible to PSC

Mapping population

- 164 F_6-derived RILs developed through Single Seed Descent method from the cross of HA 89/HA-R3

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MATERIALS & METHODS

PSC evaluation

- Environments
  - 2016: Grandin, ND; Rothsay and Crookston, MN
  - 2017: Glyndon, Rothsay and Crookston, MN
- Field design
  - Randomized complete block with 3 replications
- Field inoculation
  - No artificial inoculum applied
- Disease incidence (DI) scoring
  - Percent of plants showing phomopsis symptom

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RESULTS

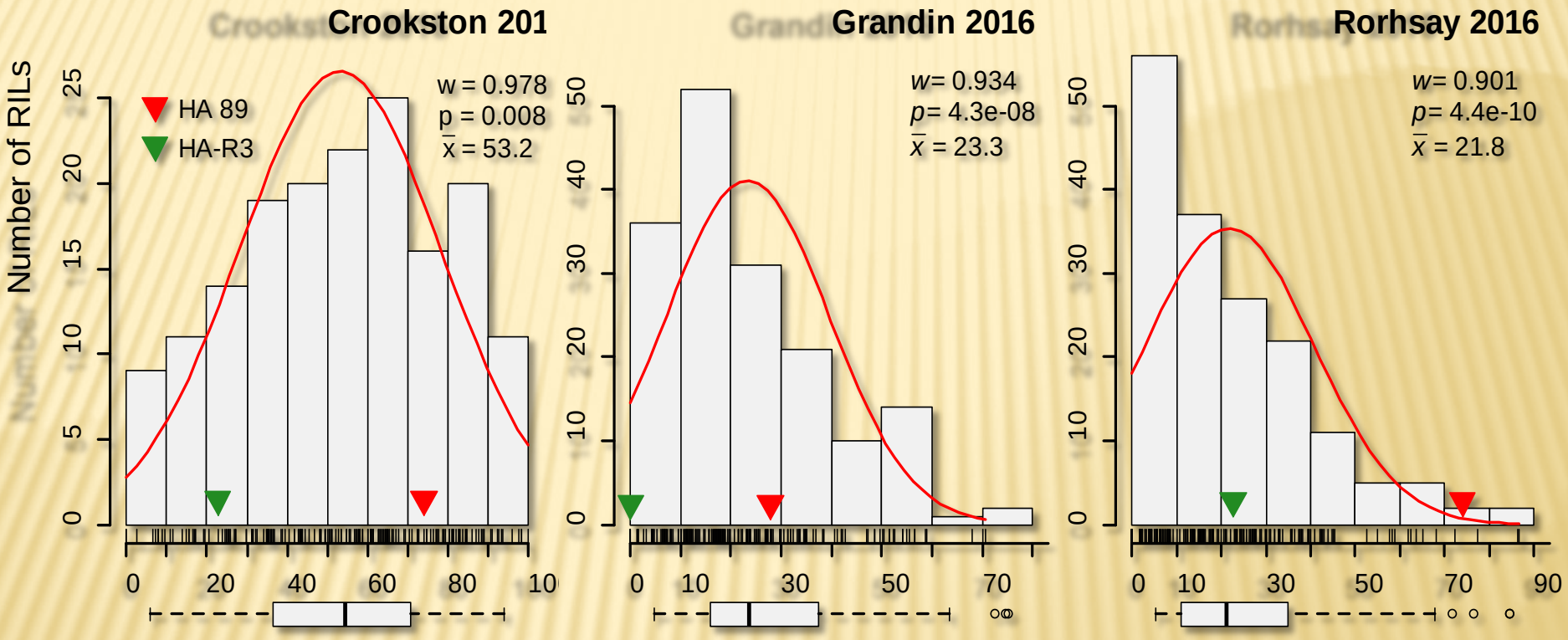

Fig 1. Phenotypic frequency distributions of PSC disease incidence (DI) for HA 89/HA-R3 RIL population evaluated in 2016

