**Analyses of Stripe rust and Leaf rust data**

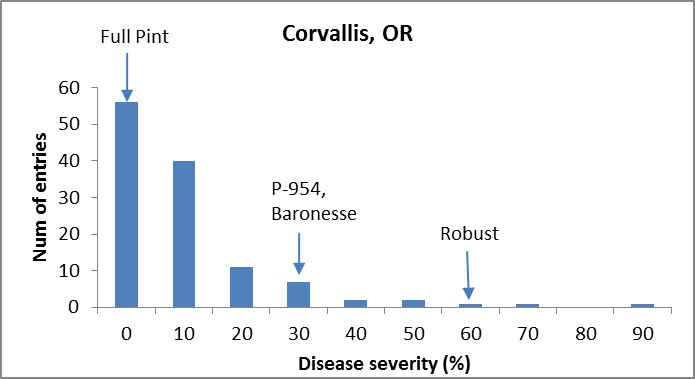
**Corvallis, OR; Davis, CA; Mt. Vernon and Pullman, WA / 2016-2017.**

**2016**

**Stripe rust:**

**Corvallis, OR** – one evaluation, disease severity.

*Phenotypic frequency distribution*: Effective epidemic development. Checks behaving as expected.

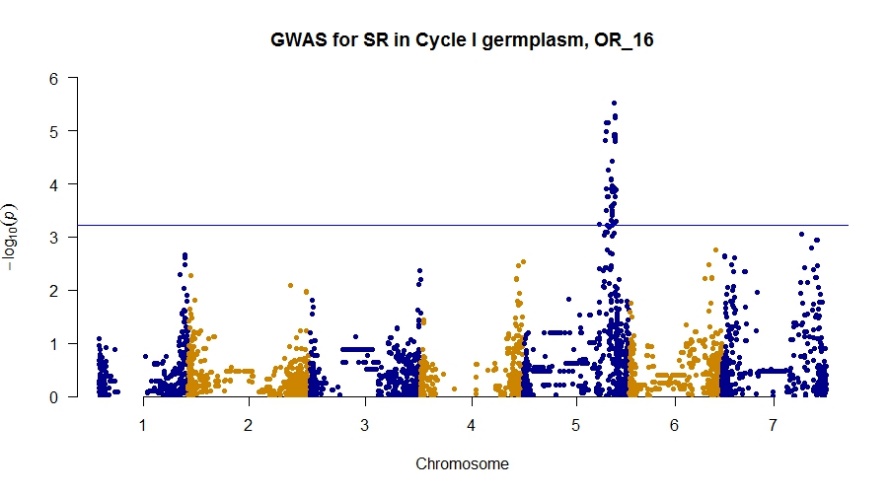


*ANOVAs*: Significant differences due to genotype. High heritability.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Response: Log(Sev) | | |  |  |  |  |
| Df Sum Sq Mean Sq F value Pr(>F) | | | | | | |
| Line 120 1.69418 0.0141182 8.2674 <2e-16 \*\*\* | | | | | | |
| Rep 1 0.00134 0.0013359 0.7823 0.3782 | | | | | | |
| Residuals 120 0.20492 0.0017077 | | | | | | |
| --- |  |  |  |  |  |  |

H2 = 0.87

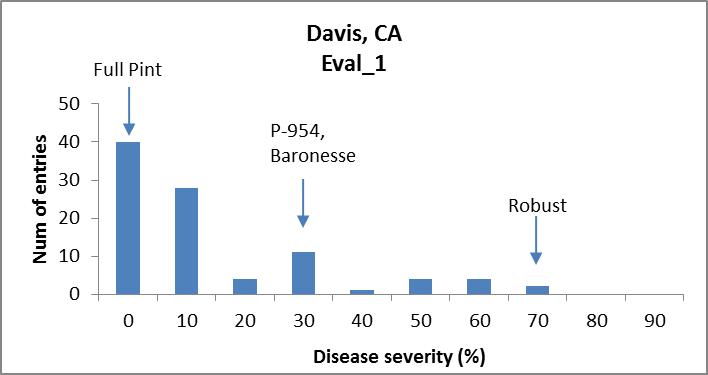
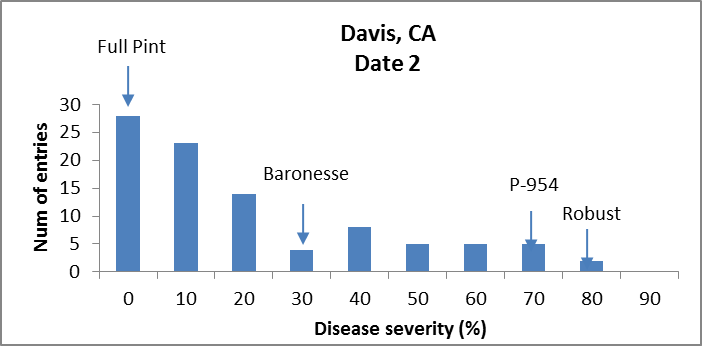
*GWAS:* Significant associations of markers with phenotype on 5H (~ 576992804 bp, marker: SCRI\_RS\_240005)



