

# MOLECULAR PLANT BREEDING CRC

## ANNUAL REPORT 2004-2005



Established and supported  
under the Australian  
Government's Cooperative  
Research Centre Program



# VISION

Australia's crop and pasture industries underpinned by innovation in molecular plant breeding.

# MISSION

Leading the conversion of genetic and molecular discoveries into innovative solutions that result in varieties to benefit Australia's crop and pasture industries.

# OBJECTIVES

Enhance collaboration among researchers and industry, and use intellectual property and other resources more effectively.

Establish, develop and undertake world class, high quality, industry focused collaborative research programs in molecular breeding for cereals and pastures.

Commercialise products of CRC research for the benefit of Australia and beyond, providing return on investment, where appropriate.

Entice and train excellent plant breeders and researchers.

Promote MPB's profile as a globally reputable organisation and foster ownership by the Participants.



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# ASSOCIATED ORGANISATIONS

## CORE PARTICIPANTS

Department of Primary Industries,  
Victoria (DPI Vic)

The University of Adelaide (UA)

South Australian Research  
and Development Institute (SARDI)

Department of Agriculture,  
Western Australia (DAWA)

Murdoch University

International Maize and Wheat  
Improvement Centre, Mexico (CIMMYT)

## SUPPORTING PARTICIPANTS

Southern Cross University (SCU)

International Centre for Agricultural  
Research in the Dry Areas, Syria (ICARDA)

Australian Grain Technologies (AGT)

ABB Grain Ltd

BASF Plant Science (BPS)

Grains Research and Development  
Corporation (GRDC)

Dairy Australia (DA)

South Australian Grains Industry Trust  
Fund (SAGITF)

Meat and Livestock Australia (MLA)

Geoffrey Gardiner

Dairy Foundation (GGDF)





# CHAIRMAN'S REPORT

It has been an eventful year for MPBCRC. Apart from consolidating all the changes from the previous CRCMPB, two very important events happened this year which will change the shape and scope of the future work of the CRC.

First, MPBCRC was successful in our bid for supplementary funding in the last round of CRC applications. Second, the CRC conducted a major review of its research portfolio in March. This review has in turn prompted a reassessment of our strategies for delivering products that benefit the pasture and grains industries, and achieve returns on investment along the chain from IP, tools, germplasm and varieties.

The supplementary funding proposal arose out of work conducted in the previous CRCMPB on lignin biosynthesis, fructan metabolism and reduced pollen allergens. In the new CRC this work was to be extended and eventually commercialised with a supporting partner, and Wrightson, New Zealand's largest agribusiness and the leading Australian seed company, was selected. However, it quickly became clear that with our patented technologies and capability in R&D, and Wrightson's strengths in plant breeding and route to global markets, a whole new business could be generated. A supplementary funding proposal was put forward and was eventually successful in providing a further \$5 million over the last five years of the current CRC. Wrightson, in collaboration with the CRC, was also successful in obtaining funding from the newly established New Zealand Trade and Enterprise Trans Tasman Fund for biotechnology collaboration. This brings the total resources for this component

of the CRC to \$20 million, or \$4 million per year in new funding – a significant program by any measure. This is an exciting venture and illustrates how the pasture industry, with fewer larger industry players that have already been through the process of consolidation, can more easily organise itself to deliver technology to the end-user. It relies on a clear vision, focus and commitment, as well as the trust and respect of everyone in the venture. Above all, the key to successful commercialisation is a very close collaboration with the commercialisation partner in all aspects of the R&D through to the market place.

MPBCRC is now in a consolidation phase, and so the review of the research portfolio conducted in early March was both timely and strategically very important. The overall objective was to assess the effectiveness of the portfolio in delivering our target products, and to identify how to capture a number of new opportunities and initiatives. This prompted questions about the long term vision for MPBCRC, and even raised the possibility of a third CRC. The review also provided an opportunity to explore the best way to create value for our industries and how to better engage the wheat breeding programs into the activities of MPBCRC. This latter point was mentioned in my last report and is still a vexed question. Although the pasture seeds model seems a straightforward approach, in cereal breeding there are more players, and the issues more complicated. Nevertheless, the short term actions arising out of the workshop will provide thorough scrutiny of the portfolio to identify high priority short term opportunities for commercialisation.

The Board has also considered two further issues. Conflicts of interest have arisen, so we have spent some time in developing generic guidelines as to how they should be handled. This is a potentially serious issue, particularly when a number of players in the industry are all involved in the same general areas of work and are often in competition with each other. This has been at times difficult but in the end very rewarding because everyone now recognises what conflicts of interest are, and what can be done about them. The Board has also spent time on assessing its own performance.

Our Education Program continues to flourish. A particularly exciting joint activity with the Australian Centre for Plant Functional Genomics (ACPGF), Get into Genes, is attracting great interest. This is a program targeted at school children to raise their interest in science and expose them to the wonders and importance of biotechnology.

My thanks go to all members of the CRC, students, researchers, the management team and Board members for another eventful and exciting year of consolidation and progress. As well I would like to acknowledge our major international core, supporting and joint venture partners (CIMMYT, BASF Plant Science, ICARDA, and Wrightson) who have brought a global perspective to our work that will have major and far reaching impacts on our industries in the future.

**Dr Tony Gregson FTSE**



# CEO'S REPORT

We are now at a very exciting stage in MPBCRC's development. Years of hard work in developing the tools, technologies and know-how required for molecular plant breeding are now starting to pay off.

Our strong patent position has stimulated the creation of new partnerships with some of the most important plant breeding organisations in the world. We have been most fortunate in drawing in major international partners such as BASF Plant Science and Wrightson. These partnerships will ensure a route to market for our technologies, and bring about real returns on Australia's investment dollar.

While we have had a number of successes there are still many more MPB products for us to see to market. With this in mind, we will be expanding our commercialisation capability next year with the addition of a new staff member. Our current Commercial Manager Cheryl McCaffery will move to the position of Commercial Director, and a new appointee will occupy the role of Commercial Officer as of September 2006.

Indeed, MPBCRC's great strength lies in the knowledge, commitment and capability of its people. We were most fortunate this year to attract one of the most respected researchers in the field of plant genetics and plant breeding – Prof Diane Mather. Joining the CRC in early 2005, Diane takes over the role of Program Leader for Program 2: new molecular technologies. Diane comes to us from the Department of Plant Science at McGill University Montreal, where she was Associate Dean. Diane's leadership is already transforming Program 2 for the

better, and her input into the overall program management of the CRC is a welcome addition to an already strong line-up of research leaders.

Now is an exciting time for all Australian agricultural industries. With new transgenic and molecular marker-derived varieties in trial plots around Australia, farmers are starting to recognise the many benefits that these new technologies can provide. As a part of MPBCRC's communication strategy I travel to many parts of Australia to talk to growers about the progress our research is making. I am happy to say that the demand for these technologies is high. Australian farmers have always recognised the need to be at the cutting edge of technology, and now that the spectre of overseas competition from countries such as Argentina and China is raising its head, this demand is now stronger than ever.

To ensure we continue focusing on research targeted at meeting the needs of industry, our Industry Advisory Committee (IAC) has been re-formed for the first time under the umbrella of the new CRC. A valuable asset for the former CRCMPB, the IAC will monitor our progress from an industry perspective, and will provide an opportunity for the Supporting Participants and key industry organisations to contribute to strategic planning. The IAC will advise the Board on industry priorities and directions, and will ensure we are on track to delivering products of use to breeders, growers, processors and manufacturers.

It is an especially exciting time for our staff and students based at La Trobe in Victoria. As the construction of the Victorian AgriBiosciences Centre reaches completion we are preparing to move into the new building. The new site will provide some much needed additional space, and will for the first time since the inception of MPBCRC see both researchers and Head Office staff co-located under the same roof.

Thank you to the many researchers and students who have, over the last year and over the life of the two CRCs, built such a strong foundation upon which our commercialisable technologies now rest. Thank you also to the Board members and Head Office staff who have helped to shape this CRC into the world class institution it is today. I look forward to your continued efforts and support.

**Dr Bryan Whan**

# HIGHLIGHTS

## Commercialisation & business development

- » MPBCRC made a successful bid for an additional \$5 million supplementary funding to support the new collaborative venture with Wrightson Ltd.
- » Total per annum resources for MPB consists of \$9.7 million general cash, \$2.4 million cash through externally funded projects, and \$16 million in kind from participants. An additional \$1 million per annum has been sourced from the New Zealand government by Wrightson Limited to contribute to our work on pasture commercialisation.
- » A portfolio review was held to discuss the future of MPB research, and how to better engage the breeding programs. We are currently exploring the potential for further collaboration with AGT and DAWA breeding programs.
- » Molecular marker research is now having a commercial impact, with all breeding programs using these technologies routinely.

## Research

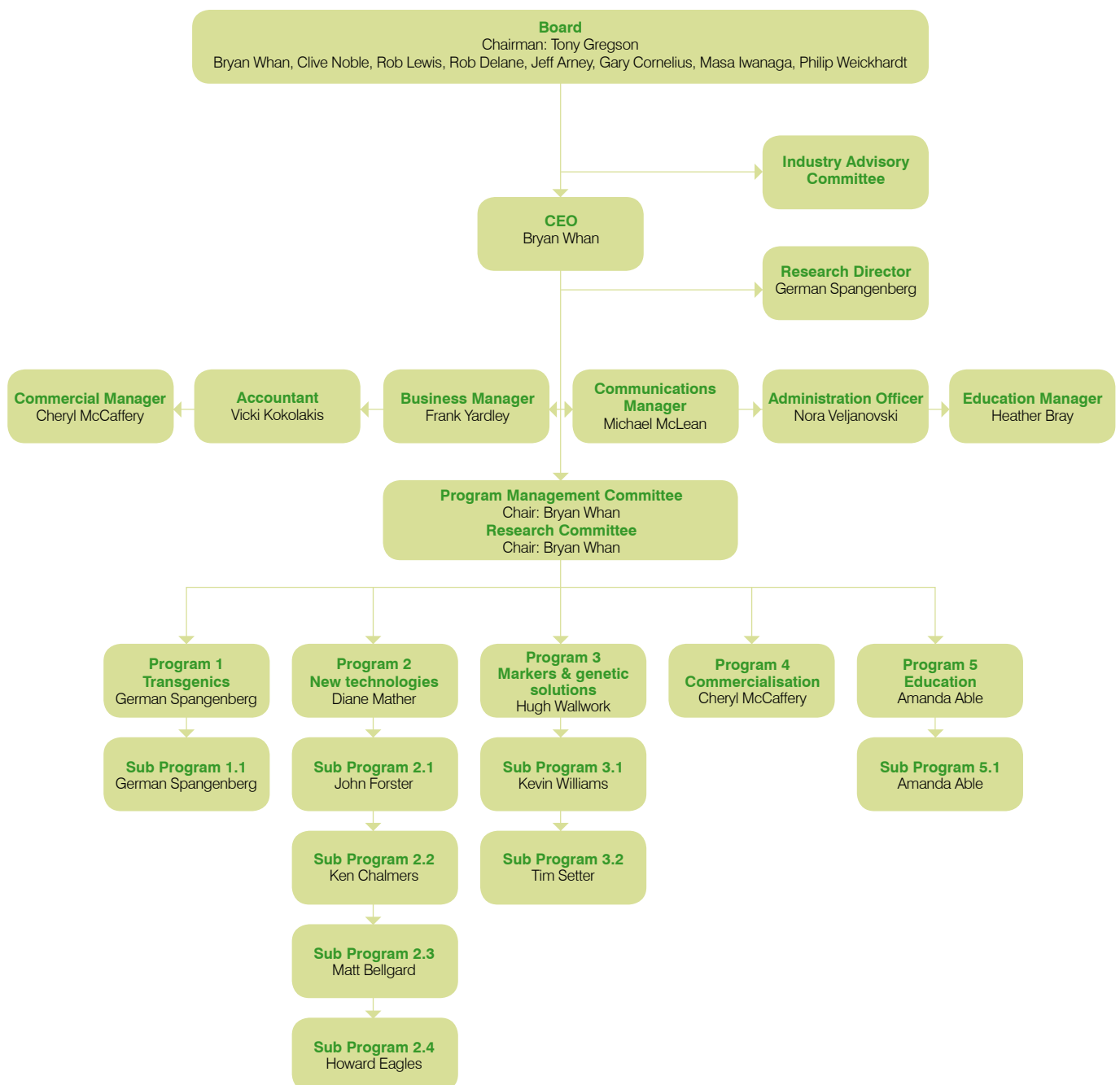
- » World's first planned field release of genetically modified (GM) ryegrass with reduced levels of pollen allergens was completed.
- » High throughput marker genotyping has been achieved using multiplex-ready SSR molecular markers. This solid phase technology has the potential to decrease the costs of marker screening to one tenth of previous costs. Already, over 2000 wheat and barley markers have been converted to multiplex-ready format.
- » Maps and new markers associated with critical traits continue to be delivered for use in cereal breeding programs. For example, a major quantitative trait locus (QTL) has been identified from Baudin for seed dormancy and pre-harvest sprouting tolerance.
- » Strategies for using molecular markers in pastures will focus on 'diagnostic' markers using single nucleotide polymorphisms (SNPs). SNPs for over 150 genes have been detected in perennial ryegrass and white clover.

- » Novel glutenin alleles that have the potential to improve wheat quality have been identified in exotic germplasm.
- » Barley lines derived from ICARDA germplasm adapted to low rainfall environments have performed exceptionally well in South Australian trials.
- » Advanced barley lines with improved malting quality and disease resistance, arising from research funded by ABB Grain, have entered S2 and S3 field trials.

## Education

- » Over 600 students have now participated in Get into Genes since its conception.
- » A new interactive display called the Gene Juice Bar was developed in an attempt to engage the community in the idea that plant products used for food contain DNA.
- » A total of 27 PhD students have now graduated from MPBCRC/CRCMPB.

# GOVERNANCE, STRUCTURE & MANAGEMENT



# THE BOARD

The Molecular Plant Breeding CRC is governed by a Board of Directors. Under their direction, the CEO conducts the day to day management of the Centre.

In the 2004–05 financial year the Board had five official meetings.

The CEO and Board are advised on industry issues and trends by an Industry Advisory Committee (IAC).

A Program Management Committee, responsible for the research activities of the CRC, converses monthly via teleconference.

## MPBCRC Board

**Roles:** Determine strategic directions for the CRC, set performance criteria, and monitor obligations of participants. Oversee management of the CRC, including staff, committees, finances, resources, intellectual property (IP) and program outcomes. Approve the Annual Operating Plan and Annual Report.

### Board Members 2004–05 (left to right)

*Dr Tony Gregson, Dr Bryan Whan, Dr Clive Noble, Dr Rob Lewis, Dr Masa Iwanaga, Mr Rob Delane, Mr Jeff Arney, Mr Gary Cornelius, Mr Philip Weickhardt*



**Dr Tony Gregson**  
Chair, Independent



**Dr Bryan Whan**  
CEO, Molecular Plant Breeding CRC



**Dr Clive Noble**  
Executive Director, Primary Industries Research Victoria



**Dr Rob Lewis**  
Executive Director, SARDI



**Dr Masa Iwanaga**  
Director General, CIMMYT



**Mr Rob Delane**  
Deputy Director General, Biosecurity & Research, DAWA



**Mr Jeff Arney**  
Independent



**Mr Gary Cornelius**  
Independent



**Mr Philip Weickhardt**  
Independent

# INDUSTRY ADVISORY COMMITTEE

**Roles:** Contribute to the strategic planning process on an ongoing basis. Advise the Board on new issues and directions. Contribute to the independent review processes of MPBCRC. Interact with the Product Focus Groups and Monitor progress of MPBCRC from an industry perspective.

# PROGRAM MANAGEMENT COMMITTEE

**Roles:** Identify and prioritise research activities. Monitor research progress, outcomes, commercialisation and transfer to end-users. Assist the CEO in developing annual budgets, and reporting on Centre activities. Advise the CEO of issues relevant to the CRC.

**DR BRYAN WHAN (CHAIR)**

CEO, Molecular Plant Breeding CRC

**PROF GERMAN SPANGENBERG**

Research Director and Leader – Program 1

**PROF DIANE MATHER**

Leader – Program 2

**DR HUGH WALLWORK**

Leader – Program 3

**DR AMANDA ABLE**

Leader – Education Program

**PROF RUDI APPELS**

WA representative

**DR KEVIN SMITH**

Pasture breeding representative

**DR STEVE JEFFERIES**

Cereal breeding representative

**DR RICHARD TRETOWAN**

CIMMYT representative

**MS CHERYL McCAFFERY**

Commercial Manager, MPBCRC

**MR MICHAEL McLEAN**

Communications Manager, MPBCRC



# COMMERCIALISATION

## PROGRAM LEADER:

**Cheryl McCaffery**

## Commercialisation strategies and activities

### TECHNOLOGY TRANSFER: DISSEMINATION OF RESEARCH OUTPUTS

There is more than one way to ensure that information concerning research outputs is made known to the kinds of people and organisations who may derive benefit from adopting these outputs, but ensuring adoption is not so straightforward. MPBCRC has engaged in at least four different mechanisms for the communication of research outputs to potential end-users:

- » formal written reporting to parties who have been involved in the selection and funding of particular areas of research focus
- » publication of scientific papers in relevant reputable journals read by the target audiences
- » presentation of research results at CRC Annual Research Meetings and at selected conferences of industry participants
- » circulation of specific research outputs to targeted recipients including, but not exclusively, core and supporting participants and other affiliated organisations.

In some instances, technology transfer is accomplished effectively via these means of wide publication of outcomes, and dissemination of information and tools to those who would derive benefit from their utilisation, and adoption follows relatively easily and rapidly.

However, on other occasions, more active facilitation of adoption is called for. This is partly because of the nature of the technology being developed. The focus of our intellectual effort is on improving cereal and pasture grass breeding, by the development and application of molecular techniques. Approximately 50% of our resources are invested in generating new molecular marker technologies for application in marker-assisted selection within breeding programs. For these research outputs to have an impact on plant breeding, their early adoption and integration into conventional breeding programs is required. Sometimes, in the absence of more direct 'hands on' intervention with target users, new technologies such as these are not easily adopted and integrated.

### TECHNOLOGY TRANSFER: COMMERCIALISATION APPROACHES

To facilitate uptake of, especially, molecular marker technologies, MPBCRC has sought alliance with end-users whose strategic focus and principles accord with our own. This involves forging closer and more actively aligned research and breeding programs, to facilitate both rapid dissemination of the latest research know-how and confidential information, and increased uptake of that information through its validation and implementation in breeding programs.

In addition, because MPBCRC is an extension of the first-round CRC, its reputation is already well established. Existing marker technologies are therefore always in demand and are disseminated routinely for specified R&D purposes under limited technology licences.

