

Introduction

Lodging, which refers to the permanent displacement of plants from their upright positions, is a constraint to wheat production since it decreases harvest efficiency and causes grain yield and quality losses (Chen et al., 2018). Lodging is influenced by genetic and environmental factors, and agronomic practices (Figure 1).

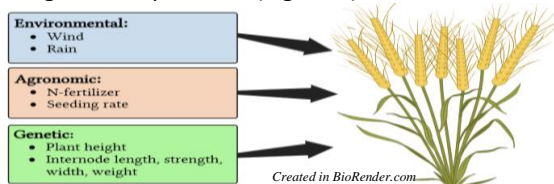


Figure 1. Factors influencing lodging in wheat.

The primary management approach of using semi-dwarfing genes causes reductions in plant height and limits yield potential by reducing canopy photosynthetic leaf area (Pearce, 2021). Therefore, genetic improvement of lodging-related stem traits plays a crucial role for improving the resistance of a wheat plant to lodging.

Objective

To identify genetic markers/genes and genomic regions for lodging resistance in spring wheat through a genome-wide association study.

Materials and Methods

- **Plant materials and trials:** A mapping population of 181 diverse wheat genotypes was tested in replicated trials under multiple environments.
- **Phenotypic data:** Main stems of ten plants were sampled from each wheat line per trial environment at the milk growth stage to examine the following traits:
 - ✓ **Breaking Strength:** Force to break the 2nd basal internode
 - ✓ **Bending Moment:** Plant height x fresh weight
 - ✓ **Lodging Index:** Bending moment/Breaking strength x 100

- **Genotypic data:** The mapping population was genotyped using an array of known genetic markers.
- **Association Mapping Analysis:** Association between phenotypic data and genetic markers was performed using a significance threshold to determine markers and genomic regions associated with lodging-related traits.

Results and Discussion

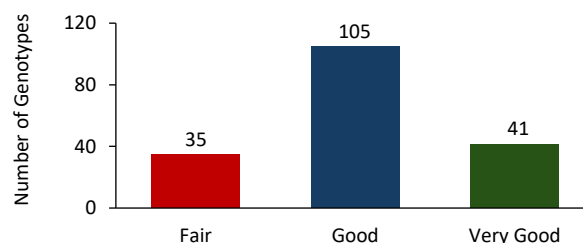


Figure 2. Grouping of genotypes from the mapping population based on lodging index values.

- Based on their lodging index values, mapping population genotypes were rated as having Very Good (2500-4300 g cm/N), Good (4301-5500 g cm/N), or Fair (5501-7500 g cm/N) lodging resistance (Figure 2).

Table 1. Effect of environment, genotype and their interaction on lodging index.

Sources of Variation	P-values
Environment	< 2e ⁻¹⁶
Genotype	< 2e ⁻¹⁶
Genotype x Environment	0.062

- Analysis of variance showed that lodging index/lodging resistance was significantly influenced by genotype and environment (P < 0.05), but not by the interaction of genotype and environment (Table 1).
- There was significant positive correlation between trial environments for lodging index (Table 2).

Table 2. Correlation between trial environments for lodging index.

Environment	WPG22	GH22	WPG23
GH22	0.27*		
WPG23	0.47*	0.43*	
WPG24	0.33*	0.38*	0.48*

- Highest correlation was observed between Winnipeg 2023 and Winnipeg 2024 trial environments (Table 2).

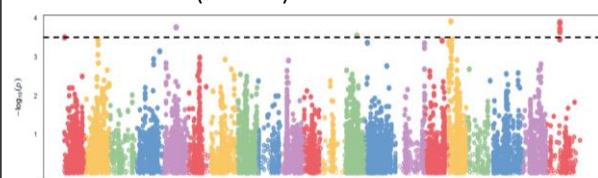


Figure 3. Association of genetic markers (dots) with lodging index. Significantly associated markers are shown above the dotted threshold line.

- Eight genetic markers across four genomic regions were found to be significantly associated with lodging index (Figure 3).

Conclusions

- Genotypes in the mapping population showed diverse lodging resistance levels.
- Lodging index/lodging resistance was influenced by both environment and genotype.
- Lodging index was positively correlated between any two trial environments.
- This study identified eight genetic markers associated with lodging index in the mapping population.

References

- Chen et al. (2018) Field Crops Research 228: 31-38.
Pearce (2021) Journal of Experimental Botany 72 (2): 157-160

Acknowledgements