

What is the impact of Blackleg on Canola yield in Australia?

M. BABIAR, L. BARRETT, S.J SPRAGUE
www.csiro.au



What is the estimated impact of Blackleg on Canola and economy ?

A few statistics...

Blackleg worldwide:

- global loss estimated “over US\$ 900M”^[1]

Blackleg (*Leptosphaeria maculans*) in Australia:

- loss estimation from <10% to 40% ^[2]
- “up to 90% yield loss” ^[3]

What is the estimated impact of Blackleg on Canola and economy ?
A few statistics...

Specific quantitative assessments, or qualitative relationship, but no quantitative relationship :

→ Is it possible to quantify this disease-yield relationship ?

What is the estimated impact of Blackleg on the Canola plant ?

A bit of biology...

According to previous studies:

- strong link between stem canker symptom and yield loss
- extreme cases : lodging causing complete yield loss
- disease development :
disease spread ~ rainfall
canker severity ~ temperature

Assessing disease development:
percentage of stem section cankered



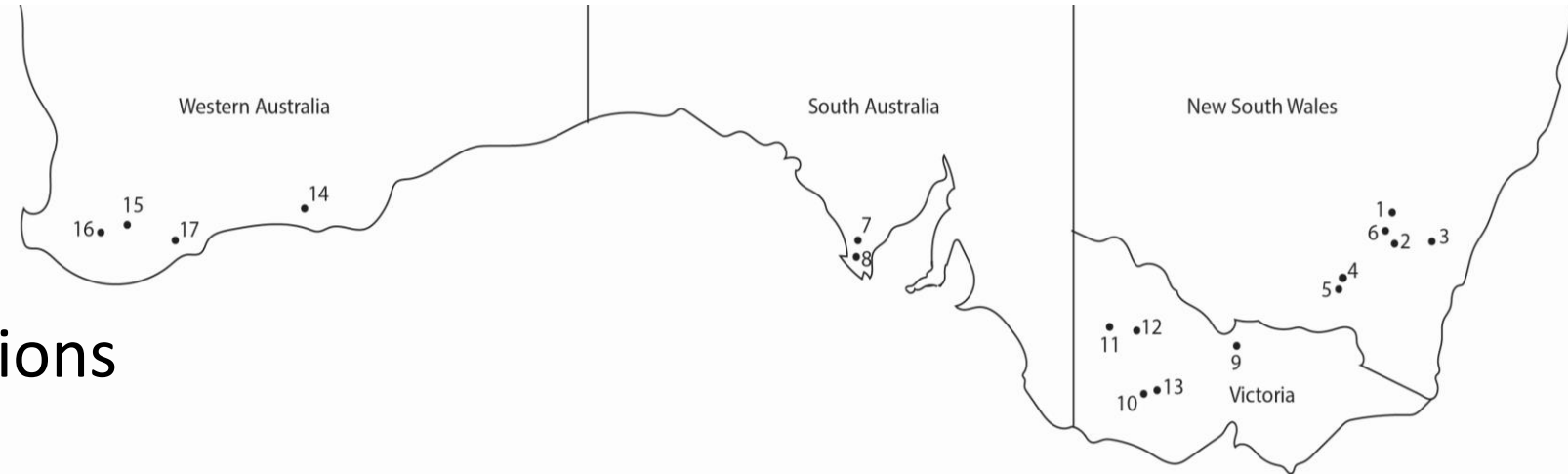
S.J Sprague

Material and methods : data collection

Yield and disease data from:

Summarizing
environmental
variables

- 16 locations
- 4 states
- 4 years (2013-2016)



Genetics & cultivation
practices variables

Parameters sampled:

- 22 varieties
- 6 genetic resistance rating levels (R ; R-MR ; MR ; MR-MS ; MS ; MS-S)
- 13 fungicide treatments (including “Nil” control treatment)

Material and methods : data collection

SARDI:
Andrew Ware
Jenny Davidson



MGP:
Steve Marcroft
Biz Sheedy
Alistair Smith
Buffy Harrison



DAFWA:
Ravjit Khangura
Andrea Hills
Ciara Beard



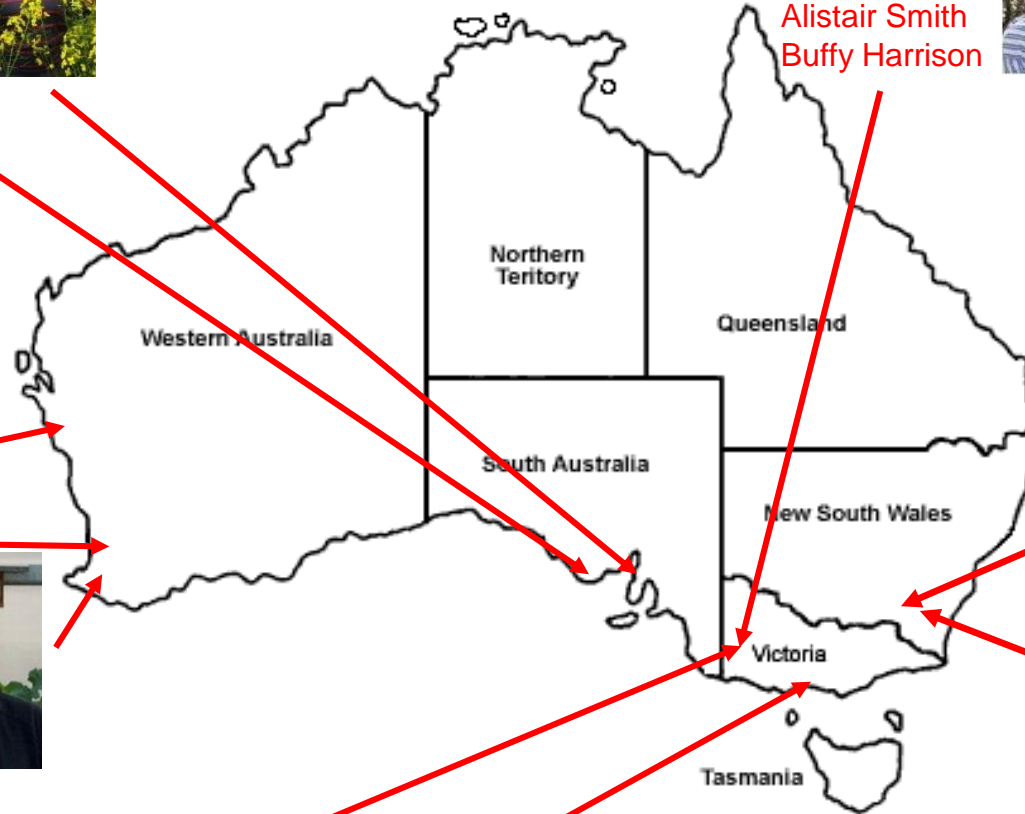
NSW DPI:
Kurt Lindbeck
Audrey Leo



CSIRO:
Susie Sprague



UM:
Alex Idnum
Barbara Howlett
Angela Van de Wouw



Material and methods : presentation of the data set

Disease data:

- Environmental variables
- Genetics & cultivation practices variables
- Disease severity (CSII)

Total : 33 356 measurements taken

Yield data:

- Environmental variables
- Genetics & cultivation practices variables
- Yield

Total : 1352 observations

Material and methods : presentation of the data set

Disease data:

- Environmental variables
- Genetics & cultivation practices variables
- Disease severity (CSII)

Total : 33 356 measurements taken

+ Rainfall data from Bureau of Meteorology ^[4]

Yield data:

- Environmental variables
- Genetics & cultivation practices variables
- Yield

Total : 1352 observations

General data frame, per observation :

- Mean disease severity
- Yield

- Location
- Variety
- Genetic resistance rating
- Treatment
- Repetition
- Year
- Rainfall data

Total : 1352 observations

Material and methods : presentation of the data set

Disease data:

- Environmental variables
- Genetics & cultivation practices variables

- Disease severity (CSII)

Total : 33 356 measurements taken

+ Rainfall data from Bureau of Meteorology ^[4]

Mean disease severity = $\Sigma (CSII)/n$

Yield data:

- Environmental variables
- Genetics & cultivation practices variables
- Yield

Total : 1352 observations

General data frame, per observation :

- Mean disease severity
- Yield

- Location
- Variety
- Genetic resistance rating
- Treatment
- Repetition
- Year
- Rainfall data

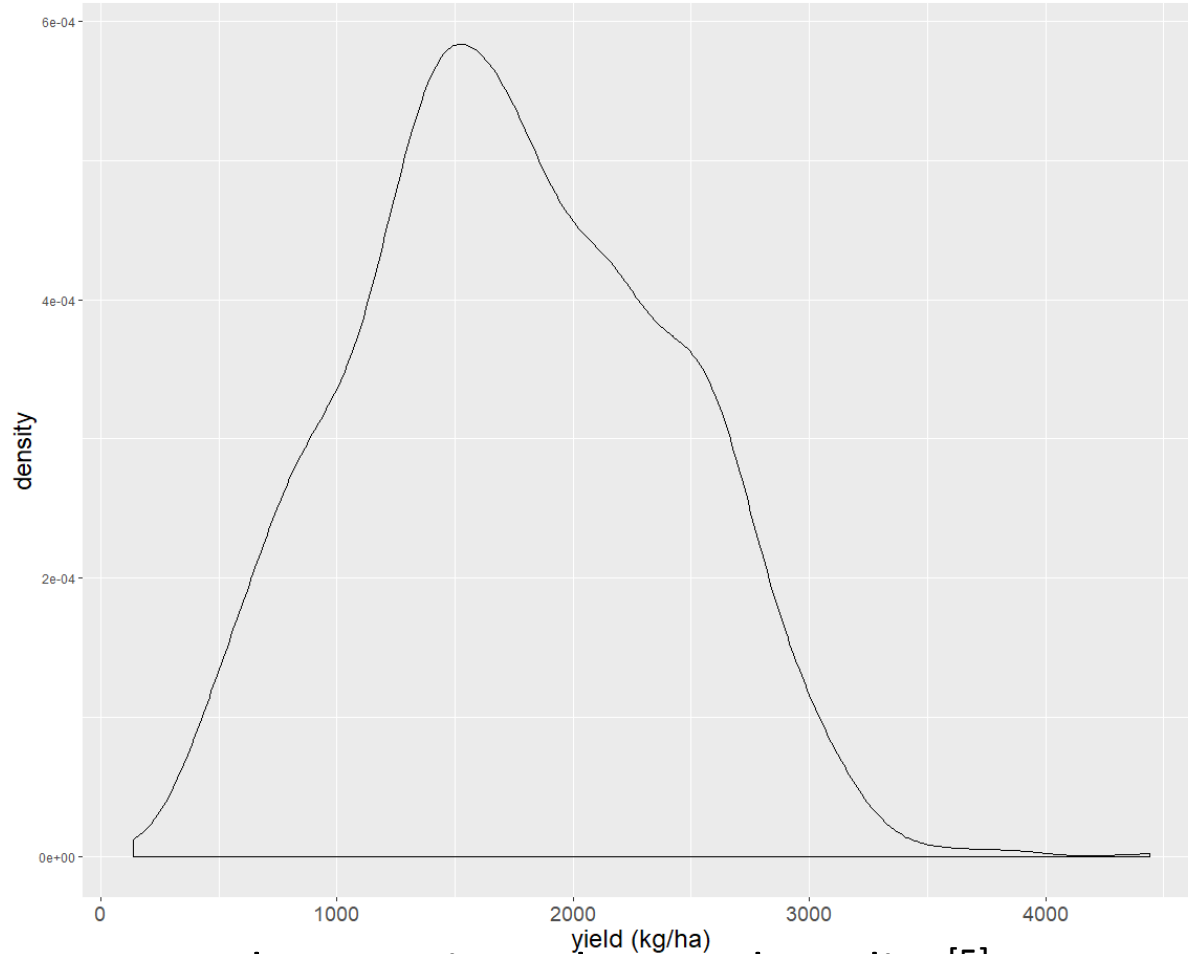
Total : 1352 observations

Questions raised :

- I) What are the parameters influencing disease severity ?
- II) How do those parameters influence the yield-disease relationship ?
- III) What is the yield response to disease presence ?

Results: disease severity and yield across Australia

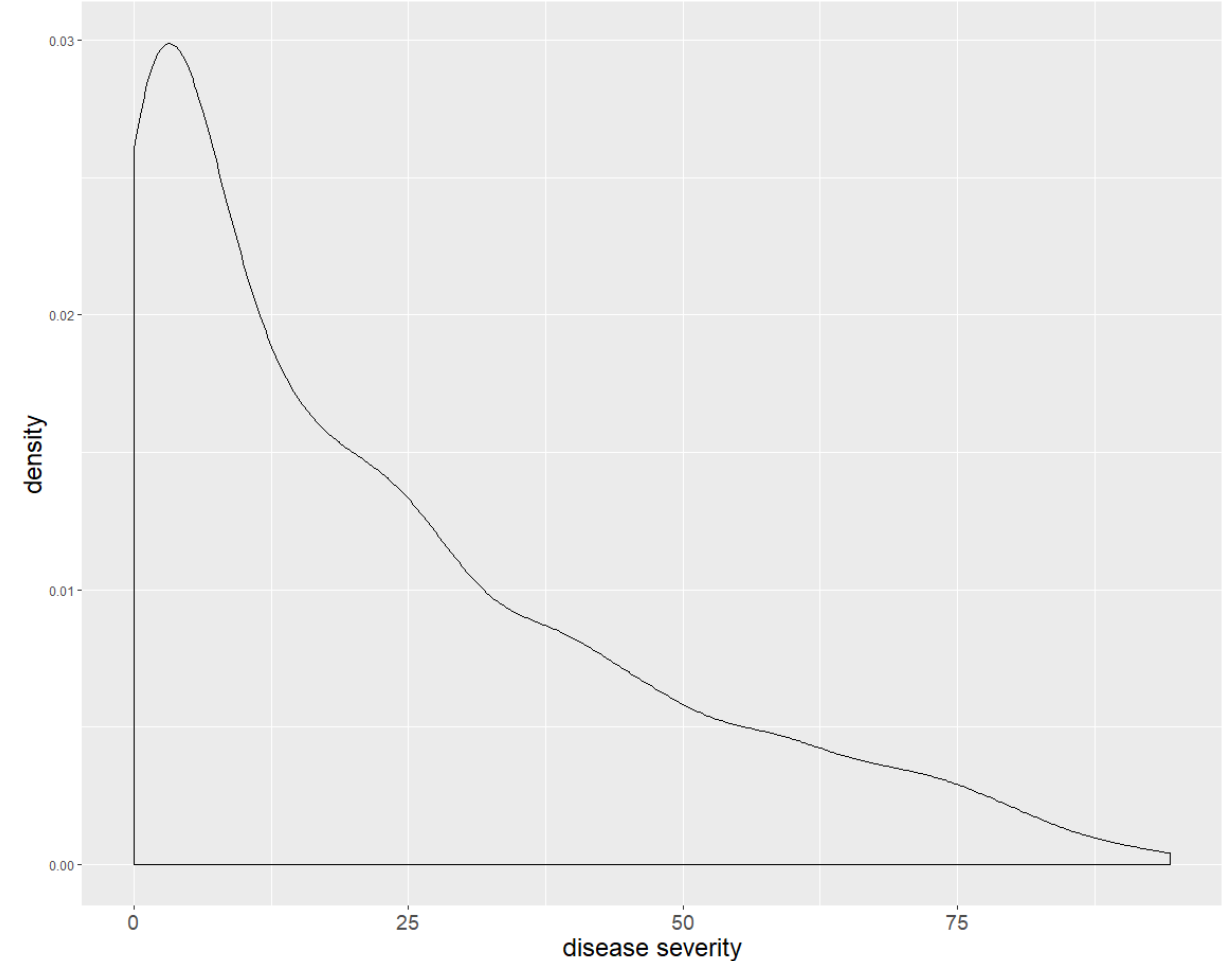
Distribution of yield (kg/ha)



Compared to previous data and studies^[5] :

- Consistent yield mean between 1,5 and 2 t/ha
- Coherent yield range sampling across Australia

Distribution of average disease severity



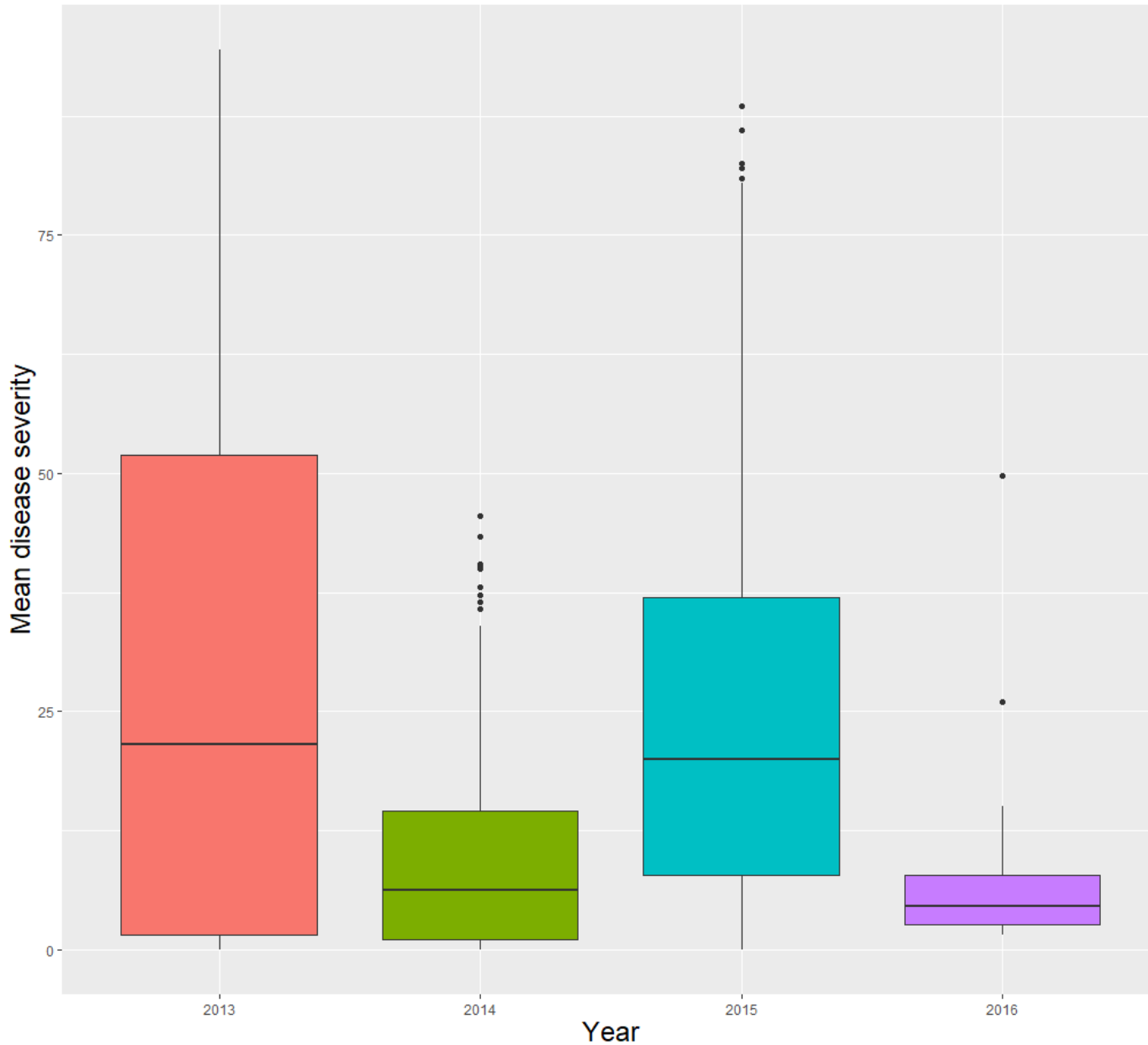
As a result of data collection :

- A large sampling of disease severity

I) What are the parameters influencing disease severity ?