In other areas of technology, adoption and utilisation of research outcomes is stimulated if the IP underpinning the outcomes is protected in some way. IP can sometimes best be protected using legal instruments such as patents and plant breeders' rights (PBR). Such approaches are particularly true of the biotechnologies that are based on the application of recombinant DNA techniques such as the development of new generation varieties via the transfer of specific genetic traits to targeted high quality recipient breeding lines. Patents and PBR provide property rights in the IP, and property rights are tradable commercial assets. Such assets allow the owner to have greater control over how the technology is used, including by granting exclusive rights to selected end-users who then have a competitive advantage in the market place. Because of the high investment required to bring these kinds of products to market, the competitive advantage afforded by IP protection is seen as almost mandatory.

MPBCRC uses both the above approaches to encourage and facilitate uptake and application of the outcomes from its research programs.

Transfer is then afforded, predominantly, pursuant to technology licensing agreements. However, if circumstances warrant, alternative mechanisms may also be considered; for example, the formation of joint ventures or start-up companies to continue the further development and eventual commercialisation of MPB research outputs. Even in this scenario, the relevant IP would be licensed from the CRC owners to the new company.

## MAJOR ACTIVITIES DURING 2004–05

The major commercial activity over the past year has been the establishment of the commercialisation pathway for research outcomes from the pasture transgenesis program. Three technologies arising from the first phase of the CRC have been further developed and are now being applied – together, and in a wider range of target species – in a development and commercialisation program with a commercial partner. MPBCRC has entered into a joint venture arrangement with the commercial partner, New Zealand-based pasture breeding and wholesaling company, Wrightson Limited, to facilitate the creation of the world's first elite high-energy, pollen allergen-free temperate grass cultivars for domestic and export use. The respective roles of each of MPB and Wrightson have been formulated and agreed. The parties have established a joint venture company – Gramina Pty Ltd – to act as the commercialisation entity for this and, potentially, other related technology in the field of pasture grasses. Gramina is an Australian-based company, established and owned by the parties in equal proportions.

Once seed-stock quantities of Gramina varieties have been generated, commercial volumes will be multiplied and distributed under licence by Wrightson Seeds Limited, either itself or via sub-licensing distributors in target markets. The proprietary seed will be protected by virtue of a range of patent assets protecting both the underlying technology and the plant

material embodying that technology, and by PBR. The latter will be used, in particular, in countries where patent rights are less well regarded, less utilised and less easily enforced. The licence between Gramina and Wrightson Seeds Limited is currently being negotiated.

During 2004–05, the CRC also finalised four major collaborative research and licensing agreements with BPS, to develop an effective and efficient wheat transformation method and to apply it to the generation of transgenic wheat 'events' that exhibit fungal resistance and drought tolerance.

## ACTIVITIES PLANNED FOR 2005–06

One of the next activities for the commercialisation of the wheat transgenesis technology is to investigate the viability of establishing a facility for providing transformation services. A fundamental project with BPS is the development of an independent wheat transformation system; that is, one that does not rely on having licence rights to third party IP. MPB will of course exploit this technology itself, together with its participating organisations, for the purposes of delivering MPB-developed products. There may also be opportunity to provide this capability more broadly, to other organisations within Australia and overseas.

Another major activity to be brought to fruition during the coming year is to establish the best way of ensuring the up-take and adoption of the latest marker technologies and methodologies that are continuously being developed by researchers in MPB's grain and pasture

programs. The work in grains is largely being implemented already, through MPB core participants and via close strategic relationships with selected private breeding organisations such as AGT. The commercialisation arrangements for these activities are in the process of being negotiated and agreed. In addition, 'third generation' marker technologies are being developed and commercial routes to market need to be established in such a way that a continuous pipeline of marker technologies can be implemented over time.

Activities in the pastures area are being undertaken jointly with representatives of the industry participants, who are co-investing in these outputs – DA, MLA GGDF. There have been many discussions with end-users, since the candidate gene-based molecular marker approach now being developed involves an entirely new paradigm for these industries. A trial implementation program is being undertaken in the coming year with one interested industry participant.



*Logo of the newly formed joint venture with Wrightson Limited*

## OTHER ACTIVITIES DURING 2004–05

Publication of information concerning MPBCRC technologies can also be effectively carried out through trade conferences and field days. Members of the CRC have participated in over 20 such events over the past year and we continue to see this outlet as a valuable means of communicating our capability and available technology.

Our very successful Get into Genes training workshops, run in conjunction with ACPFG, have continued to be run for secondary school students. The workshop involves participants in hands on activities such as isolating and manipulating DNA. Its dual purposes are to:

- » improve the level of understanding of the basic science behind the various research programs that are undertaken by MPB
- » help dispel some of the unwarranted fear surrounding the applications of these latest, more precise methods of crop improvement.

MPBCRC participants have also undertaken contract research for other external organisations.

Further needs of the market are always being assessed, with a view to identifying opportunities to use MPB expertise to provide research and education outputs of benefit to the Australian grains and pastures industries.

## IP management

### POLICIES AND PRINCIPLES

MPBCRC has a written IP Management and Commercialisation Policy which addresses all aspects of generation, protection and management of IP arising from its research programs. A significant part of the Policy deals with issues relating to the adequate and appropriate protection of all Centre IP. Any IP developed by the participants in carrying out the activities of the CRC is Centre IP. There are many fora during which key researchers may raise IP queries and identify IP, the protection of which they think worthy of consideration. The monthly Program Management Committee meetings provide just one such forum. In addition, all researchers are encouraged to communicate frequently with the commercialisation team to discuss issues that arise on a day to day basis and to seek advice as necessary. Furthermore, MPBCRC ensures that all relevant personnel are aware of and act on their responsibilities regarding IP protection.

It is the responsibility of the participant organisations to maintain all relevant information associated with MPBCRC research being undertaken, including laboratory books, photographs, videos etc. This information must be retained by the participant organisation after the conclusion of the project, and remains the property of MPBCRC. In particular, the proper use of laboratory books is critical, to substantiate possible patent claims for US purposes, and is audited on an *ad hoc* basis.

When potentially patentable IP is identified, the value of seeking to protect it is assessed and preliminary prior art searches undertaken before any decision to file an application is made. IP will only be protected where it contributes to the overall strategic direction of the CRC and where it constitutes a component of a valuable package that can be delivered to end-users.

In the context of preparing research proposals, all researchers are required to identify any existing third party IP that may be used or that it is proposed be used in the project, so that steps can be taken to ensure that either there are no constraints associated with its use, or that appropriate licences are in place to provide freedom to operate.

All matters relating to IP – whether Centre IP or third party IP – are tracked regularly, and relevant information is registered as part of the CRC's Program Management System.

To ensure that all staff and researchers are sufficiently apprised of important IP issues, and aware of their responsibilities with respect to IP being developed and/or used, regular IP training programs are provided. For example, during 2005, a half-day training workshop was held during the Annual Research Meeting for all MPB students. All students assign IP rights to MPBCRC upon beginning research projects with the CRC.



## NEW INTELLECTUAL PROPERTY

One new patent filing was made during the past year. The invention is directed to a novel technology for amplifying nucleic acid (DNA) such as molecular markers. The technology provides a means of specifically amplifying a number of nucleic acids simultaneously, in a single closed tube reaction. The method results in substantially reducing both the costs and the risks of contamination associated with multiple distinct reactions. The technology is less expensive to deploy, and allows increased genotyping throughput and flexibility for multiplex PCR setup. All marker assays are performed under identical conditions and yield relatively uniform product for each marker both within assays and between assays. The latter feature facilitates both automation of the steps in the method and subsequent analysis of the results.

The method has been reduced to practice for a range of different crop and animal species.

## INTELLECTUAL PROPERTY SOLD, TRANSFERRED OR LICENSED

A portfolio of patent families comprising pending applications and granted patents have been licensed to give effect to the further development and commercialisation of three key technologies having application in pasture grasses. These technologies include key genes involved in herbage quality (lignin and fructan metabolism) and low allergenicity (pollen allergens), and are being combined to create products featuring all three characteristics. This work is

being undertaken in a joint venture with the New Zealand-based company, Wrightson Limited, as discussed in the previous section. The overall outcome from implementation of this new program will be to address successfully the key needs of Australia's pastoral industries, thereby supporting economic growth, sustainable development and vibrant rural communities. This will be achieved through:

- » designer pastures, delivering improvements in pasture and environment, through providing enhanced herbage quality and reduced pollen allergenicity
- » accelerating delivery of technologies to global markets by extending the reach to additional key target species and by combining traits, thereby enhancing global competitiveness of our pastoral industries
- » penetrating world markets with Australian-owned technologies, through collaboration with Wrightson, thereby concomitantly maximising commercial returns regionally.

The delivery of grasses with enhanced nutrition that are readily digestible increases productivity by matching pasture feed capacity to nutritional demand. Pasture grass is a lower cost input than livestock supplements. Grasses with enhanced nutritional value, drought resistance and improved seasonal growth patterns represent a key sustainable mechanism for impacting the productivity of our livestock industries.

## End-user involvement

Delivery of outcomes from MPBCRC's research and development activities depends critically on gaining the close involvement of end-user organisations. This is partly due to the nature of our R&D: development and implementation of new technologies for improving crop breeding must of necessity involve organisations in crop breeding. Effective deployment of these technologies requires appropriate involvement at an early stage of new product development. This is because the nature of these technologies dictates that their value comes from early and rapid up-take and utilisation in the selection of improved, genetically enhanced breeding lines for new variety development.

Some of the relevant organisations are themselves either core or supporting participants in the CRC; others are not, and are therefore engaged by alternative contractual means.

Major end-users of our research outputs, and their respective relationships with MPBCRC, are identified in the table overleaf.

# END-USERS OF MPB RESEARCH OUTPUTS

ORGANISATION	RELATIONSHIP WITH MPBCRC	ACTIVITIES
DAWA	Core Participant	Wheat and barley breeding
CIMMYT	Core Participant	Wheat breeding
UA	Core Participant	Barley breeding
ICARDA	Supporting Participant	Barley breeding
AGT	Supporting Participant R&D collaborator and licensee of MPB IP	Wheat breeding
ABB Grain	Supporting Participant and licensee of MPB IP	Barley distribution and marketing
GRDC, grains industries	Supporting Participant contractual provider of research investment for grains industries	Molecular research on cereals
GGDF DA, MLA, pasture/livestock industries	Contractual providers of investment in research for the dairy industries	Molecular research on pasture grasses and clovers
BASF Plant Science	Supporting Participant licensee of MPB IP	Development of transgenic wheats
Wrightson Limited	Supporting Participant licensee of MPB IP	Development of transgenic pastures
Grain Foods CRC	Research collaborator in novel grain products for niche markets	Development of novel quality products
Advanta	Licensee of MPB marker technology	Pasture grass breeding
Numerous research organisations (26)	Users of MPB marker (SSR) technology under limited licence provisions	Research on pasture grasses



## Progress against contractual targets/milestones

The two major achievements in commercialisation revolve around the half of the CRC portfolio that is directed to producing transgenic crops. Four substantial research collaboration and licensing agreements have been negotiated with BPS to develop a wheat transformation method for the generation of transgenic wheat 'events' that exhibit fungal resistance and drought tolerance. Progress on these projects is on track. Eventually, the capability may be expanded into barley. The possibility of establishing a viable transformation service in Australia, as described above, will also be investigated in the coming year.

On the pasture side, negotiations with Wrightson Limited have been finalised. This joint venture will be undertaken with the assistance of CRC Supplementary Funding that MPBCRC was successful in obtaining, as well as funding to Wrightson from New Zealand Trade and Enterprise under the Australia New Zealand Biotechnology Partnership Fund.

Three key pasture grass technologies are the subject of pending and granted patents which are licensed for the purposes of the joint development and commercialisation program. These technologies are being combined to create superior multi-solution products, exhibiting all three characteristics simultaneously. Technology packages will be extended into perennial ryegrass, hybrid ryegrass and tall fescue, to enable the servicing of both domestic and international markets.

For the non-transgenic half of the portfolio, the most effective delivery means are still being devised. The molecular marker technologies are precision tools that allow the manipulation of genetic information for the selection and breeding of new varieties. The most appropriate way to commercialise these technologies is to develop germplasm as a tangible product. However, as MPBCRC is not itself a breeding organisation, effective deployment requires appropriate involvement of relevant breeding organisations at an early stage of new product development.

In the pasture grass area, a Commercialisation Advisory Committee comprising MPB and the other parties funding this research – DA, GGDF and MLA – has been established. Part of its role is to (i) assess and communicate research progress to key industry players and translate it into terms that the breeding organisations can understand, and (ii) determine the best and most efficacious manner in which to deploy MPB capability and tools in each organisation's program.

Since the candidate gene-based molecular marker approach involves a new paradigm for these industries, there have been many discussions with end-users to acquaint them with the details of the approach, and one has been selected for more detailed discussions with a view to running a trial program.

In the final analysis, it might eventuate that the best way to provide all players with the benefits of the technology may be to offer a genotyping and trait characterisation service. The tools available could then be applied confidentially to a particular competing breeding program's plant material, and specific requested characteristics sought for the requesting breeder. It is yet to be determined whether such a service would be viable.

For the grains industries, negotiations are in progress with MPBCRC's participating breeding programs to establish what possible legal arrangements can best be employed to deliver these tools in wheat and barley breeding. Exactly which path will eventually be possible will depend on the outcome of these negotiations.

# PROGRAM OUTPUT REPORT

DESCRIPTION OF ALL MILESTONES	MILESTONE DATE AS PER COMMONWEALTH AGREEMENT	ACHIEVEMENT DATE
<b>Commercialisation plan</b>		
Plan for IP management and commercialisation of MPBCRC IP and products developed and reviewed.	Year 1 and ongoing	December 2003 Reviewed regularly as part of commercialisation processes.
Plan for IP management and commercialisation of MPBCRC IP and products implemented.	Year 2 and ongoing	September 2004 Further commercialisation arrangements continue to be negotiated and effected.
<b>Capability in IP protection and commercialisation</b>		
Commercial manager with skills in IP management and commercialisation appointed.	Year 1 and ongoing	July 2003
Policies on IP management developed and implemented, including an audit of all research projects.	Year 2 and ongoing	IP management policy was implemented immediately; auditing occurred March and June 2005 and continues.
Commercial partners identified where appropriate.	Year 2 and ongoing	Agreements with BPS effected September and December 2004, and with Wrightson June 2005.
<b>IP commercialised – IP from research programs protected where appropriate and commercialised</b>		
Breeder software made available to breeding organisations.	Year 2 and ongoing	On a continuous basis, as improved versions are available.
New technologies such as molecular markers, breeding strategies, and database systems made available to breeding programs and other researchers.	Year 2 and ongoing	During 2004–05, novel technology for identifying new markers was developed and implemented; new markers and molecular technologies are incorporated into breeding on a continuous basis.





# RESEARCH ACTIVITIES

The Molecular Plant Breeding CRC's research programs are structured to focus on outputs – tangible products for commercialisation and delivery to end-users. Only by keeping abreast of industry need will the CRC ensure both a return on Australia's investment in research, and the ongoing competitiveness of Australian crop and pasture industries.

## Products of MPB research

The following products are delivered through three Research Programs and an Education Program. As MPB technologies will ultimately impact on new varieties, most products will be delivered through participant breeding programs and commercial organisations.

### **PASTURES – TRANSGENIC**

- » Grasses with enhanced herbage quality, nutritive value, and low pollen allergenicity
- » Clovers with improved herbage and environmental quality

### **PASTURES – NON TRANSGENIC**

- » Pasture varieties using molecular markers and technologies

### **WHEAT – TRANSGENIC**

- » Wheats with tolerance to drought and fungal disease

### **WHEAT – NON TRANSGENIC**

- » Wheats with premium Asian quality to suit sponge and dough bread baking in Singapore, Thailand, Philippines and Japan
- » Wheats tolerant to drought, salinity, waterlogging, frost, disease and pre-harvest sprouting

### **BARLEYS – NON TRANSGENIC**

- » Malting barleys with enhanced malting quality and tolerance to drought, salinity, disease and pre-harvest sprouting

### **TECHNOLOGIES, TOOLS AND BREEDING STRATEGIES**

- » New molecular markers
- » Graphical presentation of genotypes
- » Techniques and technologies for increased efficiency in the application of protein and DNA markers in breeding programs
- » Bioinformatics systems
- » Cross outcome prediction software for breeders

### **TRANSFORMATION ENTITY**

- » Transformation systems for market-ready transgenic plants including a toolbox of promoters and freedom to operate (FTO)

### **EDUCATION PRODUCTS**

- » Workshops for upper high school students on gene technology
- » Ongoing training for researchers and plant breeders
- » Tertiary plant breeding training



# PROGRAM 1

## TRANSGENICS: DEVELOPING GENE SYSTEMS AND DELIVERING TRANSGENIC TECHNOLOGIES

**PROGRAM LEADER:**  
**Prof German Spangenberg**

### Objectives

Program 1 will increase the rate of genetic gain in cereal and pasture plant improvement through the development of new transformation techniques and gene systems, and their delivery in transgenic breeding. Transformation events with new quality attributes, increased tolerance to environmental stresses such as drought, and increased disease resistance will be developed in wheat, perennial ryegrass and white clover, and delivered to breeding programs.

### Background

The primary focus of Program 1 is to develop and deploy GM, or 'transgenic', techniques to enhance cereal and pasture molecular breeding. In transgenic wheat, MPBCRC researchers are assessing candidate genes for important traits such as drought tolerance and fungal disease resistance. In transgenic grasses and clovers, genes involved in key metabolic pathways and developmental processes are being identified and evaluated to develop pastures with enhanced herbage and environmental quality.

### NOVEL TOOLS FOR TRANSGENICS (1.1.10A, 1.1.10B)

Transgenesis has been used to both analyse plant gene function as well as develop new transformation events for several decades now. However, the process of refining and improving our approaches for transgenic breeding continues.

A number of projects within Program 1 are aimed at developing novel tools for transgenic breeding in cereals and pastures. These include the development of a 'toolbox' of promoters (regulatory gene sequences) required to target the expression of transgenes to specific organs and tissues, and to regulate transgene expression in a way that is controlled by plant development and the environment.

Promoters for organ-specific, tissue-specific and inducible expression have been identified and isolated for evaluation in transgenic wheat plants. In addition, microarray-based expression profiling in wheat has led to the identification of novel candidate genes with a diversity of expression patterns for wheat promoter discovery.

A major requirement for the production of market-ready transformation events is to reduce the complexity of transgene integration patterns. For this reason, single transgene copy, selectable marker-free transformation events are required. Genetic transformation using the soil bacterium *Agrobacterium tumefaciens* has been demonstrated to result in a higher frequency of single/low copy transgene insertions, and so is the preferred method of transformation. Research undertaken within Program 1 will result in a robust and efficient, *Agrobacterium*-mediated transformation system for wheat. A baseline protocol for *Agrobacterium*-mediated transformation of wheat has already been established.

### **NOVEL GENES FOR TRANSGENICS (1.1.08, 1.1.09, 1.1.11)**

The basic process of transgenic breeding involves identifying new genes of benefit to Australian agriculture, and packaging them into novel gene systems for delivery to breeding programs.