**UC Davis** – Two evaluations, disease severity at each rating

*Disease severity*

*Phenotypic frequency distributions*: Increase in disease severity over time. Checks behaving as expected.

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

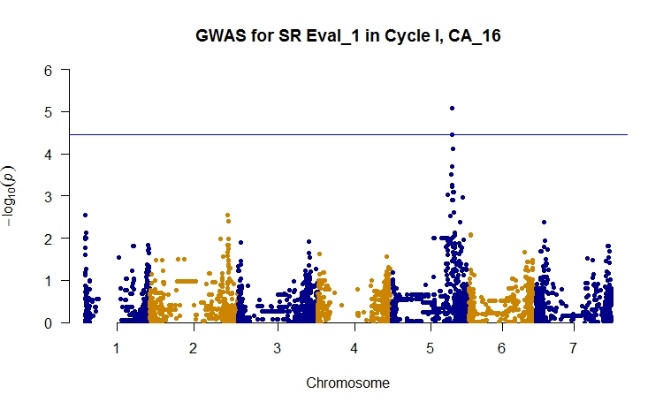
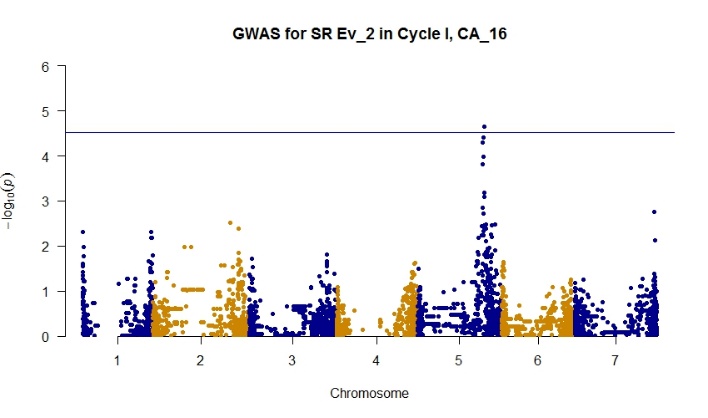
|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Eval\_1** |  |  |  |  |  |  |
| Response: Log(Sev) | | |  |  |  |  |
| Df Sum Sq Mean Sq F value Pr(>F) | | | | | | |
| Line 93 2.05362 0.022082 4.5686 1.330e-12 \*\*\* | | | | | | |
| Rep 1 0.08135 0.081348 16.8303 8.756e-05 \*\*\* | | | | | | |
| Residuals 93 0.44951 0.004833 | | | | | | |

H2 = 0.78

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Eval\_2** |  |  |  |  |  |  |
| Response: Log(Sev) | | |  |  |  |  |
| Df Sum Sq Mean Sq F value Pr(>F) | | | | | | |
| Line 93 2.81104 0.030226 4.5771 1.257e-12 \*\*\* | | | | | | |
| Rep 1 0.05730 0.057298 8.6766 0.004072 \*\* | | | | | | |
| Residuals 93 0.61415 0.006604 | | | | | | |