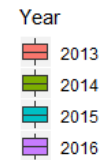
Disease severity varies amongst years

Disease severity distribution across years



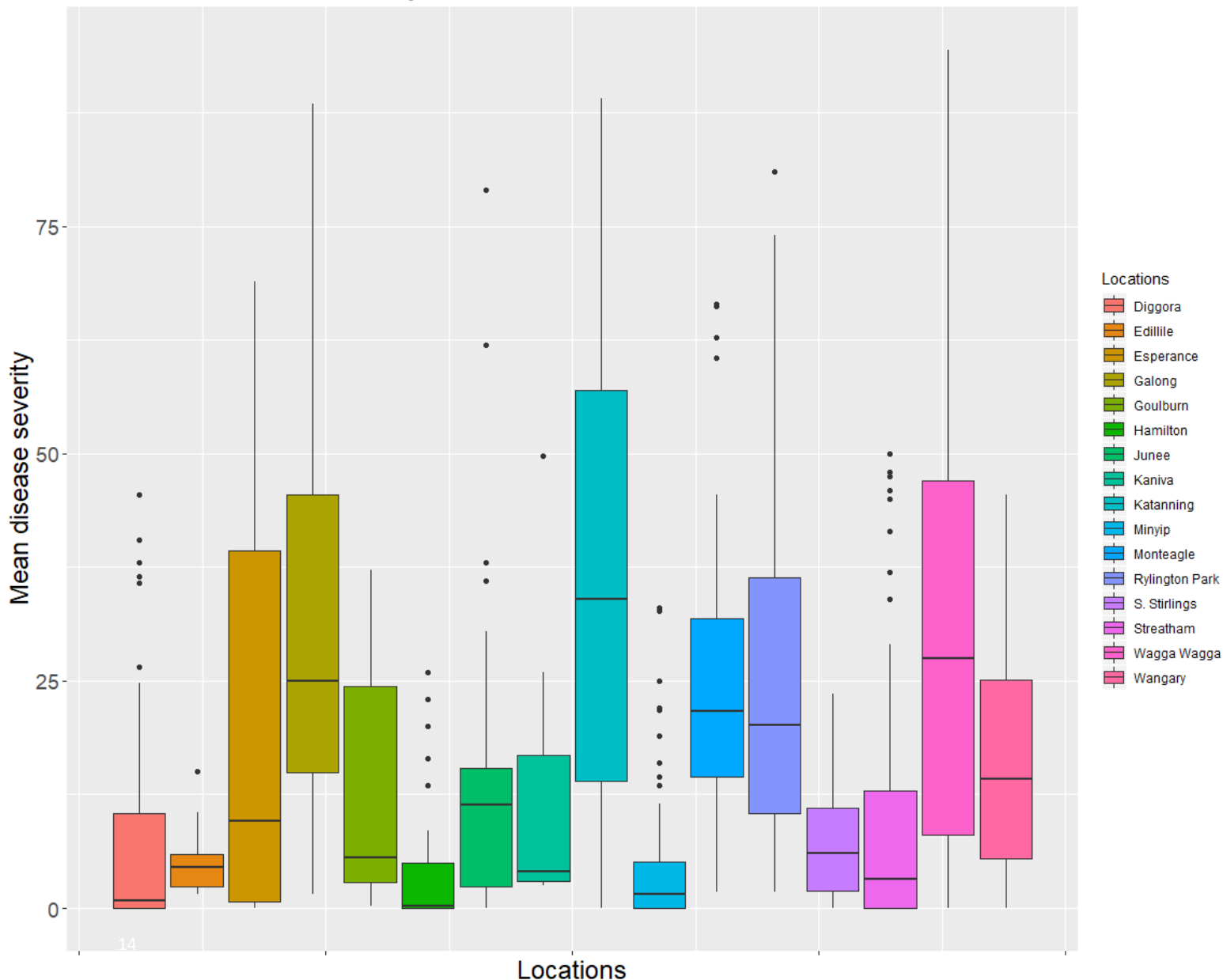
Means comparison test on disease severity :

$(2014 \sim 2016) < (2013 \sim 2015)$



Disease severity varies amongst location

Disease severity distribution across resistance locations



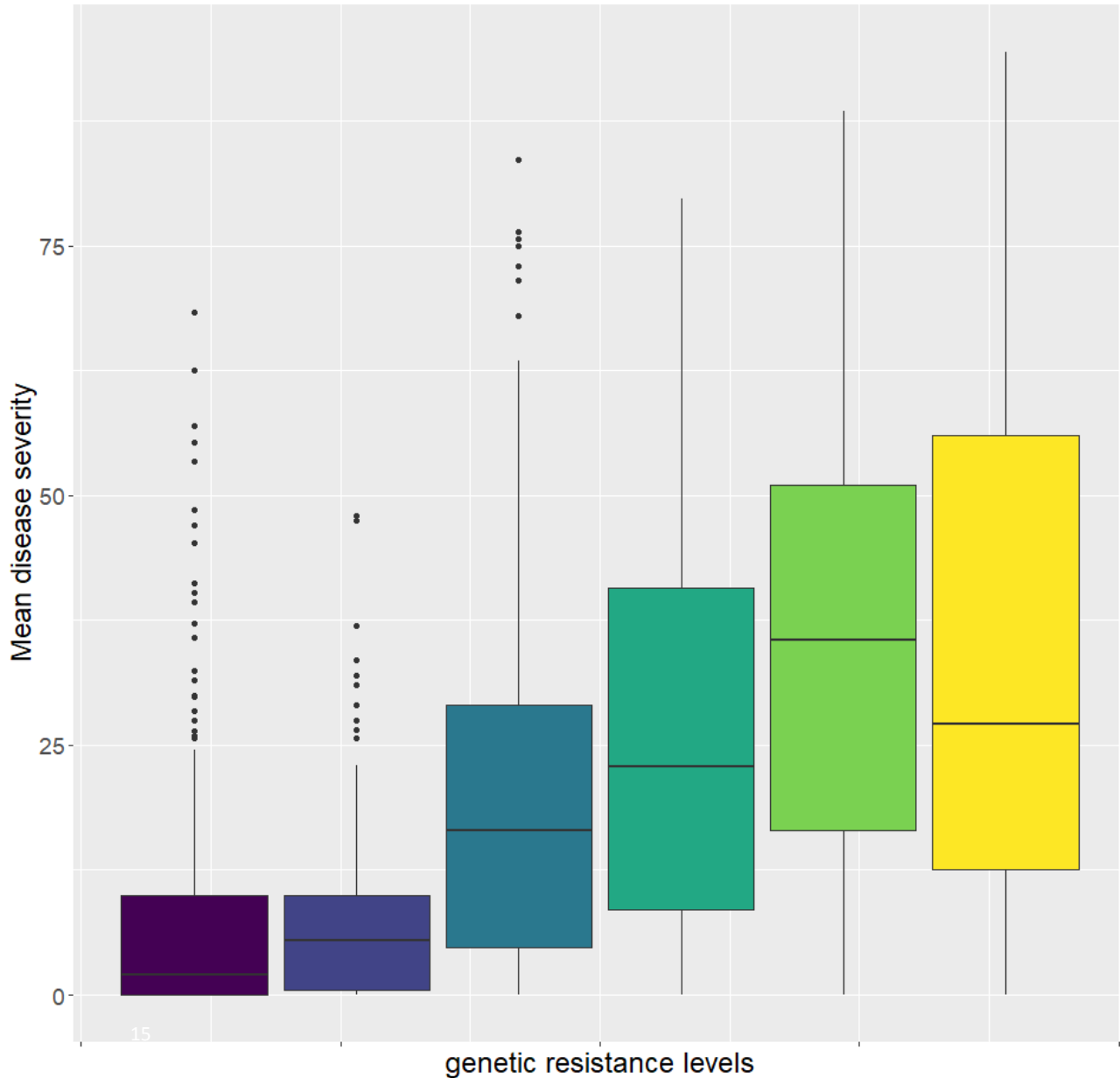
Means comparison test on disease severity :

~ 4 groups with significantly different disease levels

No obvious link between distance and significant difference

Disease severity varies amongst resistance levels

Disease severity distribution across resistance levels



Means comparison test on genetic resistance:

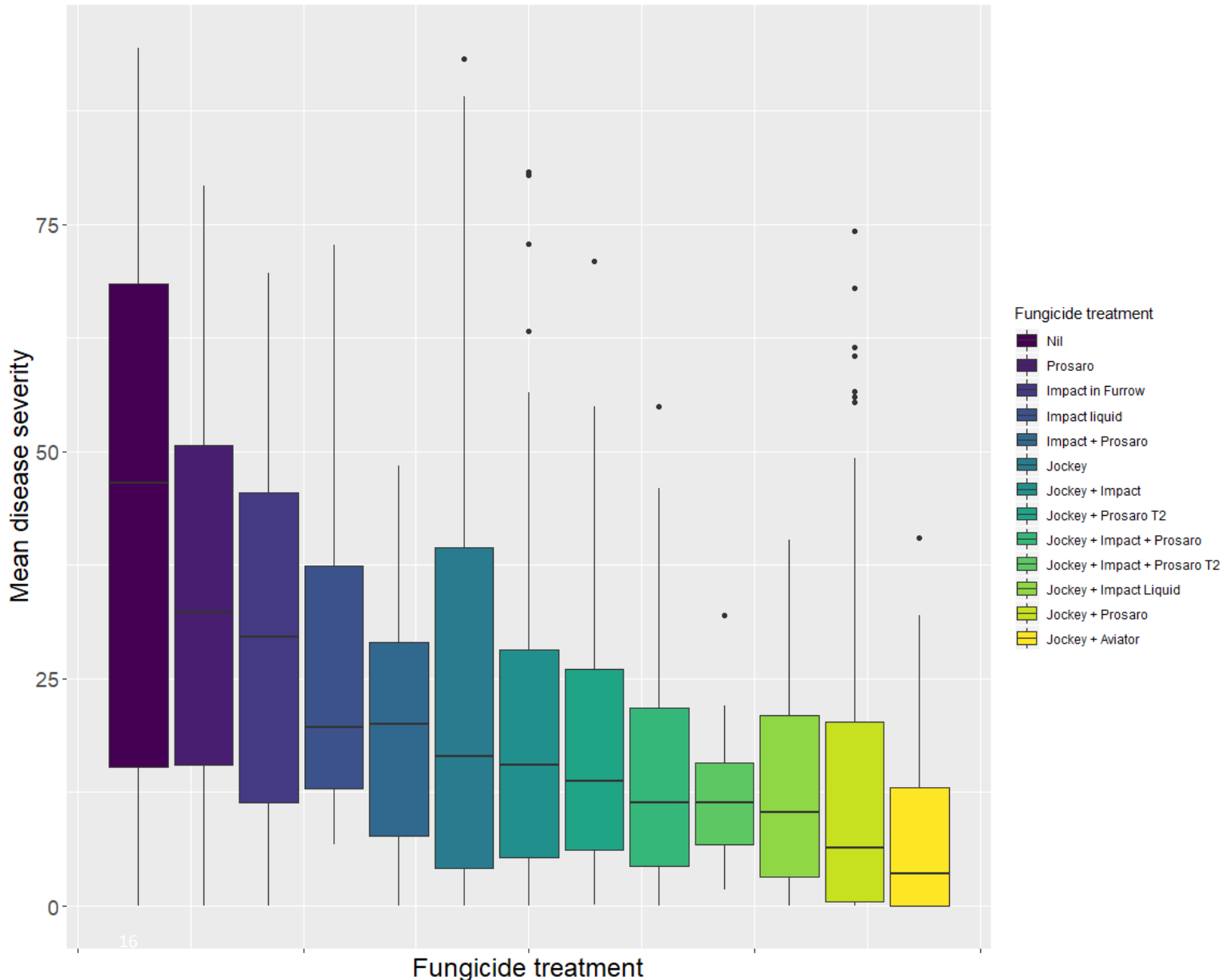
$$(R \sim R-MR) < MR < MR-MS < (MS \sim MS-S)$$

genetic resistance levels

- R
- R-MR
- MR
- MR-MS
- MS
- MS-S

Disease severity varies amongst fungicide treatments

Disease severity distribution across treatments



Fungicide treatments allow a large disease severity distribution

Disease severity distribution: importance of genetics, environmental factors, and cultivation practices

Disease severity distribution
across years, resistance levels, and treatments



In a nutshell:

- Many parameters influencing disease level
- Complex interaction between those parameters
- Incomplete, unbalanced data set

II) How do those parameters influence the yield-disease relationship ?

“Kitchen sink”/Fully-factorial analysis and sources of yield variability

```
Linear mixed model fit by REML ['lmerMod']
Formula: Yield..kg.Ha. ~ Rep.severity.means + Year + Long.term.Apr.Jun + Long.term.total + (1 | Location) + (1 | Variety)
Data: yield.disease.rainfall.cat.df
```

REML criterion at convergence: 19638.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.1824	-0.5968	-0.0234	0.5509	5.0465

Random effects:

Groups	Name	Variance	Std.Dev.
Variety	(Intercept)	107348	327.6
Location	(Intercept)	532633	729.8
Residual		109738	331.3

Number of obs: 1352, groups: Variety, 22; Location, 16

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	310.0537	239.1471	1.296
Rep.severity.means	-3.6837	0.6534	-5.638
Year2014	-19.6025	75.6778	-0.259
Year2015	-236.7615	46.3136	-5.112
Year2016	-530.1212	558.7573	-0.949
Long.term.Apr.Jun	-10.3906	0.8647	-12.016
Long.term.total	9.8900	0.4789	20.650

Correlation of Fixed Effects:

	(Intr)	Rp.sv.	Yr2014	Yr2015	Yr2016	L..A.J
Rp.svrty.mn	-0.042					
Year2014	-0.003	0.138				
Year2015	-0.140	-0.114	0.142			
Year2016	-0.265	0.008	0.027	0.048		
Lng.trm.A.J	0.005	-0.085	-0.850	-0.010	-0.006	
Lng.trm.ttl	-0.338	0.033	0.582	0.103	-0.035	-0.720

“Kitchen sink”/Fully-factorial analysis and sources of yield variability

```
Linear mixed model fit by REML ['lmerMod']  
Formula: Yield..kg.Ha. ~ Rep.severity.means + Year + Long.term.Apr.Jun + Long.term.total + (1 | Location) + (1 | Variety)  
Data: yield_disease_rainfall_cat_df
```

REML criterion at convergence: 19638.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.1824	-0.5968	-0.0234	0.5509	5.0465

Random effects:

Groups	Name	Variance	Std.Dev.
Variety	(Intercept)	107348	327.6
Location	(Intercept)	532633	729.8
Residual		109738	331.3

Number of obs: 1352, groups: Variety, 22; Location, 16

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	310.0537	239.1471	1.296
Rep.severity.means	-3.6837	0.6534	-5.638
Year2014	-19.6025	75.6778	-0.259
Year2015	-236.7615	46.3136	-5.112
Year2016	-530.1212	558.7573	-0.949
Long.term.Apr.Jun	-10.3906	0.8647	-12.016
Long.term.total	9.8900	0.4789	20.650

Correlation of Fixed Effects:

	(Intr)	Rp.sv.	Yr2014	Yr2015	Yr2016	L..A.J
Rp.svrty.mn	-0.042					
Year2014	-0.003	0.138				
Year2015	-0.140	-0.114	0.142			
Year2016	-0.265	0.008	0.027	0.048		
Lng.trm.A.J	0.005	-0.085	-0.850	-0.010	-0.006	
Lng.trm.ttl	-0.338	0.033	0.582	0.103	-0.035	-0.720

“Kitchen sink”/Fully-factorial analysis and sources of yield variability

Linear mixed model fit by REML ['lmerMod']
 Formula: Yield..kg.Ha. ~ Rep.severity.means + Year + Long.term.Apr.Jun + Long.term.total + (1 | Location) + (1 | Variety)
 Data: yield.disease.rainfall.cat.df

REML criterion at convergence: 19638.1

Scaled residuals:
 Min 1Q Median 3Q Max
 -4.1824 -0.5968 -0.0234 0.5509 5.0465

Random effects:

Groups	Name	Variance	Std.Dev.
Variety	(Intercept)	107348	327.6
Location	(Intercept)	532633	729.8
Residual		109738	331.3

Number of obs: 1352, groups: variety, 22; Location, 16

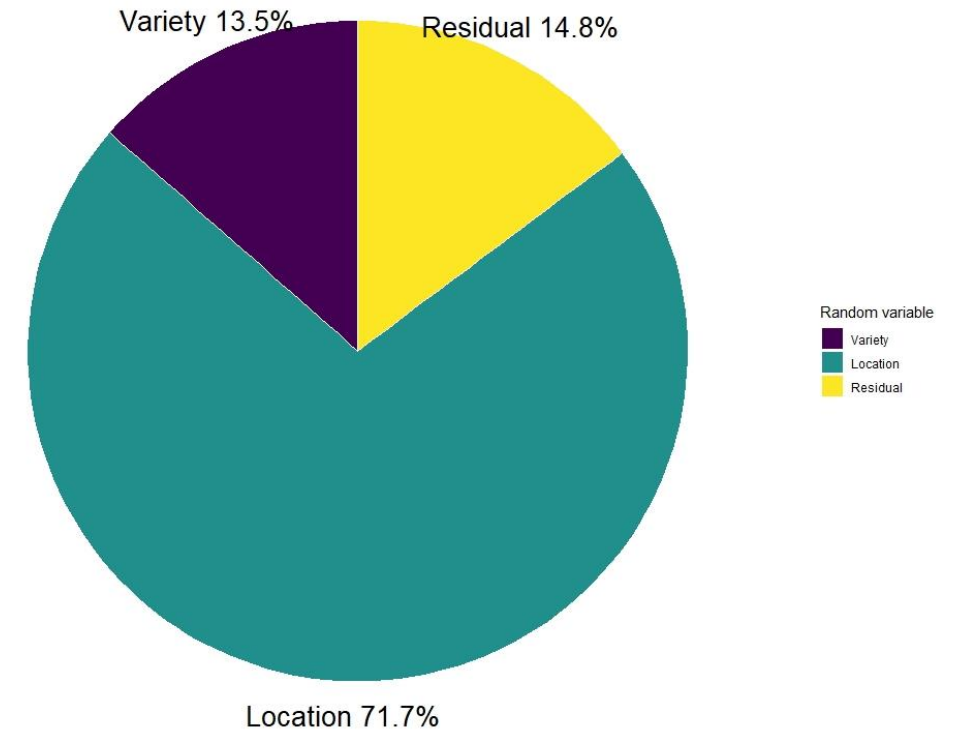
Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	310.0537	239.1471	1.296
Rep.severity.means	-3.6837	0.6534	-5.638
Year2014	-19.6025	75.6778	-0.259
Year2015	-236.7615	46.3136	-5.112
Year2016	-530.1212	558.7573	-0.949
Long.term.Apr.Jun	-10.3906	0.8647	-12.016
Long.term.total	9.8900	0.4789	20.650