Identifying and characterising genes primarily located in the pairing homoeologous (*Ph*) region of bread wheat may result in the identification of genes controlling chromosome pairing and recombination. Chromosome pairing and recombination are essential processes during early meiosis in sexually reproducing organisms. Isolation of genes derived from within the *Ph2* region could be of significant benefit to breeding programs as tools for accelerated alien gene introgression. Candidate genes within this region have now been identified, and selected candidates are being subjected to detailed functional analysis. In addition, genes identified outside the *Ph2* region, but nonetheless important due to their putative meiotic function, are also being characterised.

Further research has also led to the identification of novel candidate genes for drought tolerance and non-host fungal disease resistance. These identified and isolated genes are now being transferred to wheat to assess their performance in conferring tolerance to abiotic and biotic stresses in transgenic wheat.

In the move towards more sustainable production systems in the 21st century, increased productivity and profitability of pasture-based dairy systems is required. These increases will be best achieved by focusing molecular plant breeding efforts into increasing nutritive value and biomass production of forage grasses (such as perennial ryegrass), into improving quality for enhanced animal welfare, and increasing abiotic stress tolerance and nutrient efficiency of forage legumes (such as white clover).

Consequently, MPBCRC has already identified and isolated novel genes involved in lignin biosynthesis and fructan metabolism for their deployment in molecular breeding of GM pasture grasses with enhanced nutritive value.

Perennial ryegrass and tall fescue frequently contain endophytic fungi (*Neotyphodium lolii* in ryegrass and *N. coenophialum* in fescue) which result in both beneficial and detrimental properties. The presence of the endophyte has been shown to improve seedling vigour, persistence and drought tolerance in marginal environments as well as provide protection against some insect pests. However, endophyte-infected grasses may be toxic to livestock because the fungus produces a wide range of chemicals, many of which have a high degree of biological activity against mammalian systems.



MPB researchers have developed the world's first grass endophyte unigene microarray interrogating over 5,000 grass endophyte genes, and deployed the technology in detailed studies on the endophyte/grass interaction at the transcriptome level. In addition, the experimental basis for the analysis of the endophyte/grass interaction at the metabolome level has been established. Knowledge arising from this research on systems biology of the endophyte/grass symbiotic association is expected to lead to designer endophyte-grass combinations for enhanced pasture quality, along with safer and improved pasture production.

### **NOVEL TRANSFORMATION EVENTS FOR BREEDING (1.1.10C, 1.1.10D, 1.1.11)**

Building on novel tools and novel genes for transgenesis applications arising from the research described above, market-ready transformation events will be generated in wheat, perennial ryegrass and white clover. These novel transformation events will incorporate transgenic technologies following a sensible choice of targets for molecular breeding.

After thorough analyses under containment laboratory and glasshouse conditions, selected transformation events have been evaluated in small-scale planned field releases.

The world's first field assessment of novel transformation events in ryegrass with a down-regulation of the main pollen allergen has been undertaken as an initial step towards the evaluation of the potential for the development of hypo-allergenic ryegrass to reduce incidence of hay fever and seasonal allergic asthma.

Transformation events in perennial ryegrass for modified lignin and fructan biosynthesis are being produced as a first step towards the development of high energy ryegrass.

## Highlights

- » Novel candidate wheat genes were identified for discovery of promoters with a range of specificities and their assessment in GM wheat.
- » GM wheat plants for assessment of novel candidate genes for drought tolerance were produced.
- » GM wheat plants for assessment of novel candidate genes for fungal disease resistance were produced.
- » Novel candidate genes in barley for fungal disease resistance were identified for detailed functional analysis.
- » The grass-endophyte association was analysed at the transcriptome level based on the world's first unigene microarray for grass endophyte developed by MPBCRC.
- » World's first planned field release with GM ryegrass with reduced levels of pollen allergens was completed.

# PROGRAM OUTPUT REPORT

PROJECT	PROJECT OUTPUTS	PROGRESS
<b>Program Output 1: Novel tools and systems for breeding transgenic crops and pastures. (2006 and ongoing)</b>		
1.1.10a	Development of a robust and efficient <i>Agrobacterium</i> -mediated transformation system for the production of market-ready transformation events in wheat.	A set of 10 transformation vectors was generated for the development of an <i>Agrobacterium</i> -mediated transformation system in wheat. A baseline protocol for <i>Agrobacterium</i> -mediated transformation of wheat was established.
1.1.10b	Development of a toolbox of promoters with a range of specificities (organ, tissue, inducible) for use in transgenic breeding in wheat.	A set of five promoters for organ-specific, tissue-specific and inducible expression in wheat was identified and isolated. Microarray-based expression profiling led to the identification of novel candidate genes in wheat.
<b>Program Output 2: Novel genes and gene systems for transgenic breeding in crops and pastures. (2006 and ongoing)</b> These genes will provide tolerance to drought and resistance to diseases in cereals, and improved herbage quality and improved grass-endophyte associations in pastures.		
1.1.08	Identification, isolation and characterisation of genes involved in meiosis control and recombination in wheat.	Detailed structural analysis of the <i>Ph2</i> region was completed. Genic content of the region deleted in the <i>Ph2a</i> mutant was determined and several candidate <i>Ph2</i> genes identified. A set of candidate genes for key meiotic processes were identified and isolated.
1.1.09	Identification, isolation and characterisation of genes involved in regulatory signalling pathways of disease resistance in cereals.	Candidate genes involved in changes to the cytoskeleton, oxidative signalling and pH changes across the cell membrane in barley were identified.
1.1.10c	Identification, isolation and characterisation of genes conferring drought tolerance to plants.	A set of 19 candidate genes for drought tolerance was identified. Transformation vectors were generated.
1.1.10d	Identification, isolation and characterisation of genes conferring fungal disease resistance to plants.	A set of 11 candidate genes for fungal disease resistance was identified. Transformation vectors were generated.
1.1.11	Identification, isolation and characterisation of genes involved in lignin biosynthesis in grasses.	A set of four genes involved in lignin biosynthesis in perennial ryegrass was isolated. Transformation vectors were generated.
1.1.11	Identification, isolation and characterisation of genes involved in fructan metabolism in grasses.	A set of four genes involved in fructan metabolism in perennial ryegrass was isolated. Transformation vectors were generated.
1.1.11	Identification, isolation and characterisation of genes involved in host colonisation, nutrient exchange and biosynthesis of bioactives in the grass-endophyte association.	A genomic resource of over 12,000 ESTs of grass endophytes was established. Endophyte cDNA spotted microarrays were generated and applied to transcriptome analysis of the grass-endophyte association. The experimental basis for the analysis of the grass-endophyte association at the metabolome level was established.
<b>Program Output 3: Novel 'market-ready' transformation events for transgenic breeding in crops and pastures. (2006 and ongoing)</b>		
1.1.10c	Generation and analysis of transgenic wheat plants with enhanced tolerance to drought stress.	Transgenic wheat plants produced for functional analysis of six candidate genes.
1.1.09 1.1.10d	Generation and analysis of transgenic wheat plants with enhanced resistance to fungal disease.	Transgenic wheat plants produced for functional analysis of seven candidate genes.
1.1.11	Generation and analysis of transgenic ryegrass plants with enhanced herbage quality and nutritive value.	Modular transformation vectors for combinatorial expression of ryegrass genes for targeted modification of lignin biosynthesis and fructan metabolism were produced.
1.1.11	Generation and analysis of transgenic ryegrass plants with low pollen allergenicity.	First field-evaluation of selected transformation events in ryegrass was completed.

# FEATURED PROJECT REPORTS

## 1.1.11C TRANSGENIC PASTURES – DESIGNER ENDOPHYTES

**Leader: Prof German Spangenberg**

Perennial ryegrass and tall fescue frequently contain endophytic fungi (*N. lolii* in ryegrass, *N. coenophialum* in tall fescue and *Epichloë festucae* in red fescue) which result in both beneficial and detrimental properties. The presence of the endophyte has been shown to improve seedling vigour, persistence and drought tolerance in marginal environments as well as provide protection against some insect pests. However, endophyte-infected grasses may be toxic to livestock because the fungus produces a wide range of chemicals, many of which have a high degree of biological activity against mammalian systems. The most thoroughly studied compounds are alkaloids, including ergopeptine alkaloids, indole-isoprenoid lolitremes, pyrrolizidine alkaloids, and pyrrolopyrazine alkaloids.

Very little is known about the factors important in host colonisation or nutrient exchange between the grass plant and the fungus. Similarly, only recently have the first candidate genes involved in the biosynthesis of main toxins been isolated. The physiological mechanisms which lead to increased plant vigour and enhanced tolerance to abiotic stresses unrelated to the reduction in pest damage to endophyte-infected grasses are also unknown. Genes involved in the endophyte/grass host interaction have not yet been isolated. Their isolation and characterisation would

be critical for an effective manipulation of grass/endophyte interactions.

To date, 13,964 expressed sequence tags (ESTs) have been generated from *in vitro* and *in planta* grown *E. festucae* and the *Neotyphodium* endophytes. Two endophyte cDNA spotted microarrays have been generated, which provide a tool for comparative gene expression studies between endophyte species, as well as a tool for high throughput parallel gene expression profiling in grass endophytes. In combination with established unigene chips for the grass hosts they provide a powerful tool for the dissection of the grass-endophyte association at the transcriptome level.

*Researchers: Dr Silvana Felitti, Dr Eline van Zijll de Jong, Kate Shields (student), Marc Ramsperger (student), Pei Tian (student), Prof John Forster*

## 1.1.11A TRANSGENIC PASTURES – DESIGNER RYEGRASS

**Leader: Prof German Spangenberg**

Perennial ryegrass is the major grass species sown in temperate dairy pastures in Australia, and the key pasture grass in temperate climates throughout the world. Improving the digestibility of temperate pasture grasses has been identified as a priority for industry R&D. Improved digestibility of grass is associated with increased animal production, through both increases in pasture intake, and in the energy yield from pasture. Major contributions to the digestibility of forage grasses are made by lignins, components of plant cell walls, and

fructans, a class of highly water-soluble polysaccharides. Modification of both lignin and fructan composition (and/or content) in forage grasses would thus increase digestibility. Even small increases in digestibility are expected to have significant impact on forage quality and concomitantly on animal production. Perennial ryegrass also has significant economic impacts in that it is responsible for a major portion of grass pollen allergies, an important environmental disease that afflicts about 20% of the population in cool temperate climates.

This project is aimed at improving the digestibility of perennial ryegrass, to reduce its levels of pollen allergens and to package these desirable traits together in commercial cultivars. Genes and promoters encoding key enzymes in lignin and fructan metabolism and the major pollen allergens from perennial ryegrass have been isolated and characterised. The targeted modification of lignin, fructan and pollen allergen levels in ryegrass using transgenic technologies is proposed. Protocols for regeneration and genetic transformation of perennial ryegrass through to the recovery of fertile transgenic plants have been established. Candidate genes have been inserted into transformation vectors designed for the transfer of these genes, individually and in combination, and the production of transgenic plants is ongoing.

*Researchers: Jaye Chalmers (student), Yingying Cao (student), Natasha Petrovska (student), Dr Aidyn Mouradov, Dr Ulrik John*





# PROGRAM 2

## NEW MOLECULAR TECHNOLOGIES

**PROGRAM LEADER:**  
**Prof Diane Mather**

### Objectives

Program 2 will increase the rate of genetic gain in cereal and pasture improvement through novel marker technologies, strategies for genomic analysis, and software tools for research and plant breeding. A new generation of technologies will be delivered to breeding programs to provide major improvements in new varieties using non-GM techniques.

### Research overview

#### **CANDIDATE GENE TECHNOLOGIES (2.1.03, 1.2.05, 2.2.07)**

MPB's molecular marker strategy for pasture crops involves discovery of SNP markers within 'candidate genes' (genes thought to have direct effects on breeders' traits) and deployment of these markers for crop improvement. SNPs have been detected in over 150 genes. SNP markers have been added to genetic maps and are being screened on elite germplasm. In perennial ryegrass, several candidate genes for lignin biosynthesis have been found to coincide with QTLs for herbage digestibility. Further SNP detection work is underway in these genes to provide a 'proof-of-concept' for molecular breeding applications.

In wheat and barley, there are already several well-characterised genes that are known to affect grain quality and agronomic performance. With classification of breeding materials for these genes, existing plant breeding data and appropriate data analysis, the effects of specific genes can be estimated. Estimates obtained last year for effects of wheat puroindoline genes on grain hardness and effects of several barley genes on grain yield are now used by plant breeders to select parents and design crossing strategies. This year, wheat puroindoline genes were shown to influence dough extensibility.

In wheat, a comparative mapping approach is being used to discover new candidate genes for boron tolerance, late-maturity alpha-amylase and flour colour, with international genomic resources used to assemble physical maps and identify candidate genes. Ultimately, this research will identify key genes that determine the value of wheat varieties for growers and markets. In the short term, it provides new molecular markers for implementation in wheat breeding.

In a new student project, map-based cloning is being applied to isolate the gene(s) underlying a key QTL that affects malt quality, seed dormancy and pre-harvest sprouting in barley. This project is using mapping populations, barley-rice synteny information and high throughput genotyping.

#### **TECHNOLOGIES FOR DNA MARKERS AND PROTEIN PROFILING (2.1.04, 2.2.04)**

Molecular plant breeding requires low cost, high throughput laboratory methods for DNA markers and for protein identification.

One approach for developing low cost DNA marker assays combines the capture of markers (particularly SNPs) on reusable solid-phase platforms with simple presence/absence colorimetric assays. Existing solid-phase markers have now been validated in elite wheat germplasm and used for marker-assisted selection and new wheat and barley markers have been converted to the solid-phase format. Several solid-phase markers have been optimised for multiplexing, and robotic automation is being investigated to further increase throughput.

Exciting progress has been made in the development and deployment of a novel multiplex-ready marker system for microsatellite (SSR) markers. Over 2,000 barley and wheat markers have been converted to multiplex-ready format. The system has been successfully deployed in several laboratories, with over 70,000 marker assays performed. Users are provided with DNA primers, bioinformatic support and technical training. Multiplex marker panels are being developed for varietal identification and for rapid construction of genetic maps.

### 2.1.03 CANDIDATE GENE-BASED MOLECULAR MARKERS IN OUTCROSSING FORAGE SPECIES

**Leader: Prof John Forster**

Perennial ryegrass and white clover are important dairy pasture crop species in Australia and internationally. Improvements in the production and quality traits of these species will lead to significant economic benefits for producers and society. Molecular marker technology allows for the mapping of genes that affect these traits and for marker-assisted selection within plant breeding programs. MPB has already established a world-leading position in this area, by establishing marker systems and reference genetic maps for perennial ryegrass and white clover. Outcrossing pasture species have complex breeding systems, and linkage-based molecular breeding methods developed for inbred crops such as cereals are of limited use in these species.

To address the challenges associated with applying molecular markers in pasture crop improvement, this project is developing DNA markers within candidate genes for breeders' traits, and new systems for using these markers for direct selection of superior parents and progeny. This project is supported by GGDF, DA and MLA.

DNA sequence information has been analysed for hundreds of candidate genes, with SNPs detected in over 150 candidate genes to date. Systems for high throughput screening of SNP markers have been established, and new markers have been added to genetic maps. In parallel, extensive data have been obtained for important traits, and loci affecting those traits have been mapped.

In perennial ryegrass, variation for herbage digestibility has been associated with a region of the genome that contains genes involved in the biosynthesis of lignin (a highly indigestible structural component of plant cell walls). The SNP detection effort has been intensified for these candidate genes. These genes will now be used for proof-of-concept in molecular breeding applications.

*Researchers: Dr Kevin Smith, Prof German Spangenberg, Dr Noel Cogan, Dr Mark Dobrowolski, Dr Eline van Zijl de Jong, Nathaniel Bannan, Michelle Drayton, Kahlil Lawless, Rebecca Ponting, Peter Dracatos (student), Julie George (student), Pamela Trigg, Darren Pickett, Stephanie Lambert, Cassandra Rambousek*

### 2.2.03C WHOLE-GENOME ANALYSIS AND SELECTION IN WHEAT AND BARLEY

**Leader: Assoc Prof Ken Chalmers**

Molecular markers have gained acceptance in Australian wheat and barley breeding programs, and provide those programs with competitive advantages. Generally, markers are used to tag only one or two traits or chromosome regions

at a time, even though genetic map information is available for many traits and for the whole genome.

This project applies a whole-genome approach to marker-assisted analysis and selection, using high throughput laboratory methods to scan molecular markers throughout all regions of the barley and wheat genomes. The first phase of the project, completed this year, examined the whole-genome 'fingerprints' of wheat and barley breeding materials, tracking the effects of breeding processes in the development of new elite lines, and validating 'molecular ideotypes' that explain the success of particular lines.

In the next phase of this project, molecular ideotypes and whole-genome marker scanning will be used to develop new elite lines of wheat and barley. This will allow marker-assisted selection for numerous traits and regions of the genome. It will reduce the number of lines that need to be evaluated in the field and in quality labs, lowering costs and permitting more intensive evaluation of the lines with the most promising whole-genome fingerprints. By producing varieties in this way, cereal breeders will be able to exploit all of the current genetic knowledge from genome mapping, and combine superior genes for adaptation and quality from many sources.

