



Mapping common bunt resistance in Canadian wheat cultivar AAC Tenacious

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Canada in the World

- Produces about 4% of the global wheat supply
- Accounts for about 15% of global wheat trade
- Overall, it generates about \$7 billion annually, and about \$11 billion when value-added food processing is considered



COMMON BUNT OF WHEAT

Caused by:

- *two species of fungi genus Tilletia [T. tritici (syn. T. caries) and T. laevis (syn. T. foetida)]*

Cause:

- substantial yield losses in caused significant crop damage in the Canadian prairies

Risk level:

- listed as Priority 1 disease in the registration testing system

Preferred approach to manage:

- Growing **resistant cultivars** is the most economical and environmentally safe approach, particularly for organic farming



Previous findings

- Several major and minor genes have been identified in wheat for common bunt resistance
- In our germplasm, we detected common bunt resistance QTLs on chromosomes 1A (*QBt.lrc-1A*) and 6A (*QBt.lrc-6A*) and 7A (*QBt.lrc-7A*), which co-segregate with stem rust resistance and stripe rust resistance
- Plant height is also reported to be associated with common bunt resistance
- Canadian breeding programs utilized *Bt10*
- Reliance on one major gene presents unnecessary risk to the wheat production

AAC Tenacious Pedigree

**Highly
resistant and
stable over
environments:**

Reward

Hope

Redman

Columbus

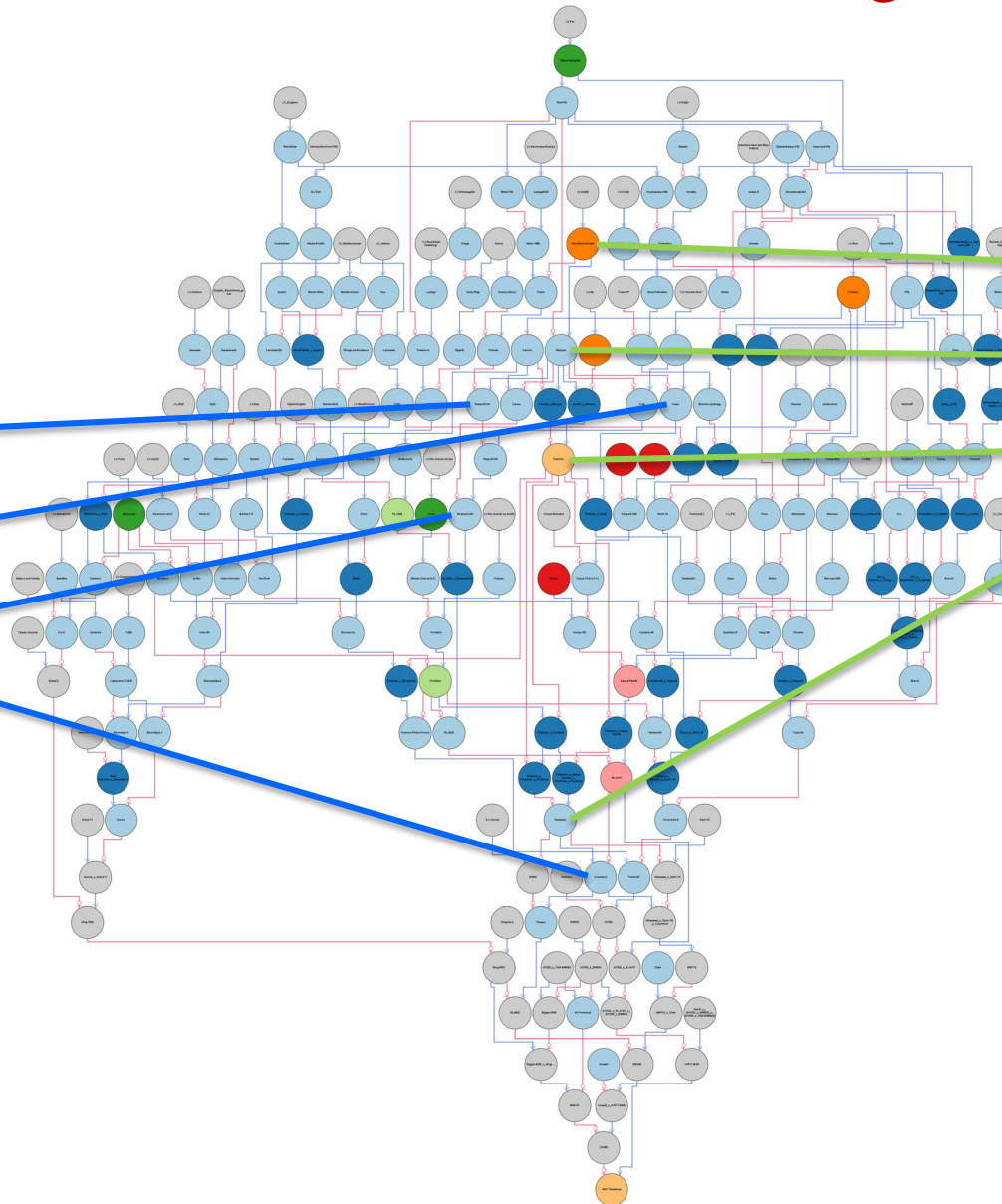
**Intermediately
resistant:**

Hard Red Calcutta

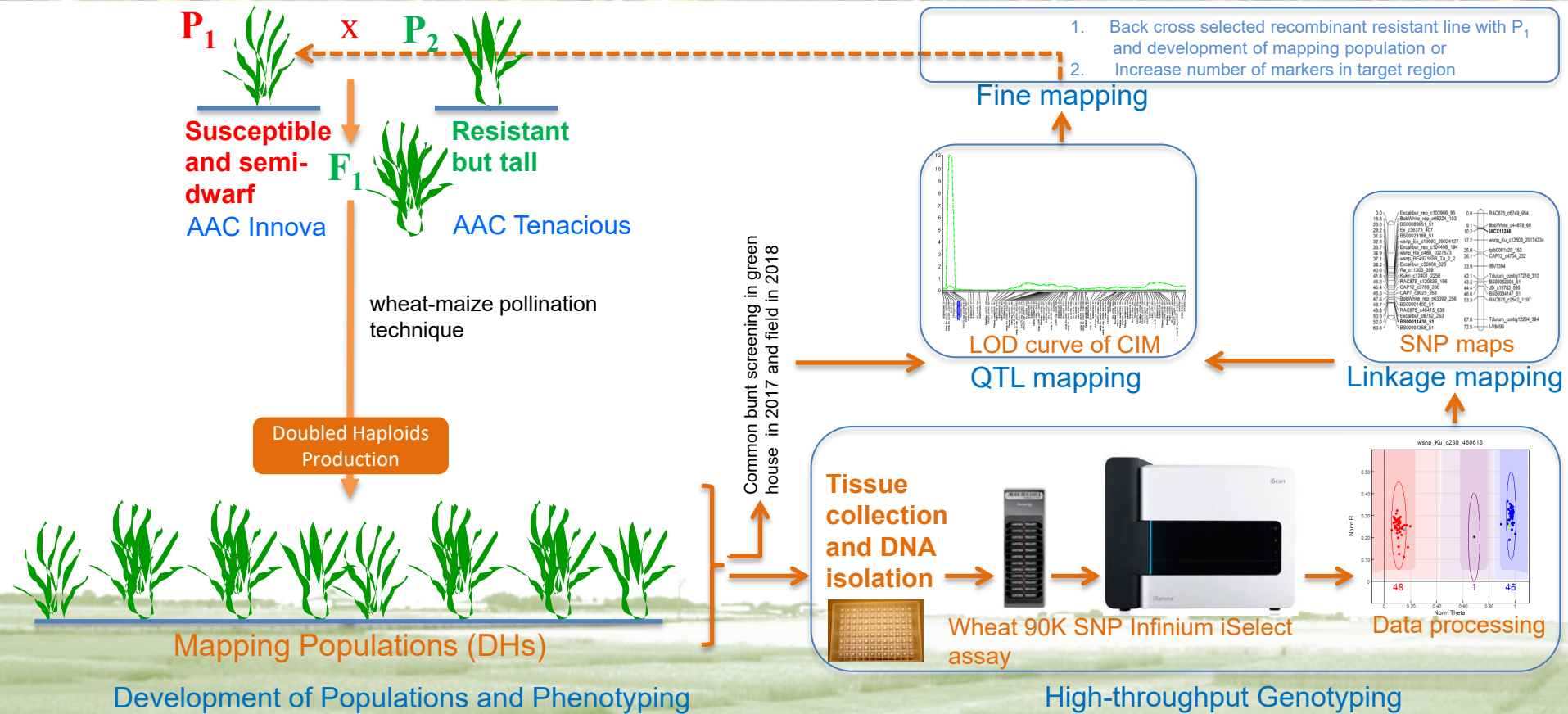
Marquis

Thatcher

