Molecular Breeding in Wheat: Challenges & Opportunities

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Outline of Lecture

• Achievements and needs in wheat production (national and international)
• Opportunities and possibilities (work done and being done in India and abroad)
• Future needs in molecular breeding
Available Literature

- DWR’s “Vision 2025” (2007);
- Euphytica Special Issue, 2007:
- CIMMYT/FAO Documents;
- “Wheat: Science & Trade” 2009 (book);
- GAP Report 2010 (Global Harvest Initiative);
- Nature & Science on Food Security

GAP = Global Agr. Prouctivity
Regular Discussions

- **Conferences:** 
  - IWGS (2008); Tribute to Borlaug, ICAR (21-22, Nov, 2009); 8th IWC St Petersburg (June 2010); 20th ITMI & 3rd ICPMB (Beijing, Sept. 2010); 3rd Intern’l Group Meeting on Wheat: Changing Climate (Feb 9-12, 11)
Funding for Wheat Improvement

- **Funding & Establishments:** DBT/ICAR/GCP; DWR; Borlaug Global Rust Initiative; Rice-Wheat Consortium; Wheat Yield Consortium (WYC); Borlaug Inst for SA; HarvestPlus

- **Intern’l Collaborations:** Australia, CIMMYT, Switzerland
Need to increase annual increment in food production from 32 to 44 MT

**Consumption of cereals will slightly exceed production of cereals in 2010-11**

World wheat production in 2010 is 646 mt; 5% lower than in 2009

**Global Harvest Initiative:**

2010 GAP (Global Agr Productivity Report) Oct 13, 2010

38% increase in the annual increment of food production, sustained for 40 years

Wheat production statistics

Area - more than two fold increase (from 13.4 m ha in 1965)
Production - more than six times increase (from 12.3 mt in 1965)
Productivity - over three times increase (from 0.9 t/ha in 1965)

From last eight years, India is maintaining its 2nd position in world
Resources Available

- ~2500 SSRs (genetic/physical maps) mapped
- ~50,000 SNPs (only few mapped)
- ~7,000 DArT (mapped) + ISBP markers
- >1,020,000 ESTs + GSS + miRNA
- RNAi and VIGS being used
- A number of mapping populations/maps
- A large number of QTL studies conducted
- A number of QTL/genes cloned
- Physical map and partial sequence of 3B
QTLs for MAS in Bread Wheat
MAS-Derived Wheat Varieties
(Disease Resistance, High GPC, Gluten Strength, etc.)

- **Bread wheat**
  - **USA**: Above, Avalanche, Ankor, BIOINTA 2004, Cataldo, Expresso, Farnum, Kern, Lassik, Mace, McNeal, Reeder, Hank, Patwin, Scarlet
  - **Canada**: Goodeve, Lilian
- **Durum wheat**
  - **USA**: Ben, UC 1113, Westmore

See Gupta et al. 2010a,b Mol Breeding; Plant Breeding Rev.
• Genetic enhancement of yield (through wheat yield consortium = WYC approach)
• Resistance to biotic stresses including Ug99
• Multi-genic traits & multi-trait improvement: abiotic stresses ((WUE, N/PUE, RUE)
• Quality traits & biofortification (GPC, PHST, GH, GW, Zn/Fe)
How to Meet the Challenge?

- Improve Complex Traits (Yield, Drought/WUE)
- Multiparental/MAGIC Populations
- Meta-QTL Analysis
- High-Throughput Genotyping
  - Marker/Sequencing-Based Genotyping
  - Genotyping Centres
- Precision in Phenotyping - Phenomics Facility
- GW Selection GWS): Breeding Value
Wheat Yield Consortium (WYC): multidisciplinary approach

CIMMYT Conf (Nov 11-13, 09)

What should be done?
• **Improve radiation use efficiency (RUE):** Rubisco, C4-like traits (CO₂-conc., light interception, & photosynthesis)
• Other associated traits (transport and lodging, etc.)