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RESULTS

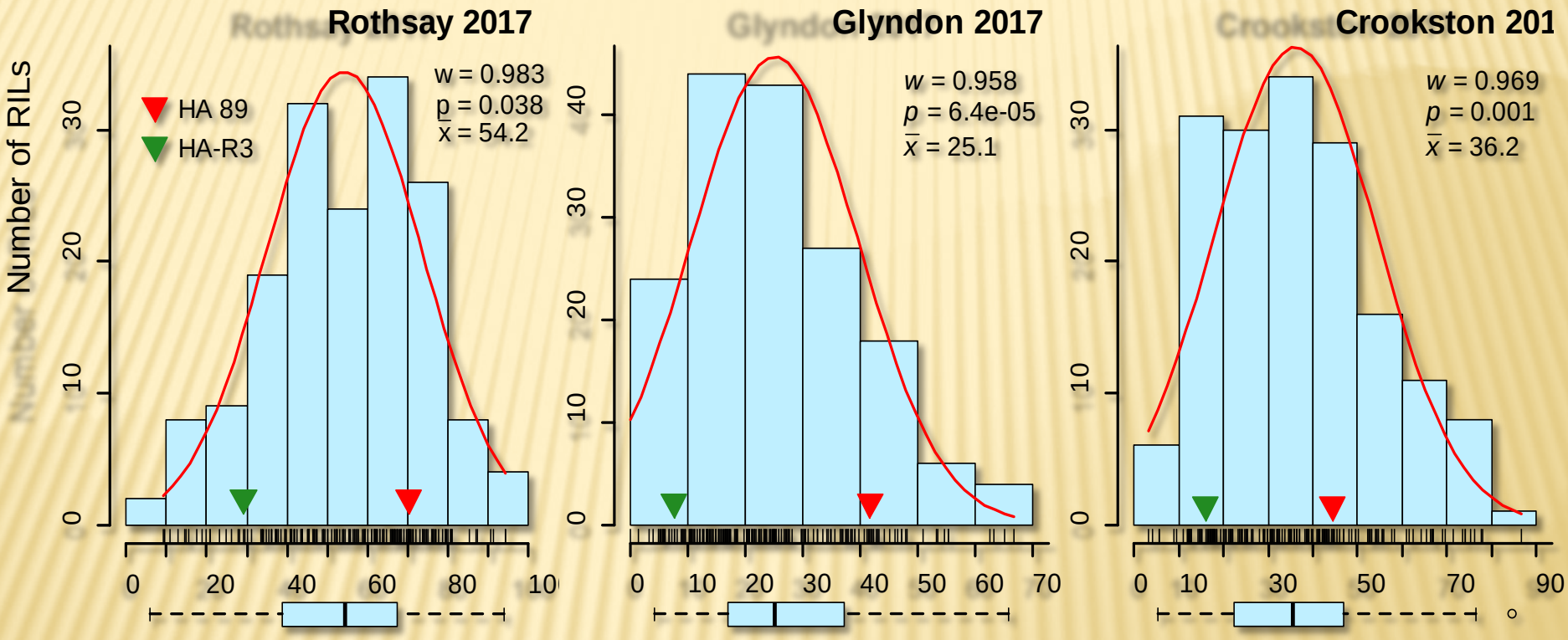

Fig 2. Phenotypic frequency distributions of PSC disease incidence (DI) for HA 89/HA-R3 RIL population evaluated in 2017

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Fig 3. Mean phenotypic frequency distributions of PSC DI for the RIL population across six environments

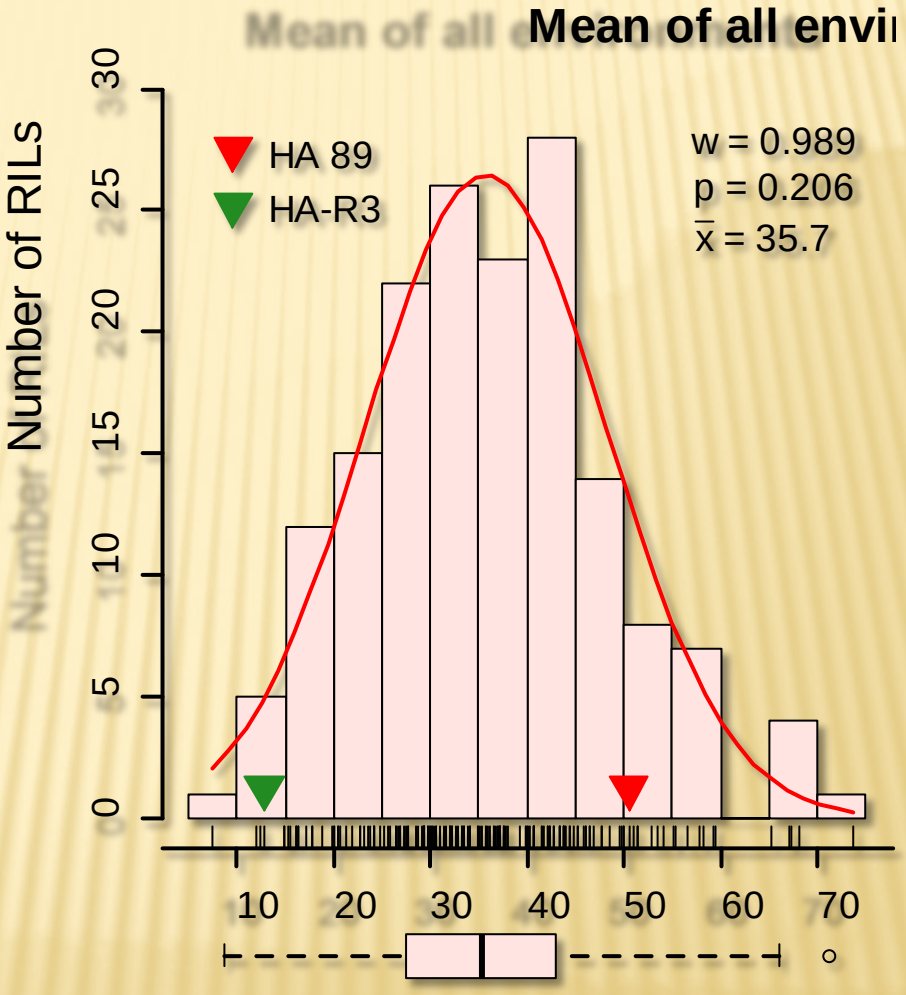

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Table 1. Analysis of variance (ANOVA) of PSC disease incidence (DI) for HA 89/HA-R3 RIL population evaluated in six environments