Neepawa



QTL mapping



Screening of Parents, Checks, and Population for Common Bunt Incidence

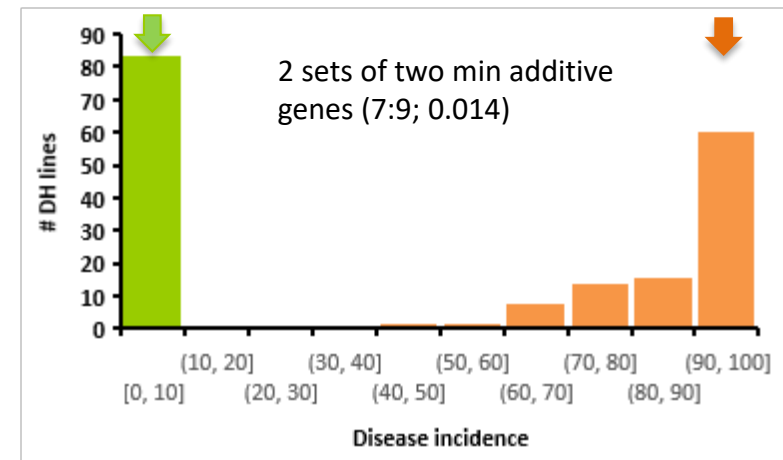
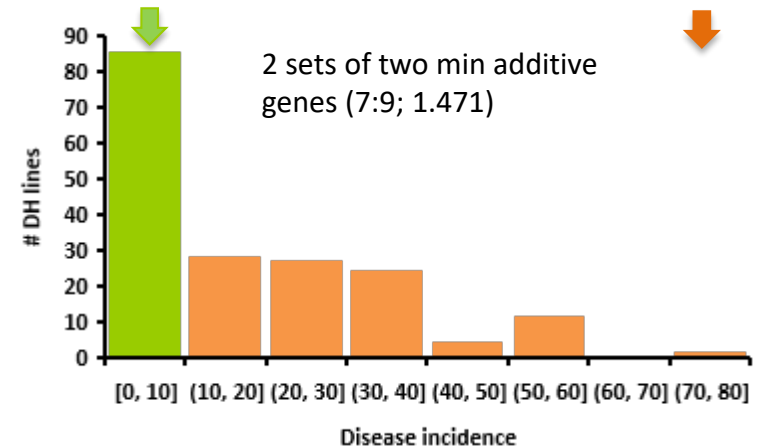
Cultivar	Disease incidence (range)
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Parents

AAC Innova	88.9 (77.71 – 100) %	↓
AAC Tenacious	0 %	↓

Check cultivars

Sadash	100 %
Indus	94.25 (75 – 100) %
Foray	93.83 (66.66 – 100) %
Neepawa	90.84 (44.44 – 100) %
Fielder	89.15 (44.44 – 100) %
Carberry	70.17 (33.33 – 92.30) %
Foremost	4.64 (0 – 30) %
Penhold	0.78 (0 – 6.25) %



$$r = 0.76$$

Disease Incidence



Healthy heads and seeds

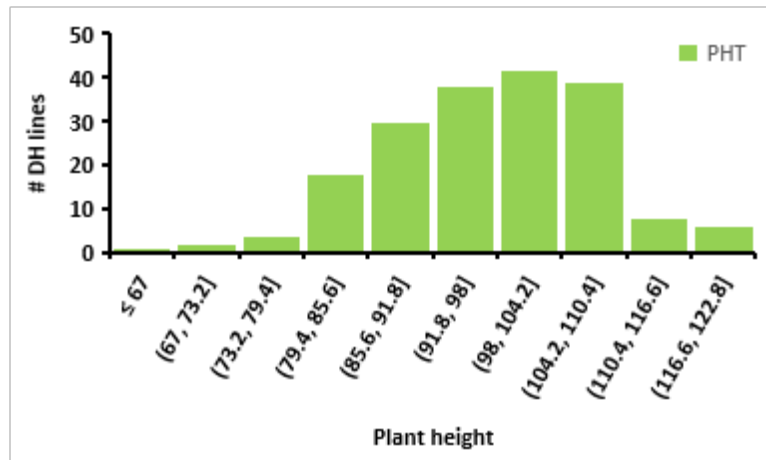



Diseased heads and seeds


A representative figure of reactions of resistant (left panel) and susceptible (right side panel) DH lines.



