Expanding the toolkit for breeding sclerotinia stem rot resistance and other traits in canola

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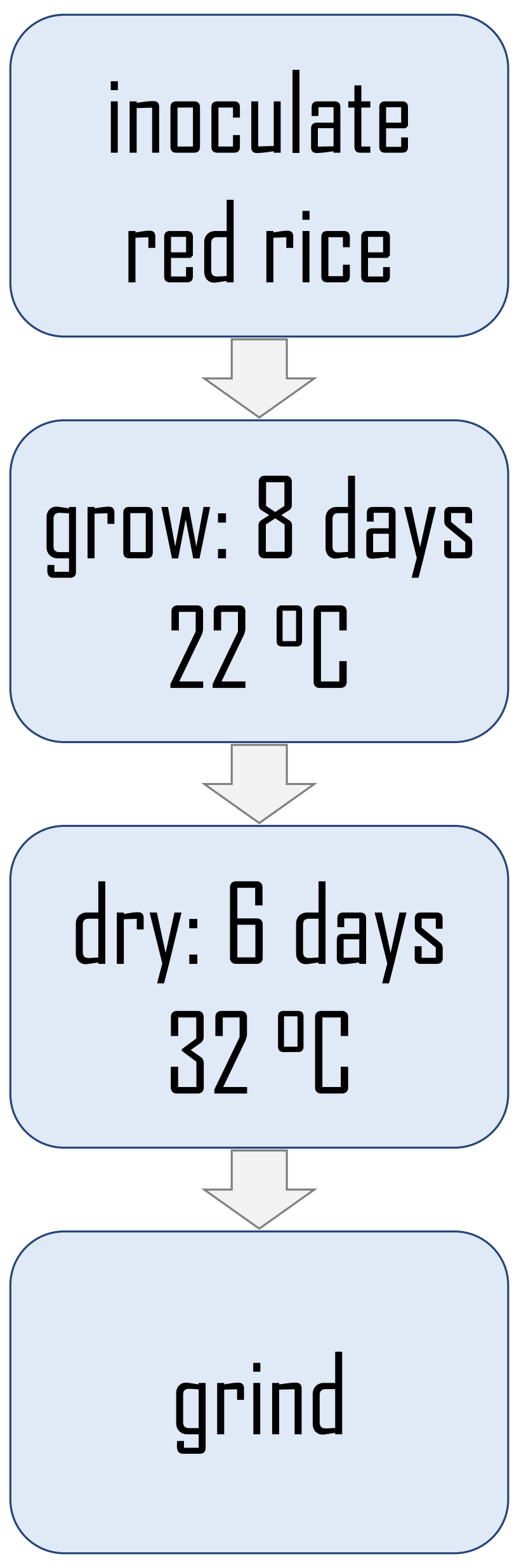
Background

Sclerotinia stem rot (SSR), caused by the fungus *Sclerotinia sclerotiorum*, is a damaging canola (*Brassica napus*) disease. Its large host-range and persistence in soil reduce the effectiveness of management with crop rotation. Furthermore, fungicides may be costly, and a single spray may not adequately cover extended SSR outbreaks.

Partial cultivar resistance is another tool for managing SSR. Ideally, partially resistant cultivars are substantially less susceptible to SSR, whilst maintaining good agronomic traits. There are few canola cultivars with partial SSR resistance globally, and none in Australia, a major canola exporter. To address this, we are developing new tools and resources for breeding partially SSR-resistant Australian canola.


inoculate red rice

grow: 8 days 22 °C

dry: 6 days 32 °C

grind

Figure 1 Above: Ground red rice inoculum used for evaluating plants in the field. **Right:** Procedure used to create large quantities of ground red rice inoculum.

Methods

To screen *B. napus* in the field, we prepare inoculum composed of ground red rice colonised with *S. sclerotiorum* mycelium (**Figure 1**). Using this method, we have compared three *B. napus* varieties, Chisaya, Chikuzen and Norin 28, which were used in early Australian canola breeding programmes, with the current Australian cultivar ATR Bonito (Nuseed). Plants were grown in six replicate plots with overhead irrigation.