*Researchers: Dr Jason Eglinton, Dr Steve Jefferies, Dr Phillippa Hearnden, Gai McMichael, Amanda Waterman*

# PROGRAM OUTPUT REPORT

PROJECT	PROJECT OUTPUTS	PROGRESS
<b>Program Output 1: High throughput, low cost SNP molecular markers developed for pasture crops using a candidate gene-based approach. (2006 and 2008)</b>		
2.1.03	Suite of reliable PCR-based candidate gene marker systems in perennial ryegrass and white clover.	SNPs identified for candidate genes in perennial ryegrass (in 80 genes) and white clover (in 70 genes).
2.1.03	QTLs mapped for key traits in perennial ryegrass and white clover; information on co-location of QTLs with candidate genes.	QTLs identified for key traits in perennial ryegrass and white clover. In perennial ryegrass, QTLs for herbage digestibility are co-located with candidate genes for lignin biosynthesis.
<b>Program Output 2: New systems for DNA marker development and for efficient application of protein and DNA markers. (2006, 2008 and 2010)</b>		
2.1.04	Low cost analysis – protein profiling to predict quality traits and solid phase diagnostics for DNA markers.	Protocols identified to bypass gene electrophoresis steps in protein profiling for wheat glutenins. Comprehensive set of malt samples produced and analysed. Wheat and barley markers converted to solid-phase format and implemented in breeding.
2.1.05	Physical maps, candidate genes and new markers for regions of the wheat genome affecting boron tolerance, late maturity alpha-amylase and disease resistance.	Comparative genomics used to develop rice-wheat syntenic maps for wheat group 7L and 3S chromosomes. Candidate genes identified and screened against BAC library.
2.2.04	New marker technologies for low cost, high throughput genotyping.	Multiplex-ready marker technology optimised for barley and wheat. Over 2000 markers converted to multiplex-ready format, Multiplex-ready panels developed for markers deployed in breeding programs.
2.2.04	New markers for use in cereal research and breeding.	New diagnostic markers for resistance to stem rust and leaf rust, tolerance to cereal cyst nematode (CCN), glutenin alleles, yellow flower colour. Multiplex-ready markers supplied to MPB researchers and breeding programs.
<b>Program Output 3: New strategies for effective genetic analysis and molecular plant breeding. (2006, 2008 and 2010)</b>		
2.2.03	Genotypic fingerprints, pedigrees and phenotypic data for key varieties and breeding lines of wheat and barley.	800 wheat lines and 1000 barley lines each genotyped for up to 265 mapped markers. Information compiled in database with pedigrees and phenotypic data for key traits.
2.2.03	Genome-wide breeding strategies for wheat and barley.	Whole-genome analysis provided successful proof-of-concept for genome-wide selection in both wheat and barley.
2.2.03	Understanding of population structure and linkage disequilibrium in wheat and barley.	Population structure analysed for barley and wheat lines. Linkage disequilibrium investigated within hardness locus in wheat and among SSR markers in wheat and barley.
2.2.07	Positional cloning of a barley malt quality QTL.	High-resolution mapping initiated.
<b>Program Output 4: GENica: Bioinformatics systems for integration of plant genetic and genomic data. (2006 and ongoing)</b>		
2.3.01	Integrated bioinformatics systems for use by MPBCRC, ACPFG and other researchers.	Comparative mapping and comparative genomic analysis systems implemented. BINNER software developed to automatically construct panels of multiplex-ready markers. Prototype informatics system developed for pedigree information and SSR marker genotypes.
2.3.01	Web-based Program Management System for MPBCRC.	MPBCRC Program Management System implemented.
<b>Program Output 5: Information and software to assist breeders to make decisions on crosses. (2006 and 2008)</b>		
2.4.01	Improved understanding of how major genes in wheat and barley affect grain yield and quality.	Wheat quality effects estimated for puroindoline (hardness) genes and a key glutenin allele. Barley yield and quality effects estimated for dwarfing genes and nematode resistance genes.
2.4.01	Cross prediction software.	New version of wheat quality predictor in use by collaborating breeding programs.

# FEATURED PROJECT REPORTS

In wheat, the importance of glutenin proteins to grain quality is well understood, yet breeders still rely upon costly gel-based assays to distinguish among glutenin variants. In barley, protein quantity and quality are known to be major determinants of malting quality, yet the roles of specific proteins are poorly understood. To address these limitations, high throughput methods (2-D gel electrophoresis, MALDI-TOF mass spectrometry, capillary electrophoresis) are being investigated. In wheat, the main objective is to develop low cost, high throughput assays for glutenins and other grain proteins. In barley, the main objective is to provide new insights into factors that determine malt quality.

## **WHOLE-GENOME STRATEGIES (2.2.03)**

New molecular technologies make it possible to simultaneously track large numbers of molecular markers, opening up opportunities for 'whole-genome' approaches in marker-based genetic analyses and marker-assisted selection.

Whole-genome marker fingerprints have been generated for elite breeding materials in barley and wheat. These have revealed the effects of breeders' selections throughout the genome and validated 'molecular ideotypes' that explain the success of particular elite lines. Whole-genome marker-based selection will now be used to assemble the best regions of the barley or wheat genome from a wide range of sources, combining favourable alleles for adaptation and grain quality traits.

In an association genetics project, a whole-genome approach has been applied to hundreds of wheat and barley lines, each genotyped for up to 265 mapped markers. The resulting data are used to investigate linkage disequilibrium and population structure, with significant associations found between markers, both within and among chromosomes. Pedigrees and trait data have been compiled for these lines and will be used to associate trait variation with marker genotypes.

In a student project initiated this year, whole-genome marker monitoring is being used to investigate responses to recurrent selection using male sterility in barley. This project will track the effects of selection and investigate the relative importance of among-chromosome assortment and within-chromosome recombination.

## **SOFTWARE AND BIOINFORMATICS (2.3.01, 2.4.01)**

A joint effort between ACPFG and MPBCRC will create an integrated bioinformatics framework (GENica) to support the management, analysis and interpretation of data for plant genomics and molecular plant breeding. Web-based software tools are being developed to support the management, analysis and interpretation of specific data types. To date, these include tools for genetic map information, genetic marker information and pedigree information. In addition, bioinformatics pipelines have been customised and used to assemble and annotate wheat sequences.

MPB cross predictor software is already intensively used by collaborating wheat breeding programs, to help choose the best parents to achieve desired outcomes for grain quality traits. A new version distributed this year includes effects of puroindoline genes, prediction for three-way crosses and changes in output format to suit user requirements.

## Highlights

- » SNPs detected in over 150 genes in perennial ryegrass and white clover.
- » Candidate genes for lignin biosynthesis coincide with QTLs for herbage digestibility in perennial ryegrass.
- » Puroindoline genes demonstrated to affect dough extensibility in wheat.
- » Screening of wheat candidate genes against bacterial artificial chromosome (BAC) libraries and sequencing of selected BAC clones.
- » Wheat and barley markers converted to solid-phase format.
- » Over 2000 wheat and barley markers converted to multiplex-ready format.
- » High throughput marker genotyping achieved using multiplex-ready SSRs.
- » Whole-genome analysis provided proof-of-concept for whole-genome selection.
- » New software tools under development and in use.



# PROGRAM 3

## MARKERS AND GENETIC SOLUTIONS

**PROGRAM LEADER:**  
**Dr Hugh Wallwork**

### Objectives

Program 3 includes projects that provide an improved understanding of the genetic control of key traits affecting wheat and barley production and grain quality. Particular emphasis is placed on traits hard to select directly by standard screening procedures, and on traits responsible for maintaining high yield under moisture limiting conditions. Different strategies being adopted for moisture stress tolerance include selection for specific plant physiological traits; selection for traits such as salt tolerance and nematode resistance that will minimise the impact of low soil moisture levels; and direct selection for yield under conditions of moisture stress. Tolerance to waterlogging, a significant problem in large areas of Western Australia, is also a focus of the Program.

Program 3 includes a number of projects involved in quality issues. We are currently investigating resistance to pre-harvest sprouting and black point, and are working to identify and quantify the effects of novel wheat and barley quality alleles.

Pathogens and host resistance genes are being investigated using both molecular and mycological techniques so that a more complete picture of pathogen variation and host resistance diversity can be obtained. The barley scald pathogen is being targeted most specifically, but resistance studies are also covering a wide range of fungal and nematode pathogen species.

Also included in this Program are projects that form part of the Australian Winter Cereal Molecular Marker Program (AWCMMP), a GRDC funded and nationally coordinated program promoting the adoption of marker-assisted selection in cereal breeding programs. These include projects identifying marker-trait associations and marker implementation projects that provide direct support for marker-assisted selection in breeding programs linked to MPB.

Using new genetic knowledge arising from MPB genetic studies, and skills in developing improved germplasm, several projects have been created to develop wheat and barley lines with improved tolerance to environmental stresses, resistance to diseases and improved quality. Lines developed in these projects will be used as parents, or developed into varieties by collaborating breeding programs associated with MPB.

### Research overview

This past year saw many of the new MPB projects get into their stride, with phenotype evaluation techniques being refined and early results looking promising. Major new initiatives on abiotic stresses in wheat have seen a project commence on terminal drought tolerance in Western Australia, on salt tolerance in South Australia, and in Mexico work will start shortly on investigating drought tolerance in a mapping population combining CIMMYT and South Australian germplasm. In barley, collaborative projects with ICARDA in Syria have led to the identification of lines that have been demonstrating high yields in low rainfall environments in South Australia. A new project with ICARDA will investigate salt tolerance whilst also continuing the evaluation of earlier ICARDA derived germplasm.

Novel quality alleles are being identified and transferred into standard isolines so that their genetic value can be more accurately determined. In wheat, QTLs have been identified that are linked to novel genes for pre-harvest sprouting resistance. In barley, a new project has just commenced that is seeking new genes for pre-harvest sprouting resistance so that the 5HL quality locus from Canadian varieties, which has been found to be linked to pre-harvest sprouting susceptibility, can be used more reliably. These projects, whilst investigating new alleles and the genetic control of each trait, will also develop improved

germplasm that will enhance the utility of these genes to breeding programs.

Wheat and barley genetic maps and marker-trait associations are being continually developed and improved. New technologies from Program 2 are being adopted, and improved quality control procedures are being implemented for mapping projects. Improved marker technologies are also being adopted for pathogen studies. These improvements, along with technologies being developed in Program 2, are being rapidly adopted for use in the marker-assisted selection labs working for MPB-associated breeding programs.

Barley germplasm projects funded by ABB Grain Ltd have used molecular makers to allow the use of novel breeding strategies to introgress quality alleles into feed barleys and fast track the improvement of disease resistance into quality barleys. These projects, initiated in the previous CRC round, have reached the stage where valuable new germplasm is now flowing into S2 and S3 trials around southern Australia.

## Highlights

### SCREENING, GENETICS AND MARKERS

» Development of a full map of Trident\* Molineux double haploid lines with 230 markers covering all chromosomes. Phenotypic data obtained leading to new markers for septoria tritici blotch, CCN, leaf rust, boron and yield components.

- » Improvements to and analysis of data from a Cascades\* RAC875-2 mapping population with new data coming from rust and septoria screening as well as yield components.
- » A major QTL has been identified from Baudin for seed dormancy and pre-harvest sprouting tolerance. The QTL accounted over 75% of phenotypic variation of pre-harvest sprouting.
- » The identification of improved markers in barley for the control of spot form of net blotch on chromosome 7H and leaf scald on 3H.
- » The improvement of existing barley mapping populations through the addition of new markers and careful curation.
- » Record levels of marker-assisted selection precision and throughput in mainstream breeding programs.
- » Importance of soil type identified for work on waterlogging tolerance. A strong influence of microelements was also observed.
- » Large infrastructure and screening systems established for work on waterlogging and drought tolerance in Western Australia. Four QTLs identified accounting for 38% of variation for waterlogging tolerance in a Dukula-4/2\* Brookton double haploid population.
- » Salt tolerance screening systems improved for discrimination of tolerance and sodium exclusion in wheat and durum.

- » Novel glutenin alleles identified in exotic germplasm.
- » Several genes related to black point tolerance have been identified and characterised.
- » QTLs with linked markers identified from *Aegilops tauschii* source of pre-harvest sprouting tolerance.
- » New populations of the scald fungus developed for detailed analysis of genotypic variation using SSRs.

### GERMPLASM DEVELOPMENT

- » Barley lines derived from ICARDA germplasm adapted to low rainfall environments perform exceptionally well in South Australian trials.
- » Advanced barley lines enter S2 and S3 trials after transfer of malting quality alleles into feed barleys.
- » Disease resistant barley lines developed from elite malting quality backgrounds enter S2 trials.
- » New wheat lines with superior combinations of disease resistance entering yield trials. One line in S3 trials throughout Australia.
- » First generation of high yielding wheat lines developed in Mexico and using Australian sources of disease resistance and stress tolerance are being multiplied and observed in trials in South Australia prior to yield evaluation in 2006.

# PROGRAM OUTPUT REPORT

PROJECT	PROJECT OUTPUTS	PROGRESS
<b>Program Output 1: Improved genetic understanding of inheritance of traits, diversity of germplasm and pathogen variation. (2006 and 2008)</b>		
3.1.03b	Knowledge of the chromosomal locations associated with useful traits and of markers linked to those loci.	Marker development work has led to an improved understanding of the genetic control of resistance for several diseases including scald, net blotch, septoria tritici blotch, and CCN.
3.1.03c	QTL analysis of phenotypic data from wheat and barley mapping populations.	Wheat and barley maps updated with 112 new markers added. QTLs identified in Trident*Molineux for, leaf rust, boron and yield components. Rust resistance QTLs have been identified from Cascades*RAC875-2.
3.1.03d	Novel alleles (and potentially novel loci) that influence malt quality identified from AB-QTL population.	BC2F2 generation developed from 3025 B2F1 plants derived from a cross using two accessions of <i>Hordeum spontaneum</i> .
3.1.04a	Optimisation of DNA fingerprinting methods to allow a more accurate investigation of molecular variation of <i>Rhynchosporium secalis</i> .	SSRs identified as the most effective marker system for analysis of pathogen variation. Protocols have been optimised.
3.1.04a	Analysis of variation amongst single spore isolates from field collections.	Scald-specific SSRs being used to fingerprint scald DNA from 168 single spores isolates collected from hotspots.
3.1.04b	Specific resistance genes identified in barley breeding lines and new introductions.	Gene identification service was successfully provided to all GRDC funded breeding programs in Australia.
3.1.04b	Improved knowledge of the genetic basis of scald resistance.	Differential isolates have been used to identify potential new sources of resistance to scald.
3.1.05a	Regions of the barley genome associated with high, and low levels of dormancy will be identified.	Synteny between barley 5H and rice has been established. Rice gibberellic acid biosynthesis genes have been positioned on a barley map.
3.1.05a	Identification of alternative dormancy loci in barley to counteract effect on pre-harvest sprouting of region of 5HL that contributes to superior quality.	Identified variation of dormancy levels in 100 elite lines, mapping population parents and international varieties.
3.1.05b	New markers for tracking pre-harvest sprouting, water sensitivity and semi-dwarf phenotypes.	25 candidate genes for the seed dormancy locus identified from rice syntenous regions and partially sequenced from various barley varieties.
3.1.05b	A marker package for high malting quality and moderate pre-harvest sprouting tolerance from Baudin.	A major QTL has been identified from Baudin for seed dormancy and pre-harvest sprouting. The QTL accounted over 75% of phenotypic variation of pre-harvest sprouting.
3.1.05b	Novel combinations of seed dormancy QTLs and malting quality QTLs.	Seed dormancy loci <i>SD1</i> and <i>SD2</i> have been backcrossed once with the malting barley lines WABAR2110.
3.1.05c	Unique black point-related proteins identified using a proteomics approach.	Proteomics techniques have been optimised and over 10 potential proteins identified. Currently being confirmed prior to sequencing.
3.1.05c	Mapping of candidate genes for tolerance to black point and association with QTLs via fine mapping.	Candidate genes have been identified.
3.2.01b	Improved knowledge of the genetic basis of stress tolerance in wheat.	New sources of tolerance to soil salinity identified and being developed into double haploid populations for phenotyping and genetic analysis.
3.2.01c	Improved knowledge of the genetic basis of waterlogging and drought tolerance in wheat.	QTLs identified for waterlogging tolerance from a Dukula/2*Brookton double haploid population. Large-scale trials sown for evaluation of terminal drought tolerance.
3.2.01f	Screening of wheat and barley varieties and breeding lines for resistance to fungal diseases. The phenotyping of genetic populations.	Field and growth room screening procedures used to screen lines for resistance to scald, leaf rust, the net blotches and common root rot in barley and yellow leaf spot, septoria tritici blotch, rusts and crown rot in wheat.

PROJECT	PROJECT OUTPUTS	PROGRESS
3.2.01g	Identify novel elite protein quality alleles from exotic or other germplasm. Develop molecular markers suitable for selection purposes.	260 landraces and 48 synthetic hexaploids screened using SDS-PAGE and SE-HPLC for protein quality and the presence of novel glutenin subunits. Some synthetic lines and related species with novel and rare alleles are being crossed into adapted wheats for further evaluation. Published markers now used in development of new germplasm.
3.2.01h	Identify genes and molecular markers conferring pre-harvest sprouting resistance in different wheat sources.	New loci for pre-harvest sprouting resistance identified from two sources that account for 50% and 35% of variation respectively. Markers are being developed.
3.2.02a	Identify chromosomal regions and markers involved in adaptation of barley to low rainfall environments.	Linkage analysis in progress on 80 lines evaluated in low rainfall environments in Australia and Syria. An advanced backcross-QTL ( <i>H. spontaneum</i> / Barque*73) population has been phenotyped in 10 low rainfall environments including Syria, and preliminary mapping has identified QTL involved in adaptation from both parents.
3.2.02b	To identify useful variation in <i>H. spontaneum</i> and our ability to access useful genes from the species.	Genetic analysis almost completed to identify wild barley derived genes for tolerance to extreme drought conditions.
<b>Program Output 2: Development of improved population maps and validation and implementation of molecular markers for marker-assisted selection. (2006 and 2008)</b>		
3.1.02a	Wheat marker validation / implementation for AGT.	Record throughput and range of loci being used for selection in wheat and barley. Commercial launch of 'Gairdner Plus' planned for spring 2005. This is the second malting barley developed using rapid marker-assisted selection backcrossing.
3.1.02b	DAWA wheat marker validation / implementation.	
3.1.02c	MBQIP marker validation / implementation.	
3.1.02d	Marker validation / implementation for the WA barley breeding program.	
3.1.03c	Genetic maps of wheat and barley with greater marker density, improved accuracy and reliability for determining and implementing marker-trait associations.	Australian wheat and barley maps updated with 112 new markers.
3.2.01b	High quality genetic maps of Trident * Molineux and Berkut * Krichauff available for QTL analysis of agronomic, disease resistance and abiotic stress tolerance traits.	A new map of a Trident*Molineux population has been produced, with 230 markers covering all chromosomes. Berkutt*Krichauff double haploid population is being multiplied.
3.2.01c	Development of wheat maps for terminal drought tolerance.	100 lines of a Westonia/Janz double haploid population for drought tolerance have been mapped with markers to create a skeletal map.
<b>Program Output 3: New germplasm developed using MPBCRC technologies will contain new alleles or gene combinations for adaptation to environmental stress, disease resistance and novel quality attributes. (2006, 2008 and 2010)</b>		
3.1.03d	Elite quality germplasm incorporating novel alleles from wild barley.	BC2F2 generation developed from 3025 B2F1 plants derived from a cross using two accessions of <i>H. spontaneum</i> with novel alpha-amylase alleles.
3.2.01b	Development of wheat germplasm with high yield under stress conditions.	Breeding lines reselected at the F8 generation from derived crosses between a CIMMYT variety and Australian sources of resistance to root diseases and hostile soils developed in Mexico.
3.2.01c	Environmental characterisations made and field constraints identified for terminal drought tolerance work. Target environments prioritised.	Environments prioritised – screening facility developed. This location is to be reviewed mid-project for possible extension to additional locations subject to resources.