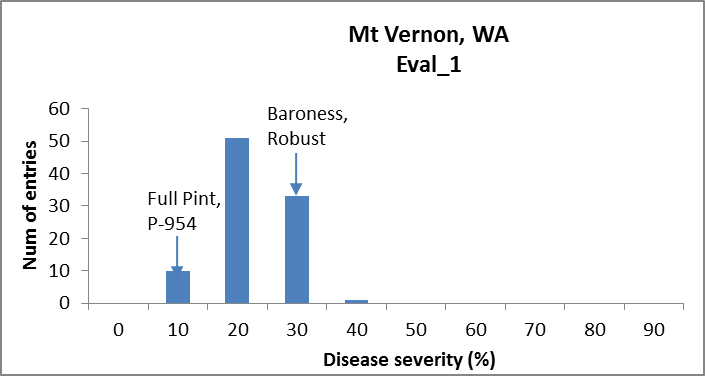
H2 = 0.78

*GWAS:* Significant associations of markers with phenotype on 5H (Eval1: ~ 521145781 bp, marker: BOPA1\_9745-628; Eval2: ~ 533551381, marker: SCRI\_RS\_233239 )

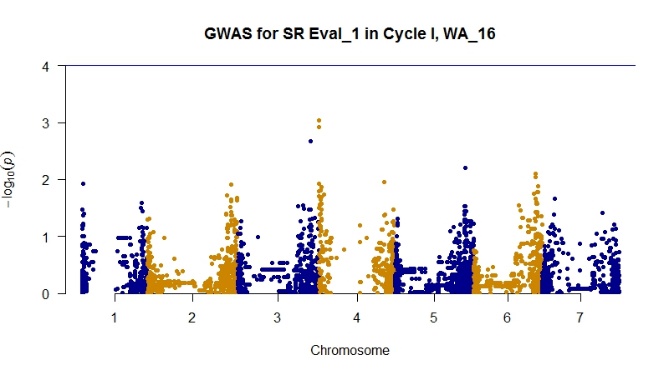
**Mt. Vernon, WA** – Spring-planted trial – One evaluation of disease severity.

*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.

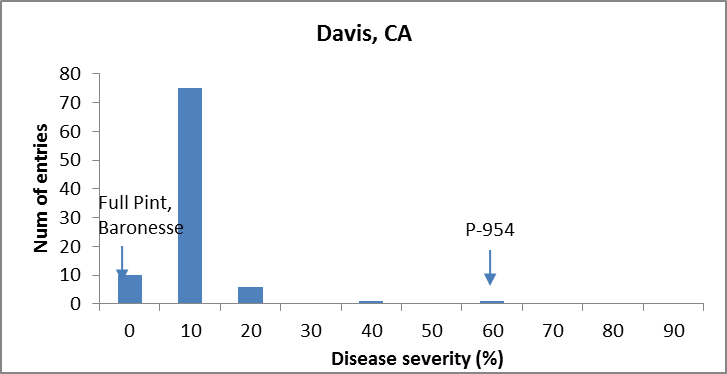
*GWAS:* No significant association between markers and phenotype.



**Leaf rust:** Effective epidemics of leaf rust observed at Davis and Mt. Vernon.

**UC Davis**

*Phenotypic frequency distributions*: Effective epidemic development, with checks behaving as expected.

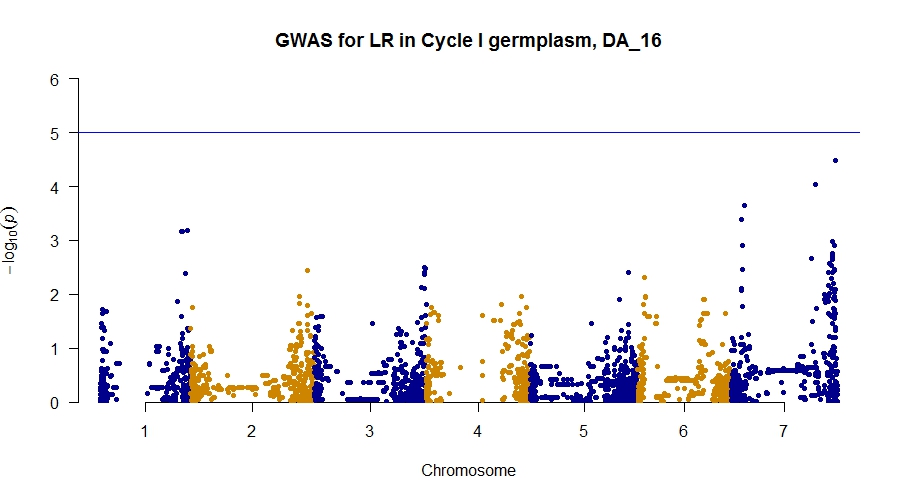


*ANOVAs*: Significant differences due to genotype. High heritability.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Response: Log(Sev) |  |  |  |  |
| Df Sum Sq Mean Sq F value Pr(>F) | | | | |
| Line 93 0.41129 0.0044225 4.3326 6.489e-12 \*\*\* | | | | |
| Rep 1 0.00240 0.0024035 2.3546 0.1283 | | | | |
| Residuals 93 0.09493 0.0010208 | | | | |

