Molecular markers for wheat quality and disease resistance for the northern region - QDPI

Summary

This project is the Department of Primary Industries and Fisheries (DPI&F) component of a suite of four closely-linked projects that form the Northern Region Wheat Molecular Marker Program (NRWMMP). Other components in the suite are those of the University of Southern Queensland (USQ), CSIRO Plant Industry (PI) and the International Maize and Wheat Improvement Centre (CIMMYT).

The aims of the project are:
1. To develop molecular markers for wheat quality attributes of importance to the northern region (high dough strength and extensibility and good sponge and dough bread quality)
2. To develop molecular markers for serious diseases of wheat in the northern region (root-lesion nematodes (RLN), crown rot (CR) and yellow spot (YS))

All phenotyping of doubled haploid (DH) populations for the above attributes, as well as genotyping for resistance to RLN and YS, have been accomplished in this project.
Conclusions

Grain Quality

1. Germplasm has been identified that has quality attributes suitable for sponge and dough style breads and with high loaf volume.

2. A DH population has been characterised by a wide range of quality attributes, and from these data quantitative trait loci (QTL) to chromosomal regions controlling these various attributes will be identified (CSIRO Plant Industry [PI]). These outputs will enable northern region wheat breeders to improve the sponge and dough bread making qualities of northern region wheat varieties. When these varieties are available to growers it will make our export grain industry more competitive with American Dark Northern Spring (DNS) wheat in Asian markets.

Multiple Disease Resistance

1. Multiple disease resistant germplasm (RLN – Pratylenchus thornei, P. neglectus; YS) and CR resistant germplasm has been identified and developed.

2. DH populations have been characterised for resistance to these diseases.

3. QTL to chromosomal regions associated with resistance to P. thornei, P. neglectus and YS have been identified in multiple disease resistant germplasm derived from a synthetic hexaploid wheat.

4. Data on disease resistance in other DH populations have been supplied to CSIRO-PI (P. thornei) and to USQ (CR) for QTL identification and marker development. These outputs will enable northern region wheat breeders to improve overall disease resistance of northern region wheat varieties. When these varieties are available to growers, it will help reduce the region’s $83 million losses from these diseases.

Outcomes
The project has the potential to develop:

1. Molecular markers for quality attributes to use in breeding wheat varieties suitable for sponge and dough style breads. The availability of such Australian Prime Hard (APH) varieties to northern region grain growers would make export wheat more competitive with United States (US) Dark Northern Spring (DNS) varieties and increase Australia's share in Asian markets.

2. Molecular markers for very effective resistance to two species of RLN, YS and CR. If these markers can be successfully developed and implemented into northern breeding programs in a cost-efficient way their use should greatly accelerate the development of multiple-resistant wheat varieties. When such varieties are available, they will be readily grown by growers who are very aware of the economic cost of these diseases. This will result in a reduction of risks from diseases and the use of fungicides, and better productivity and profitability on-farms.

Achievements/Benefits

Background

Northern region wheat producers face a number of threats to their livelihood. One medium term threat is that quality of available wheat varieties may not meet important market demands. Another more immediate threat is from several serious diseases to which only a few varieties are individually resistant, with no variety being resistant to all diseases. Wheat breeders need the most modern tools to counter these threats. The use of molecular markers to screen early generation breeding material for quality and disease resistance could greatly improve the effectiveness and efficiency of wheat breeding programs. Research providers to the northern region coordinated their efforts to develop molecular markers for high priority attributes for regional wheat breeding. This project is the Queensland (QLD) DPIF (QDPIF) component of a suite of four closely-linked projects (DPI&F, USQ, CSIRO PI and CIMMYT). The coordinated proposals arose from a GRDC-sponsored meeting held in Toowoomba on January 9-11, 2001. In particular, these projects provided a collaborative platform through which the organisations involved concentrated their efforts on markers for wheat characters of high priority.

Importance of the Issues

The aims of the projects were:

1. To develop molecular markers to wheat quality attributes of importance to the northern region (high dough strength and extensibility and good sponge and dough bread quality).

2. To develop molecular markers for resistance to serious diseases of wheat in the northern region (RLN, CR and YS).

3. To validate markers for quality traits and disease resistance before implementation into northern region wheat breeding programs.