Component	df	Variance estimate	Confidence limit (0.05)		F/Z value	Pr > F/Z
			lower	upper		
Env	5	-	-	-	39.19	<.0001
Rep (Env)	12	σ^2_r = 12.66	6.08	40.63	2.17	0.0148
Genotype	165	σ^2_g = 116.41	88.66	159.65	6.70	<.0001
Genotype x Env	825	σ^2_{ge} = 152.94	131.49	180.13	12.47	<.0001
Error	1979	σ^2_e = 264.41	248.63	281.76		

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

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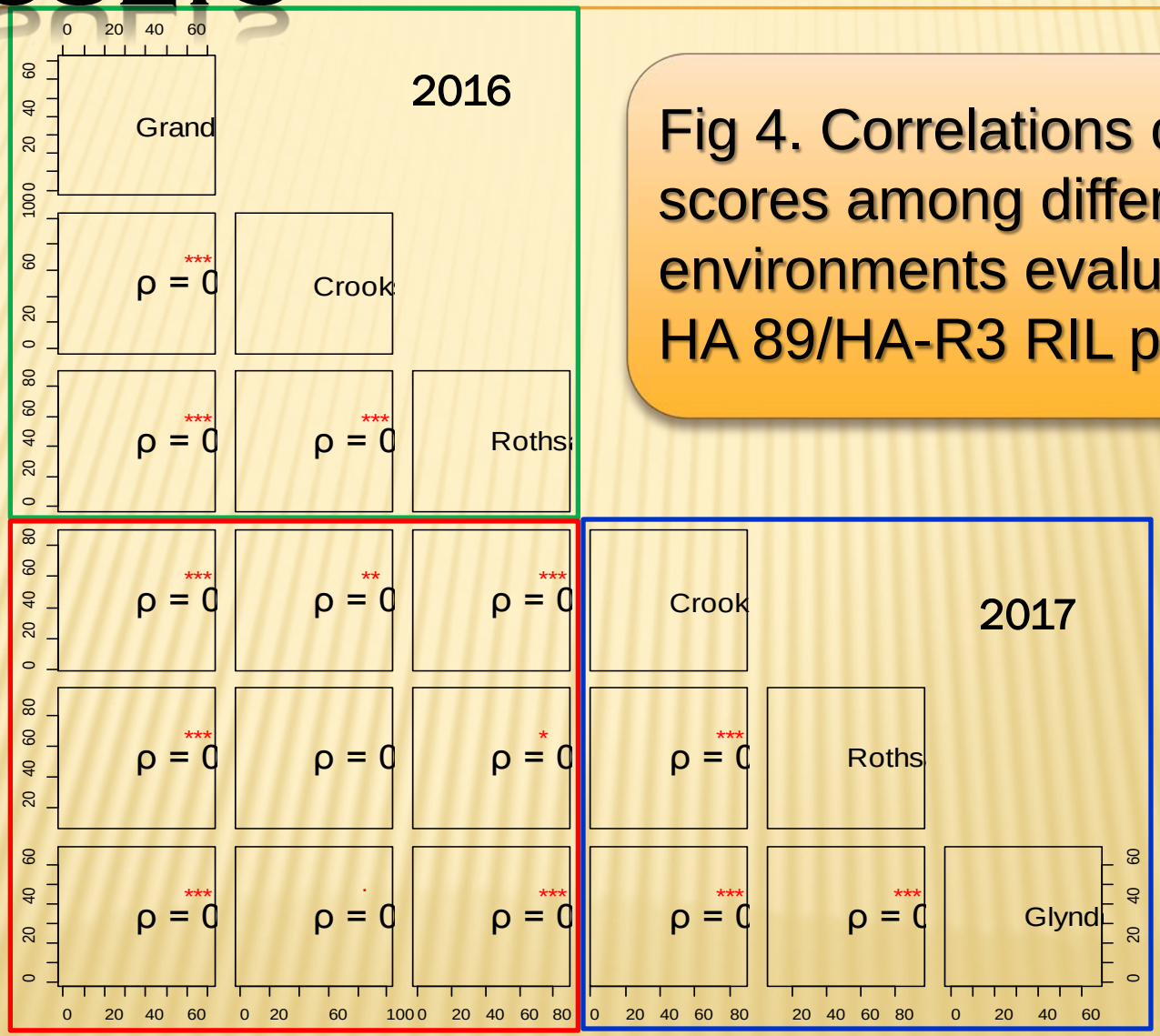

Fig 4. Correlations of PSC DI scores among different environments evaluated for HA 89/HA-R3 RIL population

FUTURE PLAN

Genotype-by-sequencing (GBS) technology will be used for genotyping of HA 89/HA-R3 RIL population with large numbers of SNP markers

Complete linkage map construction and QTL mapping in the HA 89/HA-R3 RIL population

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

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