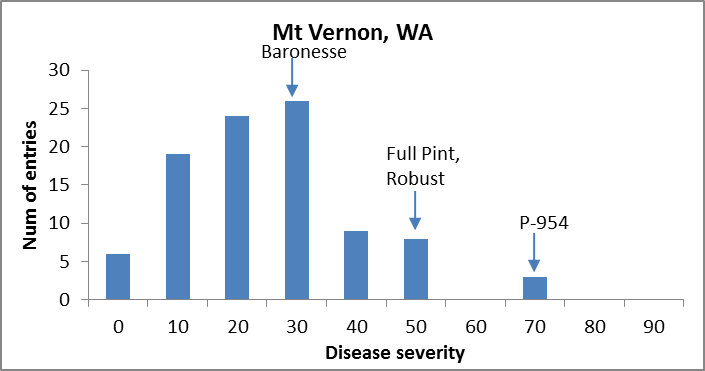
H2 = 0.76

*GWAS:* No significant association between markers and phenotype. Trend on 7H



**Mt. Vernon, WA – 1 date**

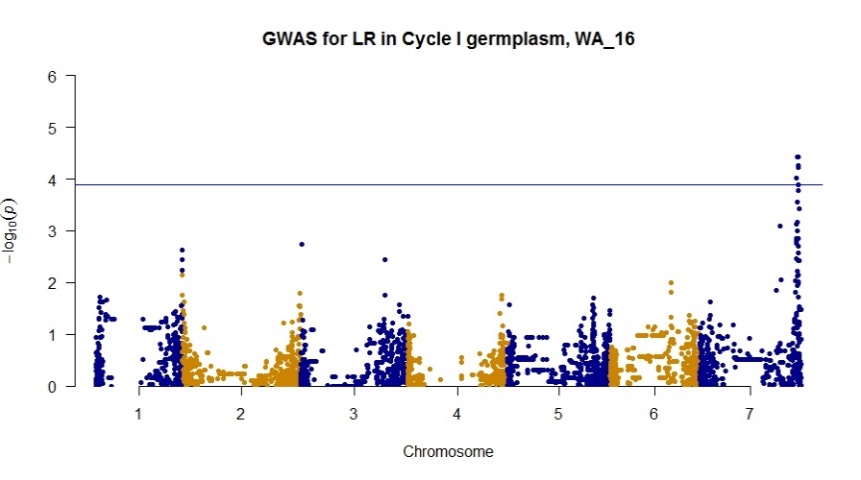
*Phenotypic frequency distributions*: Effective epidemic development. Some checks moving from tolerant to susceptible.



*ANOVAs*:

Not possible due to un-replicated assessment.

*GWAS:* Significant association of markers with phenotype on 7H (~634620797 bp, marker: BOPA1\_6868-595)



**2017**

**Stripe rust:**

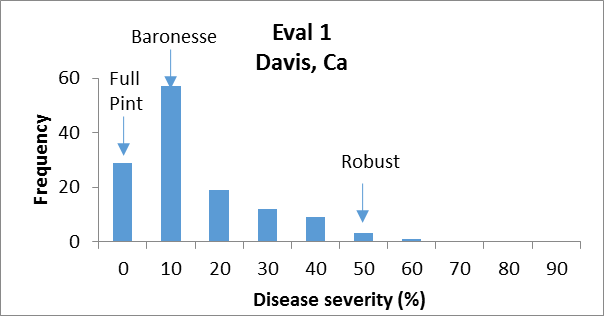
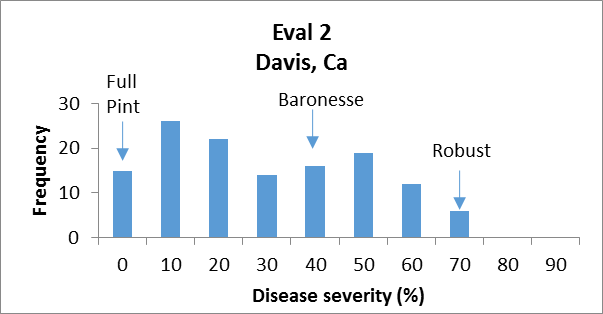
**Corvallis, OR** –

