

Deciphering the genetics of Hessian fly resistance in soft red winter wheat in the US southeast

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Introduction

- Wheat, *Triticum aestivum* L., is an important worldwide commodity grown on over 221 million hectares¹⁻³.
- Hessian fly (HF) has caused millions of dollars in damage to wheat in the US and can cause 10% losses in fields yearly^{4,5}.
- Chemical⁶, cultural⁴, and genetic control methods are used to control HF⁷.
- Resistance breeding is the most cost-effective option⁷. Few HF resistance (R) genes, like *H13*, work well in the southeast (SE)⁸.
- More sources of resistant germplasm are needed to control HF and prevent them from overcoming the few effective R genes in the US SE (Figure 1).

Objective

Identify QTL for resistance to HF a bi-parental RIL population between UGA 111729 (HF resistant) and AGS 2038 (HF susceptible) soft red winter wheat (SRWW).

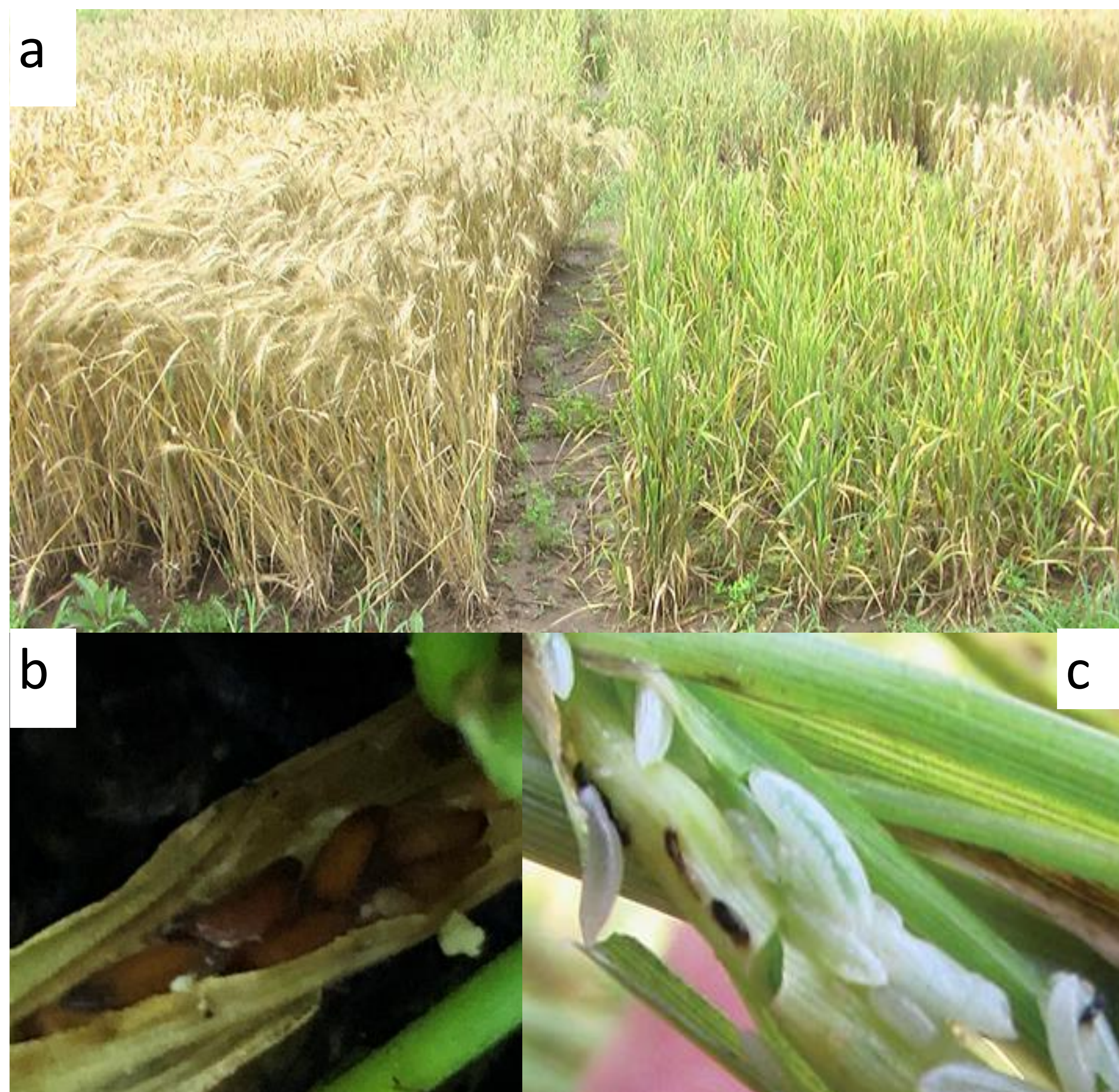


Figure 1. Symptoms and identification of Hessian fly. (a) Resistant wheat (left) vs. susceptible wheat (right)⁹, (b) Hessian fly pupae, (c) Hessian fly larvae⁹.