Expected outputs were:

- Molecular markers to genes for quality attributes and disease resistance in wheat. The projects have the potential to develop markers for quality attributes to use in breeding wheat varieties suitable for sponge and dough style breads. The availability of such APH varieties to northern region grain growers would make export wheat more competitive with US DNS varieties and increase Australia's share in valuable Asian markets.

- The potential to produce molecular markers for very effective resistances to serious soil-borne and stubble-borne diseases – namely, two species of RLN (combined loss in the northern region = $45 million/year), YS ($17 million) and CR ($21 million). If such markers can be implemented in northern breeding programs they will greatly accelerate the production of multiple disease resistant wheat varieties. Multiple disease resistant varieties will reduce risks from diseases (especially in conservation tillage systems), increase overall productivity and profitability on farms, and reduce the need for pesticides, while aiding the long term sustainability of rural enterprises and associated communities.

Achievements

Liaison:

Strong mutually beneficial linkages were established among all participants in the NRWMMP, namely DPI&F, USQ, CSIRO PI and CIMMYT. Two coordination meetings per year have been conducted and information exchanged freely. Professor Rudi
How have been passed to USQ for the development of molecular markers for CR resistance. In addition, 84 lines have been tested in one other replicated experiment. These data showed susceptibility to the disease. From the combination of these experiments, 18 of 160 lines have shown partial resistance and 28 have been confirmed. The variety Sunco possesses a useful level of adult plant resistance (APR) to CR. Two lots of 80 out of 250 lines in a Sunco/Batavia DH population were tested for their adult plant reaction to CR in replicated field tests. Due to the variability of field reactions, data from at least two experiments are necessary for accurate determination of partially resistant and susceptible lines. From the combination of these experiments, 18 of 160 lines have shown partial resistance and 28 have been confirmed.

Disease Resistance

Root lesion nematodes and yellow spot:

The synthetic hexaploid wheat CPI 133872 has an excellent level of resistance to the two species of RLN (P. thornei and P. neglectus) and to YS (Pyrenophora tritici-repentis). A DH population from a cross with Janz (a widely grown Australian variety) was used as the primary population for marker development to these diseases. Two years of phenotyping data from 100 DH lines in the synthetic hexaploid CPI 133872/Janz population to resistance to P. thornei and P. neglectus and YS were collected. Bulk segregant analysis for both P. thornei and P. neglectus identified putative markers associated with RLN resistance. These markers were used with other polymorphic markers in the construction of a framework map. The framework map consists of 169 markers with 2–15 markers per chromosome and an average distance of 15.9 cM between markers.

Single marker and interval QTL analysis in both two-stage and one-stage (combining spatial analysis of phenotypic data with genotypic data) identified chromosome regions associated with resistance to P. thornei, P. neglectus and YS. A major QTL for P. thornei resistance was detected on 6DS, explaining 22–24% of the phenotypic variation, and another on 6DL explaining 8–12% of the variation. Other QTL individually explaining 6–12% of the variation were detected on 6AS and 2BS. QTL for P. neglectus resistance were detected on 6DS, explaining 11–14% of the phenotypic variation and on 4DS, explaining 10–12% of the variation. Minor QTL for P. neglectus resistance were detected on 2BS, 3DS, and 4BS. A major QTL explaining 27–38% of the variation for YS resistance was detected on 5BL – this QTL corresponds to the location of the tns1 gene. Other QTL for YS resistance were detected on 5AL (10% variation explained), 3DL (17%), 4BS (13%) and 5AL (13%).

Four other synthetic hexaploid/Janz DH populations have been phenotyped for resistance to P. thornei and P. neglectus. Based on a half diallel analysis of P. thornei data, these synthetic hexaploid lines appear to have some resistance genes similar to CPI 133872 and some different genes. Markers flanking the QTL in the CPI 133872/Janz DH population were tested against these other synthetic hexaploids, and polymorphisms between them and Janz were identified.

Three bread wheats (GS50a, Morocco 426 and Iraq 43) selected from half diallel analysis for resistance to P. thornei were used for marker development in conjunction with CSIRO-PI. DH populations from each parent crossed to Janz were phenotyped in this project and leaf material passed to CSIRO personnel for genotyping. The data supplied was of high quality (126 DHs x 6 replications) from glasshouse experiments with a latinised design resulting in high line heritability. Marker results will be used to develop molecular markers to various quality attributes in conjunction with a genetic map of the DH population produced by CSIRO-PI (GA4). It is particularly pleasing that the data was found to cover an extensive range in loaf volume.