Correlation of Fixed Effects:

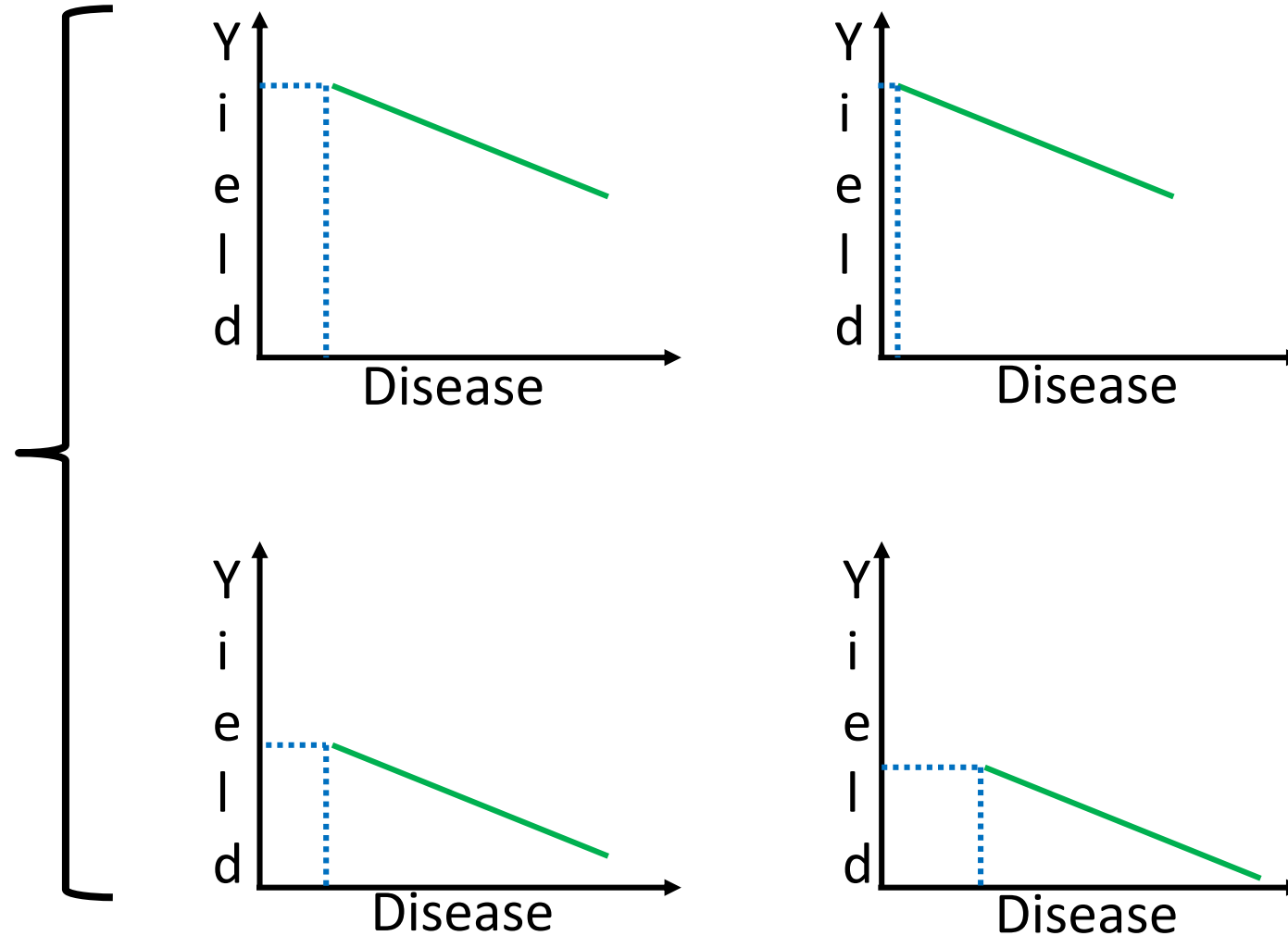
	(Intr)	Rp.sv.	Yr2014	Yr2015	Yr2016	L..A.J
Rp.svrty.mn	-0.042					
Year2014	-0.003	0.138				
Year2015	-0.140	-0.114	0.142			
Year2016	-0.265	0.008	0.027	0.048		
Lng.trm.A.J	0.005	-0.085	-0.850	-0.010	-0.006	
Lng.trm.ttl	-0.338	0.033	0.582	0.103	-0.035	-0.720

Impact of control parameters on yield-disease relationship variability



Mixed linear model : assessing yield-disease relationship

Controlling
for a
parameter

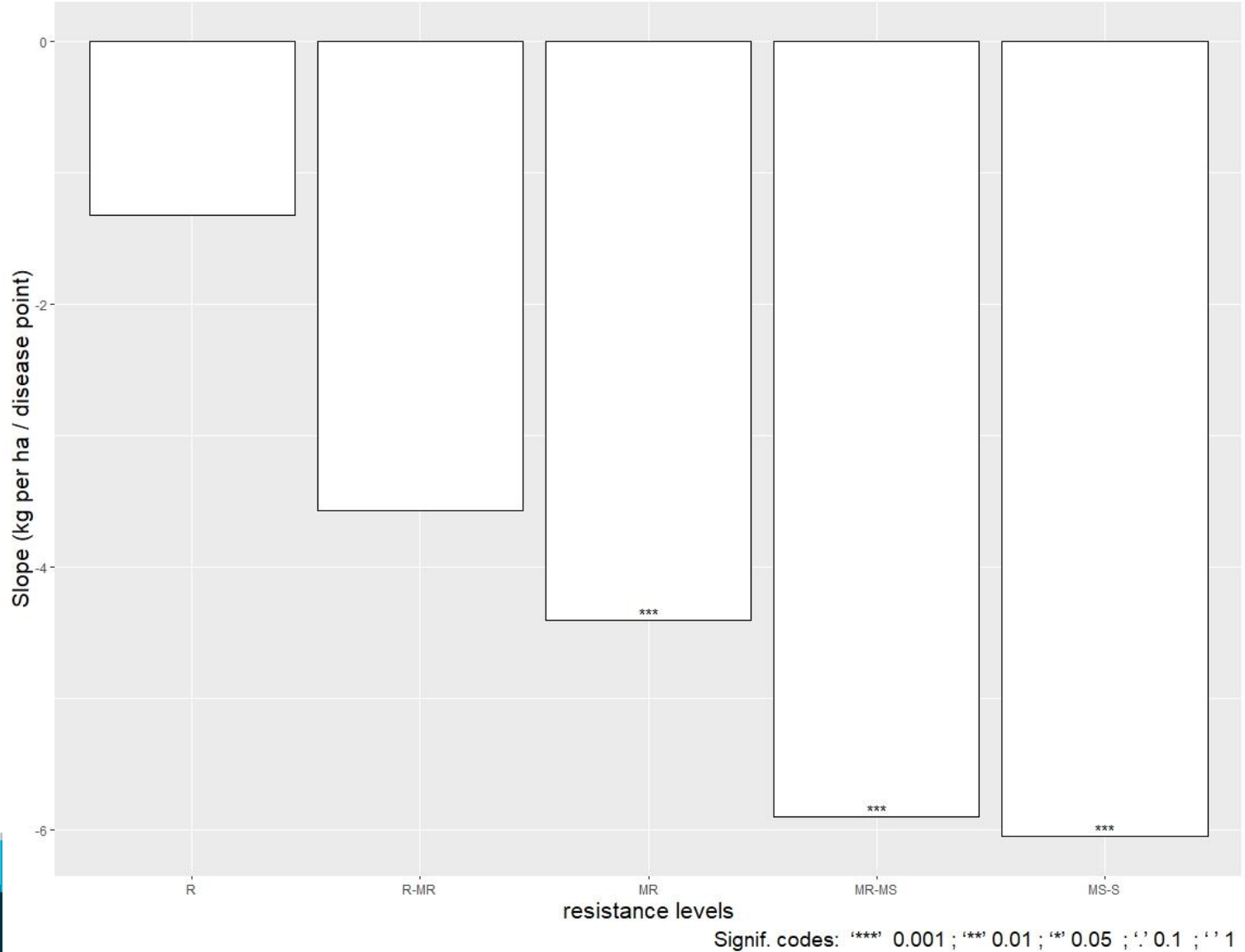


Relationship
assessed by
the **slope** :

yield loss
according to
disease
severity

Sources of yield variability : the impact of genetics and environment

Yield-disease relationship
in different resistance groups



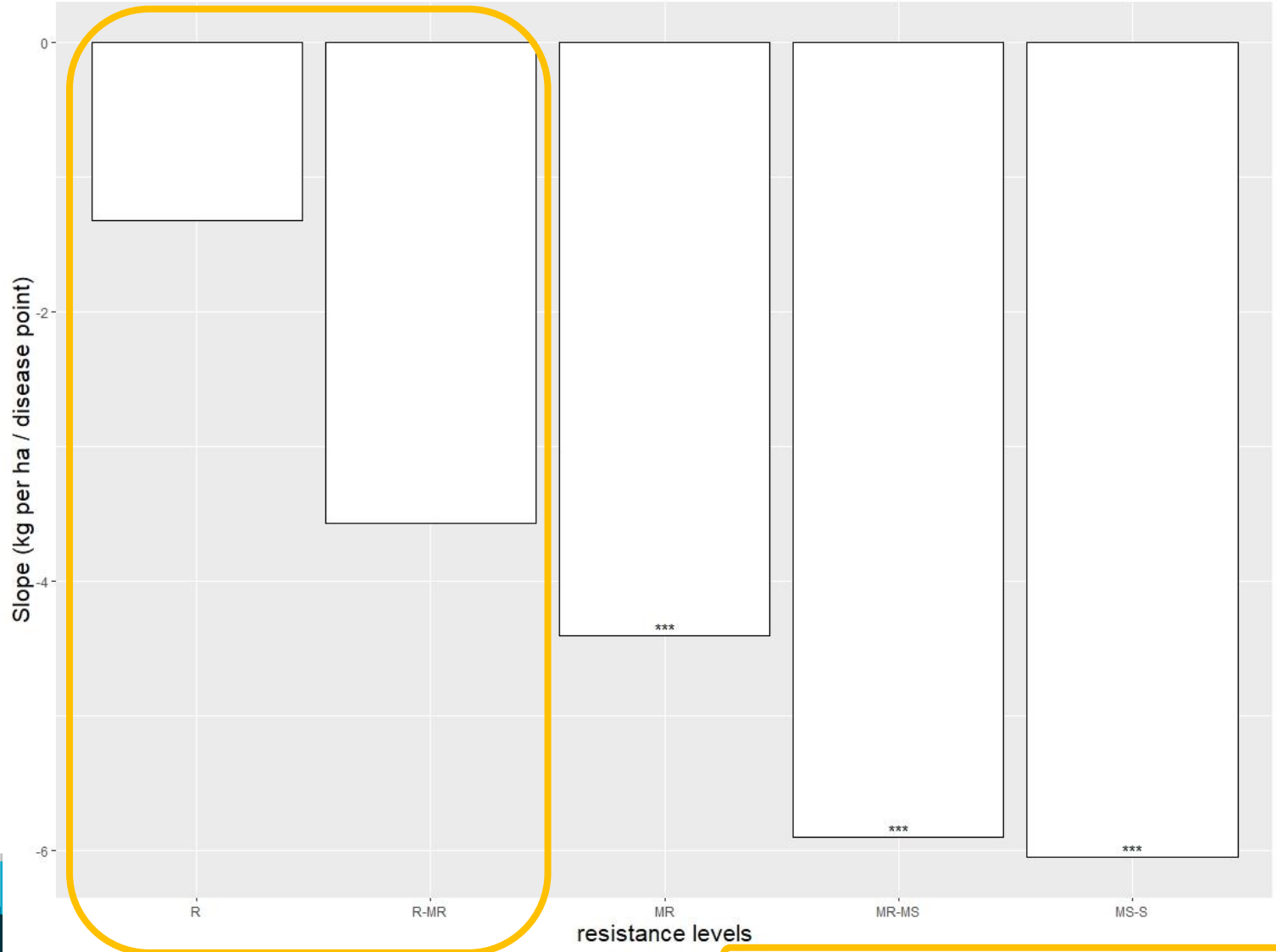
For each genetic resistance category :

```
Formula: Yield..kg.Ha. ~ Rep.severity.means + Year + Long.term.Apr.Jun  
+ Long.term.total + (1 | Location) + (1 | Variety)
```



Sources of yield variability : the impact of genetics and environment

Yield-disease relationship
in different resistance groups



For each genetic resistance category :

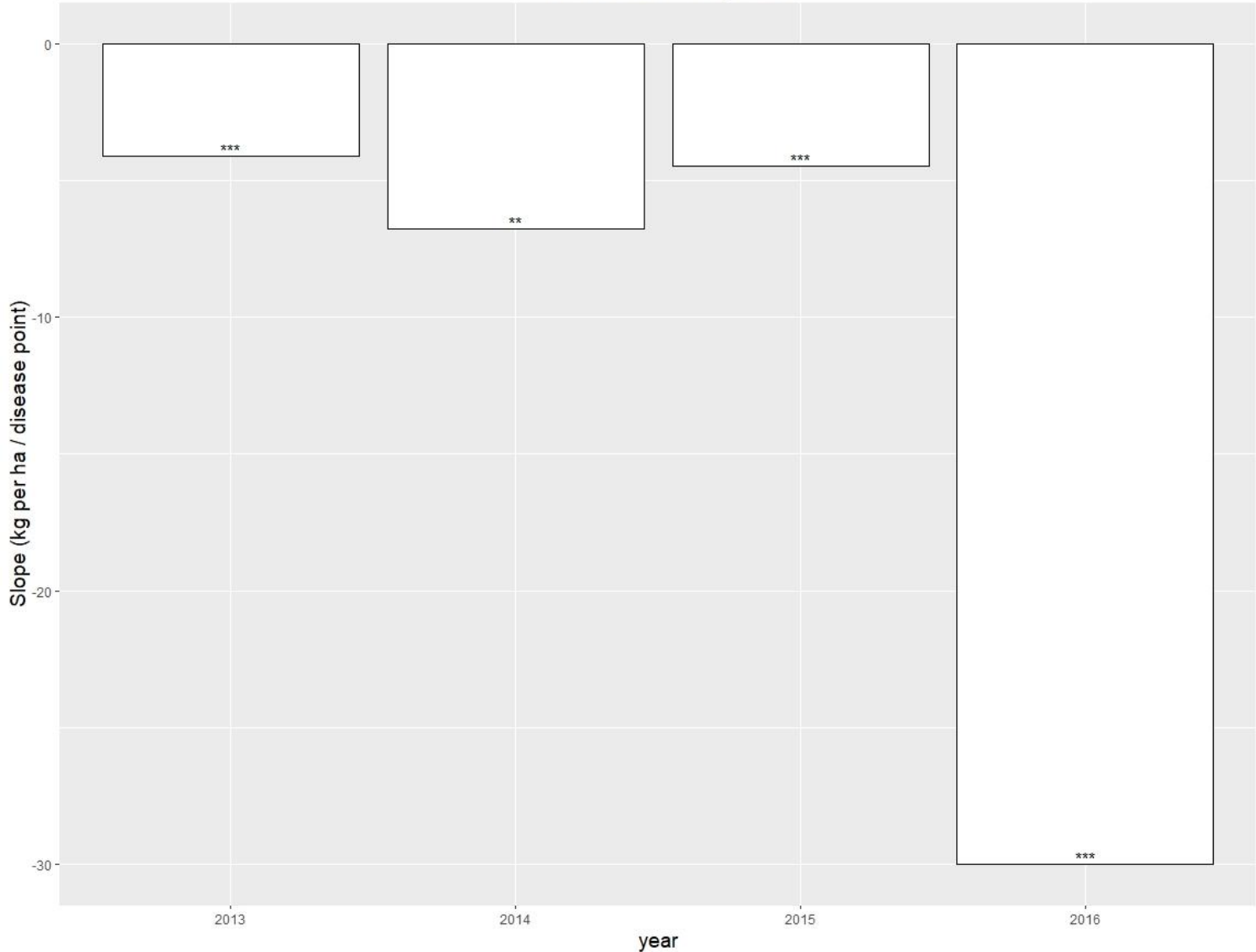
```
Formula: Yield..kg.Ha. ~ Rep.severity.means + Year + Long.term.Apr.Jun
+ Long.term.total + (1 | Location) + (1 | Variety)
```

