Identification of chromosomes responsible for crown rot resistance in durum wheat

Zheng Z[1,2], Li HB[1], Ma J[1,4], Chakraborty S[1], Faris JD[3], Xu SS[3], Liu CJ[1,4*]

1. CSIRO Plant Industry, Queensland Bioscience Precinct, 306 Carmody Road, St Lucia, QLD 4067, Australia

2. Institute of Crop Protection, Hebei Academy of Agricultural Sciences, Baoding, China

3. USDA-ARS, Northern Crop Science Laboratory, Fargo, ND 58105, USA

4. School of Plant Biology, Faculty of Natural and Agricultural Sciences, The University of Western Australia, Crawley, Perth, WA 6009, Australia

****Corresponding author: chunji.liu@csiro.au***

ABSTRACT

Crown rot (CR), caused by *Fusarium* species, is the most serious biotic threat to the Australian wheat industry. Compared with bread wheat (2n=6x=42), durum wheat (2n=4x=28) is more susceptible to CR. In an effort to understand the genetics of CR resistance in durum wheat, we have analysed three sets of Langdon-*Triticum dicoccoides* (LDN-DIC) disomic chromosome substitution lines. We found significantly different levels of CR resistance among these substitution lines. CR resistance attributed to a particular LDN chromosome differed for the 3 substitution sets, indicating that genes conferring CR resistance in the three donor parents have different chromosomal locations. With better CR resistance than either parent, LDN (PI481521-2A) was the least susceptible genotype among the substitution series. These data suggest that the 2A chromosome of LDN might harbour genes that increase CR severity/susceptibility, thus replacing it with a homologue from another genotype may be beneficial in improving CR resistance. On the contrary, the two available 3B substitutions [LDN(IsraelA-3B) and LDN(PI478742-3B)] had the lowest CR resistance among their respective sets of substitutions series, suggesting that the LDN 3B chromosome may be more important in reducing CR infection than other chromosomes. Thus, retaining LDN 3B could be beneficial in generating CR-resistant durum wheat. Further studies are required to determine if these chromosomes have similar effects in different durum genetic backgrounds.

INTRODUCTION

Growing durum wheat can be more profitable than growing bread wheat, as they have similar yield potential but the former often attracts a better price per unit of grain due to specific qualities. However, the threat of CR in Australia is so serious that many farmers are reluctant to take the risk of growing durum wheat as all existing varieties are highly susceptible to the CR pathogen. Improving crown rot resistance is among the most important breeding objective for the durum wheat industry.

We are investigating the genetics of CR resistance in durum wheat to determine ways to enhance resistance. One of our objectives is to ascertain whether the high level of CR susceptibility in durum wheat is caused by a particular chromosome. If such a chromosome does exist, replacing it with a homologue from another durum genotype or genotypes of a related species could form a strategy to breed resistant durum varieties. To address this objective, the three sets of Langdon-*T. dicoccoides* (LDN-DIC) disomic chromosome substitution lines developed by USDA-ARS scientists were analysed. Results from this analysis are reported in this paper.

MATERIALS AND METHODS

Three sets of LDN-DIC disomic chromosome substitution lines developed by scientists at the USDA-ARS Cereal Crops Unit, Fargo, ND, USA were used in this study. These substitution lines share LDN as the recipient parent,with three different donor parents all belonging to *T. dicoccoides*. They are PI481521 (set1), Israel A (set2), and PI478742 (set3). Of the three sets of LDN-DIC substitution lines, the 1st set is the only one for which both parents and their 14 possible substitution lines were all available for this study. Four of the 14 possible lines were not available for the 2nd set of substitutions. Both the recipient and donor parents and 12 of the 14 possible lines for the 3rd set of substitutions were available. CR assays were carried out in the controlled environment facility at the CSIRO Plant Industry Brisbane Laboratories, with 25°C/18°C day/night temperatures and 60%/90% relative humidity, and a 15 hour photoperiod. A highly aggressive isolate of *F. pseudograminearum,* isolate CS3096 (Akinsanmi et al. 2004), was used for CR infection following the seedling soaking method as reported by Li et al. (2008). CR severity was visually scored using a scale of 0 (no CR symptom) to 5 (dead seedlings). Three to four replicates with five seedlings each were used for each of the three sets of substitution lines in an experiment and the experiment was repeated once.

RESULTS AND DISCUSSION

Compared with the recipient parent LDN, each line within a set of substitution series differs by only a single chromosome pair. Therefore, any difference detected between a substitution line and the recipient parent LDN should be controlled by gene(s) located on the substituted chromosome. For this reason, analysing phenotypes of these substitution lines can be useful to conveniently locate genes on particular chromosomes.

As shown in Table 1, highly significant difference was detected among substitution lines for each of the three sets of LDN-DIC substitution series analysed.

Of the two parents used in set1, the recipient parent LDN was less susceptible to CR infection (Fig. 1, Table 2). Among the substitution lines, 2A had the least CR severity and was significantly more resistant than both of the parental genotypes. In contrast, the two homoeologous group 3 chromosome substitutions, 3A and 3B, developed the most severe CR, similar to the donor parent. The remaining 11 substitutions gave similar CR reaction to either one or both of their parents (Figure 1; Table 2). Results from this set of substitution lines suggest that the susceptibility of the donor parent was mainly conditioned by the two homoeologous group 3 chromosomes. The higher CR resistance reaction of the 2A substitution line compared to either parent suggests that either the 2A chromosome from the donor parent confers improved resistance compared to LDN chromosome 2A; or LDN chromosome 2A harbours genes that confer increased CR susceptibility.