# PROGRAM OUTPUT REPORT

PROJECT	PROJECT OUTPUTS	PROGRESS
3.2.01c	Germplasm characterisation for drought tolerance. Screening protocols developed for international nursery and commercial varieties. Germplasm characterised for adaptive traits.	Project work commenced in November 2004. Protocols developed in collaboration with screening trial funded by EGA/DAWA. A national and international nursery developed. Stay green, plant height and flowering dates recorded.
3.2.01d	Well-adapted Krichauff-derived lines with resistance to CCN, <i>Pratylenchus</i> , yellow leaf spot and diversified sources of leaf and stripe rust resistance	One line in interstate S3 trials with AGT. New lines with improved leaf rust resistance are being evaluated in the field in 2005.
3.2.01e	Characterisations of existing wheat lines carrying rust resistance genes <i>Sr32</i> , <i>Sr37</i> and <i>Sr39</i> .	New stem rust resistant recombinant lines carrying <i>Sr32</i> and <i>Sr39</i> have been sent to breeding programs in Perth, Narrabri and Roseworthy.
3.2.01e	New recombinant lines containing short segments of chromosomes from either <i>Triticum searsii</i> accession TE10, <i>T. uniaristatum</i> accession TA3401 or <i>T. speltoides</i> accession AEG874-60	Production of alien chromosome addition lines is proceeding well with nearly the complete set of chromosomes from <i>T. searsii</i> and <i>T. uniaristatum</i> isolated in an Angas wheat background.
3.2.01f	Development of wheat and barley germplasm incorporating new sources of disease resistance.	Durum lines with improved resistance to crown rot have reached the B1F5 stage. Lines with putative partial resistance are being checked in the field and Terraces in 2005. New sources of resistance to spot form net blotch, scald and common root rot are being crossed into malting quality barleys and resistant progeny identified.
3.2.01g	Elite germplasm with improved quality through the manipulation of novel and other glutenin alleles.	BC1 F1 seed produced to incorporate quality alleles into adapted backgrounds. Two double haploid populations are being produced from F2 selected using markers for required protein alleles.
3.2.01h	Advanced wheat germplasm lines with improved pre-harvest sprouting resistance.	BC2F7 lines have been developed with improved seed dormancy. These are being evaluated in rain simulators and at two sites by breeding programs in 2005 to check for pre-harvest sprouting resistance.
3.2.01i	Development of durum germplasm with tolerance to hostile soils, improved colour and reduced incidence of grain quality defects.	Set of four recurrent, locally adapted durums selected and initial crosses made with sources of tolerance to a range of hostile soil conditions, improved yellow pigment and sprouting and black point resistance.
3.2.02a	Improved germplasm for low rainfall environments across Australia.	Testing of 300 ICARDA lines in 24 Australian low rainfall environments has identified high yielding lines for these situations. These are being used in breeding programs.
3.2.02d	A germplasm platform for ABB and MPBCRC to access elite malting quality parents with improved disease resistance.	18 B1F6 selected lines with improved resistance to CCN, scald, spot form net blotch and leaf rust in S2 yield trials in 2005. Further backcross and topcross lines are at earlier stages of development.
3.2.02e	Pyramid malting quality alleles into a widely adapted Australian variety.	VB9104 derived germplasm developed possessing CCN resistance and boron tolerance, and carrying improved malt quality QTL. Lines in S2 and S3 yield trials in 2005. New intercross double haploid populations being multiplied in 2005.
3.2.02f	Validation of a new breeding method for barley quality. Germplasm developed possessing a combination of excellent malting and high yield derived from a feed barley variety.	Novel breeding strategy developed whereby malting alleles are transferred into feed barleys using marker-assisted selection. Extensive marker-assisted selection completed for early generation population development. 11 elite lines have been progressed to S2 trials and one in S3 trials in 2005.

# FEATURED PROJECT REPORTS

## 3.1.05C GENETIC BASIS OF BARLEY BLACK POINT FORMATION

**Leader: Dr Amanda Able**

The physiological disorder referred to as black point is a serious but intermittent problem in barley. Black point refers to a localised blackening at the germ end of the grain (mainly in the caryopses) and is often associated with the occurrence of specific environmental conditions such as rain and high humidity during grain filling and ripening. Black point has been identified as unacceptable to many members of the grains industry resulting in downgrading of barley quality at receipt once black point reaches levels greater than 5% in a sample. This downgrading from malting grade to feed grade for barley can cost growers more than \$50 per tonne. However, knowledge of the genetic and biochemical mechanisms responsible for black point in barley is limited.

We are currently using several approaches to identify genes potentially involved in either black point formation or to identify genes which confer tolerance to black point: proteomics, synteny and the study of regulatory factors.

Proteins which differ between black-pointed and healthy grain from both susceptible and tolerant varieties are currently being identified. Unique proteins will be sequenced and this information used to identify loci for use in the breeding program. In husk tissue, we have identified several proteins (of approximately 45 kDa in size) with significantly lower

expression in black-pointed tissue. Higher expression levels of some smaller proteins (approximately 20 to 25 kDa in size) were also observed in husk tissue. All of these proteins were only extractable from the cell wall. Several proteins have also been identified as unique in the husk of black-pointed grains. Proteins are currently being sequenced using mass spectrometry methods. Our group is also examining proteins present in the whole grain in relation to black point. Comparisons are being made between black-pointed and clean whole grain protein extracts to identify other proteins possibly involved in black point development as the embryo region of the grain also appears to be implicated in black point development

Using synteny with the rice genome we have identified a number of candidate genes from the black point QTL on 2H. This region is now being fine-mapped further and we are currently studying the expression of the candidate genes selected. These include a lipoxygenase, a peroxidase and a quinone reductase. We are also currently studying their regulation during black point formation through identification of the transcription factors and QTLs responsible for this regulation. Increased knowledge of the genes and proteins involved in black point formation and/or tolerance can be used in breeding programs to ensure a more economically viable malting barley industry.

*Researchers: Tim March (student), Ryan Walker (student), Prof Diane Mather, Dr Jason Able*



*Barley affected by black point*

### 3.2.01C WATERLOGGING TOLERANCE IN WHEAT

**Leader: Dr Tim Setter**

The aim of this project is to identify and phenotype specific mechanisms of waterlogging tolerance, to develop molecular markers for those mechanisms and to transfer tolerance into elite germplasm.

Three types of trials were run in 2004–05: (i) two sites were established with gradients for waterlogging, with one site resulting in a waterlogging situation; (ii) two sites were run as Row Trials with only one site resulting in a waterlogging situation, and (iii) approximately 6000 pots were used in a semi-field (pot) trial using controlled waterlogging at Katanning, Western Australia.

The overall conclusion for waterlogging gradients and Row Trials is that results in the field are highly variable and often inconsistent between sites; sometimes the ranking of genotypes for waterlogging tolerance is just the opposite in one site in comparison to another. These results may be due to differences in the soil physical properties, or the timing or severity of the waterlogging. The pragmatic approach is to classify genotypes into groups of 'stable' or 'unstable'. The mechanistic approach is to identify the mechanism of tolerance to waterlogging in these different soils and conditions. We are focusing on the latter, since it is inappropriate to group together as one what are in fact different environments.

This year was the first year that we have been able to obtain accurate statistically significant differences in genotypes for waterlogging tolerance in pots that are consistent with field observations. This was done at the Katanning Waterlogging Tolerance Facility after we designed and mass-produced 10,000 of our own pots to eliminate root escape, and we ensured that soils were completely mixed to eliminate any spatial variations. The low errors in data indicate that protocols are now developed to reproducibly screen for waterlogging tolerance.

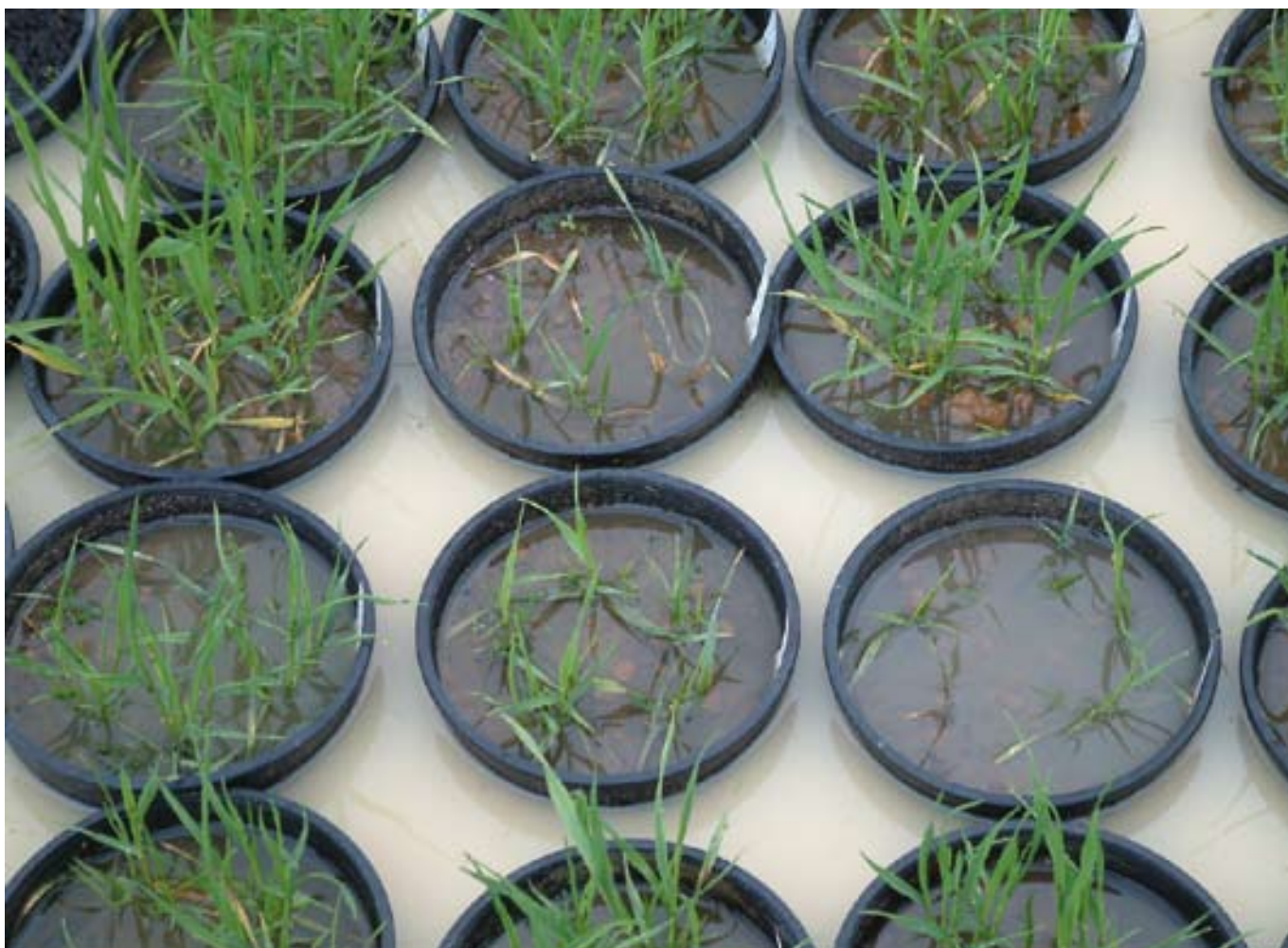
Data obtained at Katanning in 2004 have identified a new cross for varietal improvement and for molecular marker development. This cross of EGA Tammarin Rock / EGA Eagle Rock incorporates recently released varieties with one of the highest ranges in waterlogging tolerance (3-fold based on shoot biomass); with EGA Tammarin Rock having the highest waterlogging tolerance of 39 varieties. Doubled haploid lines are expected to be available for MPBCRC trials in 2006.

Evaluating the mechanisms of waterlogging tolerance is a key part of this project. The current hypothesis is that waterlogging tolerance is a product of tolerance to anaerobiosis and tolerance to specific microelements. Preliminary evidence for the importance of microelements under waterlogging is already available for aluminium, magnesium and iron in Australia, and for sodium and boron in India. It is likely that all these microelements are important across the waterlogging-prone regions of Australia, in that waterlogging exacerbates the predisposition of soils for microelement toxicities. The use of molecular markers to support breeding programs for these complex environments is a highly achievable and an exciting goal for germplasm improvement.

To identify molecular markers for waterlogging tolerance from the CIMMYT variety Ducula, a molecular map of a Ducula-4/2\*Brookton population was constructed using 184 SSR markers. Analysis of this map with the phenotypic data from one soil type has identified four QTLs corresponding to 38% of the variation for this trait. The analysis of the second year phenotypic data is being conducted, and in 2005 data

for waterlogging tolerance from three soil types will be available. Application of new high throughput technologies developed by MPBCRC has increased the genotyping capacity for this research.

*Researchers: Dr Mehmet Çakir, Dr Glenn McDonald, Irene Waters, Paul Barnett, Robin Wilson, Dr Iain Barclay, Dr Robyn McLean, Prof Rudi Appels*



Waterlogging tolerance trials at Katanning, WA



# PROGRAM 4

## EDUCATION

### PROGRAM LEADER:

**Dr Amanda Able**

### Objective

The primary mission of the Education and Training Program is to ensure that Australian cropping industries are internationally competitive by having world-class plant breeders who use innovative biotechnologies and enjoy strong community support. We are currently addressing this aim through three sub-programs: schools and community education, tertiary education and MPB professional training. By providing this continuum of education to all groups, we hope to provide career paths to agriculture (and in particular, plant breeding and biotechnology) and knowledge to the community about our research.

### Program overview

#### SCHOOLS

Outreach activities with the wider community and schools have involved a significant collaboration with ACPFG to develop a number of educational packages including Get into Genes, the Gene Juice Bar and Beer: Barley to Bottle. Get into Genes became fully operational in South Australia in early 2005 for secondary school students, with over 600 students participating in the workshop since its inception. Our involvement in numerous professional development workshops and conferences for secondary school teachers has meant that we have had significant demand for Get into Genes participation.

#### COMMUNITY

In an attempt to raise awareness among the community that plant products used for food contain DNA, we developed an interactive display called the Gene Juice Bar. This bright, fun display involves the extraction of DNA from various fruits and vegetables as well as the provision of fact sheets on what DNA is and what we can do with DNA.

During National Science Week 2004, Beer: Barley to Bottle was run as a quiz night for adults. In addition to tasting different styles of beer, workshop participants explored concepts of barley breeding, malting and brewing. ACPFG and MPBCRC are now exploring avenues for distribution of these packages nationally.

MPBCRC has also been involved in numerous field days such as Eyre Peninsula, Cleve and Horsham/Wimmera field days. Displays at these field days have involved mini DNA extraction experiments and a display of the role that gluten plays in bread dough development. A number of our scientists were also involved in open forums on GMOs, events such as Science in the Pub, career fairs and hosting work experience students. For use at such events, the education team has also developed a series of recruitment posters and postcards showing catch phrases including 'Make your own luck', 'Be part of the solution', 'We offer more than just dough' and 'Cracking the code'.





Filming the educational DVD on molecular markers

### UNIVERSITY

Over the summer of 2004–05, two summer scholarships were awarded to undergraduate students. The program is designed to expose students to research and provide opportunities for them to network and develop contacts within plant breeding and plant biotechnology. In 2004–05, there were nine Honours students working within MPBCRC, with four of these receiving scholarships. Interestingly, two of the students had received a summer scholarship the year before. Of these nine Honours students, two are continuing their Honours into the next financial year and four have started their PhDs with us. Two PhD students have finished in the last year bringing the total number of students graduated from MPBCRC/CRCMPB to 27. Another 21 students are due to submit, with 16 students having started their PhD with MPBCRC since July 2003. Please see designated tables in the following pages for more details of individual students' locations and project titles.

A postgraduate student retreat was held in conjunction with the Annual Research Meeting in July 2004. The program included media and communication, scientific communication, intellectual property management, networking and grant application writing. This involved the development of material by the Education Officer and the Education Program Leader. Honours students were included in this training to add more value to the Honours program and to try to retain all current Honours students.

### MPB TRAINING

MPB Training has been active, with three major workshops/short courses being run this year: Molecular Mapping Techniques in Diagnostic Biotechnology (Murdoch), Molecular Marker Short Course (UA), Systems Biology: From Genome to Phenome (DPI-PBC). We have filmed an educational DVD on molecular marker techniques with TAFE SA due for release later in 2005 once the production stage is finalised. We envisage that the DVD will become a key teaching and learning tool within the biotechnology industry and will enhance the value of current training activities. A marketing/commercialisation strategy is currently being developed while the final product is being completed.

This last year has been a whirlwind of activity particularly in addressing community and school educational needs but the Education team has had a lot of fun in the pursuit of addressing learning outcomes for each group of learners. We are looking forward to another action-packed year full of more educational ideas and their delivery with the help of our MPB scientists.