Signif. codes: '***' 0.001, '**' 0.01, '*' 0.05, '.' 0.1, ' ' 1



Sources of yield variability : the impact of genetics and environment

Yield-disease relationship
across different years



Signif. codes: '***' 0.001; '**' 0.01; '*' 0.05; '.' 0.1; ' ' 1

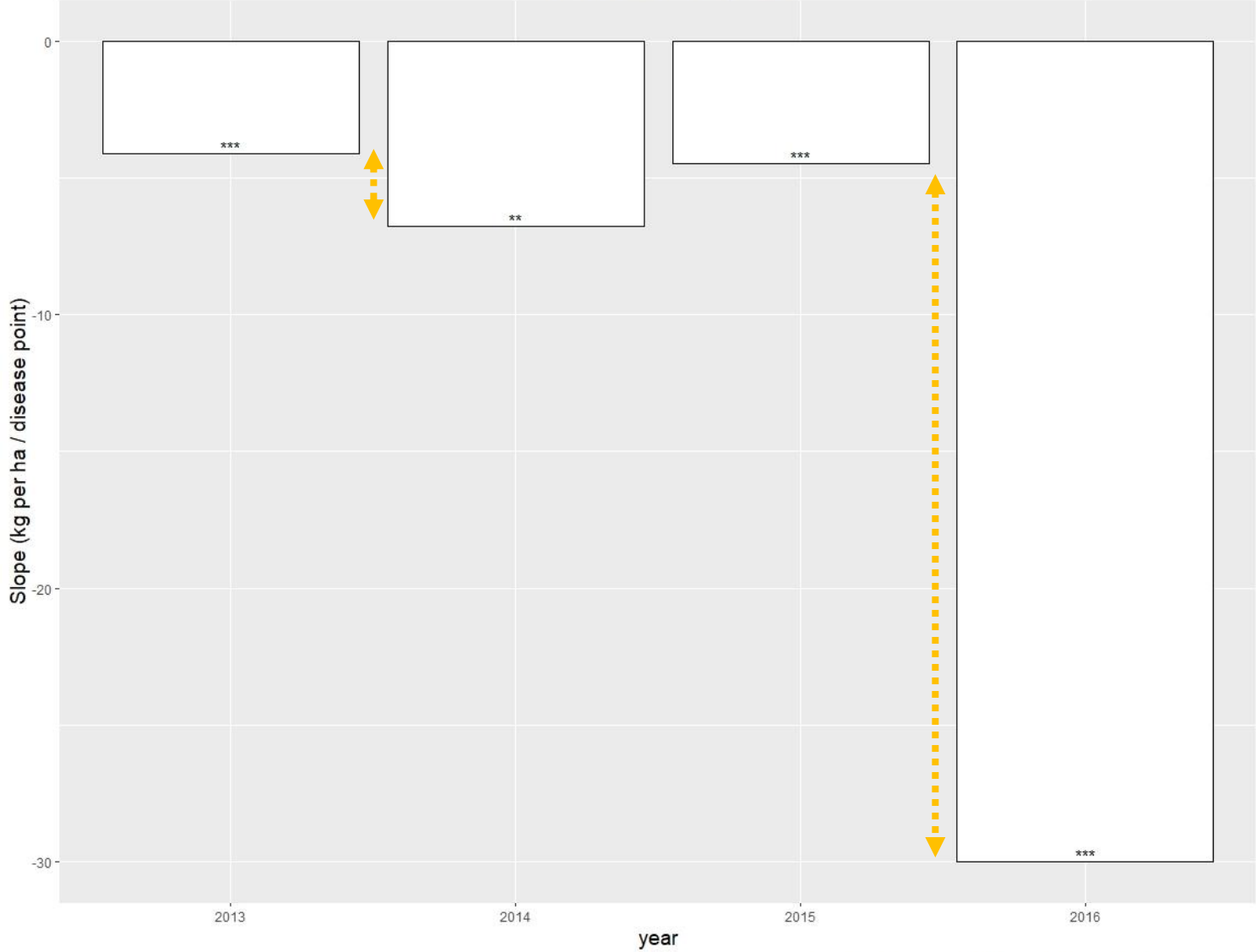
For each “Year” category :

Formula: `Yield..kg.Ha. ~ Rep.severity.means + Long.term.Apr.Jun + Long.term.total + (1 | Location) + (1 | Variety)`



Sources of yield variability : the impact of genetics and environment

Yield-disease relationship across different years

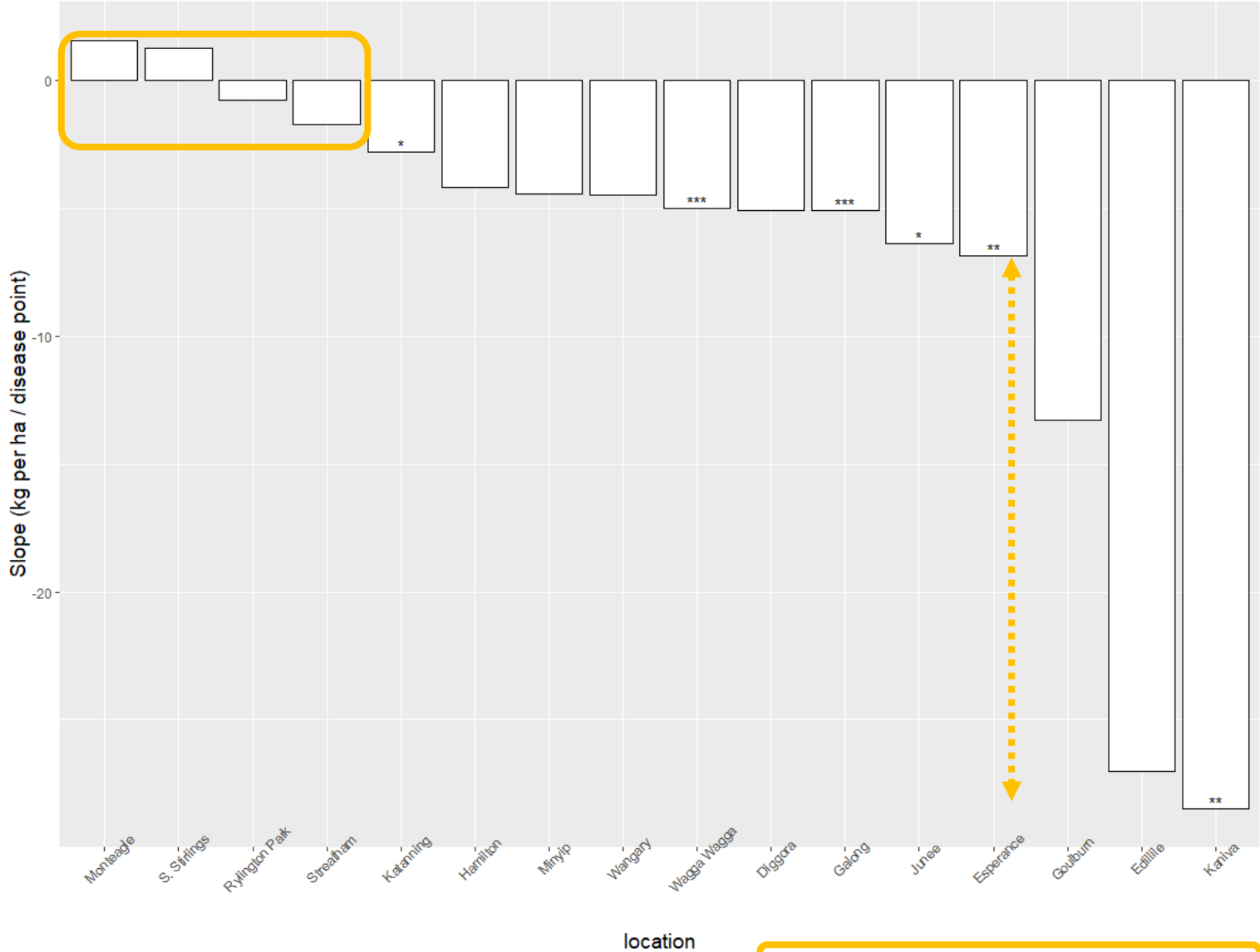


For each “Year” category :

```
Formula: Yield..kg.Ha. ~ Rep.severity.means + Long.term.Apr.Jun +
Long.term.total + (1 | Location) + (1 | Variety)
```

Sources of yield variability : the impact of genetics and environment

Yield-disease relationship
across different locations



For each “Location” category :

Formula: `Yield..kg.Ha. ~ Rep.severity.means + Year + (1 | Location)`

Signif. codes: '***' 0.001; '**' 0.01; '*' 0.05; '.' 0.1; ' ' 1



III) What is the yield response to disease presence ?

Yield-disease relationship : a distribution across significant observation

For each Year*Location*Variety observation :

$\text{lm}(\text{Yield}.. \text{kg}.\text{Ha}.\sim \text{Rep}.\text{severity}.\text{means})$

Simple linear equation of the form :

$$Y = a + bX$$

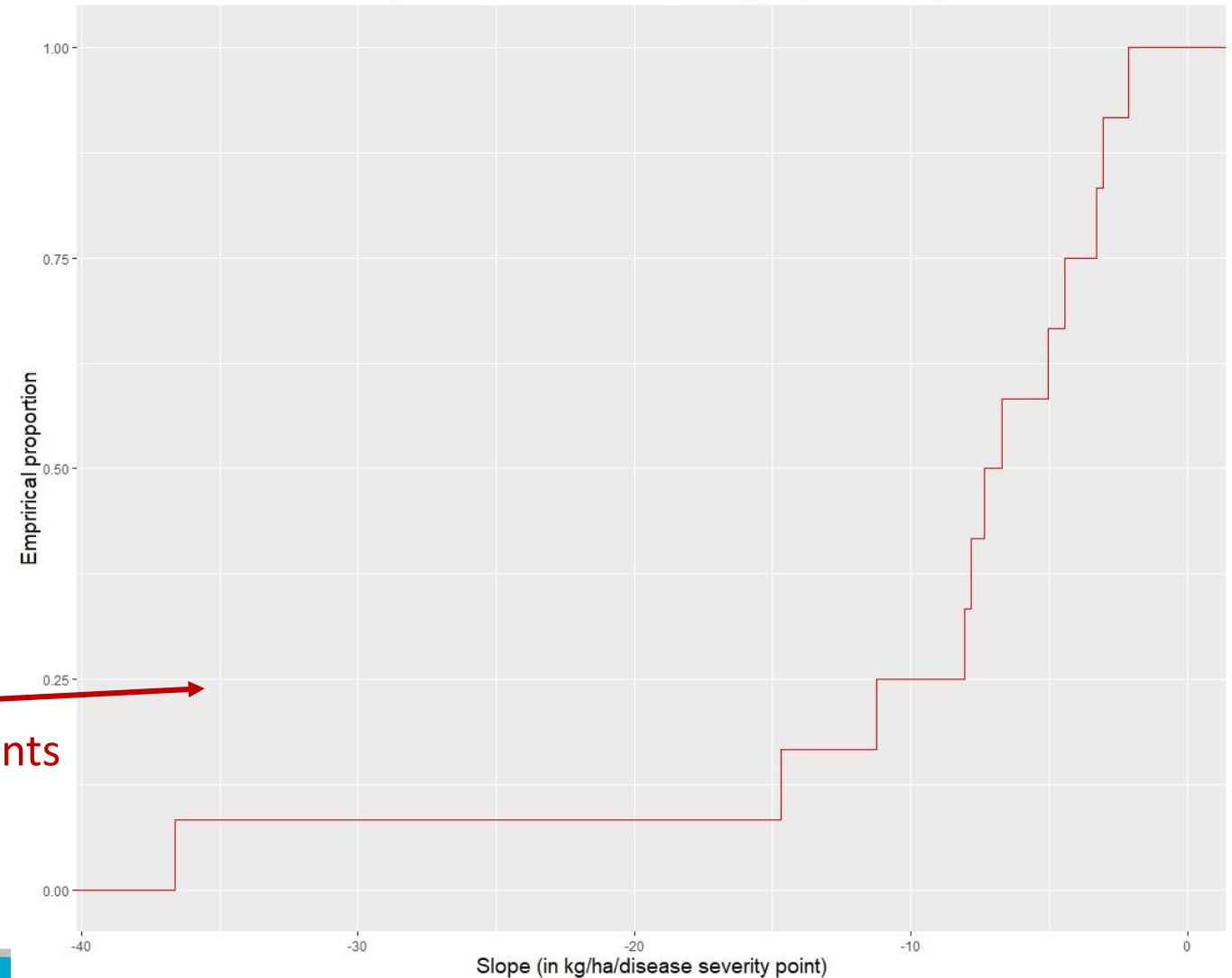
Distribution of all significant “b” coefficients

With :

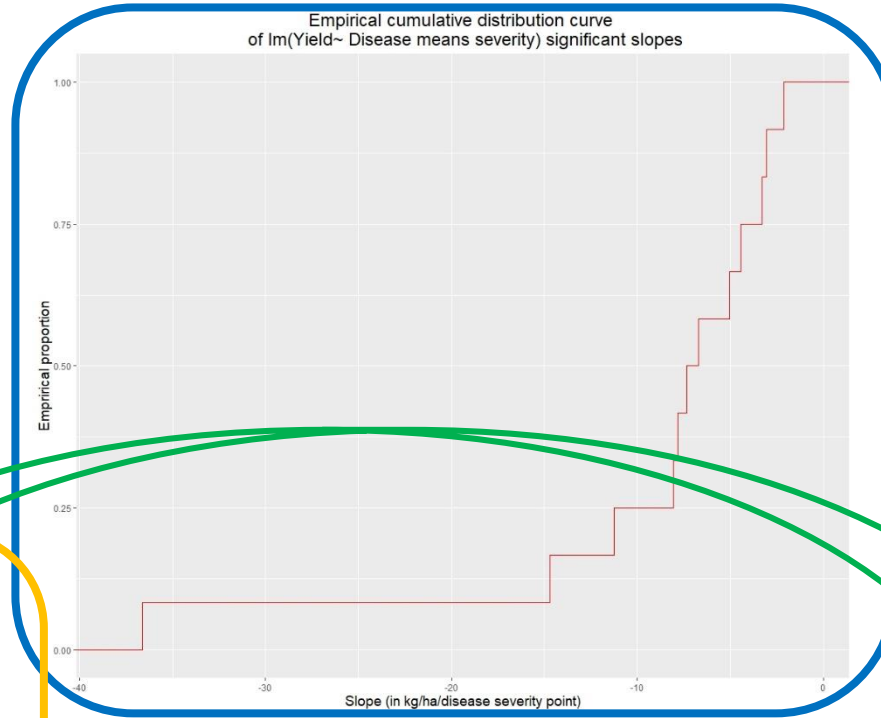
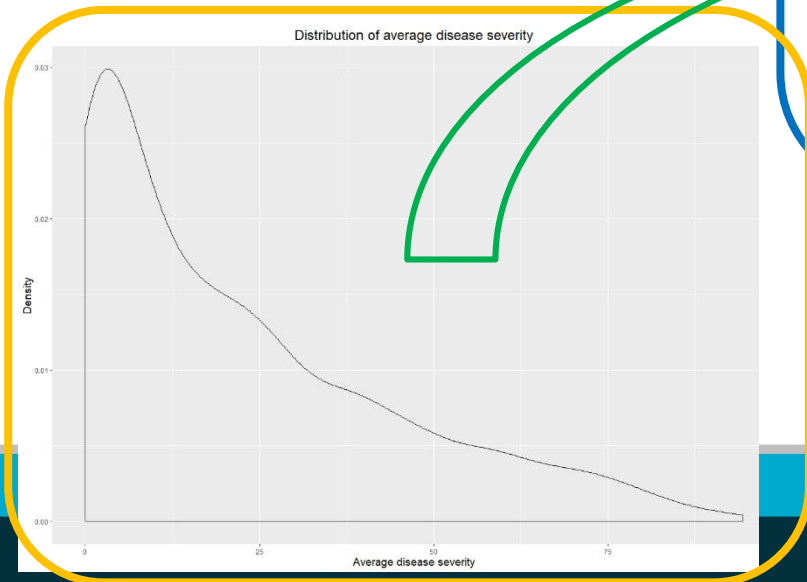
Y representing the yield, and

X the mean severity score

Empirical cumulative distribution curve
of $\text{lm}(\text{Yield} \sim \text{Disease means severity})$ significant slopes



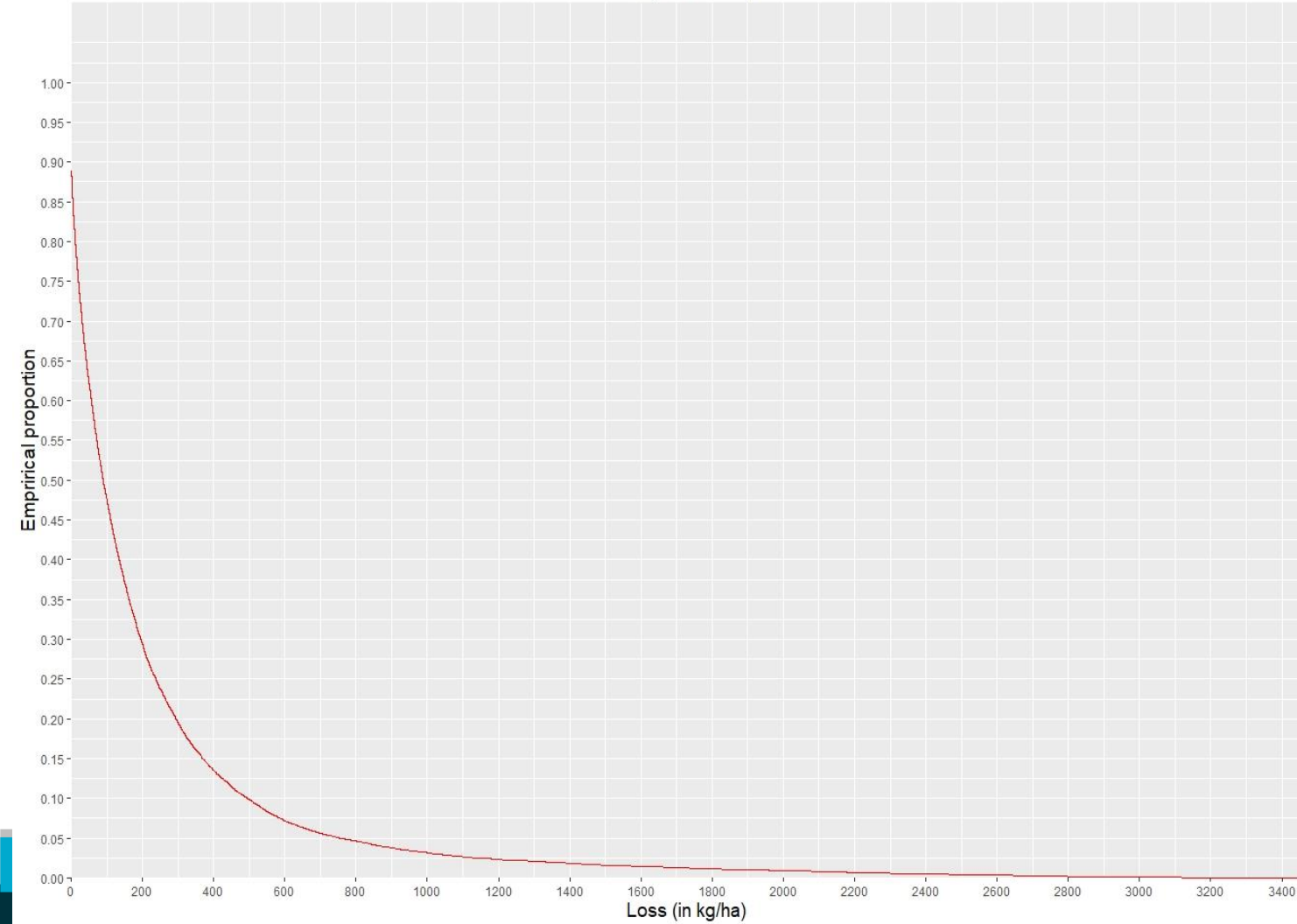
Yield-disease relationship : an estimation of the loss



Potential loss i,j (kg/ha) =
Repetition Disease Severity means i (%age) * Potential relationship slope j (kg/ha/ %age point)