Materials and methods

Plant material:

- 237 lines (F_6) generated from a cross between UGA 111729 (HF resistant) and AGS 2038 (HF susceptible)
- Checks: AGS 3030 (HF resistant), USG 3555 (HF susceptible)

Field 2021:

- Field locations: Williamson, GA and Plains, GA
- Randomized complete block design (RCBD)
- HF trap crops planted: late August 2020; RIL population planted: November 2020
- Data collection conducted at Feekes stage 10.5¹⁰
- 20 plants per entry and replicate; 2 replicates in each location.
- Number of larvae/pupae (NOP): average HF count over several plants in a sample¹¹
- Percent infested tillers (PIT): number of infested stems over total stems in the sample¹¹

Growth chamber 2021:

- RCBD; 3 replicates; University of Georgia (UGA), Griffin Campus
- Growth chamber parameters: 14 h, 20°C, 500 μ Mol fluorescent light/10 h, 15°C, no light
- Placed in growth chamber with HF-infested wheat stubble at ~2 weeks old
- Data on NOP and PIT collected 3 weeks after start of HF infestation with the same protocol as in field trials

QTL data analysis:

- QTL IciMapping¹² parameters: 1 cM walk speed, 0.001 stepwise regression probability, 1000 permutations, 0.05 type 1 error

Results

- Field 2021:** Significant QTL for NOP and PIT identified between marker IWB65911 (132.5 cM) and marker IWB37580 (134.5 cM), spanning a region of 2 cM and explaining 11% and 14% of the trait, respectively (Figures 2a and 2b; Table 1).
- Growth chamber 2021:** Significant QTL for NOP identified between marker IWB65911 (132.5 cM) and marker IWB37580 (134.5 cM), spanning a region of 2 cM, and explaining 49% of the trait. Significant QTL for PIT identified between marker IWB26378 (130.5 cM) and marker IWB45704 (132.5 cM), spanning a region of 2 cM, and explaining 57% of the trait (Figures 2c and 2d; Table 1).