Genetic variation for plant height



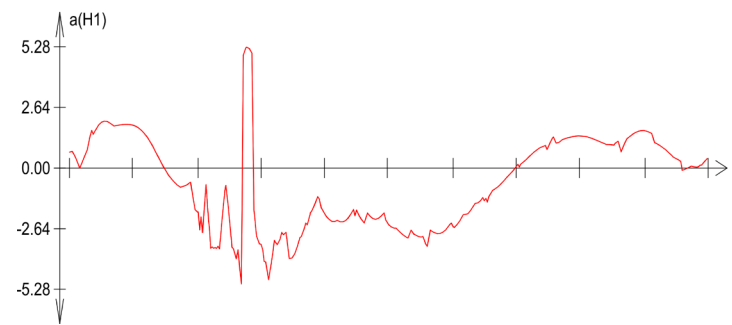
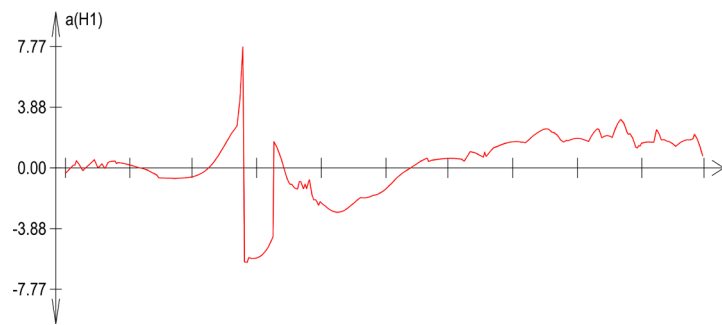
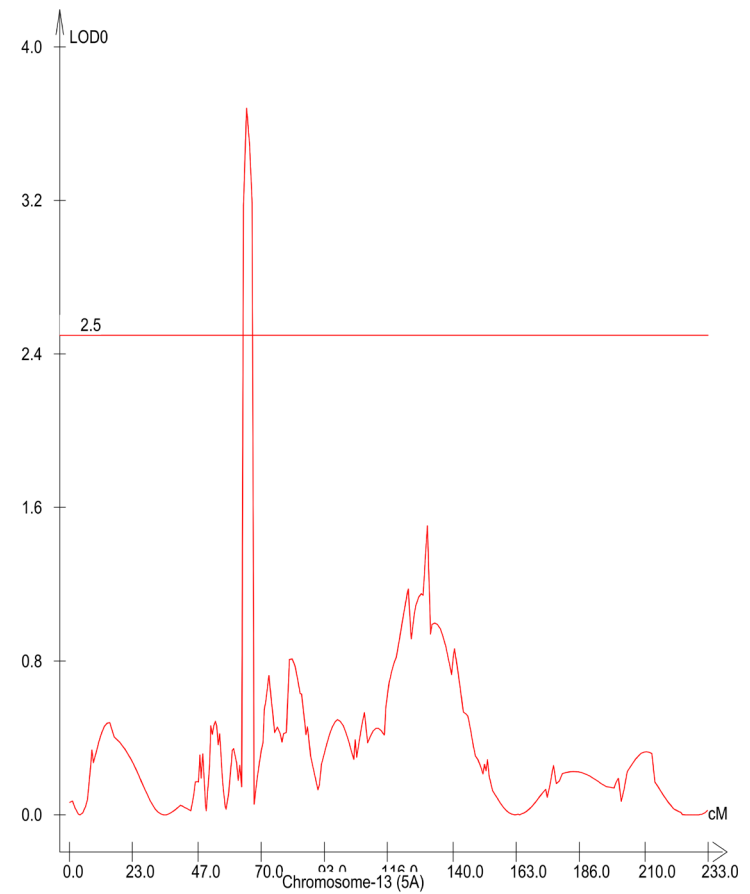
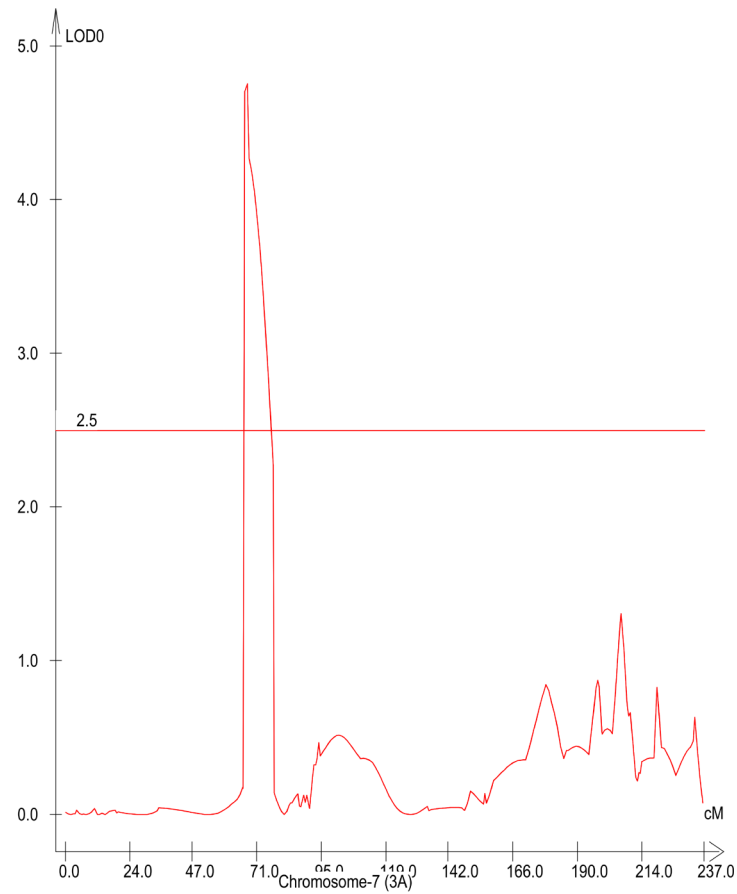
 AAC Tenacious (tall)
- carry a gibberellic acid (GA)-sensitive (*Rht-B1a*), tall allele
- the brassinosteroid-sensitive tall allele *Rht8a*