How should it be achieved?
• **Screen for genetic variation & make crosses** for RUE/C4 traits
• **Genome-wide selection (GWS)** for complex traits

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Strategy to Improve Yield Potential

Basic research platforms: complementary traits

Applied research platforms: germplasm

RUE
- C₄ like traits
  - Carbon concentrating mechanisms
- Rubisco
  - RuBP regeneration
  - Thermally stable Rubisco activase
  - Rubisco engineering

RUE
Spike/ canopy photosynthesis
- Estimate contribution of spikes to canopy RUE
- Identify a range of optimal canopy structures/ N-profiles

RUE
Partitioning
- Identify optimal Rht, Ppd, Vm, EPS deployment
- Optimize partitioning among organs
- Reduce kernel abortion associated with sensitivity to environment cues
- Increase kernel weight potential

Partitioning
Lodging resistance
- Validate stem and root lodging models in range of genetic backgrounds & environments
- Estimate trade-offs between lodging resistance and improved HI

Physiological tools:
- Develop conceptual models, phenotyping protocols, & molecular markers

Genetic resources:
- Explore wheat collections/alien species for desired traits

Pre-breeding:
- Trait-based & wide crossing: amphiploids, synthetics, genetic transformation
- Test alternate physiological models to harmonize traits in a common genetic background
- Determine interaction of traits with abiotic stress

Breeding:
- Introgress high-yield phenotype into elite genetic backgrounds
- Multi-location yield testing to determine relative impact in diverse target environments
- Combine with local adaptation requirements including disease resistance and end-use quality
- Deploy finished product through international nurseries
Genetic Variation for Drought Tolerance in Wheat

Differences in relative yield under low water supply, plotted against mean of ~50 genotypes at 25 environments/several years

QTLs for drought and heat on 1B, 4A, 7A, 7B: CS/SQ1 & Seri/Babax RILs (Quarrie et al. 2005, 06; Pinto et al. 2010)
Resistance Against Abiotic Stresses (Including Climate Change)

- **Drought Tolerance** (Meerut & DWR, Karnal)
  Donors: SQ1, Exccalibur, RAC875, C306, NP846, Dharwar Dry, Kundan
  Markers: 7AL, 7BS, 4AL (PVE: 18-32%)
  Quarrie et al. (2005), Kirigwai et al. (2007), Peleg et al. (2009), Pinto et al. (2010)

- **Heat Tolerance** (Meerut, & DWR, Karnal)
  Donors: WH730, Raj3765, NI5439
  Markers: 1BS, 2DS, 5BL, 7BL: PVE= upto 45%
  Mohammadi et al. (2008b)

- Genetic variation available; more markers needed
Selection for Long Root (WUE)

Michelle Watt, CSIRO (2010)
Depth of Root System & Yield

Red = CSIRO Vigour Line
Black = CIMMYT Synthetic
Others = Common wheats

Michelle Watt, CSIRO (2010)
Second Green Revolution for Climate Change: New Dwarfing Genes

The current dwarf varieties
-unresponsive to low input
-deep sowing for drought

New dwarfing genes may help develop varieties for drought & other stresses;
JIC and Rothamsted in UK +
WSU in USA with PAU &
CCSU, India are looking for
These new dwarfing genes
GWS in Wheat
(Crossa et al. Genetics, Oct. 2010)

- Parametric & semi-parametric models were tried for GS using wheat data (>599 genotypes and ~1447 DArT markers)
- Models with markers had higher predictive ability than pedigree-based models.
- Gains in predictive ability (relative to pedigree data), 7.7% to 35.7%.

Mark Sorrells at Cornell & Others at CIMMYT are currently using GWS.
Improvement in GPC Using MAS: But?