*The Education Team: Dr Amanda Able, Dr Heather Bray, Michael McLean*



DNA extraction demonstration at Esperance Crop Updates

# PROGRAM OUTPUT REPORT

PROJECT OUTPUTS	PROGRESS
<p>Increased community and school student awareness of the importance of plant biotechnology, plant breeding and agriculture</p>	<p>Exceeding target and ongoing.</p> <p>Five fact sheets have been prepared for the website. Website views have increased significantly since redesign. Educational pages for children to be designed.</p> <p>Numerous events such as field days attended with more than 1,000 people engaged.</p> <p>Get into Genes is in the final stages of development. 584 students attended Get into Genes. More than 100 teachers have attended workshops in the last year. Participation in the Open access web forum on GMOs also occurred.</p> <p>Currently developing Year 10 genetics interactive with Liz Hope from Urrbrae Agricultural High School.</p> <p>The Gene Juice Bar was developed in conjunction with ACPFG and has already engaged more than 100 people.</p> <p>Beer: Barley to Bottle developed for National Science Week in conjunction with ACPFG and engaged 70 people. Currently being redesigned for broader community use. MPB staff also participated in events such as 'Science in the Pub'.</p>
<p>Coordinated delivery of tertiary breeding courses and quality of training for postgraduate students.</p>	<p>There were nine Honours students working within MPBCRC, with four of these receiving scholarships.</p> <p>Two summer scholarships were awarded.</p> <p>Tertiary programs in Australia have been reviewed. Resource development will need to be approached through MPB participants.</p> <p>MPB staff have been integral to the development of a Masters in Plant Biotechnology at the University of Adelaide which will be coordinated by the Education Program Leader, and starts July 2006.</p> <p>Two PhD students finished in the last year (total of 27 graduates in MPBCRC/CRCMPB). 21 students due to submit, 16 students started PhD with MPBCRC since July 2003.</p> <p>Students rated the 2004 student retreat highly. The 2005 retreat has been developed using suggestions from this evaluation.</p>
<p>Provision of professional training (branded as MPB training).</p>	<p>Filming and script writing of the DVD on molecular marker techniques developed in conjunction with TAFE SA completed. Narration and production of animation currently underway. Commercialisation strategies under development.</p> <p>Initial survey of industry needs for training to be conducted.</p> <p>Three workshops provided this year with positive feedback.</p> <p>The student retreat is also considered an MPB training exercise. We are currently packaging material used into an appropriate format for delivery elsewhere.</p>

# STUDENT LIST

## STUDENTS COMPLETED 2004–2005

Name	Title	Institution	Supervisor	Funding	Project
Eline van Zijl de Jong	Molecular marker analysis of <i>Neotyphodium</i> spp.	DPI - PBC La Trobe	Prof German Spangenberg	MPBCRC	1.1.11
Yohei Norimatsu	Electrophysiological characterisation of the effects of necrosis inducing proteins from the barley scald fungus	Flinders	Dr Peter Anderson Prof Steve Tyerman	OPRS MPBCRC	CG1.02

## STUDENTS COMPLETED EXPERIMENTAL WORK – SUBMISSION PENDING

Name	Title	Institution	Supervisor	Funding	Project
Paul Eckermann	Analysis of quantitative trait loci	UA	Dr Ari Verbyla	APA MPBCRC	CM3.04
Linh Nguyen	Isolation and characterisation of barley <i>p450</i> genes	SCU	Prof Robert Henry	MPBCRC	CG3.03
Maria-Jane Appelbee	Assessment of the quality potential of endosperm storage protein alleles in hexaploid bread wheat relatives	UA SARDI	Dr Geoff Cornish	MPBCRC	3.2.01g
Stewart Coventry	Improving drought and heat tolerance in cereals	UA	Dr Glenn McDonald	MPBCRC	3.2.02a
Jacinda Rethus	Transformation of wheat with a gene of industry significance and studies on the expression of that gene	DPI - Horsham MU	Prof Geoff Fincher Dr Jim Kollmorgen	APA MPBCRC	CG5.01
Lorraine Watson	Gene expression profiles in germinating barley	SCU	Prof Robert Henry	MPBCRC	1.1.01
Juan José Olivares-Villegas	Development of molecular markers associated with genomic regions controlling components of drought and heat tolerance in bread wheat	CIMMYT UA	Dr David Hoisington Dr Manilal William Dr Glenn McDonald	MPBCRC	CM1.20
María Magdalena Salgado	Characterisation of anti-fungal genes and corresponding transgenic wheat plants	CIMMYT UA	Dr David Hoisington Dr Alessandro Pelligreneschi Prof Geoff Fincher	MPBCRC	CG1.04
Jaye Chalmers	Functional genomics of fructan biosynthesis in grasses	DPI - PBC La Trobe	Prof German Spangenberg	MPBCRC	1.1.11a
Natasha Petrovska	Functional genomics of reproductive development in grasses	DPI - PBC La Trobe	Prof German Spangenberg	MPBCRC	1.1.11d
Nathaniel Bannan	Strategies for marker assisted selection in out-crossing pasture species	DPI - Hamilton La Trobe	Dr Kevin Smith	MPBCRC	2.1.02
Marc Ramsperger	Grass endophyte genomics	DPI - PBC La Trobe	Prof German Spangenberg	MPBCRC	1.1.11c
Kate Shields	Grass endophyte genomics	DPI - PBC La Trobe	Prof German Spangenberg	MPBCRC	1.1.11c
Paul Bogacki	Gene expression profiling in the incompatible interaction between barley and the net blotch pathogen <i>P. teres</i>	UA SARDI	Dr Kevin Williams	GRDC MPBCRC	1.1.04
*Emma Ludlow	Virus induced gene silencing in white clover as a tool in functional genomics	DPI - PBC La Trobe	Prof German Spangenberg	DA	1.1.11

# STUDENT LIST

2001					
Name	Title	Institution	Supervisor	Funding	Project
Haydn Kuchel	Whole genome analysis of a wheat breeding strategy	UA AGT	Prof Peter Langridge Dr Steve Jefferies	AGT MPBCRC	CM2.28
2002					
Name	Title	Institution	Supervisor	Funding	Project
Sherri Kruger	Development of association mapping technologies	UA	Prof Peter Langridge Dr Jason Able	MPBCRC	2.2.03b
Nicholas Cummings	Functional genomics of fructan biosynthesis in grasses	DPI - PBC La Trobe	Prof German Spangenberg	GGDF MPBCRC	1.1.05
Berhane Lakew Awoke	Genetic potential of wild barley ( <i>H.v. ssp. spontaneum</i> ) to improve adaptation to low rainfall environments	SCU ICARDA	Prof Robert Henry Dr Stephania Grando Dr Salvatore Ceccorelli Dr Jason Eglinton	MPBCRC	3.2.02b
*Marcel Labandera	Development and evaluation of transgenic lucerne and clover plants for enhanced aluminium tolerance and phosphorus acquisition efficiency	DPI - PBC La Trobe	Prof German Spangenberg	La Trobe	1.1.11
*Meredith Carter	Genome-level studies on agronomically important regions in wheat	Murdoch DAWA	Prof Rudi Appels Prof Mike Jones	GRDC	2.1.05
2003					
Name	Title	Institution	Supervisor	Funding	Project
Julie George	Candidate gene-based marker development and validation in white clover	DPI - PBC La Trobe	Prof John Forster Prof Roger Parish	GGDF	2.1.03
Pei Tian	Grass endophyte functional genomics	DPI - PBC La Trobe	Prof German Spangenberg Prof Charles Pallaghy	MPBCRC	1.1.11e
Andrew Craig	An investigation of cytoskeletal movement in the <i>R. secalis</i> / barley interaction	UA	Dr Amanda Able Dr Klaus Oldach	MPBCRC	1.1.09a
2004					
Name	Title	Institution	Supervisor	Funding	Project
Yingying Cao	Fructan metabolism in perennial ryegrass	DPI - PBC La Trobe	Prof German Spangenberg Prof Roger Parish	MPBCRC	1.1.11a
Timothy March	Genetic basis of black point in barley	UA	Dr Amanda Able Dr Jason Able	UA MPBCRC	3.1.05c
Elysia Vassos	Conversion of feed barley to malting types	UA	Dr Jason Eglinton Prof Diane Mather Prof Andrew Barr		3.2.02f
Joanne Elsdon	Map-based cloning of a quantitative trait locus in barley	UA ACPFPG	A Prof Ken Chalmers Dr Nick Collins Dr Jason Eglinton Prof Peter Langridge	GRDC	2.2.07
Yumiko Bonnardeaux	Seed dormancy in cereals	UWA Murdoch	Prof Rudi Appels Prof Krishnapillai Sivasithamparam	APA MPBCRC	3.1.05b
Peter Dracatos	Development and implementation of candidate gene-based molecular markers in outcrossing forage species	DPI - PBC La Trobe	Prof John Forster Dr Tony Gendall	GGDF	2.1.03

2005					
Name	Title	Institution	Supervisor	Funding	Project
Reetinder Gill	Male sterile facilitated recurrent selection in barley breeding	Murdoch	Dr Reg Lance Prof Rudi Appels	Murdoch MPBCRC	2.2.03d
Allen Tarr	Protein profiling for predicting barley malting quality traits	Murdoch DAWA	Prof Rudi Appels Dr Reg Lance Prof Mike Jones	MPBCRC	2.1.04a
Jingjuan Zhang	Abiotic stress in wheat with a special reference to terminal drought	Murdoch	Dr Tim Setter Prof Rudi Appels Dr Mehmet Çakir	Murdoch MPBCRC	3.2.01c
Scott Boden	<i>TaASY1</i> : Complementation analysis and identification of protein-protein interactions	UA	Dr Jason Able Dr Andrew Milligan Dr Chunyuan Huang Prof Peter Langridge	GRDC MPBCRC	1.1.08
Ryan Walker	Regulation of black point formation in barley	UA	Dr Amanda Able Dr Jason Able Prof Diane Mather	UA MPBCRC	3.1.05c
Yi Tu	Transgenic pastures – Deployment of transgenic technologies in forages a) Designer perennial ryegrass (with particular emphasis on the lignin modification component)	DPI - PBC La Trobe	Prof German Spangenberg Dr Tony Gendall	MPBCRC	1.1.11a
Shamila Abeynake	Transgenic pastures – Deployment of transgenic technologies in forages b) designer white clover	DPI - PBC La Trobe	Prof German Spangenberg Dr Tony Gendall Prof Roger Parish	MPBCRC	1.1.11b
HONOURS 2004–2005					
Name	Title	Institution	Supervisor	Funding	Project
Scott Boden	Understanding the role of an <i>SSRP1</i> orthologue in wheat and barley	UA	Dr Jason Able Prof Peter Langridge	MPBCRC	1.1.08
James Chand	Functional characterisation of an <i>Arabidopsis Asy1</i> homologue isolated from bread wheat ( <i>Triticum aestivum</i> L)	UA	Dr Jason Able Prof Peter Langridge	MPBCRC	1.1.08
Ryan Walker	Isolation and characterisation of genes expressed during black point formation	Flinders UA	Dr Amanda Able		3.1.05c
Danielle Cash	Identification of <i>Arabidopsis</i> and wheat ERF orthologues using rice as a 'bridging' species and determining their significance in response to pathogen infection in wheat	Murdoch	Dr Michael Francki Prof Rudi Appels	MPBCRC	
Jingjuan Zhang	Rice-wheat-barley comparative genomics to identify new molecular markers for dwarfing	Murdoch	Prof Rudi Appels Dr Chengdao Li		3.2.01c
Wayne Altmann	Investigating the effects of matrix attachment regions (MARs) in a canola transformation system	Flinders UA	Dr Jason Able		CG4.03
Wayne Crismani	Preliminary characterisation of <i>TaRAD26</i>	UA	Dr Jason Able	MPBCRC	1.1.08
Andrew Lloyd	Functional analysis of <i>TaMSH7</i> in transgenic barley	UA	Dr Jason Able Dr Andrew Milligan	MPBCRC	1.1.08
John Russell	Analysis of barley genes in transgenic plants	SCU	Prof Robert Henry Dr Agnelo Furtado	Paul Johnson Memorial Fund	

\* Students joined CRC after commencing PhD.



# COLLABORATION

The Core and Supporting Participant organisations of the CRC continued this year to share knowledge and resources in the spirit of true collaboration. Breeders and researchers from industry, university, government department and research centre came together to share know-how, data, germplasm and other resources.

While the majority of our CRC's research projects have involvement from multiple participant organisations, a number of recent collaborations are worthy of note. The collaborative efforts outlined in past Annual Reports are ongoing. The following are examples of linkages developed within the centre and with other organisations within Australia and internationally.

## Linkages within the CRC

'GENica', the integrated genetics and genomics system is an initiative about which we can be particularly proud. Not only has this project involved collaboration between all the participant organisations of the CRC, but close ties with ACPFG have also been forged so that a pooling of our joint knowledge and resources might be possible. While still under development, GENica is already in use and is already providing the benefits of collaboration. As an online database GENica is accessible to all CRC participants anywhere in Australia and around the world.

The MPBCRC Annual Research Meeting was held in Ballarat in July 2005. This event was attended by over 100 CRC participants from Victoria, South Australia, Queensland, Western Australia, Syria and Mexico. The Research Meeting

always provides an ideal opportunity to network, and serves to strengthen ties between individuals from different locations, research projects and disciplines. This year, additional educational and networking opportunities were provided to students via means of the first MPBCRC Student Retreat.

## Linkages to end users

The ongoing support of the AGT and DAWA breeding programs has kept MPBCRC research focused and relevant to the needs of Australian industry. This year, at the Portfolio Review held in the Yarra Valley Victoria, key researchers and staff met to discuss the future of our research portfolio, and how to better engage the breeding programs. A number of models proposing different ways to ensure both the maximum uptake of MPBCRC technology, and appropriate returns to the CRC were explored. The meeting sparked additional discussions, and negotiations are currently underway to develop a collaborative model whereby MPBCRC technologies are delivered via the breeding programs. The Review was a valuable forum in which to explore some thorny issues, and as always, the contribution of the breeding programs was invaluable.

## External linkages

This year MPBCRC fostered valuable relationships with a number of other CRCs. Of particular note was the collaborative discussions initiated with the Grain Foods CRC. With MPBCRC's strong transgenic capability, and the Grain Foods CRC's broad knowledge of

health, taste and convenience-related grain characteristics, a partnership between our two organisations promises to yield real benefits to Australia's grain industries.

Links have been established with the Value Added Wheat CRC that are also proving beneficial. The ongoing development of cross-outcome prediction software, conducted by Howard Eagles and his team, has been strengthened by the inclusion of wheat quality data supplied by the Value Added Wheat CRC. It is hoped that this project will continue to forge links with other organisations to further increase the predictive power of this software.

Members of the Education Program formed valuable links with local secondary school teacher Elizabeth Hope of Urrbrae Agricultural High School in South Australia. Ms Hope visited the Education Team for a 10 day placement through the Premier's Industry Awards for Teachers of Science and Mathematics. Liz worked with Education Manager Heather Bray to produce educational materials on gene technology for high school students.

As in past years, MPBCRC participants formed new links with researchers from numerous overseas institutions. This year MPBCRC worked with research groups from the United States, Japan, Syria, Uruguay, the Philippines, Canada and the United Kingdom. Continued collaboration with BPS in Germany, and new links with Wrightson in New Zealand have further strengthened the CRC's commercialisation capability.

# SPECIFIED PERSONNEL



**Dr Bryan Whan**  
Chief Executive Officer



**Dr Heather Bray**  
Education Manager



**Ms Vicki Kokolakis**  
Accountant



**Ms Cheryl McCaffery**  
Commercial  
Manager



**Mr Michael McLean**  
Communications  
Manager



**Mrs Nora Veljanovski**  
Administration Officer



**Mr Frank Yardley**  
Business Manager

The administration of the Molecular Plant Breeding CRC is conducted by a small team spread across two locations:

- » Technology Enterprise Centre, Bundoora, Vic
- » University of Adelaide, Waite Campus, Urrbrae, SA.

The CEO, Bryan Whan, is supported by an Education Manager, an Accountant, a Commercial Manager, a Communications Manager, an Administration Officer, and a Business Manager.

Together, they work closely with and

support 200 staff who contribute to the activities of the Centre. Of this group, 110 are funded by MPBCRC and 58 are in-kind contributions made by partners of the Centre. Thirty-three participants are funded through grants provided by bodies such as GRDC.

## Specified Personnel

TITLE AND NAME	ROLE IN CRC	ORGANISATION	TIME ALLOCATION
Amanda Able	Program Leader	UA	0.25
Diane Mather	Program Leader	UA	1.00
Warwick Green	Commercialisation/ Utilisation	Wrightson Limited	0.10
Cheryl McCaffery	Commercial Manager	MPBCRC	1.00
German Spangenberg	Research Director	DPI Vic	0.70
Hugh Wallwork	Program Leader	SARDI	0.65
Bryan Whan	CEO	MPBCRC	1.00

*Specified Personnel as determined under schedule 4 of the Commonwealth Agreement.*

# PUBLICATIONS & PATENTS

## Refereed journal articles

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**Eagles HA, Eastwood RF, Hollamby GJ, Martin EM, Cornish GB (2004)**

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**Furtado A, Henry R (2005)**

The wheat *Em* promoter drives reporter gene expression in embryo and aleurone tissue of transgenic barley and rice. *Plant Biotechnol J* 3: 421-434.

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Exploiting genotypic variation in plant nutrient accumulation to alleviate micronutrient deficiency in populations. *J Trace Elem Med Bio* 18: 319-324.

**Henry RJ (2004)**

Genetic improvement of cereals. *Cereal Food World* 49: 122-129.

**John UP, Spangenberg G (2005)**

Xenogenomics: genomic bioprospecting in indigenous and exotic plants through EST discovery, cDNA microarray-based expression profiling and functional genomics. *Comp Funct Genom* 6: 230-235.

**Love C, Robinson A, Lim G, Hopkins C, Batley J, Barker G, Spangenberg G, Edwards D (2005)**

Brassica ASTRA: an integrated database for brassica genomic research. *Nucleic Acids Res* 33: D656-D659.

**Lyons GH, Judson G, Ortiz-Monasterio I, Genc Y, Stangoulis J, Graham R (2005)**

Selenium in Australia: selenium status and biofortification of wheat for better health. *J Trace Elem Med Bio*: Published online 2 August 2005, (<http://www.sciencedirect.com>).

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**Martin EM, Eastwood RF, Ogonnaya FC (2004)**

Identification of microsatellite markers associated with the cereal nematode resistance gene *Cre3* in wheat. *Aust J Agric Res* 55: 1205-1211.

**Moghaddam E, Trethowan RM, William HM, Rezaei A, Arzani A, Mirlohi AF (2005)**

Assessment of genetic diversity in bread wheat genotypes for tolerance to drought using AFLPs and agronomic traits. *Euphytica* 141: 147-156.

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**Monneveux P, Reynolds MP, Trethowan RM, Zapata F (2005)**

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**Mortimer J, Batley J, Love C, Logan E, Edwards D (2005)**

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Using computer simulation of the selection process and known gene information to assist in parental selection in wheat quality breeding. *Aust J Agric Res* 56: 465-473.

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Investigating the effects of dominance and epistasis on selection using QuCim. *Crop Sci* 44: 2006-2018.

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Genetics and molecular breeding in the *Lolium/Festuca* pasture grass species complex. *Grassland Science* 51: 89.

## Conference proceedings – invited and contributed papers

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**Appels A, Çakir M, Francki M, Carter M, Li D, Lance R, Wilson R, McLean R, Barclay I, Loughman R, Ryan K (2004)**

Molecular markers and accelerated breeding technologies. Wheat Breeding and Cereal Chemistry Conference, Canberra, Australia, 20-24 September.

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**Batley J, Love C, Hopkins CJ, Burgess B, Keniry A, Mountford H, Teakle G, King G, Grant N, Spangenberg GC, Edwards D (2005)**

Characterisation of simple sequence repeat markers derived from *Brassica oleracea* shotgun sequences. Plant and Animal Genome XIII, San Diego, California, USA, 15-19 January.

**Batley J, Love C, Hopkins CJ, Burgess B, Keniry A, Mountford H, Teakle G, King G, Grant N, Spangenberg GC, Edwards D (2005)**

Characterisation of simple sequence repeat markers derived from *Brassica oleracea* shotgun sequences. Brassica 2004, Daejeon, Sth Korea, October.

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Molecular tools for Plant Biology. The 2004 Annual Conference of the Korean Society of Plant Biotechnology, Busan, Sth Korea. (Invited Plenary Lecture), Sth Korea, October.

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Development of robust allele specific PCR based SNP markers for barley. Plant and Animal Genome XIII, San Diego, California, USA, 15-19 January.

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**Cogan NOI, Vecchies AC, Ponting RC, Drayton MC, George J, Dumsday JL, Dobrowolski M, Spangenberg GC, Sawbridge TI, Smith KF, Forster JW (2005)**

Gene-associated SNPs for superior allele identification in applied breeding of outbreeding pasture species. Plant and Animal Genome XIII, San Diego, California, USA, 15-19 January, W096.

**Cornish GB, Vawser M-J, Tonkin RE (2004)**

Extra-strong dough properties associated with over-expression of HMW glutenin subunit Glu-B1 7x. Proceedings of the 54th Australian Cereal Chemistry Conference and 11th Wheat Breeders Assembly, Canberra, Australia, 21-24 September.

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**Coventry SJ, Sayed H, Baum M, Grando S, Ceccarelli S, Barr AR, Eglinton JK (2004)**

The genetic basis of adaptation to low rainfall environments in Australia. Proceedings of the 9th International Barley Genetics Symposium, Brno, Czech Republic, 20-26 June, pp 920-926.

