**Analyses of Stripe rust using Infection Type (IT)**

**Davis, CA; Mt. Vernon and Pullman, WA / 2016-2017**

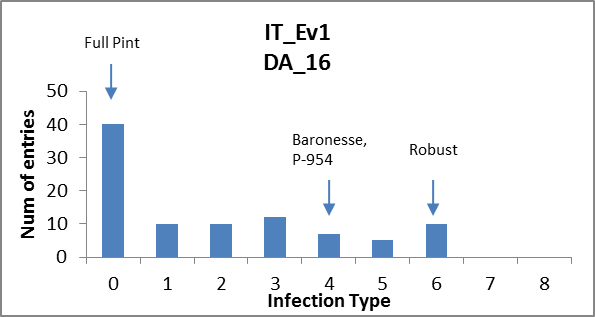
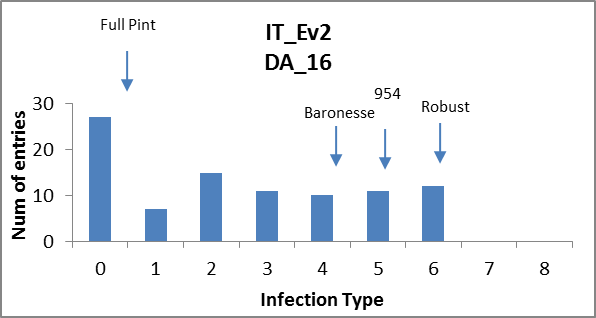
**2016**

**Stripe rust:**

**UC Davis** – Two evaluations, disease infection type at each rating

*Infection Type*

*Phenotypic frequency distributions*: Increase in infection type over time. Checks behaving as expected.

*ANOVAs*: Significant differences due to genotype. High heritabilities.

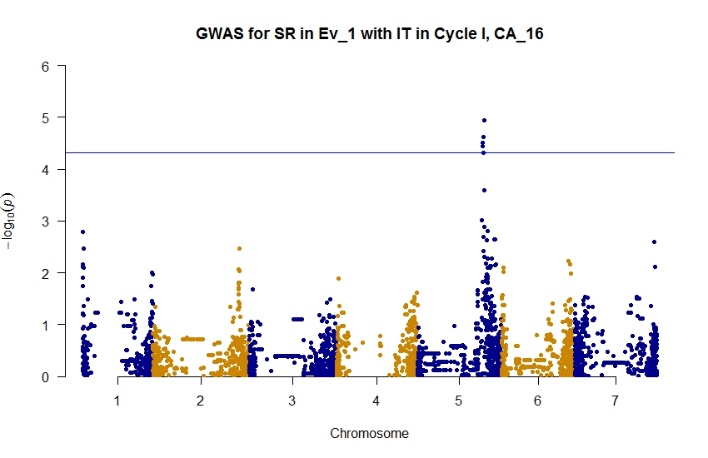
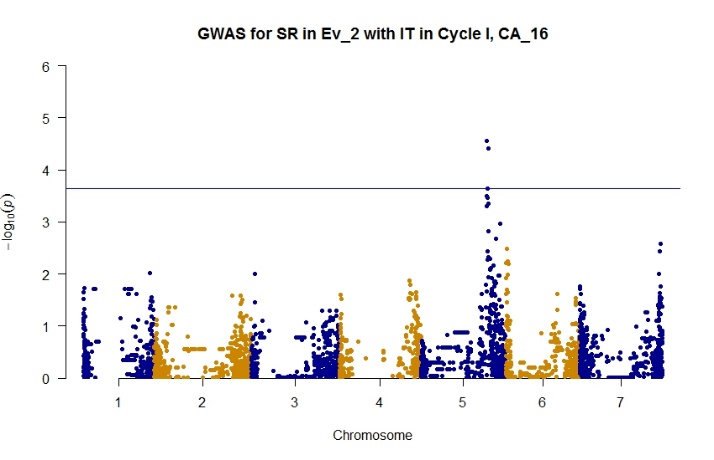
|  |  |
| --- | --- |
| **Eval\_1** |  |
| Response: Log\_IT\_E1 |  |
| Df Sum Sq Mean Sq F value Pr(>F) |  |
| Line 93 30.9210 0.33248 3.4769 3.041e-09 \*\*\* |  |
| Rep 1 1.0131 1.01308 10.5943 0.001583 \*\* |  |
| Residuals 93 8.8932 0.09563 |  |