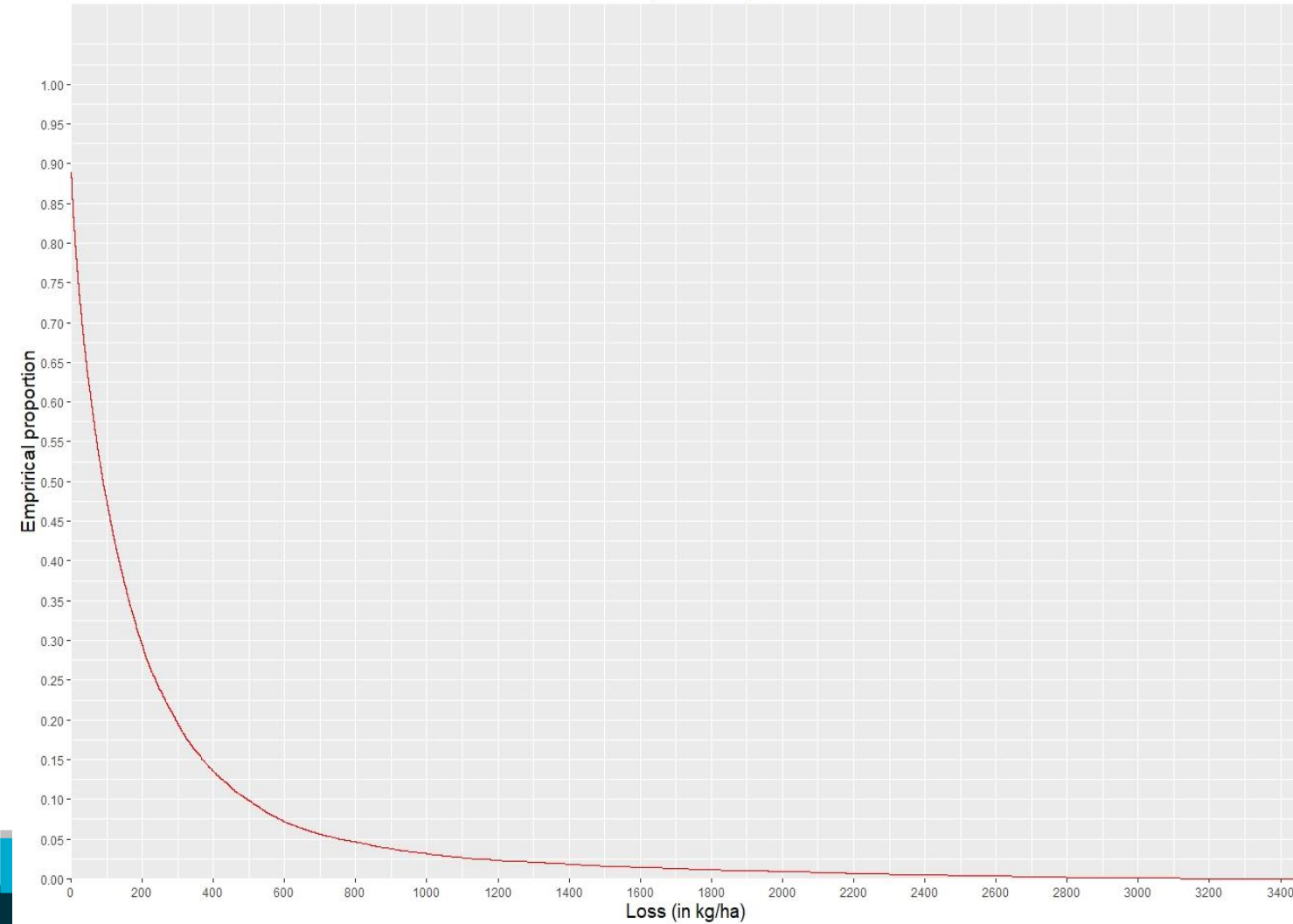
Yield-disease relationship : a distribution of estimated loss across samples

Empirical cumulative distribution curve
 $\Pr(\text{loss} \geq x)$

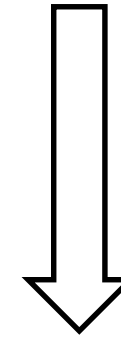


Yield-disease relationship : a distribution of estimated loss across samples

Empirical cumulative distribution curve
 $\Pr(\text{loss} \geq x)$



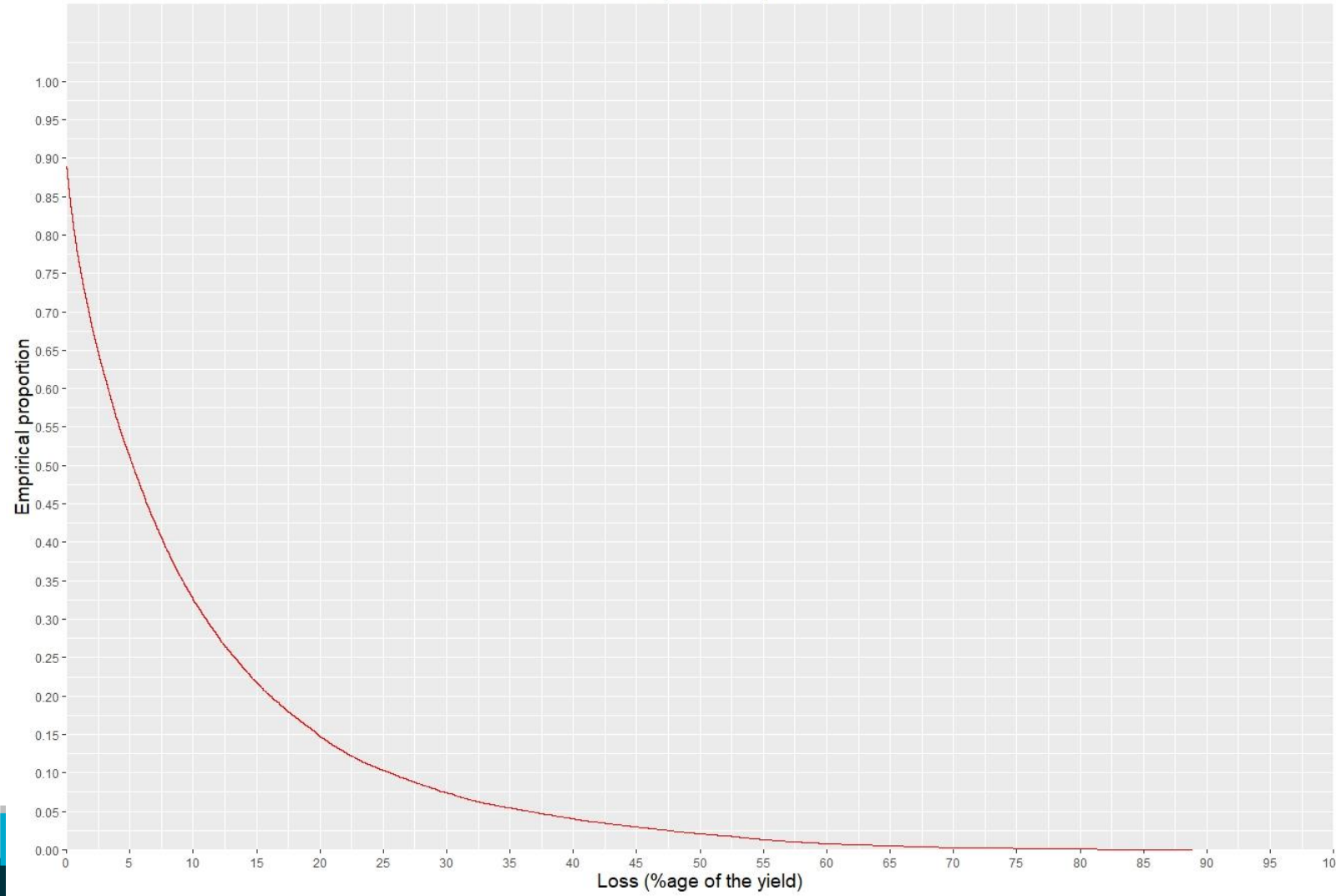
Potential loss i,j (kg/ha) =
Repetition Disease Severity means i (%^{age}) *
Potential relationship slope j (kg/ha/ %^{age} point)



Potential loss i,j (percentage of potential yield) =
Potential loss i,j (kg/ha) /
(Yield i (kg/ha) + Potential loss i,j (kg/ha))

Yield-disease relationship : a distribution of estimated loss across samples

Empirical cumulative distribution curve
 $\Pr(\text{loss} \geq x)$

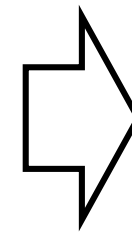
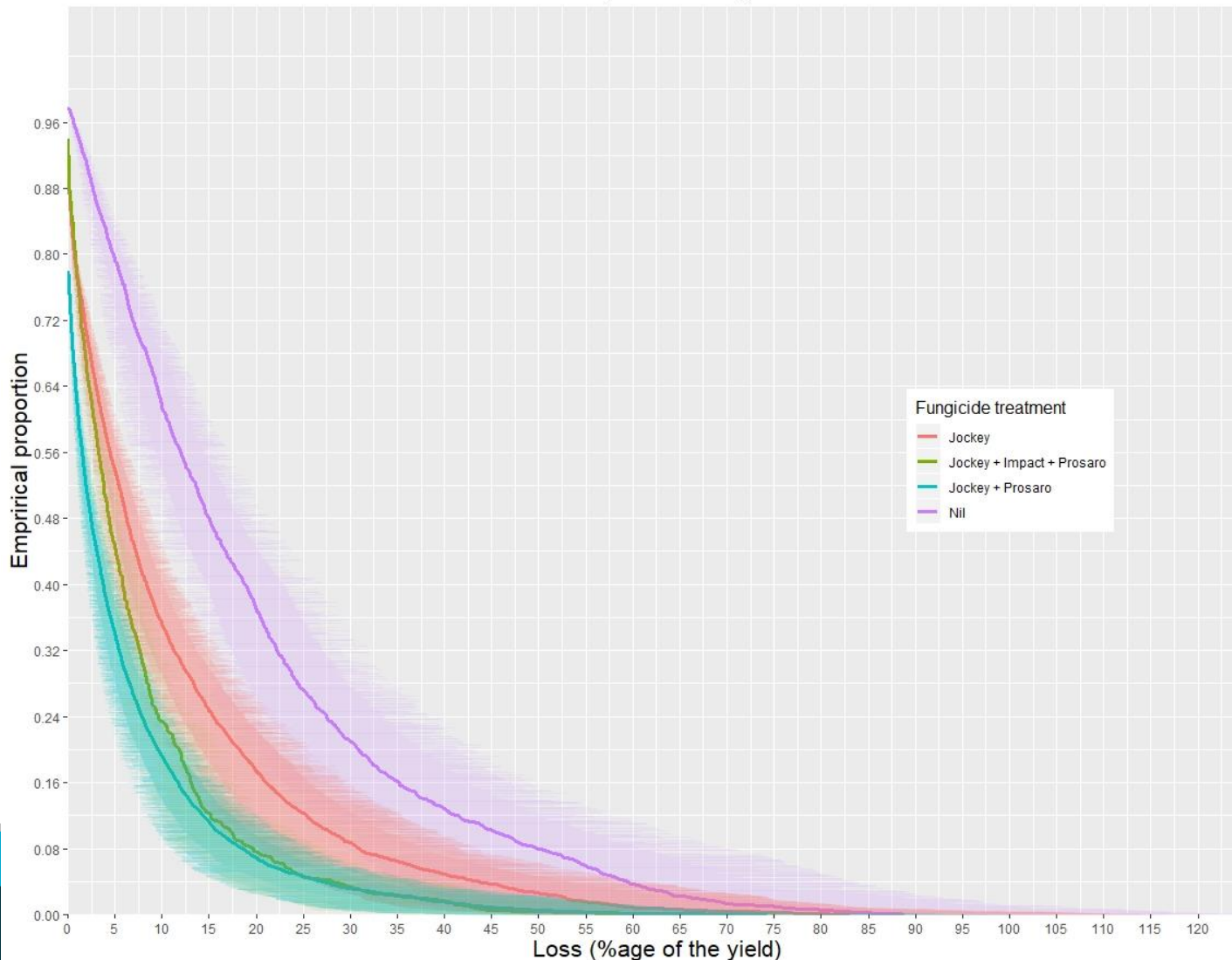


Under the assumption of significant
yield-disease relationship conditions :

Empirical cumulative distribution curve
of loss close to a linear function of
 $\log(\text{percentage loss})$

Yield-disease relationship : a distribution of estimated loss weighted by fungicide treatment type

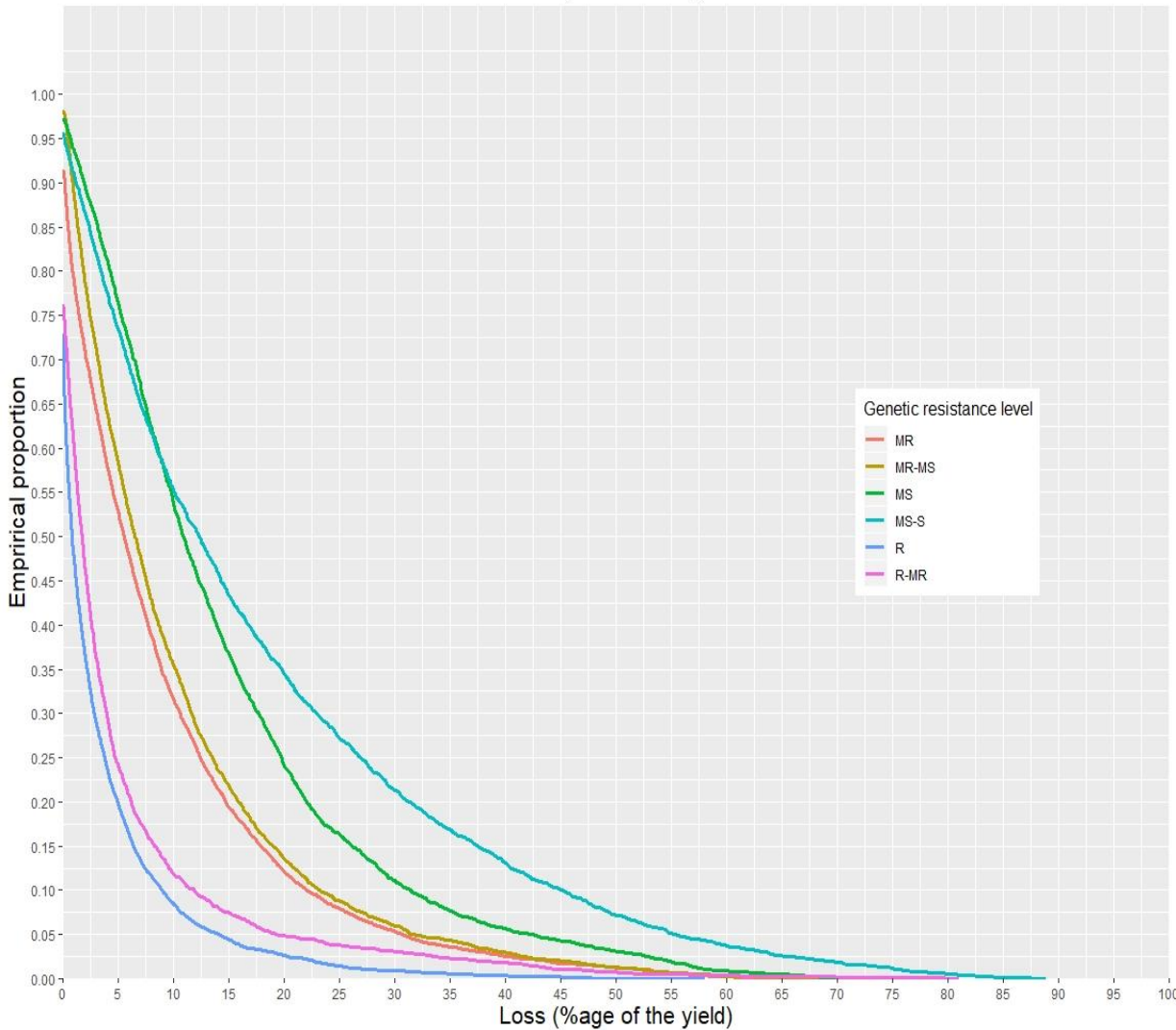
Empirical cumulative distribution curve
 $\Pr(\text{loss} \geq x)$



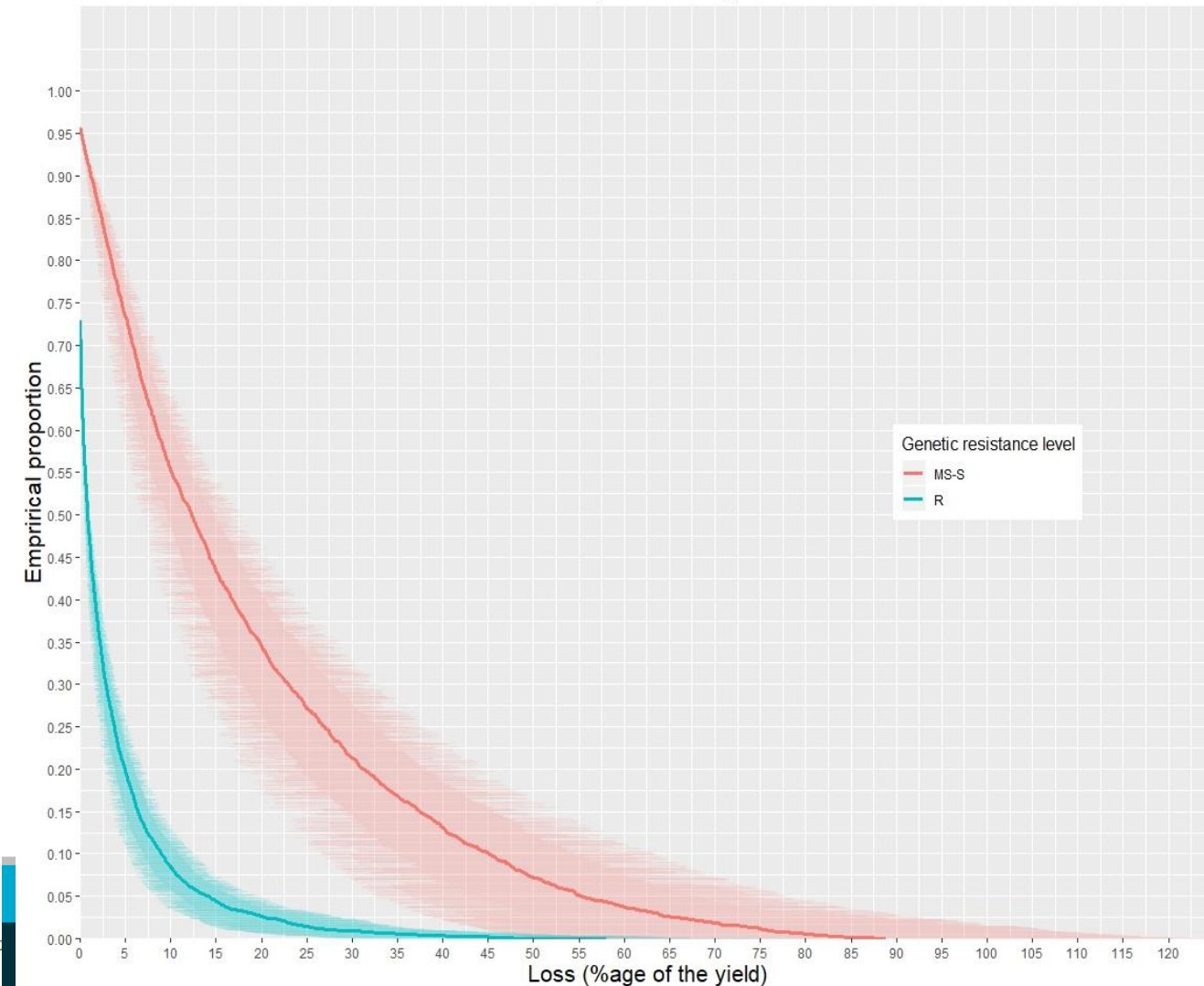
Difference between all three fungicide treatments distribution curves is never greater than the associated standard error.