We have developed long read PacBio and Oxford Nanopore P2 sequencing data for 21 *B. napus* varieties in the founding Australian canola breeding pedigree (Cowling et al., 2007). We have also developed short read sequencing data for 399 diverse spring and winter *B. napus*.

Results

Previous glasshouse and controlled environment studies suggested Chisaya, Chikuzen and Norin 28 are more resistant than ATR Bonito (Derbyshire et al., 2021; Newman et al., 2023). We found the same result using whole plant field inoculations. This was most strongly apparent in reduction of severe disease with a score > 3 (**Figure 2**).

Analysis of the whole genome sequencing data is ongoing. We aim to use it to identify causal variants for improving genomic prediction and gene editing for SSR resistance.

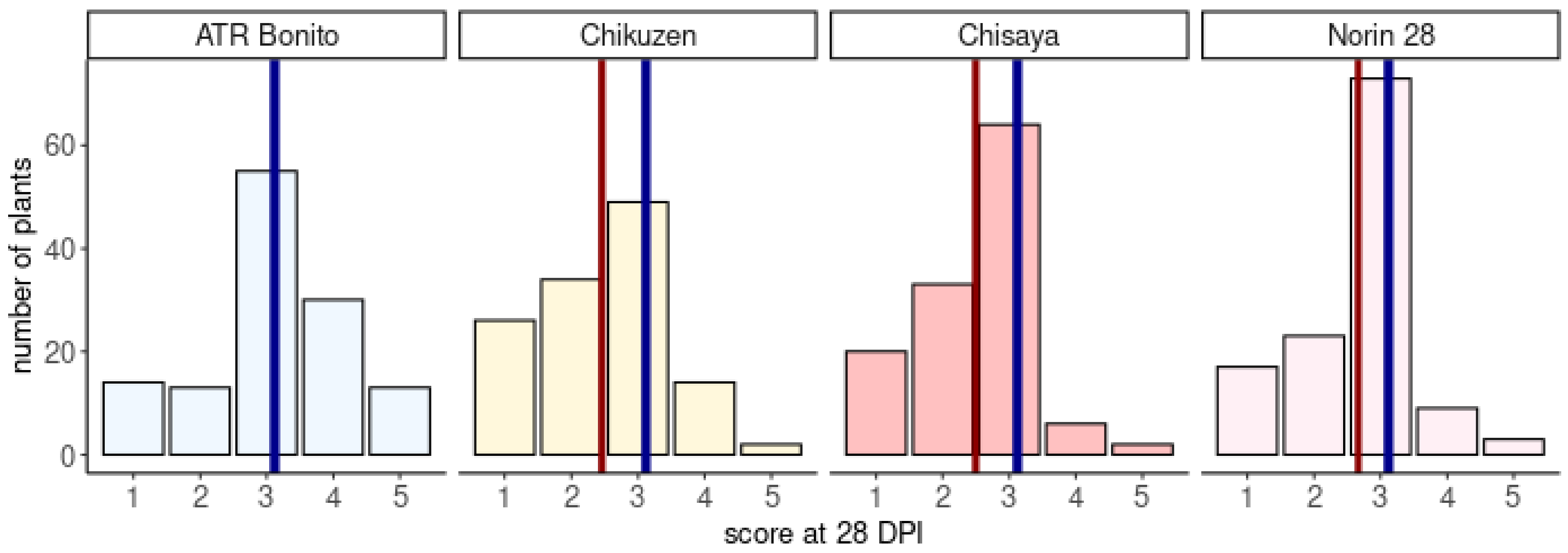
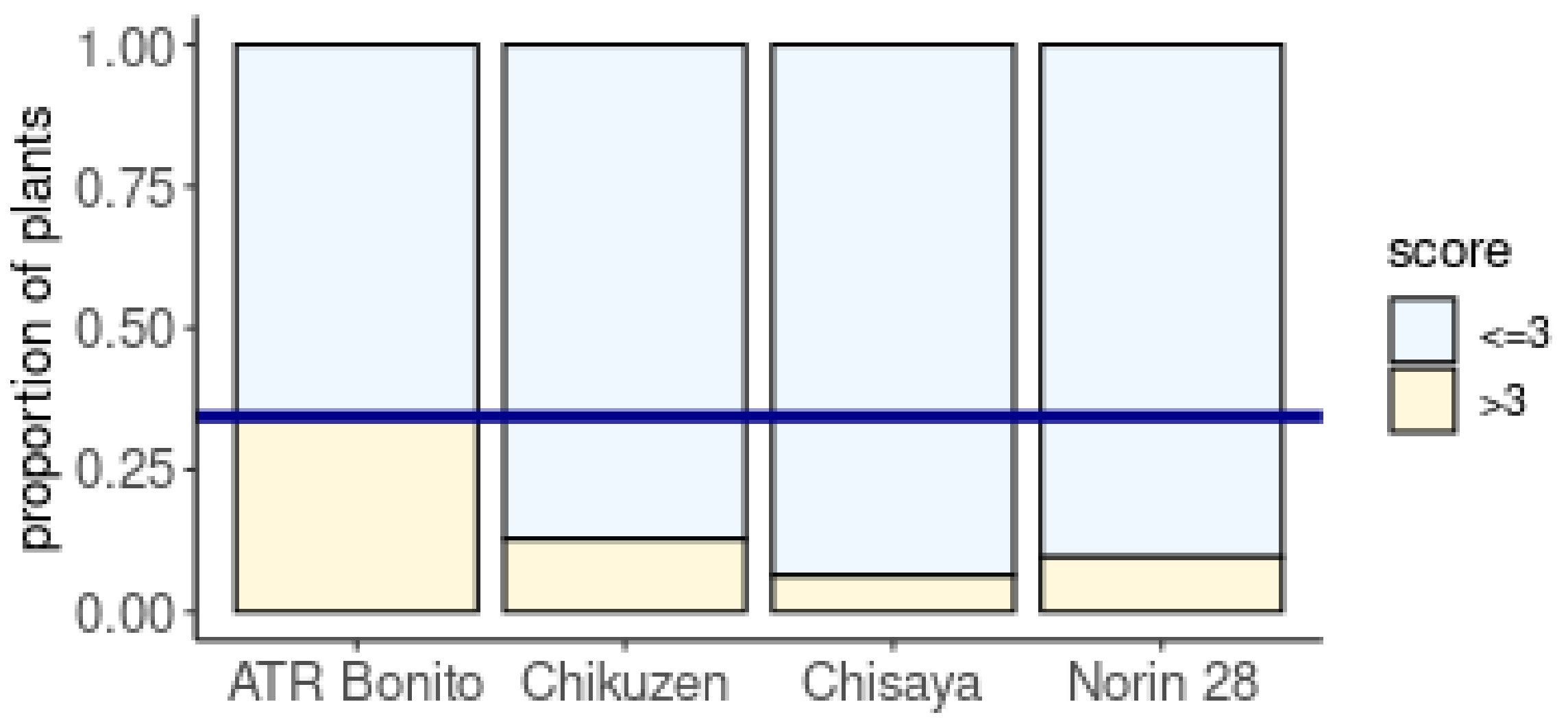


Figure 2 Above: Disease scores (x axis) for the four varieties. The y axis is the number of plants. Blue vertical lines show mean score for ATR Bonito and red vertical lines show means for the three SSR-resistant varieties. **Right:** The proportion of plants (y axis) with SSR severity scores > 3 (yellow bars) for each of the varieties. These were markedly reduced in the three SSR-resistant lines.



References

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