The Yield - Protein Relationship

<table>
<thead>
<tr>
<th>Location</th>
<th>No. of lines (out of &gt;200)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ludhiana</td>
<td>39</td>
</tr>
<tr>
<td>Meerut</td>
<td>30</td>
</tr>
<tr>
<td>Pantnagar</td>
<td>31</td>
</tr>
<tr>
<td>Pooled</td>
<td>6</td>
</tr>
</tbody>
</table>
PHST in Parents (P1, P2) and MAS Derived LR Resistant Lines (1-7)

Major Issue: Combine White Grain With PHST
Data Scoring in GW Population

Chinese spring × RS 111

1000 GW for CS = 26g

1000 GW for RS 111 = 56g
QTL Analyses for GW

**Single-locus analysis** = 10 QTL (PV= 4.37 to 23.27%)
- 4 major (3 stable) QTL: 1A, 5A, 6A and 6B

**Two-locus analysis** = 24 QTL
- (3 M-QTL; 21 E-QTL; 12 QQ interactions)
- PV: M-QTL (28.11%); E- QTL (43.36%)

- Total fixable PV= >50%
<table>
<thead>
<tr>
<th>Trait</th>
<th>Gene/QTL</th>
<th>Donor genotype</th>
<th>Recipient genotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grain protein content; Leaf rust resistance</td>
<td>GPC-B1</td>
<td>PBW343 (GPC-B1+Lr24), GluPro/3*PBW568 (13-16%)</td>
<td>Lok1, HD2967, UP2338, UP2382, PBW550, DBW17, HUW234, HUW468, MACS2496, NI 5439; 9-11%</td>
</tr>
<tr>
<td>PHS tolerance-white grained</td>
<td>Qphs.dpivic.4A2</td>
<td>CN19055, AUS1408 D7925sws</td>
<td>Lok1, HD2967, PBW550, DBW17</td>
</tr>
<tr>
<td>1000 Grain weight</td>
<td>QGw.ccsu-1A, QGw.ccsu-7A.1</td>
<td>Rye Selection 111, PBW343 (HGW+Lr24+Lr28); &gt;50g</td>
<td>UP2338, UP2382, PBW550 DBW17, HUW234, HUW468; ~35g</td>
</tr>
<tr>
<td>Gluten strength</td>
<td>LMW &amp; HMW–GS alleles (Glu-A1x, Glu-B1xy, Glu-D1x)</td>
<td>K9107 (HMW-GS)</td>
<td>UP2338, UP2382, MACS2496, NI 5439</td>
</tr>
<tr>
<td>Kernel hardness</td>
<td>Pina-D1, Pinb-D1</td>
<td>K9107</td>
<td>HUW234, HUW468</td>
</tr>
<tr>
<td>Starch properties</td>
<td>Waxy</td>
<td>Triple Null mutant (waxy mutant line)</td>
<td>MACS2496, NI 5439</td>
</tr>
<tr>
<td>Trait</td>
<td>Gene/QTL</td>
<td>Donor genotype</td>
<td>Recipient genotypes</td>
</tr>
<tr>
<td>------------------------</td>
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</tr>
<tr>
<td>Grain protein content</td>
<td><em>Gpc-B1</em></td>
<td>UC1113 (GPC-B1+Lr24)</td>
<td>MACS3125, HI8498</td>
</tr>
<tr>
<td>Yellow pigment</td>
<td><em>QYp.macs-7A</em></td>
<td>PDW233</td>
<td>MACS3125, HI8498</td>
</tr>
<tr>
<td>Lipoxygenase</td>
<td><em>Lpx-B1.1, Lpx-A3</em></td>
<td>Kofa, UC1113</td>
<td>MACS3125, HI8498</td>
</tr>
</tbody>
</table>
## Gene Pyramiding for Quality Traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>Gene/QTL</th>
</tr>
</thead>
<tbody>
<tr>
<td>GPC, PHS tolerance, GW, Gluten strength, LR resistance</td>
<td>Gpc-B1+Qphs.dpivic.4A2+, QGw.ccsu-1A, QGw.ccsu-7A.1, Glu-A1x, Glu-B1xy, Glu-D1x+Lr24, 28</td>
</tr>
<tr>
<td>GPC, GW, Kernel hardness</td>
<td>Gpc-B1+QGw.ccsu-1A, QGw.ccsu-7A.1+Pina-D1, Pinb-D1</td>
</tr>
<tr>
<td>GPC, Gluten strength, Starch properties</td>
<td>Gpc-B1+Glu-A1x, Glu-B1xy, Glu-D1x+Waxy</td>
</tr>
<tr>
<td>GPC, Yellow pigment content, Lipoxygenase activity</td>
<td>Gpc-B1+QYp.macs-7A+ Lpx-B1.1, Lpx-A3</td>
</tr>
</tbody>
</table>