Yield-disease relationship : a distribution of estimated loss weighted by genetic resistance

Empirical cumulative distribution curve
 $\Pr(\text{loss} \geq x)$



Empirical cumulative distribution curve
 $\Pr(\text{loss} \geq x)$



Conclusion : Effect of Blackleg on Canola

- Disease progression, severity, and yield-disease relationship all depend on environmental factors and genetics.
- Using this data, we could get economic parameters to fit into disease management models.

Acknowledgements :

to the multi-organisation team who collected this data, acknowledging their thorough work,

to Tim Capon and Ann Seitzinger, for their kind support and advice,

to Luke Barrett and Susie Sprague, for supervising this project,

to Sorada Tapsuwan, for her tips on statistics,

and all CSIRO Black Mountain A & F team for their warm welcoming.

Bibliography

- [1] Fitt BDL, Hu BC, Li ZQ *et al.* , 2008. *Strategies to prevent spread of Leptosphaeria maculans (phoma stem canker) onto oilseed rape crops in China; costs and benefits. Plant Pathology* **57**, 652–64.
- [2] R. Khangura, A. Hills, C. Beard, Updated 15th August 2019, *Managing blackleg in canola*, Department of Primary Industries and Regional development website, available at : <<https://www.agric.wa.gov.au/canola/managing-blackleg-canola?page=0%2C0>>
- [3] Sprague SJ, Balesdent MH, Brun H, Hayden HL, Marcroft SJ, Pinochet X, Rouxel T, Howlett BJ (2006) Major gene resistance in Brassica napus (oilseed rape) is overcome by changes in virulence of populations of Leptosphaeria maculans in France and Australia. *European Journal of Plant Pathology* 114, 33–40. doi:10.1007/s10658-005-3683-5
- [4] Commonwealth of Australia 2020, Bureau of Meteorology, Climate Data Online, available at : <<http://www.bom.gov.au/climate/data/>>
- [5] D.E. Seberry, D.W. McCaffery, T.M. Kingham (2017) *Quality of Australian Canola*, Volume 23, ISSN 1322-9397

Other references :

Australian Bureau of Agricultural and Resource Economics and Sciences, *Australian crop report* No. 187 , September 2018

Sprague *et al.*, 2007, *Pathways of infection of Brassica napus roots by Leptosphaeria maculans*, available at: < <https://nph.onlinelibrary.wiley.com/doi/full/10.1111/j.1469-8137.2007.02156.x> >

Bibliography

Means comparison test for treatments

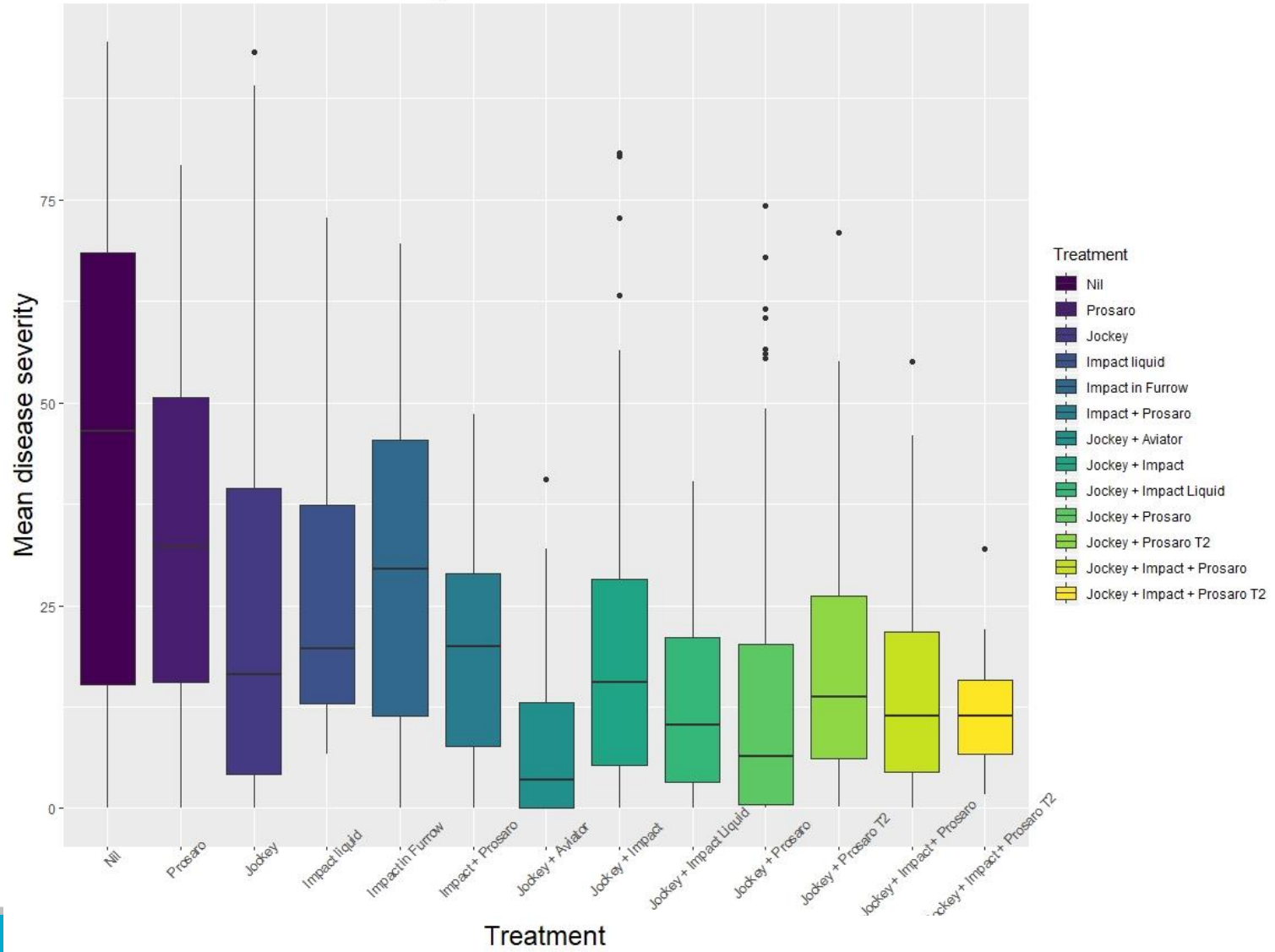
Pairwise comparisons using wilcoxon rank sum test

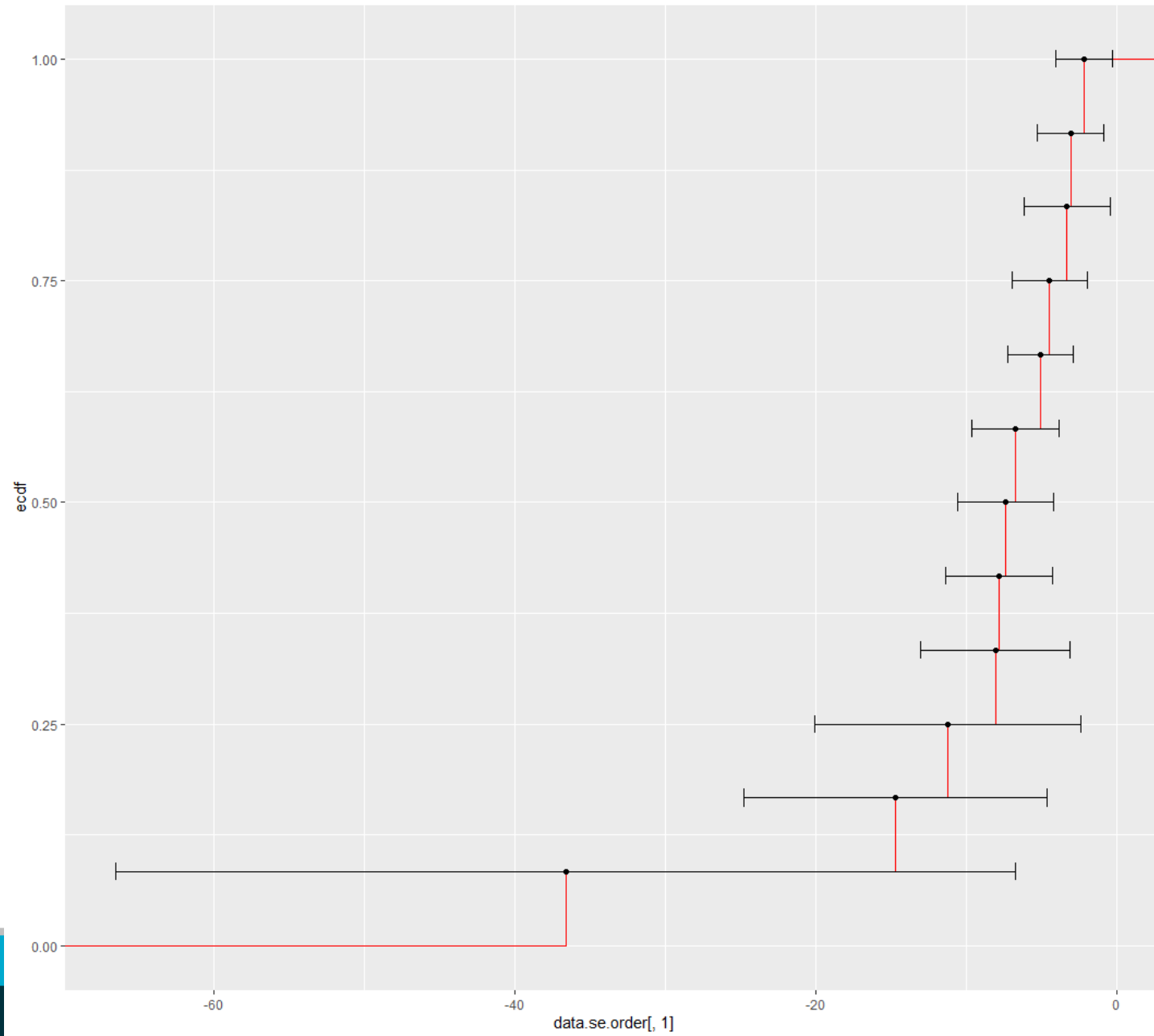
data: yield.disease.rainfall.cat.df\$Rep.severity.means and yield.disease.rainfall.cat.df\$treatment

	Impact + Prosaro	Impact in Furrow	Impact liquid	Jockey	Jockey + Aviator	Jockey + Impact	Jockey + Impact + Prosaro
Impact in Furrow	0.02115	-	-	-	-	-	-
Impact liquid	0.49290	0.67929	-	-	-	-	-
Jockey	0.91594	0.01542	0.40769	-	-	-	-
Jockey + Aviator	3.2e-05	8.3e-10	0.00062	7.0e-07	-	-	-
Jockey + Impact	0.65300	0.00284	0.24780	0.61632	6.8e-06	-	-
Jockey + Impact + Prosaro	0.03744	8.6e-06	0.03163	0.03163	0.00176	0.10781	-
Jockey + Impact + Prosaro T2	0.13775	0.01660	0.06425	0.34086	0.05563	0.33780	0.89032
Jockey + Impact Liquid	0.08460	0.00145	0.04210	0.13463	0.03744	0.17285	0.70782
Jockey + Prosaro	0.00074	2.4e-12	0.00480	2.6e-10	0.06425	2.4e-05	0.05563
Jockey + Prosaro T2	0.43894	0.00959	0.16386	0.48880	0.00068	0.71807	0.39783
Nil	2.6e-05	0.00068	0.11612	2.6e-10	8.6e-14	1.7e-08	2.6e-10
Prosaro	0.00137	0.26138	0.34812	0.00021	2.3e-11	3.2e-05	6.7e-08
	Jockey + Impact + Prosaro T2	Jockey + Impact Liquid	Jockey + Prosaro	Jockey + Prosaro T2	Nil		
Impact in Furrow	-	-	-	-	-	-	-
Impact liquid	-	-	-	-	-	-	-
Jockey	-	-	-	-	-	-	-
Jockey + Aviator	-	-	-	-	-	-	-
Jockey + Impact	-	-	-	-	-	-	-
Jockey + Impact + Prosaro	-	-	-	-	-	-	-
Jockey + Impact + Prosaro T2	-	-	-	-	-	-	-
Jockey + Impact Liquid	0.75131	-	-	-	-	-	-
Jockey + Prosaro	0.36398	0.37417	-	-	-	-	-
Jockey + Prosaro T2	0.54246	0.40879	0.02616	-	-	-	-
Nil	0.00145	2.4e-05	< 2e-16	2.2e-05	-	-	-
Prosaro	0.00306	0.00024	5.9e-16	0.00068	0.01893	-	-