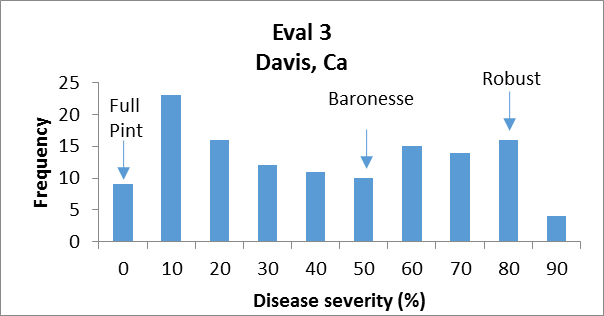
No epidemic development, no data

**UC Davis** – Three evaluations – disease severity at each rating. Checks behaving as expected

*Disease severity*

*Phenotypic frequency distributions*: Increase in disease severity over time.



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

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Eval\_1** |  |  |  |  |  |  |  |
| Response: Sev(%) | |  |  |  |  |  |  |
| Df Sum Sq Mean Sq F value Pr(>F) | | | | | | |  |
| Line 126 1.55893 0.0123725 8.2399 <2e-16 \*\*\* | | | | | | |  |
| Rep 1 0.00286 0.0028593 1.9043 0.17 | | | | | | |  |
| Residuals 128 0.19220 0.0015015 | | | | | | |  |
| Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 | | | | | | | |

H2 = 0.87

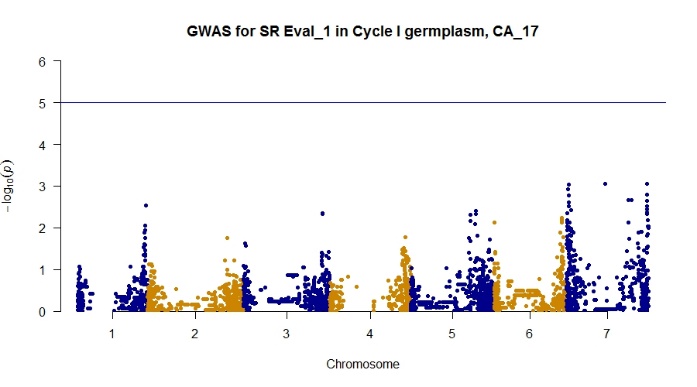
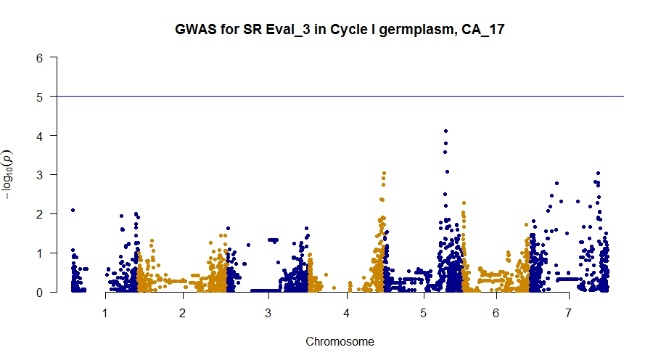
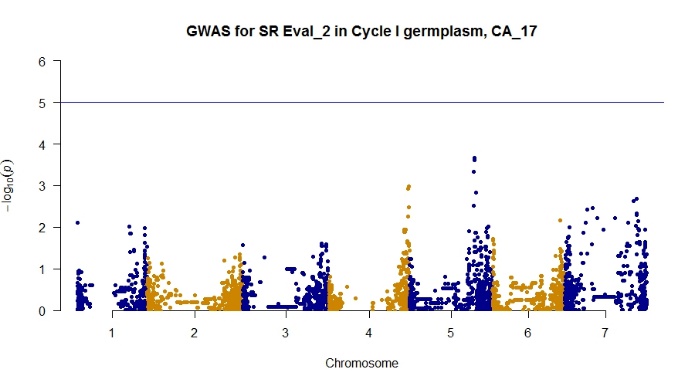
|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Eval\_2** |  |  |  |  |  |  |  |
| Response: Sev(%) | |  |  |  |  |  |  |
| Df Sum Sq Mean Sq F value Pr(>F) | | | | | | |  |
| Line 126 3.1972 0.025375 10.907 < 2.2e-16 \*\*\* | | | | | | |  |
| Rep 1 0.2980 0.297988 128.084 < 2.2e-16 \*\*\* | | | | | | |  |
| Residuals 128 0.2978 0.002327 | | | | | | |  |
| Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 | | | | | | | |