Table 1. Analysis of variance for the 1st set of LDN-DIC substitutions

Source of Variation	Sum of Squares	d.f.	Mean Squares	P
between	79.36	15	5.291	<0.0001
error	211.1	304	0.69	
total	290.5	319		

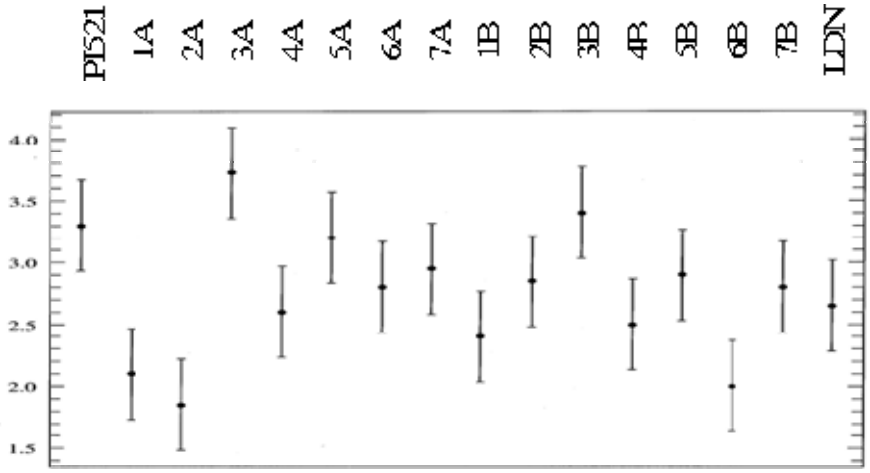

Figure 1. Crown rot reaction of the 1st set of LDN-DIC substitutions. A scale of 0 (no crown rot symptom) to 5 (dead seedling) was used for scoring crown rot severity.

Table 2. Crown rot reaction of three sets of LDN-DIC substitution lines*

	LDN	donor	1A	2A	3A	4A	5A	6A	7A	1B	2B	3B	4B	5B	6B	7B
Set1	b	c	ab	a	c	b	bc	bc	bc	ab	bc	c	ab	bc	ab	b
Set2	a	x	x	x	b	c	x	c	bc	bc	x	c	b	bc	a	bc
Set3	b	ab	ab	x	c	ab	ab	ab	ab	a	ab	x	b	c	b	ab

'*' different letters within a set of substitution lines denote significantly different disease severities; 'x' denotes missing data.

Among the 2nd set of substitution lines tested, 6B had the least CR severity, but its performance was not significantly different from LDN. All of the other lines were more susceptible than LDN, with 4A, 6A and 3B lines having the highest level of severity. Clearly, the CR reaction of this set of substitution lines is different from those in the 1st set, suggesting that the two different donor genotypes may carry different genes conferring CR reaction.

It is worthy to note that both 3B lines of the above two substitution series showed the most susceptible CR reactions in their respective set of substitutions. As mentioned earlier, this could indicate that the chromosome 3B of LDN harbours genes conferring CR resistance. Thus, replacing LDN 3B with chromosome 3B from either of the donor parents resulted in more susceptible CR reactions. However, the poor performance of the two 3B substitutions could simply be a coincidence as a result of both of the donor chromosomes potentially harbouring genes conferring increased CR susceptibility. Further studies are required to determine if retaining the 3B chromosome of LDN is beneficial for breeding CR resistant varieties.

The CR reactions of this set of substitution lines seem to be different from their reactions to Fusarium head blight (FHB). In a study reported by Stack et al. (2002), the 3A substitution line was consistently less susceptible and 2A was more susceptible than LDN. Thus, similar to the results derived from a panel of hexaploid genotypes (Liu et al. 2004), results from this set of substitution lines also suggest that genes conferring resistance to CR and FHB may be controlled by different genes.

The two parents of the 3rd set of substitution lines gave different CR reactions but the difference was not significant. Among their substitutions, 1B had the best CR resistance, which is significantly better than that of LDN and similar to the donor parent PI478742. The substitution lines 3A and 5B had the highest CR susceptibility. They were more susceptible to CR than any of the other substitution lines and the two parental genotypes in this substitution set. CR reactions of the remaining nine substitutions were not significantly different from one or both of the parental genotypes (Table 2).

Comparing the 3 sets of substitution lines showed that substitutions for any of the LDN chromosomes did not consistently increase or decrease CR resistance. The performance of the substitution lines often varied depending on the donor genotypes. The best and the worst performers in each of the three sets of substitution series are often different, suggesting that the three donors may have different genes conferring CR reaction. As one of the 3B substitutions and two of the 2A substitutions were not available for this study (Table 2), it is not clear whether substituting the former would consistently enhance resistance and whether substitution of the latter would consistently reduce resistance. Importantly, interactions between chromosomes/genes could contribute significantly to the CR reaction of the substitution lines but we were not able to estimate such effects in this study.

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