 AAC Innova is semi-dwarf
- carry a gibberellic acid (GA)-insensitive (*Rht-B1b*), semi-dwarf allele
- the brassinosteroid-sensitive semi-dwarf allele *Rht8c*

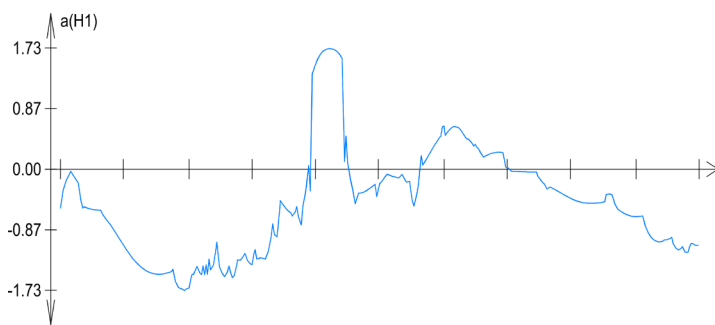
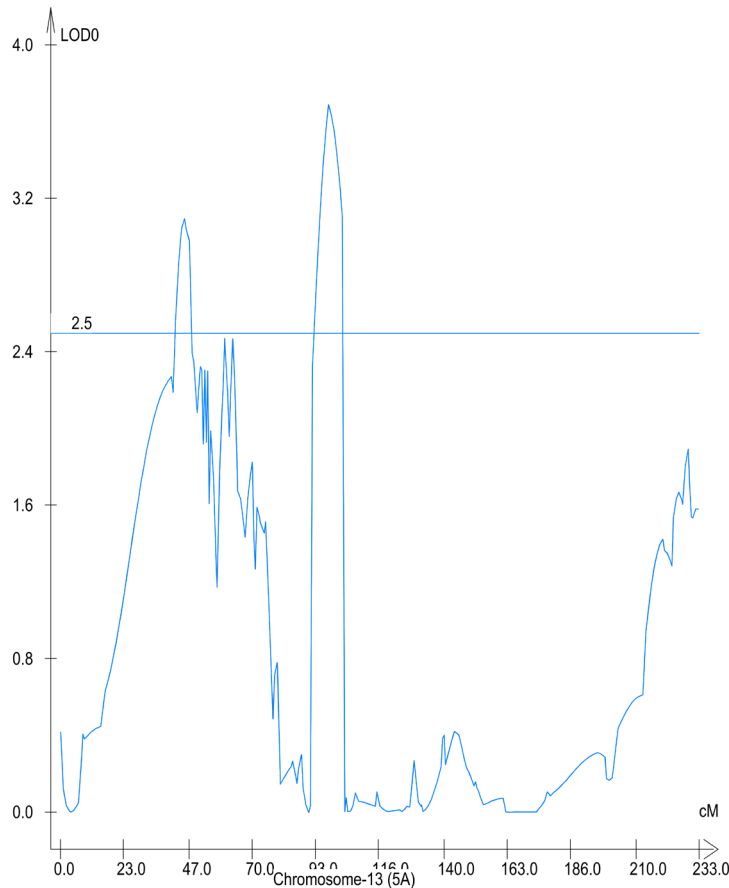
Quantitative trait loci