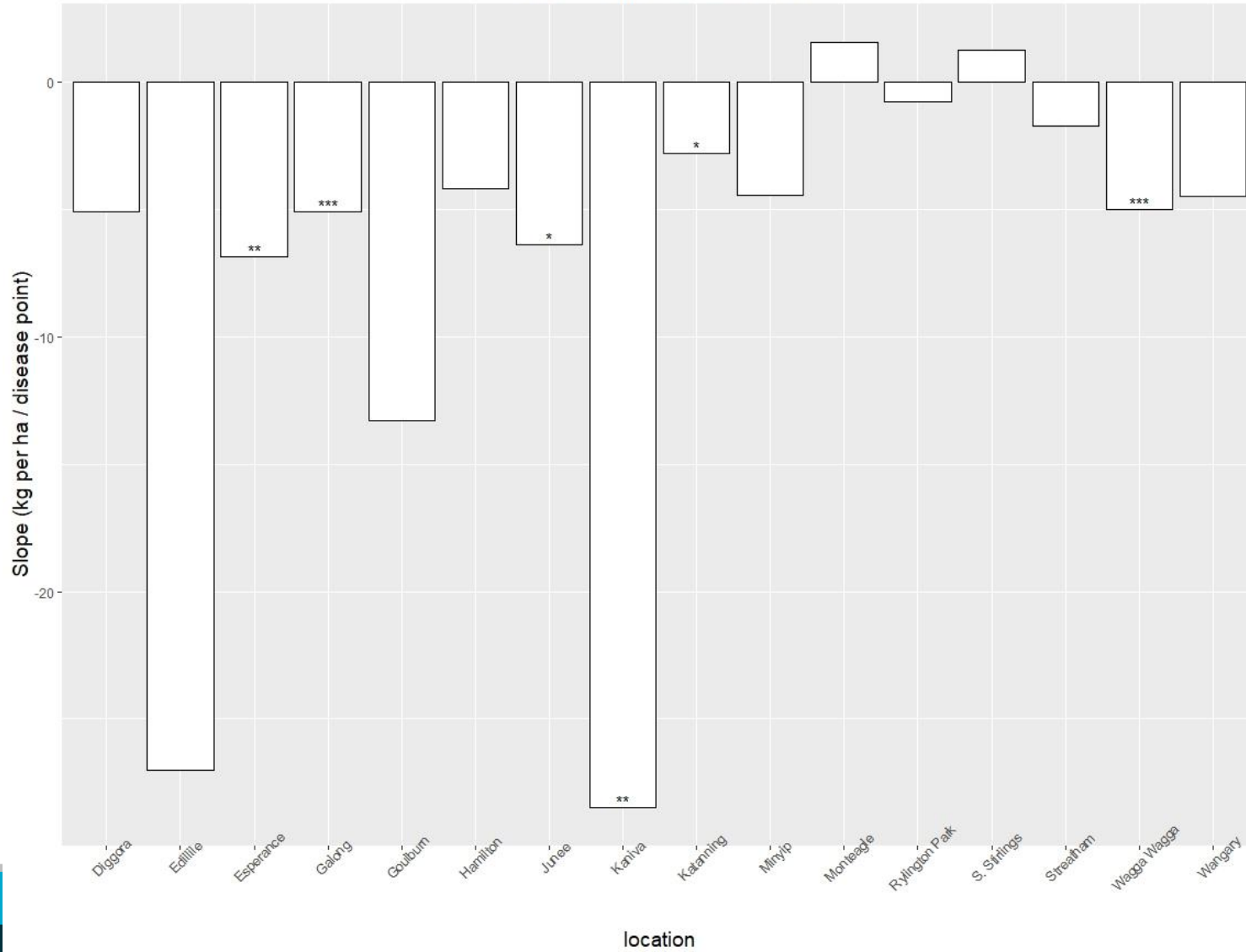
P value adjustment method: BH

Disease severity distribution across treatments



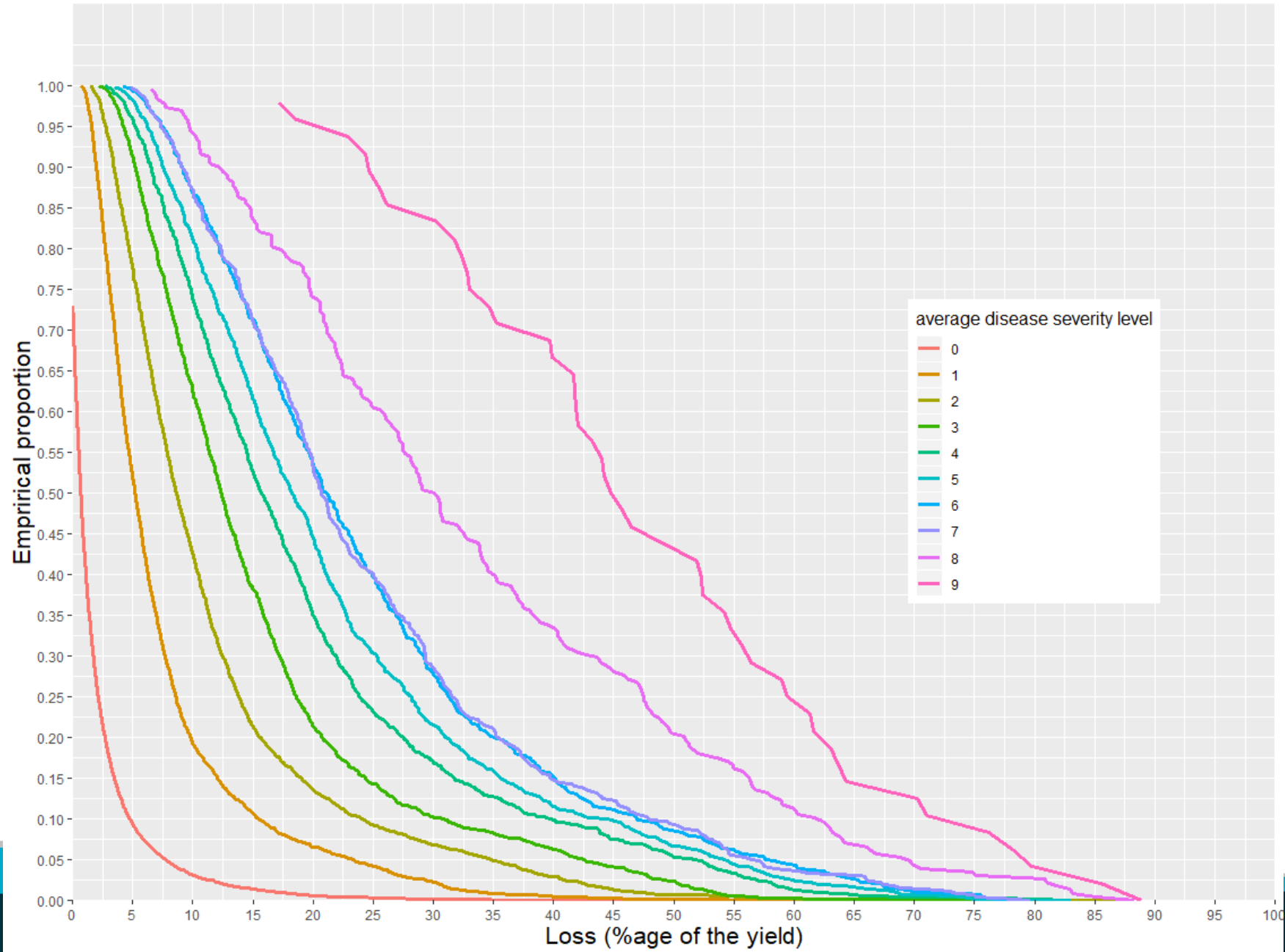


Yield-disease relationship
across different locations

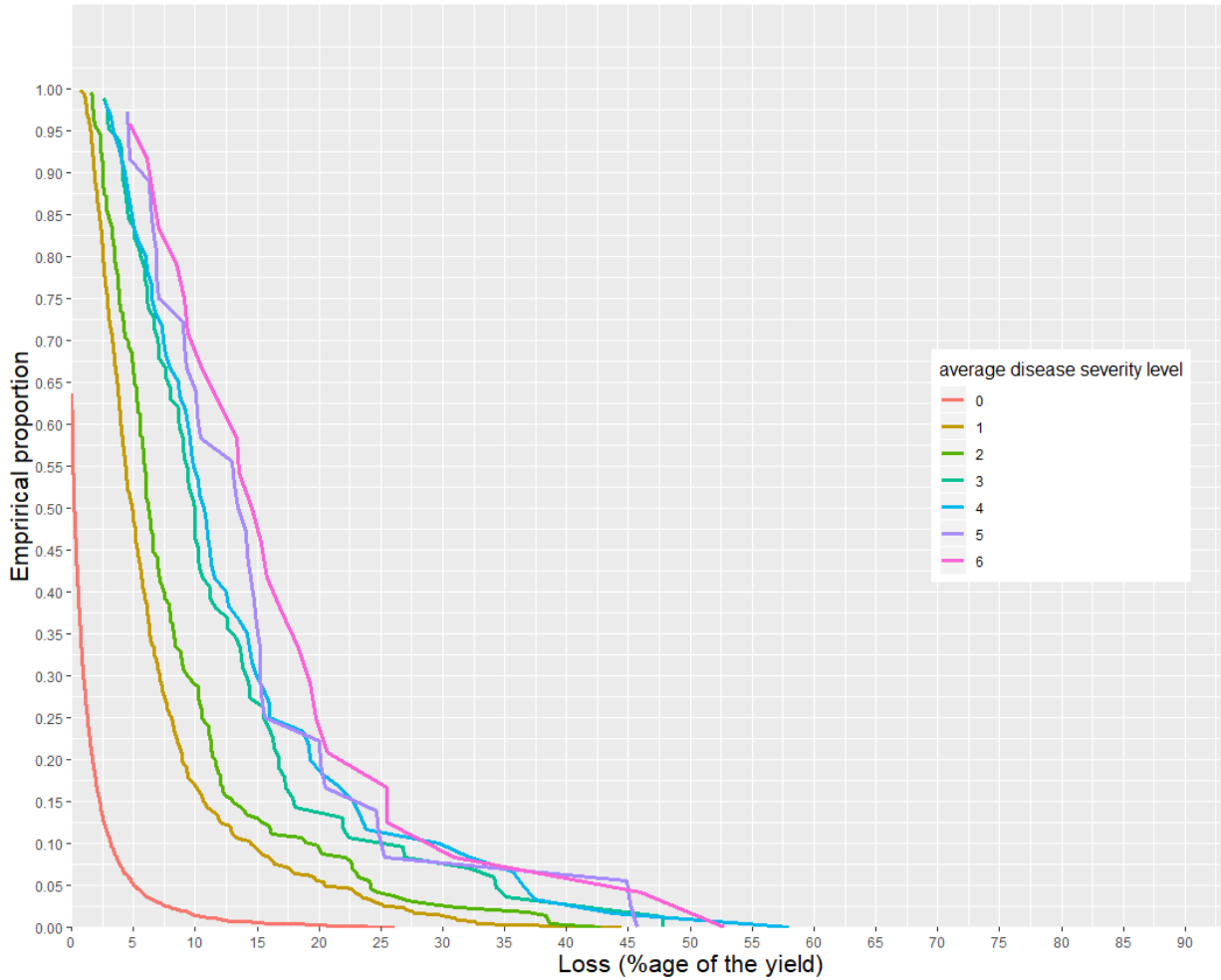


Signif. codes: '***' 0.001; '**' 0.01; '*' 0.05; '.' 0.1; ' ' 1

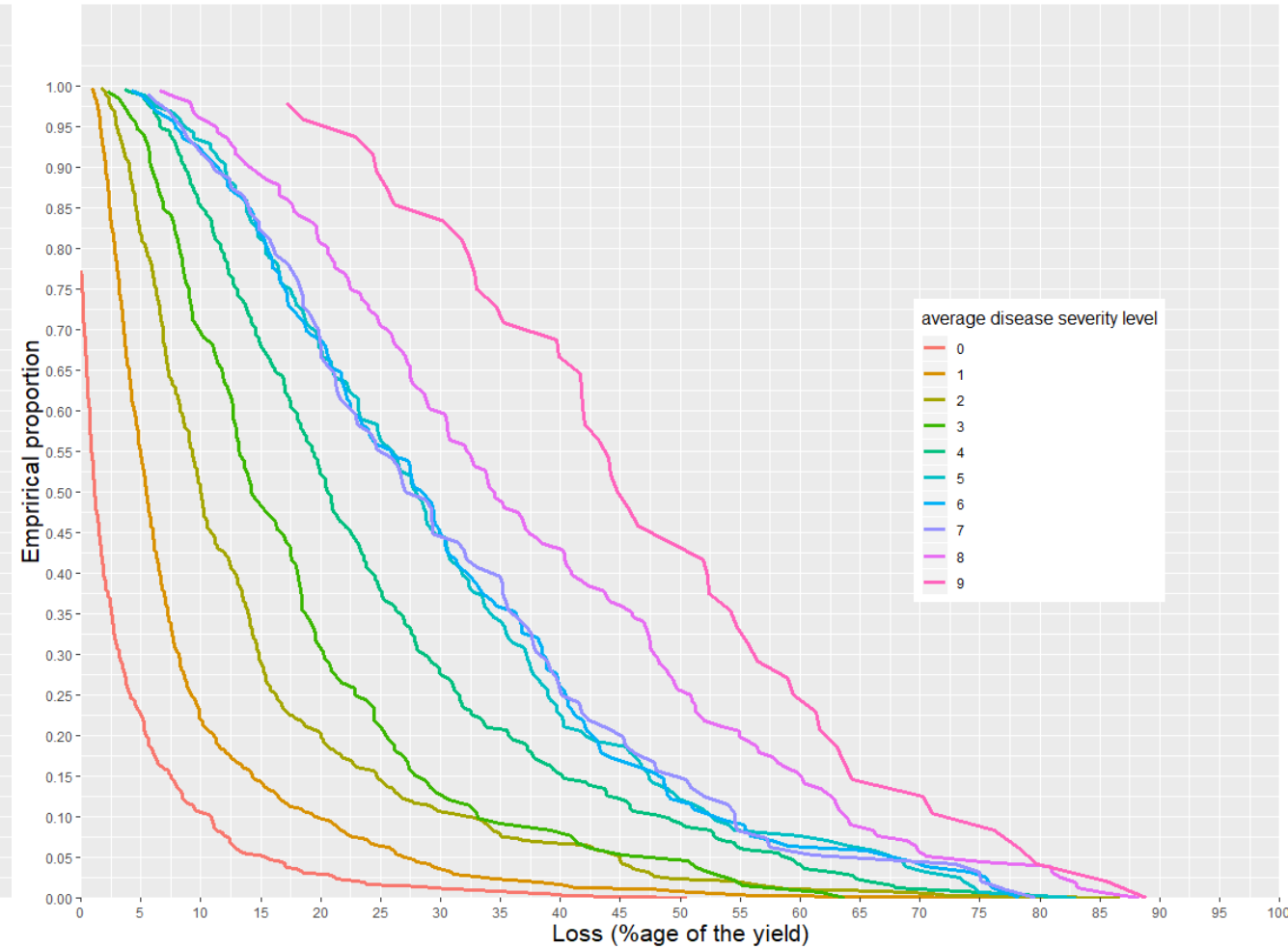
Empirical cumulative distribution curve $\Pr(\text{loss} \geq x)$



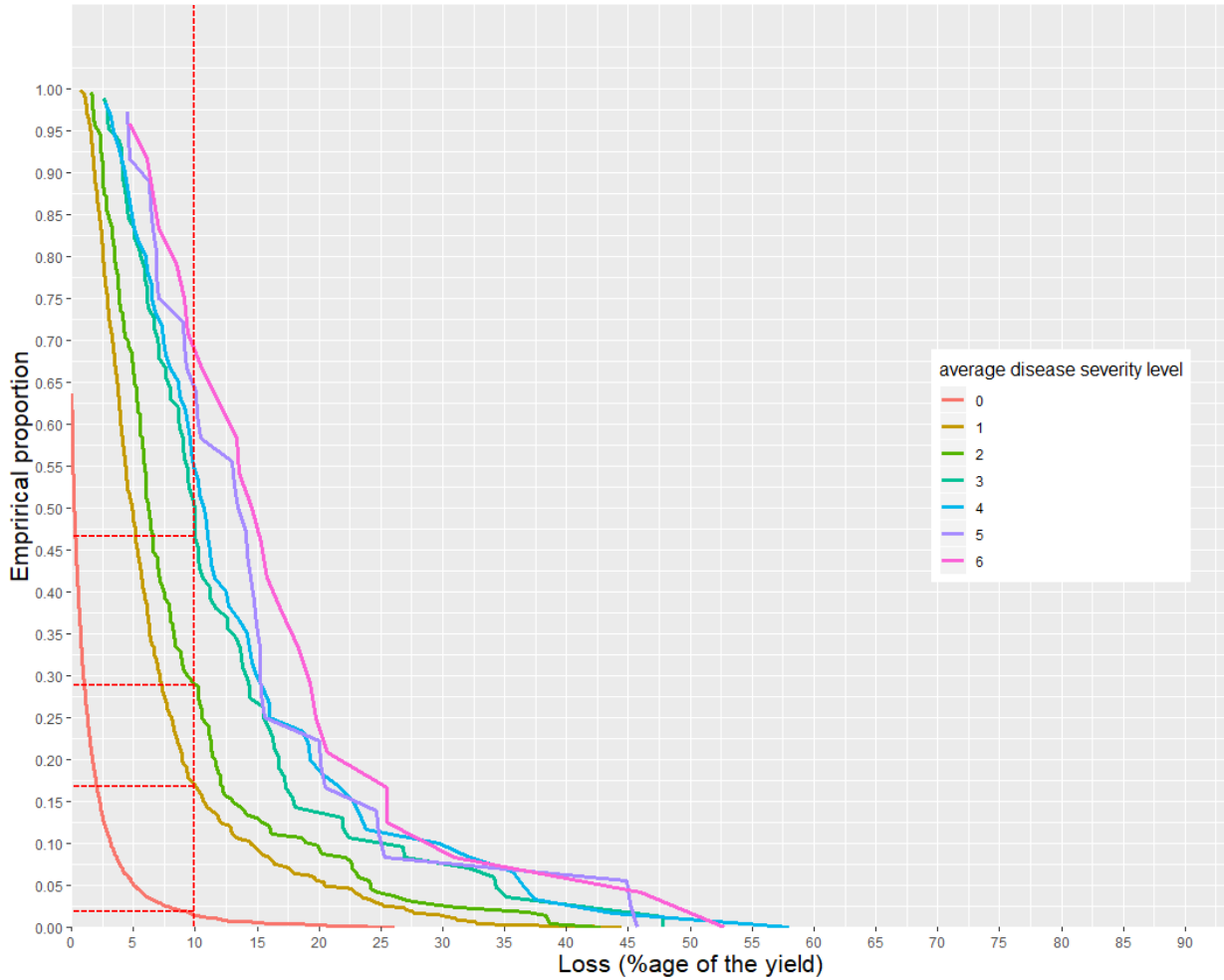
Empirical cumulative distribution curve
Pr(loss >= x) for R cultivars



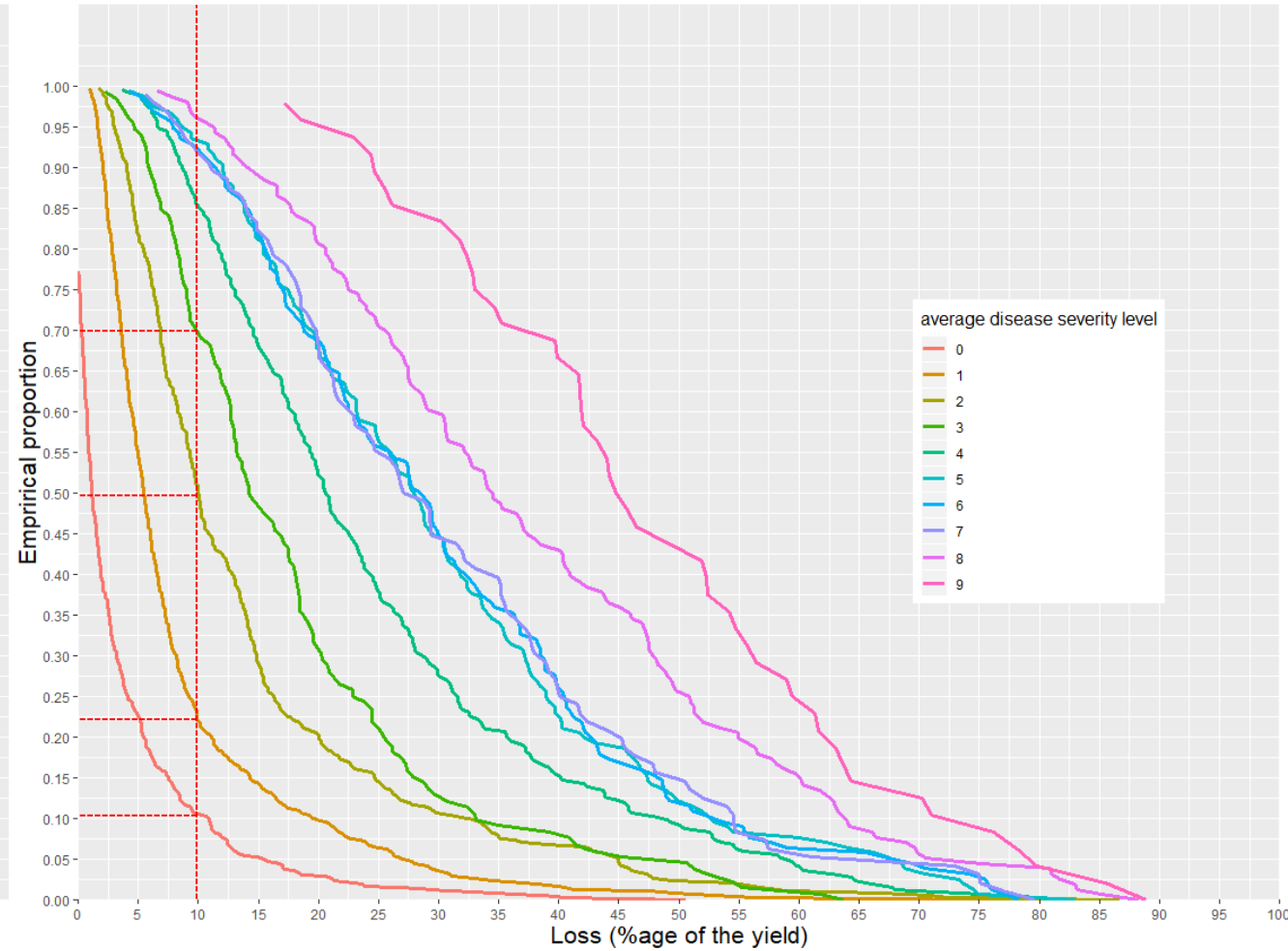
Empirical cumulative distribution curve
Pr(loss >= x) for MS-S cultivars