H2 = 0.90

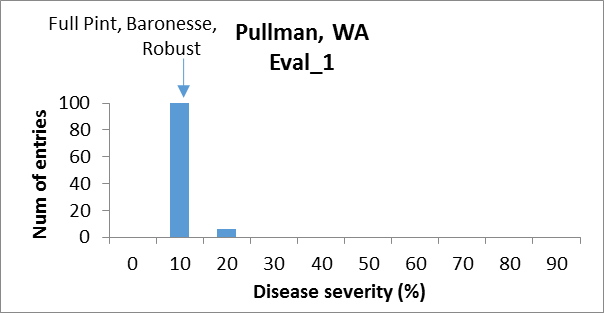
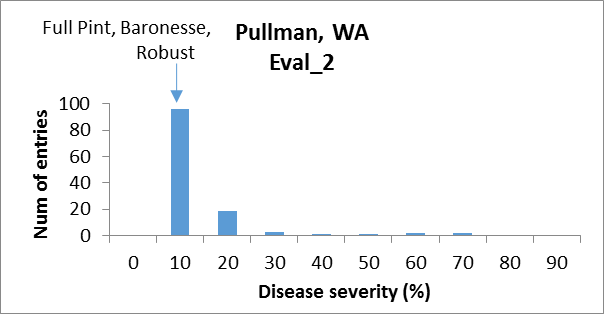
|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Eval\_3** |  |  |  |  |  |  |  |
| Response: Sev(%) | |  |  |  |  |  |  |
| Df Sum Sq Mean Sq F value Pr(>F) | | | | | | |  |
| Line 126 4.7359 0.037586 14.935 < 2.2e-16 \*\*\* | | | | | | |  |
| Rep 1 0.0733 0.073305 29.128 3.17e-07 \*\*\* | | | | | | |  |
| Residuals 128 0.3221 0.002517 | | | | | | |  |
| Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 | | | | | | | |

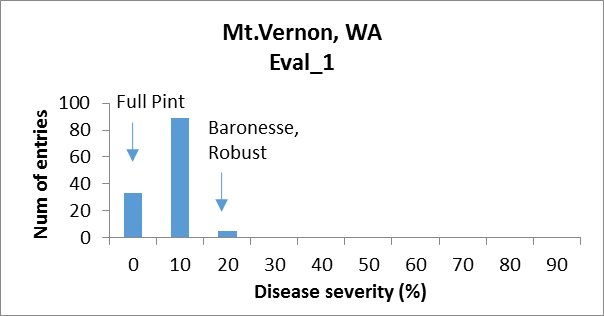
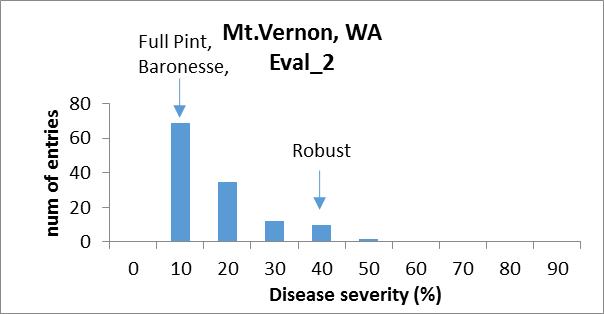
H2 = 0.93

*GWAS:* No significant associations of markers with phenotypes. Trends on 4H and 5H.