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Barley cytoskeleton movement in response to *Rhynchosporium secalis* challenge. ComBio 2004, Perth, western Australia, 26-30 September.

**Dreccer F, Ogbonnaya FC, Borgognone G, Wilson J (2004)**

Variation in shoot and root growth in primary synthetic wheat – implications for overcoming water deficits in marginal environments. 4th International Crop Science Congress, 26 September - 1 October, Brisbane, Queensland, Australia, Published online ([www.cropscience.org.au/icsc2004/](http://www.cropscience.org.au/icsc2004/)).

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**Hearnden PH, McMichael GL, Hayden M, Eglinton JK, Chalmers KJ (2005)**

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**Hopkins CJ, Mogg R, Gororo N, Salisbury P, Burton W, Love C, Spangenberg G, Edwards D, Batley J (2005)**

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**March TJ, Schultz C, Lahnstein J, Able JA, Able AJ (2004)**

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**Mrva K, Mares DJ, Williams KJ, Cheong J (2004)**

Molecular markers associated with late maturity  $\alpha$ -amylase (LMA) in wheat. Proceedings of the 54th Australian Cereal Chemistry Conference, Canberra, Australia, 21-24 September, pp 150-151.

**Nazari K, Keiper FJ, Wellings CR (2004)**

Analysis of molecular and pathogenic variability of *Puccinia striiformis* f.sp. *tritici* pathotype (104E137A-) in Australia. 11th International Cereal Rust and Powdery Mildew Conference, Norwich, United Kingdom, 22-27 August.

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Spectrum of disease resistance in synthetic hexaploids. 11th Wheat Breeding Assembly, Canberra, Australia, 21-24 September, pp 155-158.

**Smart A, Bray H, McLean M, Able AJ (2004)**

Grain growers' perspectives on genetically modified organisms. Abstracts of the 4th International Crop Science Congress, Brisbane, Australia, 26 September - 1 October, p 292.

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Gene discovery, functional genomics and molecular breeding of forage and turf plants. Baires Biotech 2005, REDBIO/FAO International Congress, Buenos Aires, Argentina, 7-10 June.

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Xenogenomics: genomic bioprospecting in indigenous and exotic plants using EST discovery, cDNA micro-array based expression profiling and functional genomics. Plant and Animal Genome XIII, San Diego, California, USA, 15-19 January.

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Genetic, physiological and breeding approaches to wheat improvement under drought. In 'Drought tolerance in cereals'. (Ed J-M Ribaut). (Haworth's Food Products Press: New York) (in press).

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## Other reports and publications

**Wang J, van Ginkel M, Basford K, Cooper M, DeLacy I, Pfeiffer W, Podlich D, Trethowan R, Ye G (2004)**

QuCim, software that simulates breeding programs for self-pollinated crops (Version 1.1). (CIMMYT: Mexico DF). CD-ROM.

# PATENTS

TECHNOLOGY AREA	APPLICATION TITLE	COUNTRIES WHERE PROTECTION IS BEING SOUGHT: APPLICATION NUMBER	STATUS
SSR markers	Molecular markers in ryegrass and fescues	Australia: 72468/00	Granted and sealed
		New Zealand: 509193	Accepted
Lignin genes	Modification of lignin biosynthesis	New Zealand: 523033	Granted and sealed
		New Zealand: 532000 New Zealand: 532001 Australia: 2001 265670 Europe: 01942874.7 USA: 10/311450	Applications in various stages of prosecution
Fructan genes	Fructosyl transferase homologues from ryegrass and fescue species	New Zealand: 523032	Granted and sealed
		Australia: 2001 265676 Europe: 01942880.4 USA: 10/311193	Applications in various stages of prosecution
Disease resistance	Modification of plant resistance to diseases and/or pests	New Zealand: 523538	Granted and sealed
		Australia: 2001 276169 Europe: 01953687.8 USA: 10/333091	Applications in various stages of prosecution
Lifecycle genes	Manipulation of plant life-cycles and/or growth phases	New Zealand: 525585	Granted and sealed
		Australia: 2002 213672 Europe: 01981971.3 USA: 10/416316	Applications in various stages of prosecution
Gene promoters	1. Use of bi-functional alpha amylase-subtilisin inhibitor promoter to direct expression in pericarp of plants	Australia 2003: 271420	National Phase entered April 2005
Gene promoters	2. Pollen-specific promoter	In 'International' phase PCT/AU2004/000802	Complete application filed: Now in unpublished PCT stage
Multiplex-ready marker technology	Method of amplifying nucleic acid	Australia: 2005 901191	Provisional filing



# COMMUNICATION

Effective communication is essential to the success of any organisation, but for a Cooperative Research Centre, with its numerous and geographically separated partners, communication is critical. MPBCRC recognises three key areas of emphasis within its communication strategy.

- » Internal: MPB researchers, students and commercial partners
- » External: general public, schools, media
- » Research: other researchers and potential collaborators.

This year saw the re-introduction of our quarterly newsletter 'On the Mark'. Primarily an internal publication designed to highlight events, research developments and community outreach activities, On the Mark is also a good tool for communicating with potential students and collaborators. The newsletter is distributed to MPB participants via email, posted on the MPB website and produced in hard copy for distribution at MPB events.

MPBCRC's newly re-vamped website ([www.molecularplantbreeding.com](http://www.molecularplantbreeding.com)) went live this year, and the increase in traffic to the site has been dramatic. In the previous financial year the total number of page views for the site was 1,700. The new site was uploaded in late 2004, and this year the figure has jumped to 46,300. Interestingly, using our newly implemented web traffic monitoring software, we now know that the majority of the individuals accessing the website are from 'biotech mega-countries' (countries growing 50,000 hectares or more biotech crops) including the United States, India, Canada and China.

Additional online resources are being developed by Prof Matt Bellgard's group based at the Centre for Bioinformatics and Biological Computing at Murdoch, Western Australia. In response to participant requests for online tools to share information, a 'Wiki'-based secure website has been established to allow participants to upload files and enter content without the requirement for specific software or web editing skills. The Wiki is an offshoot of the GENica database, and will include forms, templates and guidelines for MPB procedures, as well as specific information relating to MPB research projects. Elements of the Wiki are currently under development, with a more extensive version to be made available next year.

A number of printed resources were developed this year, including a brochure highlighting the core activities of the CRC, and a series of fact sheets on MPB research. These materials are distributed at the many field days, public events and school visits in which the CRC participates. Copies of these materials are available on the MPB website.

The Annual Research Meeting is a highlight of MPBCRC's yearly calendar, and is always an opportune time for researchers and stakeholders to be updated on the activities of the other CRC participants. This year a new element was added to the meeting in the form of a two day student retreat. In addition to the many educational outcomes of the retreat, students were given the opportunity to meet and interact with their peers from across the country and internationally. Student participation in outreach activities has noticeably increased over the past year since the retreat. The meeting was held in Ballarat in July 2004.

To date, MPB has maintained a modest media profile. A number of the technologies the CRC has been working to produce have been the subject of patent applications or commercial agreements, and as such limited publicity has been possible. However, as MPB moves into the commercialisation phase of its life cycle such restrictions are no longer required. Next year we have set the target of at least doubling the amount of media coverage on MPB research and activities.



# MEDIA COVERAGE

Print

DATE	MPB PARTICIPANT	COVERAGE	PUBLISHED BY	SUBJECT
01/07/2004		South Australia	Stock Journal	High-tech science hub opens at Waite.
08/07/2004	Whan B	South Australia	Stock Journal	Researchers push top malt barley breeds.
12/2004	Hayden MJ	National	Ground Cover Issue 53	Work starts to fast track marker delivery. Interview with Helen Olsen.
30/12/2004		South Australia	Stock Journal	Roseworthy bringing the bacon home.
13/01/2005		New South Wales	The Land	Research help boost.
02/2005	Eglinton J / Moody D	National	Ground Cover Issue 54	Breeding barley to excel. Interview with Emma Leonard.
14/02/2005	Mather D	Web	University of Adelaide press release	Uni lures world-class scientists.
19/02/2005	Mather D	Adelaide	The Advertiser	Uni drives brain drain in reverse. Interview with Andrea Stylianou.
03/03/2005		Web	Australian Biotechnology News	Cash up for grabs from NZ fund.
10/03/2005	Pellegrineschi A	Web	New Agriculturalist	The quest for drought tolerance.
03/2005	Mather D	Adelaide	The Adelaidean	Top guns of science attracted to Adelaide. Interview with Lisa Edwards.
04/2005	Coventry SJ	National	Ground Cover Issue 55	Global ties lift barley traits.
05/05/2005	Able JA	South Australia	Stock Journal	Scientists look for wheat revolution.
06/05/2005	Able JA	Queensland	Rural Weekly	Gem of an idea for wheat research.
20/05/2005	Petrovska N	Melbourne	Herald Sun	An end to sneezing. Interview with Milanda Rout.
21/05/2005	Petrovska N	Melbourne	Herald Sun	New grass to end sneezing. Interview with Milanda Rout.
21/05/2005	Petrovska N	Web	ABC online	Rye grass research reaps allergy-free benefits.
06/2005	Eglinton JK	National	Grain Business. Issue 11	Converting feed barley to malt quality.
15/06/2005	Gregson T	Victoria	Weekly Times	Grower access to GM.
15/06/2005	McLean M	Victoria	Weekly Times	Foods of the future take shape.
07/2005	Able JA	National	Australasian Science	Digging for DNA diamonds.

Radio

DATE	MPB PARTICIPANT	COVERAGE	PUBLISHED BY	SUBJECT
13/03/2005	Mather D	Adelaide	Radio Adelaide	Molecular plant breeding research. Interview with Ewart Shaw.
23/05/2005	Spangenberg G	Western Australia	ABC Radio	Low allergen ryegrass.
08/2004	Smith K	Queensland	ABC Country Hour	GM pastures.
12/08/2004	Bray H	South West South Australia	ABC West Coast	Seeing DNA at the Eyre Peninsula Field Days. Interview with Kendall Jackson.
07/09/2005	Bray H	North and West South Australia	ABC North and West SA	Gene technology at the Royal Adelaide Show. Interview with Alice Plate.
11/03/2005	Bray H	Kalgoorlie-Boulder region, Western Australia	ABC Goldfields-Esperance	Genetic Engineering for Growers. Interview with Kellie Dolan.

# GRANTS & AWARDS

Grants	RESEARCHER	ORGANISATION	TITLE	SOURCE	PERIOD	AMOUNT Y/E 30 JUNE 2005 \$000'S	AMOUNT TOTAL \$000'S
	Wallwork H	SARDI	Germplasm barley biotic – Enhancement of disease resistance in elite malting quality barleys	ABB Grain	2004-2007	86	335
Eglinton J	UA	Germplasm barley quality – Conversion of feed barley to malting types	ABB Grain	2004-2007	104	321	
Moody D	DPI-Vic	Germplasm barley quality – Enhancement for malting quality in barley	ABB Grain	2004-2007	112	341	
Spangenberg G	DPI-Vic	Perennial ryegrass biotechnology and molecular breeding	DA	2003-2007	50	743	
Spangenberg G	DPI-Vic	Molecular breeding of pasture grasses with improved digestibility	DA	2003-2005	6	60	
Forster J	DPI-Vic	Development and implementation of candidate gene-based molecular markers in outcrossing forage species	DA, MLA, GGDF	2004-2007	1,034	3,122	
Spangenberg G	DPI-Vic	Manipulation of fructan metabolism in pasture grasses	GGDF	2002-2005	23	69	
Able J	UA	Genome structure manipulation	GRDC	2002-2005	65	265	
Eglinton J	UA	Collaborative barley breeding with ICARDA for low rainfall environments	GRDC	2003-2005	216	624	
Chalmers K	UA	Whole genome-based selection in backcross families in wheat and barley	GRDC	2004-2005	250	500	
Chalmers K	UA	Map-based cloning of a quantitative trait loci in barley	GRDC	2004-2007		172	
Wallwork H	SARDI	Control of cereal fungal diseases	GRDC	2004-2008	190	1,003	
Appels R	Murdoch	AWCMMP component: rice, wheat and barley comparative genomics for key agronomic traits	GRDC	2005-2007	100	309	
Chalmers K	UA	AWCMMP: association mapping	GRDC	2005-2007	260	802	
Lance R	DAWA	AWCMMP: Barley breeding west – Molecular genetic validation and implementation	GRDC	2005-2007	135	417	
Wallwork H	SARDI	AWCMMP: Genetic analysis and marker-trait linkage	GRDC	2005-2007	400	1,236	
Eglinton J	UA	AWCMMP: MBQIP marker implementation and validation	GRDC	2005-2007	250	772	
Eastwood R	AGT	AWCMMP: Wheat marker implementation / validation for AGT	GRDC	2005-2007	250	772	
Wallwork H	SARDI	Disease genetics: Genetic evaluation of barley scald resistance	GRDC	2005-2007	120	389	

## Grants

RESEARCHER	ORGANISATION	TITLE	SOURCE	PERIOD	AMOUNT Y/E 30 JUNE 2005 \$000'S	AMOUNT TOTAL \$000'S
Hayden M	UA	Novel Marker Systems – Multiplex PCR technologies to accelerate the use of SSR's in cereal breeding and genetic research	GRDC	2005-2007	132	410
Appels R	DAWA	Winter cereal improvement: Implementation/validation of molecular markers in NWBP	GRDC	2005-2007	152	469
Able J	UA	Developing gene systems and delivering transgenic technologies	GRDC	2005-2008	11	90
Dundas I	UA	Development of new rust genes for Australian wheat breeders for alien species	GRDC	2005-2008	150	654
Chalmers K	UA	SAGIT Plant Breeding Scholarship	SAGIT	2005-2008	18	153
Mares D	UA	Germplasm wheat quality – Durum industry development	GRDC	2005-2009	206	1,138
Wallwork H	SARDI	Fast tracking of wheat with combined disease resistances	SAGIT	2004-2006	58	205
TOTALS					4,378	15,371

## Awards

RECIPIENT	AWARDING ORGANISATION	AWARD
Able J	Grains Council of Australia	Young Leader Scholarship. For attendance and accommodation in Brisbane for Grains Week 2005.
Able J	Bio Innovation SA	Travel Scholarship 2005.
Eglinton J	Grains Council of Australia	Young Leader Scholarship. For attendance and accommodation in Brisbane for Grains Week 2005.
Hearnden P	GRDC	Travel award.
Spangenberg G	Zonamerica Foundation	Zonamerica Foundation Award for contribution to plant biotechnology. Appointed to the International Advisory Board of Zonamerica Foundation, Uruguay, 2005.
Spangenberg G	Chilean Society of Animal Production	Chilean Society of Animal Production Award for contribution to animal production, Chile, 2004.
Spangenberg G	Universidad Nacional del Sur, Bahia Blanca, Argentina	Appointed Visiting Professor.
Vassos E	Grains Council of Australia	Young Leader Scholarship. For attendance and accommodation in Brisbane for Grains Week 2005.

# PERFORMANCE MEASURES

These performance measures are based on those listed in the Schedule 1 of the Commonwealth agreement, but rationalised for clarity of reporting.

PERFORMANCE MEASURE	03-04	04-05	PERFORMANCE MEASURE	03-04	04-05
<b>1. Collaborative arrangements</b> <b>Objective:</b> Enhance collaboration among researchers and industry, and use IP and other resources more effectively.			<b>3. Technology transfer</b> <b>Objective:</b> Commercialise products of CRC research for benefit to Australia and beyond, providing return on investment, where appropriate.		
Extent of collaboration of participants within MPBCRC programs			Effective procedures to assess research portfolio		
Number of projects with more than one participant (%)	72	77	Number of refereed conference papers	85	57
Extent of national and international collaboration with non-participant organisations			Number of book chapters	13	16
Agreements	1	0	Number of books	0	0
National collaborations	7	18	Progress reports submitted (%)		
International collaborations	17	24	Progress reports submitted (%)	100	100
Interactions with R&D Corporations and other funding bodies			Reviews conducted	1	1
Number of projects with funding from R&D Corporations	15	25	New projects developed		
Interactions and involvement of industry			Reviews conducted	1	1
Number of projects with industry funding	3	9	Number of new projects developed	10	6
Number of projects with industry involvement	9	9	Achievements of research outputs according to target milestones for current year		
Attendance at Annual Research Meetings			Output milestones met (%)	90	95
Number attending	104	118	Number of events demonstrating national and international recognition of Centre staff		
<b>2. Research and development</b> <b>Objective:</b> Establish, develop and undertake world-class, high-quality, industry-focused collaborative research programs in molecular breeding for cereals and pastures.			Invited lectures and conference participations	38	78
Effective research portfolio that is output-focused and relevant to industry needs			Involvement in advisory roles	10	14
Number of refereed journal publications	88*	26	Success in attracting research and commercial funding from external bodies		
			Number of new external grants	3	12
			Value of additional external grants	\$1,110,000	\$2,051,837
			Total value of external grants	\$3,942,000	\$4,378,307
			<b>3. Technology transfer</b> <b>Objective:</b> Commercialise products of CRC research for benefit to Australia and beyond, providing return on investment, where appropriate.		
			Capture of IP using legal means		
			Internal disclosures for patentability/protection assessment	2	2
			New provisional patent filings	0	1

PERFORMANCE MEASURE	03-04	04-05
Complete applications filed	1	1
Patent applications in prosecution/being maintained	22	23
Patents accepted/allowed	0	4
<b>Commercialisation: technology development and licensing</b>		
Research licences for MPB technology entered into	4	0
Confidentiality agreements executed for the purposes of confidential negotiations regarding business development	5	5
Collaborative R&D agreements entered into	1	10
Licensing agreements entered into	1	6
Agreements with end-users vis-à-vis technology development and commercialisation	2	4
<b>Impact on varieties developed using MPB technologies</b>		
Number of objectives met by germplasm development	11	19
<b>4. Education and training</b> <b>Objective: Entice and train excellent plant breeders and researchers.</b>		
<b>Effective training of post graduate students</b>		
Postgraduates enrolled	41	39
Total postgraduates completed (CRCMPB/MPBCRC)	25	27
Additional training opportunities provided	1	1
Students with non-university co-supervisor (%)	83	59

PERFORMANCE MEASURE	03-04	04-05
<b>Training for people already working in plant breeding</b>		
Training opportunities provided	2	2
<b>School activities</b>		
School education activities	7	32
Teacher training activities	3	9
<b>Community awareness activities</b>		
Community education activities	4	4
<b>Overseas experience</b>		
Number of overseas visits for staff and students supported	3	3
<b>5. Communications</b> <b>Objective: Promote MPB's profile as a globally reputable organisation and foster ownership by the Participants.</b>		
<b>Internal communication activities</b>		
Newsletters issued	0	3
Staff surveys/formal feedback forums	0	2
<b>External communication activities</b>		
MPB publications	1	7
Sponsorship of MPB-related activities	3	4
Visits to Centre website (page views)	1,731	46,347
<b>Activities of Centre staff in media, field days and other communication activities</b>		
Media appearances (print, radio and TV)	19	27
Attendance at field days and industry forums	8	21

\* 03-04 column includes refereed journal articles that had been submitted for publication, but not yet published by June 30 2004. Subsequent years include only published articles.