H2 = 0.71

|  |  |
| --- | --- |
| **Eval\_2** |  |
| Response: Log\_IT\_E2 |  |
| Df Sum Sq Mean Sq F value Pr(>F) |  |
| Line 93 32.550 0.35001 3.8632 1.748e-10 \*\*\* |  |
| Rep 1 0.678 0.67786 7.4819 0.007464 \*\* |  |
| Residuals 93 8.426 0.09060 |  |

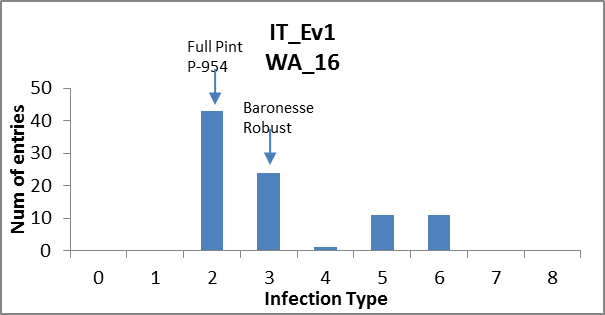
H2 = 0.74

*GWAS:* Significant associations of markers with phenotype on 5H (Eval1\_2: ~ 520992168 bp, marker: BOPA1\_9745-628)

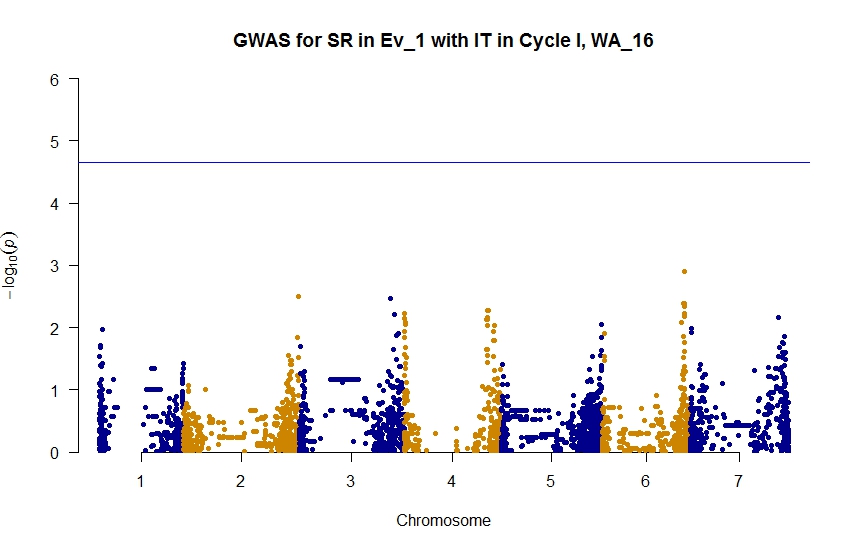
**Mt. Vernon, WA** – Spring-planted trial – One evaluation of disease severity.

*Phenotypic frequency distribution: Effective epidemic development in first evaluation of spring trial, with checks behaving as expected.*



*ANOVAs*: Not possible due to un-replicated assessment.

*GWAS:* No significant association between markers and phenotype.

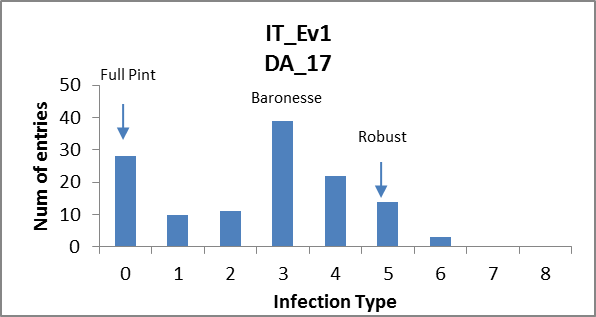
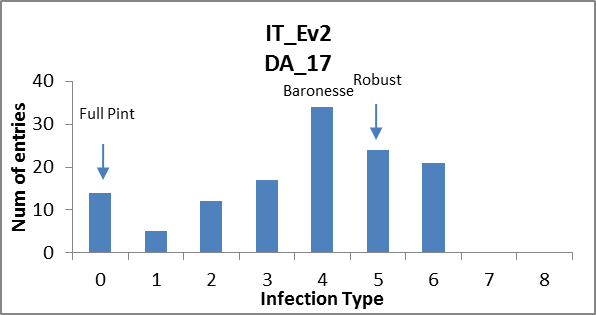