**Mt. Vernon, WA** – Limited epidemic development. Checks behaving as expected in most of locations and times

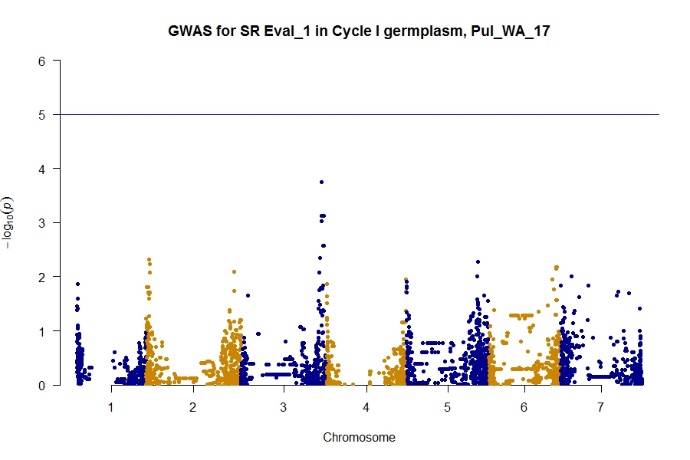
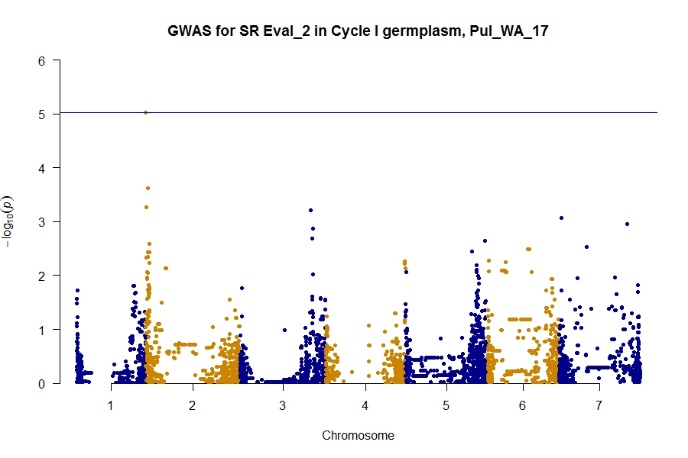
 

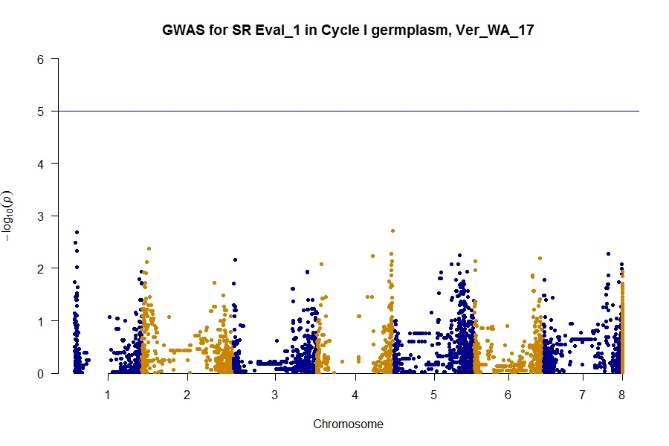
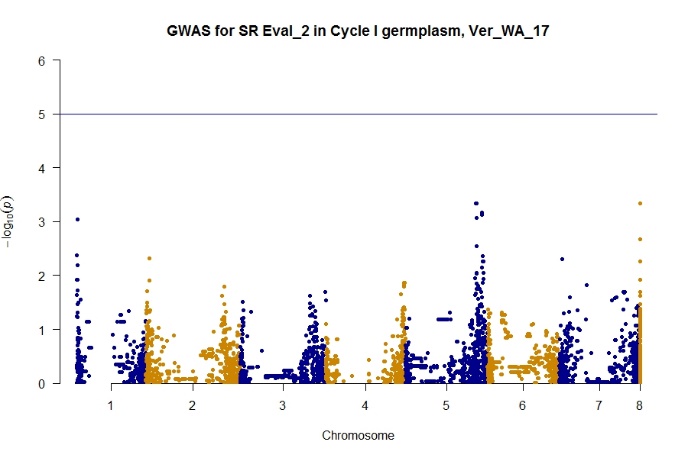
* *

*ANOVA*:

Not possible – un-replicated assessment.

*GWAS:* No significant association of markers with phenotypes.

** **

**Leaf rust:**

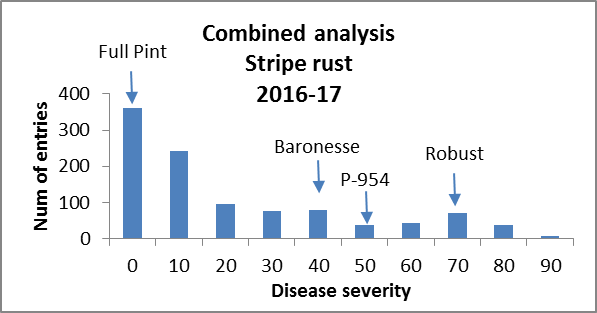
No disease reported in this year.

