

Strategies for genetic enhancement of resistance to yellow spot and stagonospora nodorum blotch in wheat

¹Manisha Shankar, ²Diane Mather, ¹Michael Francki, ¹Dorthe Jorgensen, ¹Hossein Golzar, ²Ken Chalmers, ¹Esther Walker, ³Grant Hollaway, ³Mark McLean, ⁴Stephen Neate and ¹Rob Loughman

¹Department of Agriculture and Food, Western Australia

²The University of Adelaide, South Australia

³Department of Primary Industries, Victoria

⁴Department of Agriculture, Fisheries and Forestry, Queensland

KEY MESSAGES

In Western Australia yellow spot and stagonospora nodorum blotch frequently occur together and present important resistance breeding targets. Research on the two diseases has focused on (i) identification of new resistance genes, (ii) improved germplasm and associated genetic knowledge that enhance resistance expression and diversity and (iii) improved parental stocks which can be readily utilised within breeding programs.

Yellow spot

- Yellow spot (YS) (syn. tan spot) is an important foliar disease of wheat in Australia and can cause losses exceeding 50% when conditions are favourable for disease development. Although good progress has been made internationally to understand YS resistance, relatively few resistance genes have been identified and mapped in Australian germplasm and only one (*tsn1* on chromosome 5BL) is in general and known use in Australian breeding programs. Although *tsn1* is an important YS resistance gene, it doesn't explain the full spectrum of resistance and there is a significant opportunity to enhance expression of YS resistance through identification of resistance factors other than *tsn1*.
- Six doubled haploid (DH) mapping populations (five of which were fixed for *tsn 1*) were screened for YS resistance from 2009 to 2012 at the seedling/tillering and adult plant stages at the Department of Agriculture and Food, Western Australia (DAFWA) and the Department of primary Industries Victoria (DPIVic). Four of the above populations were screened at the Department of Agriculture, Fisheries and Forestry (DAFF) Queensland. Frequency distribution of individuals within each population for various levels of YS resistance was continuous indicating that resistance is conditioned by several genes with partial effects. A few lines within each population consistently showed high levels of resistance probably resulting from a combination of several genes with additive effects.
- Eight new loci for YS resistance were mapped by the Australian Wheat and Barley Molecular Marker Program (AWBMMP) on chromosomes 1AS, 2AS, 5A, 2B, 4B, 6BS, 7BL and 2D in five of the six populations screened so far. Of these, six loci (1AS, 2AS, 5A, 6BS, 7BL and 2D) were detected in more than one population with each locus accounting for 8 to 17% of phenotypic variation within a population.
- Of the 44 lines tested under a ring test, 27, 32 and 12 lines showed good levels of broad spectrum resistance at various growth stages and environments in Western Australia, Victoria and Queensland respectively. Four lines showed good levels of broad spectrum resistance at various growth stages, environments and across all national sites and are important new sources of resistance that can be used by breeders for developing resistant varieties (Shankar et al 2013).
- Efforts are now focused on (i) identifying additional YS resistance genes using newly developed populations and rapid phenotyping methods (Shankar et al 2012b) and (ii) developing a series of fixed lines, each carrying YS resistance genes from various sources, in elite Australian backgrounds starting with 2 or 3 resistance sources, applying molecular markers and phenotypic selection as appropriate and progressing selections through single seed descent. These materials will provide proof-of-concept for achieving better resistance by pyramiding resistance genes, and they should be directly useful as parents for wheat breeding.

Stagonospora nodorum blotch

- *Stagonospora nodorum blotch* (SNB) is one of the most severe fungal diseases affecting wheat production in the Western Australia. A 30-50% reduction in grain yield has been reported in wheat growing regions with high disease pressure. Only partial control of the disease can be achieved in the field with fungicides, adding substantial cost to on-farm wheat production systems. There has been no significant genetic gain for flag leaf and glume resistance in Australian wheat cultivars and considerable effort has been made in identifying suitable levels of adult plant resistance (APR) from unadapted spring and winter wheat genotypes.
- Based on a worldwide survey of 3500 wheat lines and sequential field testing (evaluating SNB leaf disease severity, plant maturity and height over a number of years) several elite resistant lines were identified. Final selection of SNB resistant donors included assessment of grain quality, avoiding soft grained lines with low flour yield and high α -amylase activity as these factors were likely to impact on future use in breeding. Some of these resistant donors were used for population development, identification of molecular markers and mapping of novel resistance genes while some others were directly incorporated into breeding programs.
- Research focussed on 3 different resistant sources for SNB. A spring wheat resistance source 6HRWSN125 from CIMMYT, winter wheat sources P91193D1 and P92201D5 from Purdue University (USA) and a locally bred hard wheat source EGA Blanco. Based on the anticipated quantitative resistance to SNB, the following three mapping populations of around 250 individuals each were developed: (a) DH population 6HRWSN125/IGW2074 (b) DH population EGA Blanco/Millewa and (c) Recombinant Inbred Line population P92201D5/P91193D1.
- The three mapping populations were screened for flag leaf resistance and glume resistance over multiple years (2002-2008) and in different environments. A continuous distribution was observed in all three populations, indicating the quantitative inheritance of resistance to this disease. A few lines within each population showed high levels of resistance probably resulting from a combination of several genes with additive effects.
- New loci for *Stagonospora nodorum* flag leaf resistance on chromosome 1BS, 2AS, 2DL and 5BL and glume resistance on 4BL and 2DL were mapped in three mapping populations in at least 2 environments (Francki et al 2011; Shankar et al 2008, 2012a; Uphaus et al 2007).
- The deployment of various genes for SNB resistance in susceptible genetic backgrounds relevant to Western Australian environments has been successfully achieved. Newly developed fixed lines with different gene combinations were evaluated in the field at South Perth in 2011 and twelve lines with gene combinations that increase genetic gain for APR to leaf blotch were identified. Of these seven lines show good levels of resistance to both leaf and glume blotch.
- Efforts are now focussed on identifying additional SNB resistance genes using newly developed DH populations and rapid phenotyping methods (Shankar et al 2012b).

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KEY WORDS

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