QTL	Chr	Position	Interval	Additive			Closest marker	Donor
				LOD	effect	PVE		
Common bunt								
<i>QBnt.Irdc-3A</i>	3A	67.7	66.4 - 76.5	4.76	-6.11	9.8	GENE-1533_226	AAC Innova
<i>QBnt.Irdc-5A</i>	5A	64.7	63.2 - 67.0	3.68	5.22	7.8	wsnp_BE443187A_Ta_2_3	AAC Tenacious
Plant height								
<i>QPhI.Irdc-5A</i>	5A	45.3	41.7 - 47.9	3.1	-1.77	0.8	RAC875_c25072_389	AAC Innova

Quantitative trait loci



Quantitative trait loci

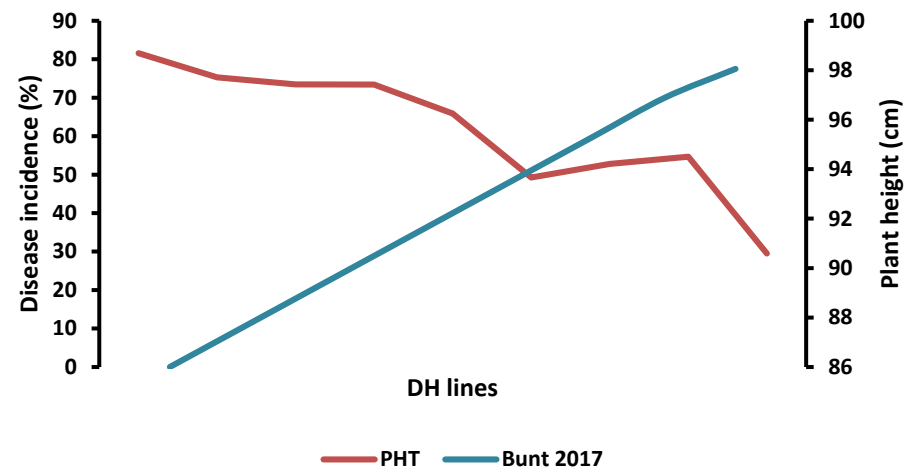


QPh.t.Irdc-5A.1 overlap almost same region as *QBnt.Irdc.5A*

QPh.t.Irdc-5A.1 detected only in disease nursery

QPh.t.Irdc-5A.2 is stable QTL and detected in multiple environments

Common bunt and plant height relationship



Future Perspectives

- 🌾 QTL mapping involving multiyear data.
- 🌾 Fine mapping of identified QTLs.



2021 Spring Wheat Bunt Nursery

Summary

- Both AAC Tenacious and AAC Innova contribute resistance QTL for common bunt
- Resistance is governed by minor additive genes/QTLs; however large scale study is required
- Though it is not clear but it seems 3A QTL pleiotropically reduces plant height



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