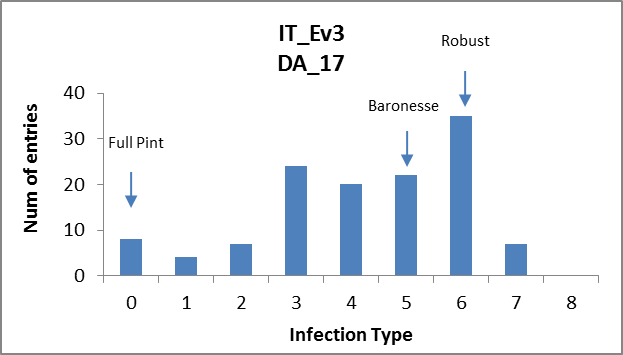
**2017**

**Stripe rust:**

**UC Davis** – Three evaluations –Infection type at each rating. Checks behaving as expected

California 2017



*ANOVAs*: Significant differences due to genotype. High heritabilities.

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| --- |
| **Eval\_1** |
| Response: Log\_IT\_E1 |
| Df Sum Sq Mean Sq F value Pr(>F) |
| Line 126 37.405 0.296861 7.6693 < 2e-16 \*\*\* |
| Rep 1 0.175 0.175078 4.5231 0.03539 \* |
| Residuals 126 4.877 0.038708 |

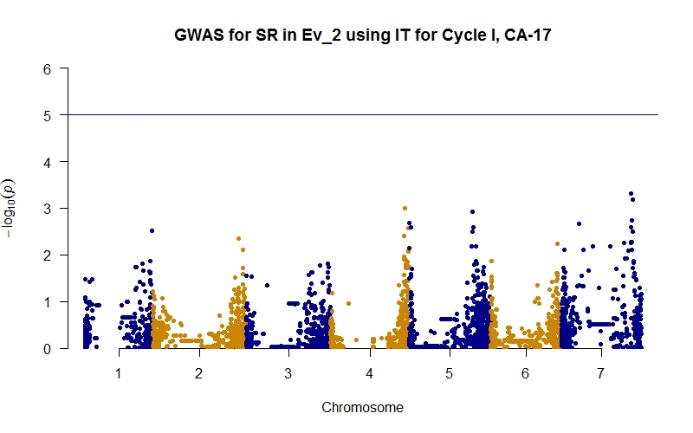
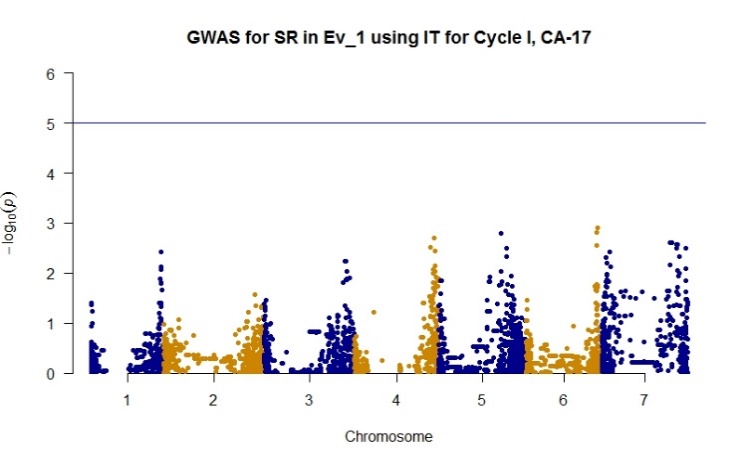
H2 = 0.86