**Combined analysis of 2016, 2017**

**Stripe Rust data**

*Disease severity*

*Phenotypic frequency distribution*: Effective distribution of the disease. Checks behaving as expected across different environments.



*ANOVA*:

Models:

BLUP\_SR: SR ~ 1 + (1 | Lines) + (1 | Loc) + (1 | Year) + (1 | Rep) + (1 |

BLUP\_SR: Lines:Year)

BLUP\_SR\_lines: SR ~ Lines + (1 | Loc) + (1 | Year) + (1 | Rep) + (1 | Lines:Year)

Df AIC BIC logLik deviance Chisq Chi.Df Pr(>Chisq)

BLUP\_SR 7 8799.3 8834 -4392.7 8785.3

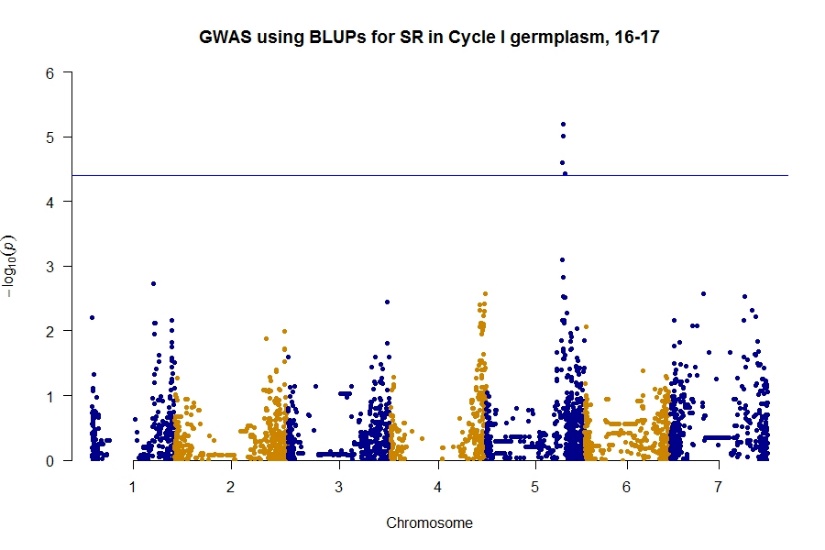
BLUP\_SR\_lines 122 8722.3 9327 -4239.2 8478.3 306.99 115 < 2.2e-16 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

H2 = 0.61

*GWAS:* Significant associations of markers with phenotype on 5H (~525964746 bp, marker: SCRI\_RS\_191145).

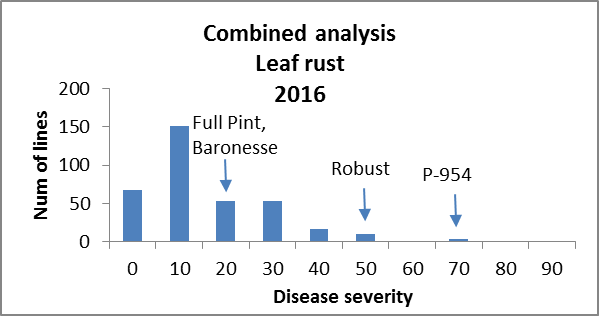


**Combined analysis of 2016**

**Leaf Rust data**

*Disease severity*

*Phenotypic frequency distribution*: Effective distribution of the disease. Checks behaving as expected across different environments. Some checks moving from tolerant to moderate susceptible



*ANOVAs*:

Models:

BLUP\_LR: LR ~ 1 + (1 | Lines) + (1 | Loc) + (1 | Rep) + (1 | Lines:Loc)

BLUP\_LR\_lines: LR ~ Lines + (1 | Loc) + (1 | Rep) + (1 | Lines:Loc)

Df AIC BIC logLik deviance Chisq Chi.Df Pr(>Chisq)

BLUP\_LR 6 1944.9 1966.4 -966.45 1932.9

BLUP\_LR\_lines 94 1958.8 2296.3 -885.38 1770.8 162.13 88 2.569e-06 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

H2 = 0.17

*GWAS:* Significant associations of markers with phenotype on 7H in two sites (~ 625633406 bp, marker: BOPA2\_12\_31374; ~522444718 bp, marker: SCRI\_RS\_122512).