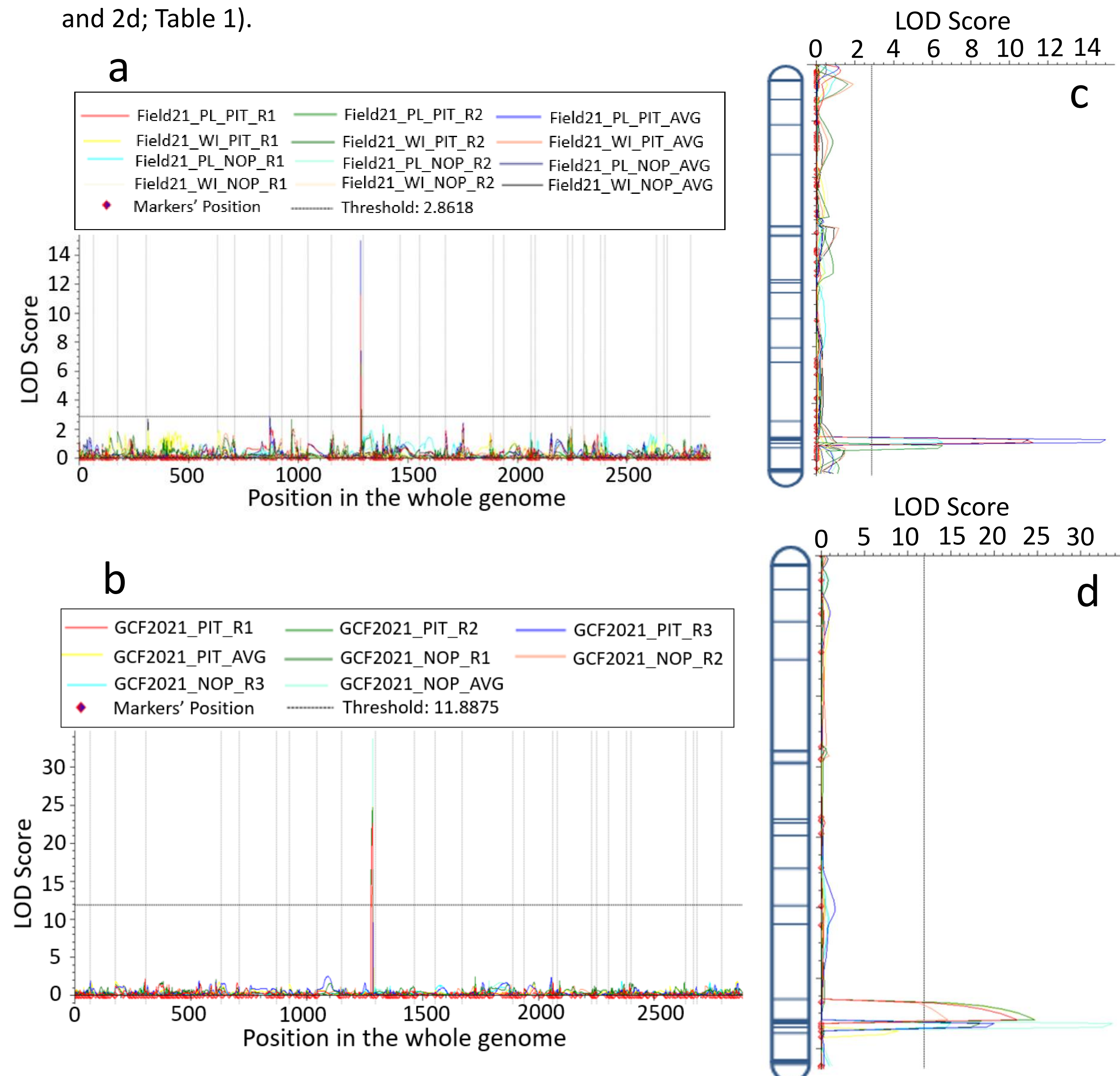


Figure 2. Results showing significant QTL for Hessian fly resistance in SRWW in 2021 trials. Manhattan plot results from field (a) and growth chamber (b) experiments; Significant QTL for Hessian fly resistance identified on the long arm of Chromosome 3D from field (c) and growth chamber (d) experiments.

Table 1. Summary of significant QTL for Hessian fly resistance in SRWW in 2021 trials.

Location	TraitName	Chromosome	Position	LeftMarker	RightMarker	LOD	PVE(%)	Add	LeftCI	RightCI
Plains	Field21_PL_PIT_R1	3D	134	IWB37580	IWB19161	11.2184	12.3632	3.9743	132.5	134.5
Plains	Field21_PL_PIT_R2	3D	135	IWB19161	IWB15577	6.5152	10.4053	3.814	134.5	136.5
Plains	Field21_PL_PIT_AVG	3D	133	IWB65911	IWB37580	14.9828	14.6071	4.1389	132.5	134.5
Plains	Field21_PL_NOP_R1	3D	134	IWB37580	IWB19161	6.5195	9.8143	0.0771	132.5	134.5
Plains	Field21_PL_NOP_R2	3D	136	IWB15577	IWB19391	5.5809	9.715	0.0908	134.5	136.5
Plains	Field21_PL_NOP_AVG	3A1	2	IWA6387	IWB52332	2.9064	2.7155	-0.041	1.5	5.5
Plains	Field21_PL_NOP_AVG	3D	133	IWB65911	IWB37580	11.0318	11.0105	0.0829	132.5	134.5
Growth Chamber	GCF2021_PIT_R1	3D	132	IWB26378	IWB45704	22.6385	37.2859	22.7968	130.5	132.5
Growth Chamber	GCF2021_PIT_R2	3D	132	IWB26378	IWB45704	24.6694	37.1388	22.8332	130.5	132.5
Growth Chamber	GCF2021_PIT_R3	3D	133	IWB65911	IWB37580	19.9688	34.4175	22.1623	132.5	134.5
Growth Chamber	GCF2021_PIT_AVG	3D	132	IWB26378	IWB45704	24.7481	57.2053	15.4746	130.5	132.5
Growth Chamber	GCF2021_NOP_R1	3D	133	IWB65911	IWB37580	18.3588	31.8961	1.3449	132.5	134.5
Growth Chamber	GCF2021_NOP_R2	3D	132	IWB26378	IWB45704	14.5777	26.4765	1.2457	130.5	132.5
Growth Chamber	GCF2021_NOP_R3	3D	133	IWB65911	IWB37580	14.8816	25.6483	2.2048	132.5	134.5
Growth Chamber	GCF2021_NOP_AVG	3D	133	IWB65911	IWB37580	33.6998	48.6416	1.609	132.5	134.5

Conclusions

- Significant QTL for HF resistance detected in SRWW, potentially co-localizing with H32¹³
- More studies will be conducted in the field using 2 other biparental populations to supplement this data and find more valuable sources of HF resistance in SRWW.

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