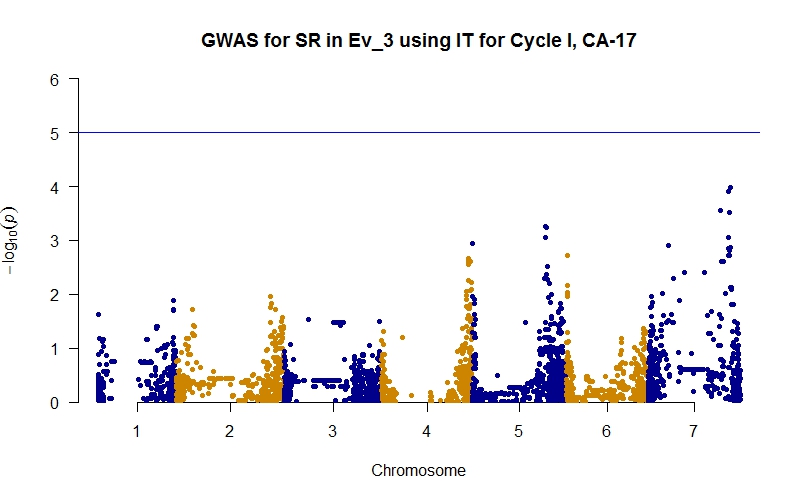
|  |
| --- |
| **Eval\_2** |
| Response: Log\_IT\_E2 |
| Df Sum Sq Mean Sq F value Pr(>F) |
| Line 126 30.4564 0.24172 8.1804 < 2.2e-16 \*\*\* |
| Rep 1 0.6197 0.61974 20.9735 1.103e-05 \*\*\* |
| Residuals 126 3.7231 0.02955 |

H2 = 0.87

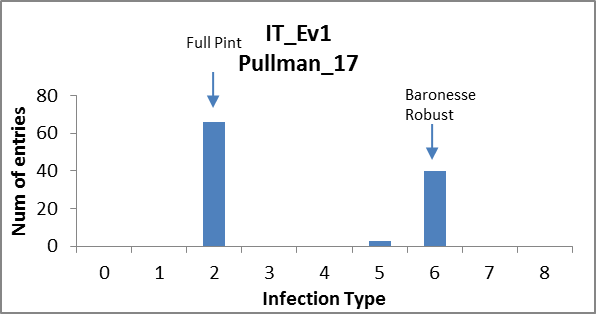
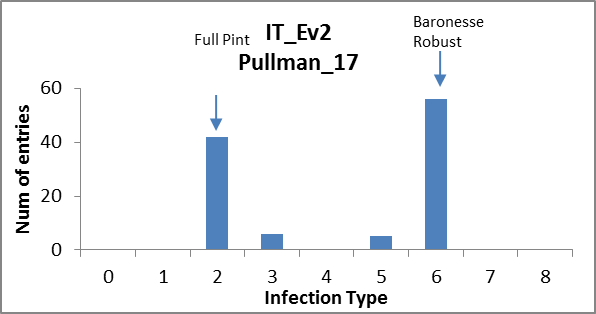
|  |
| --- |
| **Eval\_3** |
| Response: Log\_IT\_E3 |
| Df Sum Sq Mean Sq F value Pr(>F) |
| Line 126 25.3910 0.201516 7.4625 < 2e-16 \*\*\* |
| Rep 1 0.1365 0.136540 5.0564 0.02627 \* |
| Residuals 126 3.4025 0.027004 |

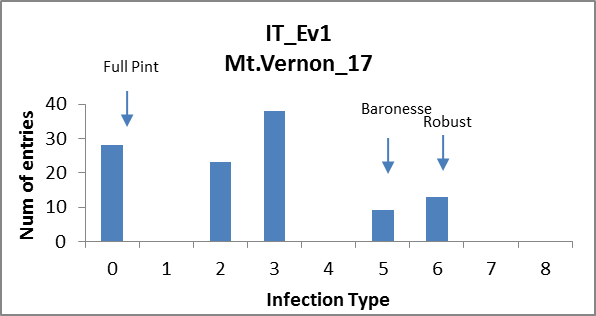
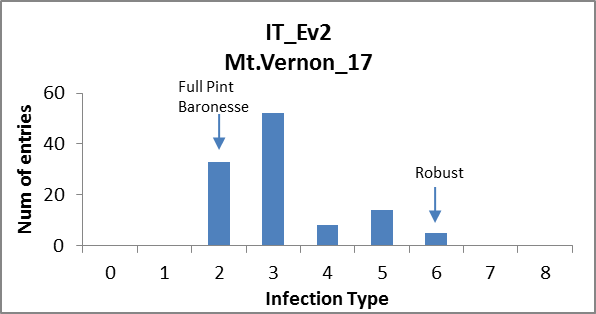
H2 = 0.86





**Mt. Vernon, WA** – Two evaluations in two locations – infection type at each rating. Checks behaving as expected. Limited epidemic development.

*ANOVA*:

Not possible – un-replicated assessment.

*GWAS:* No significant association of markers with phenotypes. Trend on 5H in Evaluation 2, Mt.Vernon