## Financial Information - TABLE 1 (Accrual Basis) In-kind Contributions (dollars in \$'000)

	ACTUAL				PROJECTED												TOTALS TO 2004-05				TOTALS FOR 7 YEARS					
	2003-04		2004-05		2005-06			2006-07			2007-08			2008-09			2009-10			Actual	Agr'mt	Diff	Actual/Proj	Agr'mt	Diff	
	Actual	Agr'mt	Actual	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected									
<b>Core participants</b>																										
International Maize and Wheat Improvement Centre (CIMMYT)																										
Salaries	235	247	244	189	189	189	190	190	189	189	189	189	189	189	189	189	189	189	189	189	479	436	43	1,425	1,382	43
Capital	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Other	812	872	1,073	774	774	774	773	773	774	774	774	773	774	774	774	774	729	729	729	729	1,885	1,646	239	5,664	5,425	239
Total	1,047	1,119	1,317	963	963	963	963	963	963	963	963	918	918	918	918	918	918	918	918	2,364	2,082	282	7,089	6,807	282	
Murdoch University																										
Salaries	59	123	178	140	140	140	140	140	139	139	139	139	139	139	139	139	139	139	139	237	263	-26	934	960	-26	
Capital	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Other	758	974	1,331	1,067	991	854	854	854	710	710	623	623	623	623	623	527	527	527	527	2,089	2,041	48	5,794	5,746	48	
Total	817	1,097	1,509	1,207	1,131	994	994	994	849	849	762	762	762	762	666	666	666	666	666	2,326	2,304	22	6,728	6,706	22	
South Australian Research and Development Institute (SARDI)																										
Salaries	164	143	203	149	150	150	149	149	150	150	149	149	149	149	149	149	149	149	149	367	292	75	1,114	1,039	75	
Capital	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Other	1,108	1,076	1,511	1,491	1,474	1,474	1,501	1,501	1,214	1,214	1,037	1,037	1,037	1,037	763	763	763	763	763	2,619	2,567	52	8,608	8,556	52	
Total	1,272	1,219	1,714	1,640	1,624	1,624	1,650	1,650	1,364	1,364	1,186	1,186	1,186	1,186	912	912	912	912	912	2,986	2,859	127	9,711	9,595	127	
The University of Adelaide																										
Salaries	53	73	137	57	50	50	50	50	51	51	50	50	50	50	50	50	50	50	50	190	130	60	441	381	60	
Capital	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Other	2,316	2,638	3,413	2,702	2,134	2,147	2,147	2,147	1,291	1,291	1,125	1,125	1,125	1,125	856	856	856	856	856	5,729	5,340	389	13,282	12,893	389	
Total	2,369	2,711	3,549	2,759	2,184	2,197	2,197	2,197	1,342	1,342	1,175	1,175	1,175	1,175	906	906	906	906	906	5,918	5,470	448	13,722	13,274	448	
Department of Primary Industries VIC																										
Salaries	533	687	601	650	651	651	651	651	830	830	651	651	651	651	651	651	651	651	651	1,134	1,337	-203	4,389	5,491	-1,102	
Capital	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Other	3,552	4,606	4,840	5,086	5,213	5,536	5,136	5,460	2,836	3,160	2,468	2,792	1,950	2,274	8,392	9,692	-1,300	25,995	28,914	-2,919
Total	4,085	5,293	5,442	5,736	5,864	6,367	5,787	6,291	3,487	3,990	3,119	3,623	2,601	3,105	9,527	11,029	-1,502	30,385	34,405	-4,020
Department of Agriculture WA																				
Salaries	209	168	249	175	168	167	168	168	168	168	168	168	169	169	458	343	115	1,299	1,184	115
Capital	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Other	676	522	1,297	886	884	884	885	885	834	834	717	717	604	604	1,937	1,408	565	5,897	5,332	565
Total	885	690	1,546	1,061	1,052	1,052	1,053	1,053	1,002	1,002	885	885	773	773	2,431	1,751	660	7,196	6,516	660
Total in-kind from core participants																				
Salaries	1,253	1,441	1,612	1,360	1,348	1,528	1,348	1,528	1,348	1,527	1,346	1,526	1,347	1,527	2,865	2,801	64	9,602	10,437	-835
Capital	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Other	9,222	10,688	13,464	12,006	11,470	11,793	11,296	11,620	7,659	7,983	6,699	7,023	5,429	5,753	22,686	22,694	-8	65,239	66,866	-1,627
Total	10,475	12,129	15,076	13,366	12,818	13,321	12,644	13,148	9,007	9,510	8,045	8,549	6,776	7,280	25,551	25,495	56	74,841	77,303	-2,462

### Supporting participants

#### ABB Grain Ltd

Salaries	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Capital	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

#### Australian Grain Technologies Pty Ltd

Salaries	29	0	43	0	0	0	0	0	0	0	0	0	0	0	72	0	72	72	0	72
Capital	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Other	147	15	180	15	15	15	15	15	15	15	15	15	15	15	327	30	297	402	105	297
Total	176	15	224	15	15	15	15	15	15	15	15	15	15	15	400	30	370	475	105	370

#### BASF Plant Science

Salaries	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Capital	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

#### Dairy Australia

Salaries	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Capital	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Other	0	696	0	959	924	924	937	937	800	800	800	800	800	800	0	1,655	-1,655	4,261	5,916	-1,655
Total	0	696	0	959	924	924	937	937	800	800	800	800	800	800	0	1,655	-1,655	4,261	5,916	-1,655





Financial Information - TABLE 2 (Accrual Basis)  
Cash Contributions (dollars in \$'000)

	ACTUAL				PROJECTED												TOTALS TO 2004-05				TOTALS FOR 7 YEARS							
	2003-04		2004-05		2005-06			2006-07			2007-08			2008-09			2009-10			Actual	Agr'mt	Diff	Actual/Proj	Agr'mt	Diff			
	Actual	Agr'mt	Actual	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt										
<b>Core participants</b>																												
International Maize and Wheat Improvement Centre (CIMMYT)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
Murdoch University	215	215	215	215	215	215	215	215	215	215	215	215	215	215	215	215	215	215	215	215	215	215	430	430	1,507	1,507	-2	
South Australian Research and Development Institute (SARDI)	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	200	200	700	700	0		
The University of Adelaide	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	300	300	1,050	1,050	0		
Department of Primary Industries VIC	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	200	200	700	700	0		
Department of Agriculture WA	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	300	300	1,050	1,050	0		
Total cash from core participants	715	715	715	715	715	715	715	715	715	715	715	715	715	715	715	715	715	715	715	715	715	1,430	1,430	5,007	5,007	-2		
<b>Supporting participants</b>																												
ABB Grain Ltd	197	250	339	250	250	308	250	250	317	250	250	250	250	250	250	250	250	250	250	250	250	250	536	500	36	1,911	1,750	161
Australian Grain Technologies Pty Ltd	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	30	30	105	105	0		
BASF Plant Science	0	825	1,249	836	847	847	847	859	859	871	0	883	0	895	0	1,249	1,661	-412	5,604	3,367	2,237	0	0	0	0	0		
Dairy Australia	463	0	618	0	618	0	618	0	155	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1,854	
Geoffrey Gardiner Dairy Foundation	270	0	360	0	360	0	360	0	90	0	0	0	0	0	0	0	0	0	0	0	0	630	0	0	1,080	0	1,080	
Grains Research and Development Corporation	0	750	2,029	750	1,346	750	1,361	750	1,361	750	750	750	750	750	750	750	750	750	750	750	750	1,500	1,500	5,250	5,250	1,736		
SAGIT	0	0	58	0	60	0	60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58	0	58	118	0	118	
Gramina Pty Ltd	0	0	0	0	90	0	90	0	125	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	215	
Heritage Seeds Pty Ltd	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
International Center for Agricultural Research in the Dry Areas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Meat and Livestock Australia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	



Financial Information - TABLE 3 (Accrual Basis)  
Resources (dollars in \$'000)

	ACTUAL		PROJECTED												TOTALS TO 2004-05			TOTALS FOR 7 YEARS		
	2003-04		2004-05		2005-06		2006-07		2007-08		2008-09		2009-10		Actual	Agr'mt	Diff	Actual/Proj	Agr'mt	Diff
	Agr'mt	Actual	Agr'mt	Actual	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt	Projected	Agr'mt						
<b>Summary of resources applied to activities of centre</b>																				
Grand total (in-kind) from table 1 (T1)	13,941	16,810	18,217	16,967	16,045	17,071	15,807	16,809	11,897	13,201	10,919	12,453	9,648	11,281	32,158	33,777	-1,619	96,474	104,592	-8,118
Grand total (cash expenditure) from table 2 (T3)	5,916	6,605	8,103	6,616	10,102	7,743	9,489	7,764	8,449	6,945	6,954	5,991	5,945	5,010	14,019	13,221	798	54,988	46,674	8,314
Total resources applied to activities of centre (T1 + T3)	19,857	23,415	26,320	23,583	26,147	24,814	25,296	24,573	20,346	20,146	17,873	18,444	15,593	16,291	46,177	46,998	-821	151,462	151,266	196
<b>Allocation of total resources applied to activities of CRC between heads of expenditure</b>																				
Total salaries (cash and in-kind)	4,748	5,312	6,768	5,760	7,398	6,310	7,013	6,296	6,380	5,715	5,562	5,217	4,580	4,446	11,516	11,072	444	42,449	39,056	3,393
Total capital (cash and in-kind)	224	287	31	73	23	38	10	20	10	10	10	5	10	0	255	360	-105	318	433	-115
Total other (cash and in-kind)	14,885	17,816	19,520	17,750	18,726	18,466	18,273	18,257	13,956	14,422	12,301	13,221	11,033	11,845	34,405	35,566	-1,161	108,694	111,777	-3,083
Total	19,857	23,415	26,320	23,583	26,147	24,814	25,296	24,573	20,346	20,147	17,873	18,443	15,623	16,291	46,177	46,998	-821	151,462	151,266	196

Financial Information - Table 4 (Accrual Basis)  
Allocation of resources between categories of activity for the 2004-05 financial year (dollars in \$'000)

	RESOURCE USAGE		
	CASH (\$'000) <sup>1</sup>	IN-KIND (\$'000)	CONTRIBUTED STAFF <sup>2</sup>
	CASH FUNDED STAFF <sup>2</sup>		
Research	6,899	18,020	42.3
Education	101	197	0.2
External communications	186		1.0
Commercialisation/Tech. transfer	287		1.0
Administration	630		3.8
Total	8,103	18,217	42.5
	[T3]	[T1]	
<b>[1] Cash from all sources, including CRC programme [2] Full time equivalent staff</b>			



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## INDEPENDENT AUDIT REPORT TO THE DEPARTMENT OF EDUCATION, SCIENCE AND TRAINING, REPRESENTING THE COMMONWEALTH, IN RESPECT OF THE MOLECULAR PLANT BREEDING COOPERATIVE RESEARCH CENTRE FOR THE YEAR ENDED 30 JUNE 2005

### Scope

We have audited the financial information of the Molecular Plant Breeding Cooperative Research Centre, as set out in Tables 1, 2 and 3 prepared on an accrual basis for the Annual Report for the year ended 30 June 2005, together with having addressed the specific contractual requirements of the Cooperative Research Centre under the Agreement dated 9th September 2003 with the Commonwealth of Australia (the Commonwealth Agreement) as specified by the Commonwealth of Australia's representative the Department of Education, Science and Training. The parties to the Cooperative Research Centre are responsible for the preparation and presentation of the financial information and for its adherence to the Commonwealth Agreement. We have conducted an independent audit of the financial information and of the specific contractual requirements of the Cooperative Research Centre under the Commonwealth Agreement as specified by its representative the Department of Education, Science and Training, in order to express an opinion on the financial information and on those specific contractual requirements of the Cooperative Research Centre under the Commonwealth Agreement to the Department of Education, Science and Training.

The financial information has been prepared for the purposes of fulfilling the Cooperative Research Centre's annual reporting obligations to the Department of Education, Science and Training under Clause 13 of the Commonwealth Agreement. We disclaim any assumption of responsibility for any reliance on this report, or on the financial information to which it relates, to any person other than the Department of Education, Science and Training or for any purpose other than that for which it was prepared.

Our audit has been conducted in accordance with Australian auditing standards to provide reasonable assurance as to whether the financial information is free of material misstatement and to address the specific contractual requirements of the Cooperative Research Centre under the Commonwealth Agreement as specified by its representative the Department of Education, Science and Training. Our procedures included examination, on a test basis, of evidence supporting the amounts and other disclosures in the financial information and the evaluation of accounting policies and significant accounting estimates, together with addressing the specific contractual requirements of the Cooperative Research

Centre under the Commonwealth Agreement as specified by its representative the Department of Education, Science and Training. These procedures have been undertaken to form an opinion whether, in all material respects, the Cooperative Research Centre's sources of funding and the application of that funding for the year ended 30 June 2005 and its financial position as at 30 June 2005 are presented fairly in accordance with Australian accounting concepts and standards and the Commonwealth Agreement and that the Cooperative Research Centre has complied with the following specific contractual requirements of the Cooperative Research Centre under the Commonwealth Agreement as specified by the Department of Education, Science and Training:

- Contributions, both cash and in-kind, have been made and recorded in accordance with the Budget, being Schedule 3 to the Commonwealth Agreement;
- Cash contributions have been paid into and expended from the Cooperative Research Centre's account as required by Clauses 4 and 7 of the Commonwealth Agreement;
- The application of Commonwealth Funding and Contributions for the Activities of the Cooperative Research Centre has been as specified in Clause 5 of the Commonwealth Agreement;
- The Cooperative Research Centre has met its obligations in relation to the treatment of Heads of Expenditure and Capital Items under Clauses 3 and 5 of the Commonwealth Agreement and Intellectual Property under Clause 9 of the Commonwealth Agreement; and
- In accounting for Commonwealth Funding and Contributions, the Cooperative Research Centre has exercised proper accounting standards and controls as required under Clause 7 of the Commonwealth Agreement.

The audit opinion expressed in this report has been formed on the above basis.

### Audit Opinion

In our opinion, the financial information presents fairly, in accordance with Australian accounting concepts and standards, the Molecular Plant Breeding Cooperative Research Centre's sources of funding and the application of that funding for the year ended 30 June 2005 and its financial position as at 30 June 2005.

It is further our opinion, in relation to the specific contractual requirements of the Cooperative Research Centre under the Commonwealth Agreement with the Commonwealth of Australia as specified by the Department of Education, Science and Training that:

- Contributions, both cash and in-kind, have been made and recorded in accordance with the Budget, being Schedule 3 to the Commonwealth Agreement, with the following exceptions where the Contributions were below the amount committed:

Organisation	Amount Committed \$	Amount Contributed \$
Department of Primary Industry, Victoria	5,836,000	5,542,000
Dairy Research and Development Corporation	959,000	618,000
Geoffrey Gardiner Dairy Foundation	379,000	360,000
Heritage Seeds Pty Ltd	200,000	-
Southern Cross University	343,000	286,000

- Cash contributions have been paid into and expended from the Cooperative Research Centre's account as required by Clauses 4 and 7 of the Commonwealth Agreement;
- The application of Commonwealth Funding and Contributions for the Activities of the Cooperative Research Centre have been as specified in Clause 5 of the Commonwealth Agreement;
- The Cooperative Research Centre has not met its obligations in relation to the treatment of Heads of Expenditure under Clause 3.5 of the Commonwealth Agreement in that the Researcher's allocations of the budgetary resources between the Heads of Expenditure has been lower or higher than the allocation in the budget by \$100,000 or 20%, whichever is the greater amount, without the prior approval of the Commonwealth. The variations relate to salaries expenditure, where actual expenditure of \$5,046,000 exceeded budgeted expenditure of \$4,360,000 by \$686,000, and other expenditure, where actual expenditure of \$3,026,000 exceeded budgeted expenditure of \$2,183,000. The Cooperative Research Centre has met its obligations in relation to the treatment of Capital Items under Clause 5.3 of the Commonwealth Agreement in that Capital Items acquired from the Grant and Contributions have been vested as provided in the Joint Venture Agreement, and in relation to Intellectual Property under Clause 9.1 of the Commonwealth Agreement in that we have seen a statement by the Chief Executive Officer to the effect that Intellectual Property in all Contract Material is vested as provided in the Joint Venture Agreement and no Intellectual Property in any Contract Material having the potential for Commercialisation has been assigned or licensed without prior approval of the Commonwealth; and
- In accounting for Commonwealth Funding and Contributions the Cooperative Research Centre has exercised proper accounting standards and controls as required under Clause 7 of the Commonwealth Agreement.

PKF  
Chartered Accountants

I J Painter  
Partner

Signed at Adelaide, this 29th day of September 2005.

# GLOSSARY

<b>MPBCRC</b>	Molecular Plant Breeding Cooperative Research Centre
<b>ACPGF</b>	Australian Centre for Plant Functional Genomics
<b>AGT</b>	Australian Grain Technologies
<b>AFLP</b>	Amplified fragment length polymorphism
<b>ANU</b>	Australian National University
<b>APA</b>	Australian Postgraduate Award
<b>AWCMMP</b>	Australian Winter Cereal Molecular Marker Program
<b>BAC</b>	Bacterial artificial chromosome
<b>BPS</b>	BASF Plant Science
<b>CCN</b>	Cereal cyst nematode
<b>CIMMYT</b>	International Maize and Wheat Improvement Centre
<b>DA</b>	Dairy Australia
<b>DAWA</b>	Department of Agriculture Western Australia
<b>DPI Vic</b>	Department of Primary Industries Victoria
<b>EGA</b>	Enterprise Grain Australia
<b>FTO</b>	Freedom to operate
<b>GGDF</b>	Geoffrey Gardiner Dairy Foundation
<b>GM</b>	Genetically modified / genetic modification
<b>GRDC</b>	Grains Research and Development Corporation
<b>ICARDA</b>	International Centre for Agricultural Research in the Dry Areas
<b>IP</b>	Intellectual property
<b>MBQIP</b>	Malting Barley Quality Improvement Program
<b>MLA</b>	Meat and Livestock Australia
<b>MU</b>	Melbourne University
<b>OPRS</b>	Overseas Postgraduate Research Scholarship
<b>PBC</b>	Plant Biotechnology Centre
<b>PBR</b>	Plant Breeders' Rights
<b>PCR</b>	Polymerase chain reaction
<b>QTL</b>	Quantitative trait locus
<b>SAGIT</b>	South Australian Grains Industry Trust
<b>SARDI</b>	South Australian Research and Development Institute
<b>SCU</b>	Southern Cross University
<b>SNP</b>	Single nucleotide polymorphism
<b>SSR</b>	Simple sequence repeat
<b>UA</b>	The University of Adelaide



# MOLECULAR PLANT BREEDING COOPERATIVE RESEARCH CENTRE

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