Quality:

The wheat variety Kukri has strong dough properties similar to requirements for the sponge and dough style bread market in south-east Asia. A Kukri/Janz DH population was grown in two replicate field trials at three sites in 2001 and 2002. Two trials have been selected each year for quality analyses. Phenotypic data was obtained on Kukri/Janz DH lines from the four trials for grain/dough quality attributes of test weight, protein, hardness, test milling, flour colour, Farinograph water absorption, Extensograph resistance and extensibility. This data has been statistically analysed to account for both field and laboratory variation. It will be used to develop molecular markers to various quality attributes in conjunction with a genetic map of the DH population produced by CSIRO-PI (GA4). It is particularly pleasing that the data was found to cover an extensive range in loaf volume.

How these achievements will benefit the industry
The outputs from this project on markers for wheat quality will enable northern region wheat breeders to improve the sponge and dough bread making qualities of northern region wheat varieties. When these varieties are available to growers it will make our export grain industry more competitive with US DNS wheat in Asian markets.

The outputs from this project on multiple disease resistance will enable northern region wheat breeders to improve overall disease resistance of northern region wheat varieties. When these varieties are available to growers it will help reduce the region's $83 million losses from these diseases.

Other research

Dough quality

Water absorption:

At the northern region AWCMMP meetings on 22–23 September 2003, it was reaffirmed by northern wheat breeders that development of molecular markers to the grain quality parameter flour water absorption and to the resistance genes for RLN and YS are high priorities. Subsequently, at a QDPI-QLD domestic flour millers' meeting on 24 September, millers confirmed the need for APH varieties with improved water absorption. Similar assessments of the need to improve water absorption have been offered by the Australian Wheat Board (AWB) (international) representatives on previous occasions. The importance of molecular markers to water absorption was recognised at the outset of the current project and a DH population from a Lang⁶/Qt 8766 cross has been developed for the purpose of mapping QTL controlling water absorption in a follow-on project. Lang has very good overall processing quality while QT 8766 has generally good quality combined with very high flour water absorption.

Multiple Disease Resistance

More closely linked markers in CPI 133872:

The CPI133872/Janz DH linkage map will be saturated with markers in the regions associated with disease resistance by exhausting new sources of chromosome-specific microsatellite markers for targeted mapping as they become available. Essential links could be made with the emerging technology projects in the northern region ET7 (BAC technology) and ET5 (SNP technology) to improve genome coverage in these target areas and also provide alternative polymorphic markers to increase the usability of the markers in different genetic backgrounds.

Effective markers for backcrossing RLN and YS resistance:

Screening of the CPI133872/Janz DH population has identified individual lines in which a high level of resistance to all three diseases (P. thornei, P. neglectus and YS) has been recovered. Development of the framework map in a DH (F infinity) population from a cross between a synthetic hexaploid and an adapted bread wheat has had advantages of homozygous individuals that can be replicated, more polymorphisms between the chosen parents, and a greater probability of detecting chromosomes bearing resistance QTL. It is important that the markers that are developed are capable of tracking the QTL as they are moved via backcrossing into more adapted backgrounds. This will be used to develop the markers in crosses between these multiple resistant DHs and adapted varieties/lines by assessing in parallel the phenotypes and genotypes of F2s and BC1F2s. For this purpose, a multiple disease phenotypic test – recently developed by project staff at the Leslie Research Centre – for single plants inoculated with P. thornei, P. neglectus and P. tritici-repentis will be employed. Leaf material from these same plants will be tested with the best available marker set and the process repeated until reliable, more closely linked molecular markers are developed that will be effective in adapted bread wheat backgrounds. As the phenotypic test is non-destructive, the procedure can be applied iteratively to the progeny of individual plants through successive generations, generating more opportunities for crossovers and the need for markers to be more closely linked to resistance loci. Research opportunities for further phenotyping and genotyping to identify markers for CR resistance will be reported in GA11.

Intellectual property summary
The DPI&F has legal expertise to develop any commercial products if required.

**Additional information**