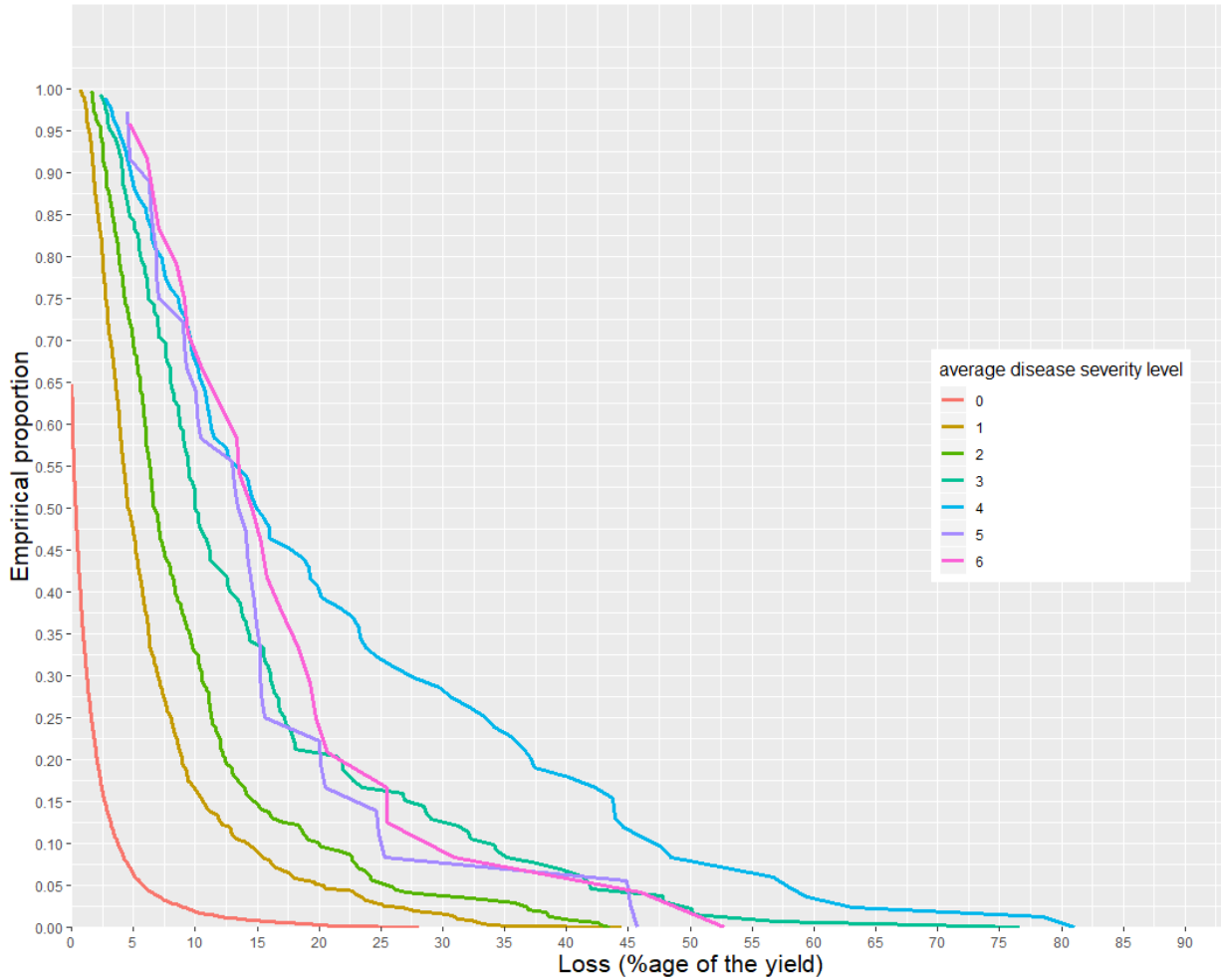
Empirical cumulative distribution curve
Pr(loss >= x) for R cultivars



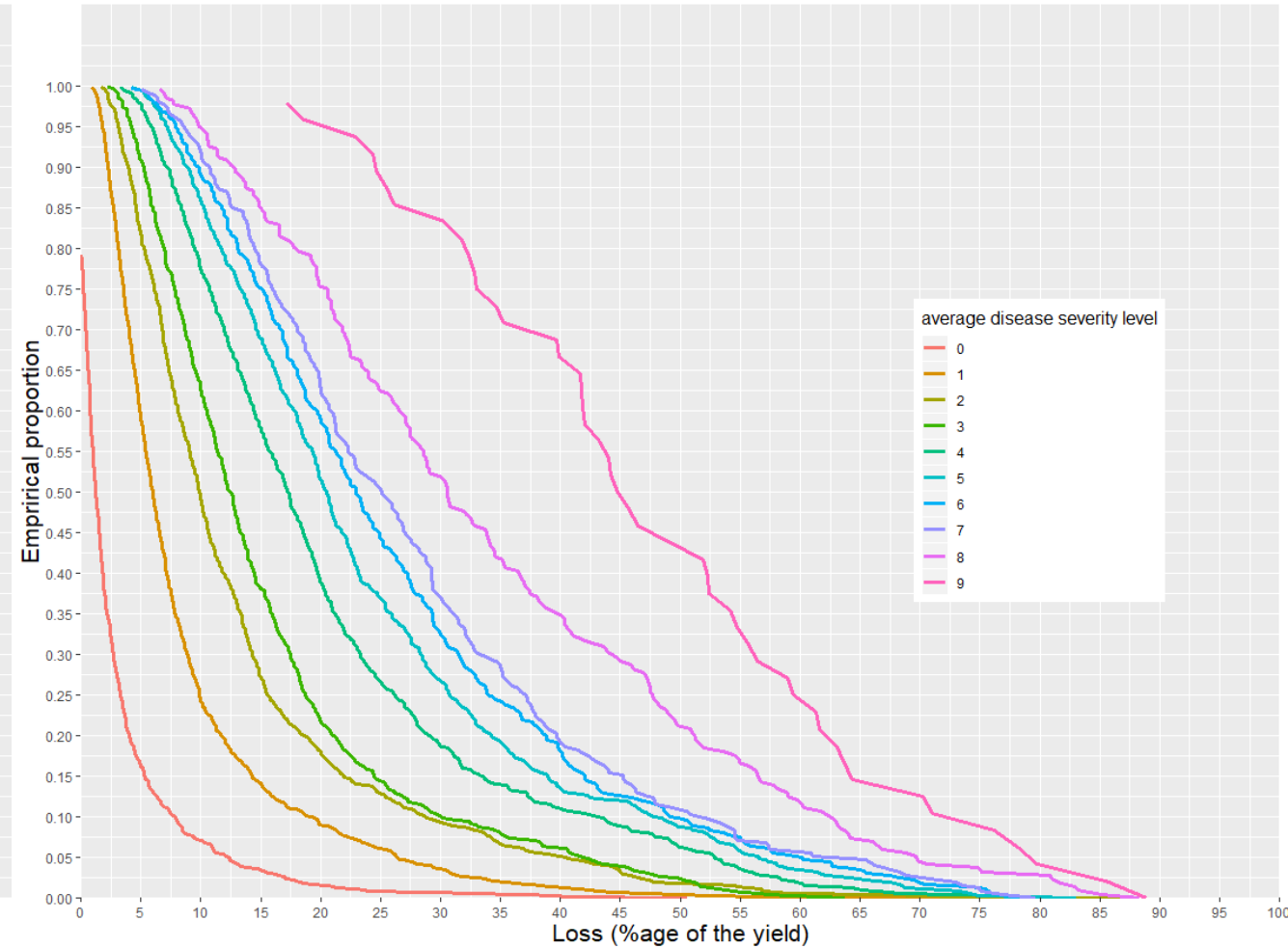
Empirical cumulative distribution curve
Pr(loss >= x) for MS-S cultivars



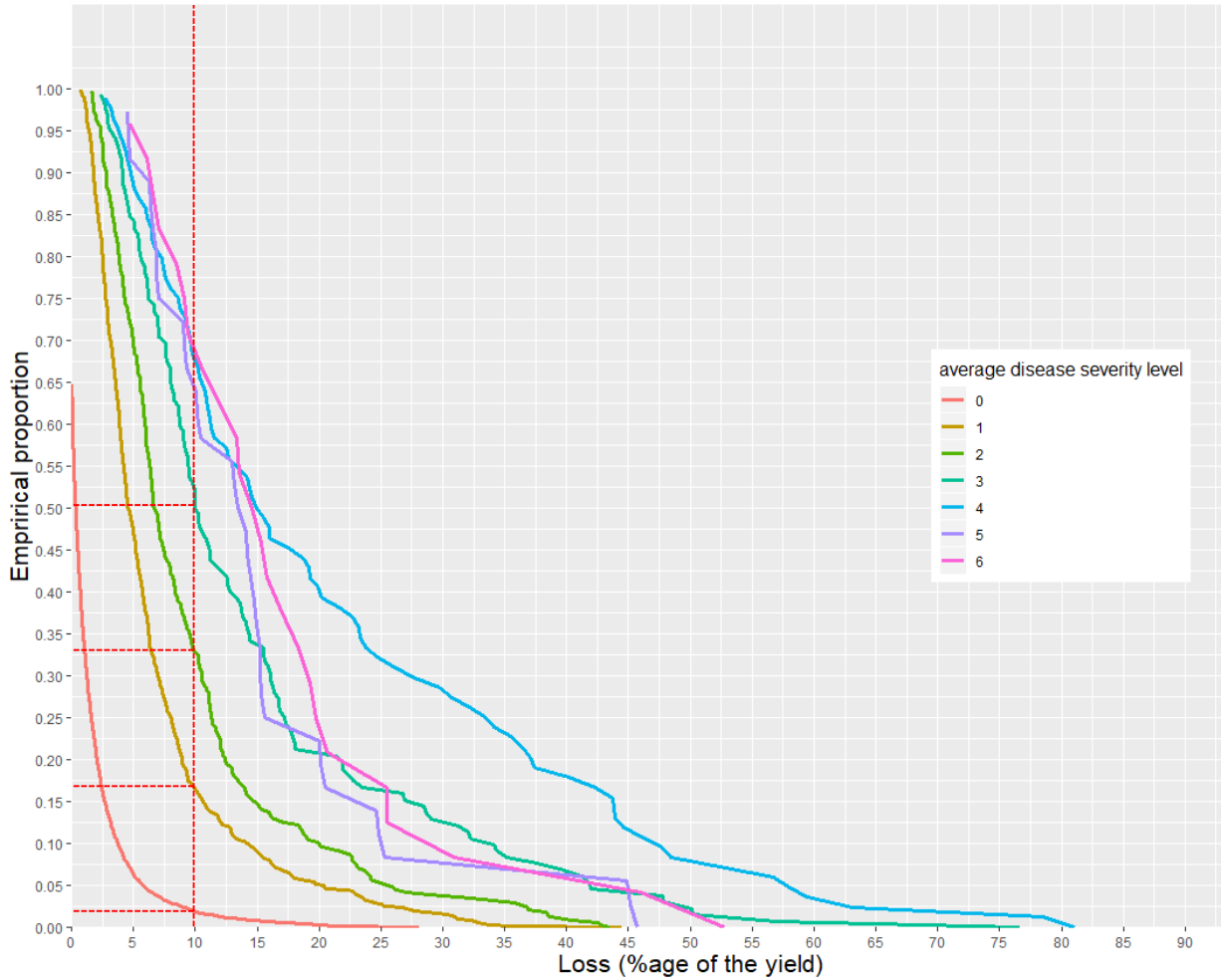
Empirical cumulative distribution curve
Pr(loss \geq x) for R and R-MR cultivars



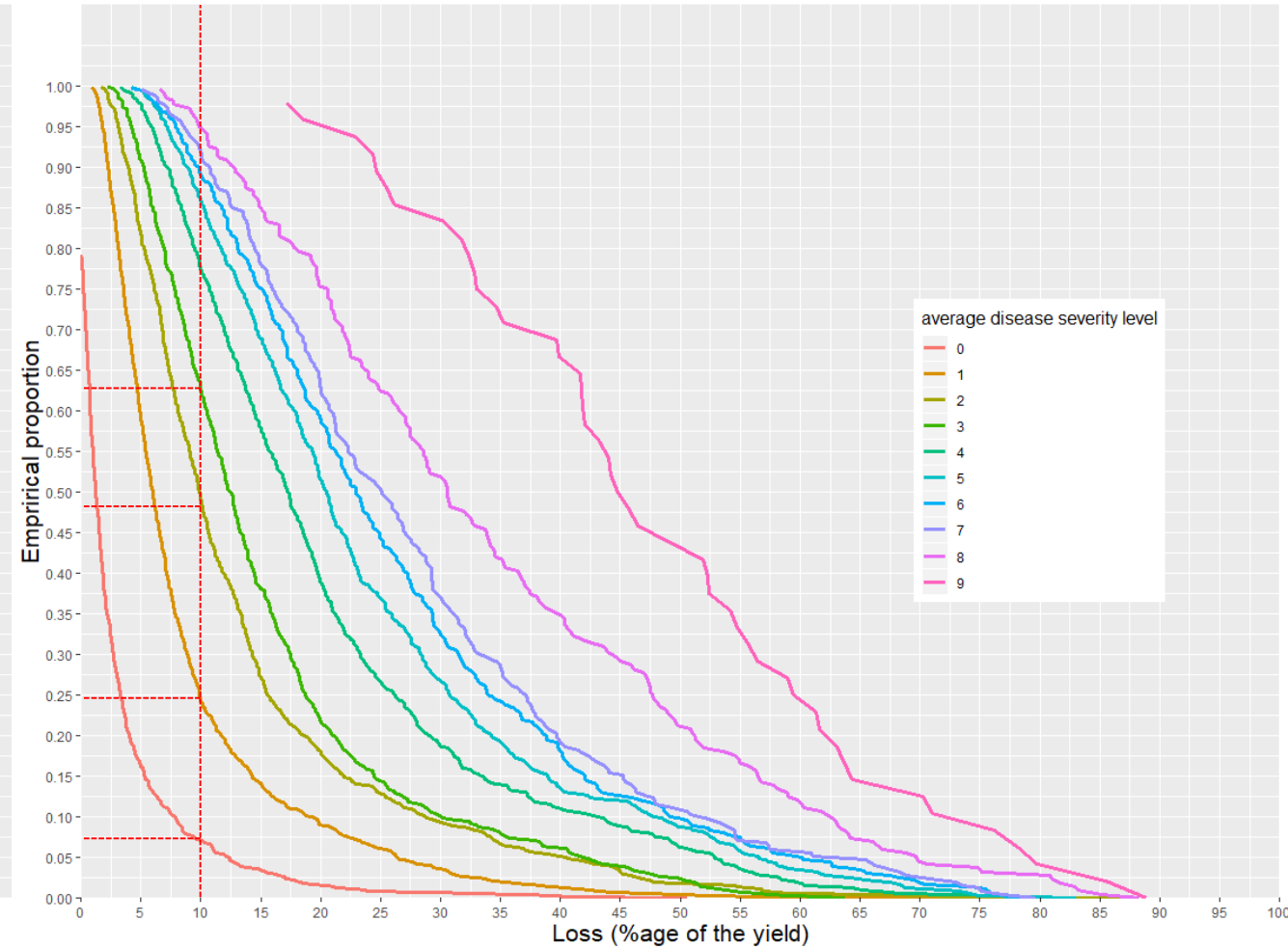
Empirical cumulative distribution curve
Pr(loss \geq x) for MS and MS-S cultivars



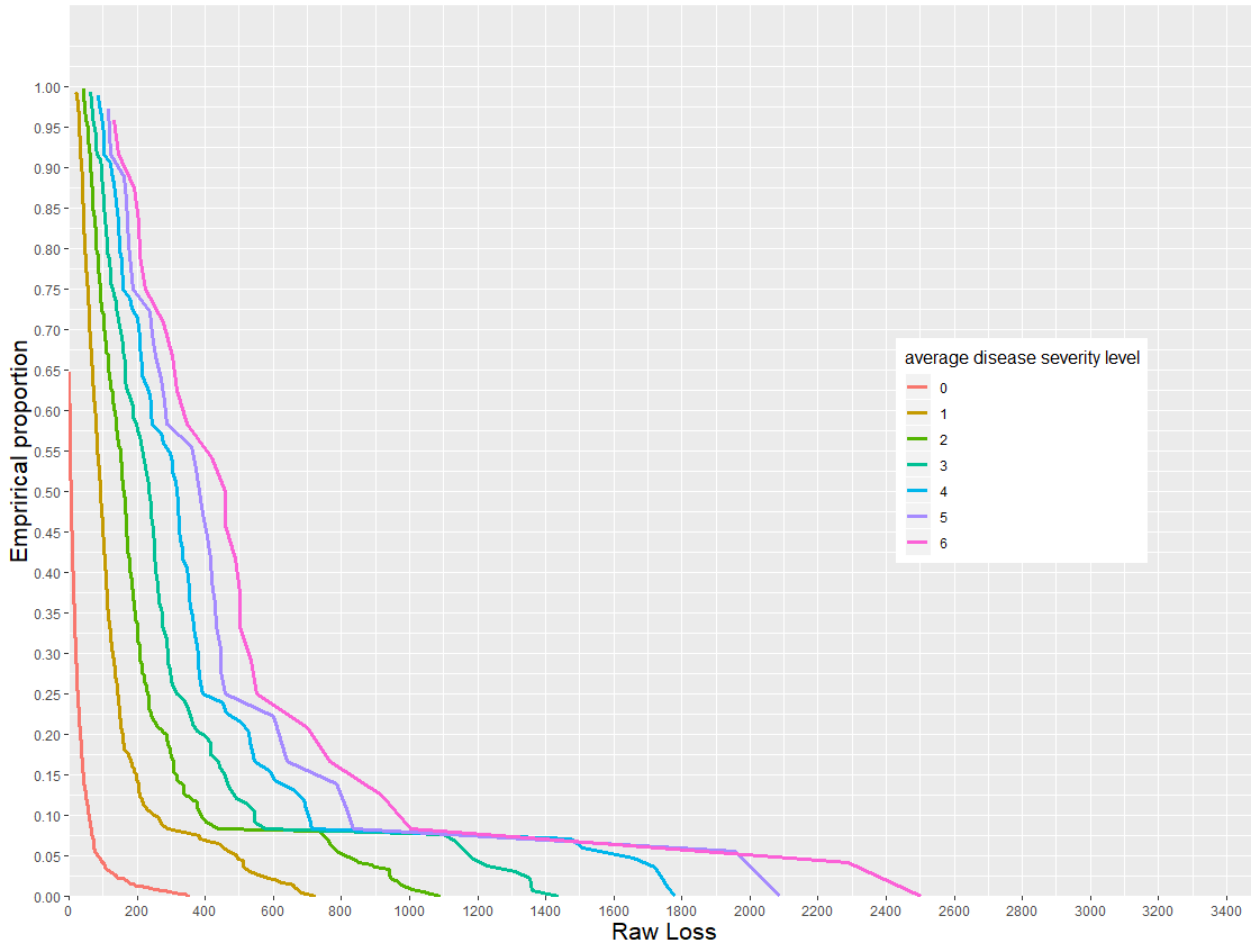
Empirical cumulative distribution curve
Pr(loss \geq x) for R and R-MR cultivars



Empirical cumulative distribution curve
Pr(loss \geq x) for MS and MS-S cultivars



Empirical cumulative distribution curve
 $\Pr(\text{loss} \geq x)$ for R and R-MR cultivars



Empirical cumulative distribution curve
 $\Pr(\text{loss} \geq x)$ for MS and MS-S cultivars