3. Indo-Australian Programs (ICIAR: Molecular markers for faster wheat breeding in India (2007-12), PAU, DWR, NRCPB

4. GCP for drought and heat tolerance

5. Two DH Populations (RAC875 x Kukri; Excalibur x Kukri) for Drought from Australia to DWR (Fleury et al., 2010)

6. Germplasm with longer roots received from Australia
Biofortification—A Sustainable Agricultural Strategy for Reducing Micronutrient Malnutrition in the Global South

Howarth E. Bouis and Ross M. Welch

CROP SCIENCE, VOL. 50, MARCH–APRIL 2010

H.E. Bouis, HarvestPlus

Zn fortified wheat for India by 2012-13

15th International Symposium on Iron Nutrition and Interactions in Plants
26-30 June 2010, Budapest, Hungary

BIOFORTIFICATION

The First Global Conference: From Discovery to Delivery
Nov. 9-11, 2010 Washington, D.C.
TILLING in Wheat

246 alleles detected in waxy genes: WxA1 (7A); WxB1 (4A), WxD1 (7D)

Triangles up indicate mutations in coding region; those down indicate mutations in noncoding regions.

Slade et al. 2005, Nature Biotechnology

OTHER TILLING POPULATIONS

- UK (RRes, JIC): 4500 lines in M6 generation after EMS treatment
- USA (BS Gill’s Lab): 2x (716 M2 plants), 6x wheats (518 M2 plants); waxy locus, GBSS1 studied
- USA (UC, Davis, J Dubcovsky): Two M2 populations (1536 plants each)
- USA (SDSU, Wanlong Li)
- Australia (Peter Sharp): 1,025 EMS-treated M2 plants (Waxy gene)
- Denmark (Copenhagen): Six TILLING populations
Selection of Parents for MAGIC Populations

4-Way & 8-Way MAGIC Popul’ns in UK, Australia (1500-5000 RILs)

Principal Component Analysis
High Throughput in Modern Research

Field Trials by
Australian Grains Technology
University of Adelaide

Measurements of expression of all genes in a genome
ACPFG; University of Adelaide

NGS Technology for
High-throughput Genotyping
Australian Plant Phenomics Facility

The Plant Accelerator™
Adelaide
Mark Tester (mark.tester@acpfg.com.au)

High Resolution Plant Phenomics Centre
Canberra
Bob Furbank (robert.furbank@csiro.au)

Bridging the gap – linking physiology to genetics by use of remote sensing, computing and robotics
Future Wheat Breeding in India

1. Desired Research Agenda

- Yield potential through improved RUE
- Productivity & yield under abiotic stress (Water & N/P Use Efficiency)
- Quality and speciality traits (protein/starch, Zn/Fe, protective compds)
- Genome-wide selection (GWS) using breeding values of marker alleles
- Functional genomics: gene/allele mining
1. Facilities Needed

- High-throughput genotyping centres
- Phenomics facilities for phenotyping
- Bioinformatics (ICIS, IWIS, LIMS, ISMAB, BLUP and others)
- Regular training programmes in molecular breeding and bioinformatics
- Public-private partnership
- Effective International collaboration
National Agri-Food Biotechnology Institute (NABI),

- Large Scale Development of SNPs using cDNA and 454 NGS technology
- Association mapping for MAS: drought & heat (WUE); N/P use efficiency (NUE); Quality traits (PHST, bread/chapati making; biofortification and other traits
Borlaug Institute for South Asia

Overview of the Borlaug Institute

Borlaug Institute for South Asia

World germplasm
Wheat and maize for biotic, abiotic, and quality priority traits suited to regional needs

International staff
- IRS
- Visiting scientists
- Post-docs
- Students

Conventional labs
State-of-the-art labs:
- Hi-thru-genotyping
- Transgenics
- Double haploids
- Bioinformatics
- Climate change/GIS

Ready to use material for product development and technologies for testing and use

Participatory testing and adaptive trials on ecosystem/technology platforms for scaling out and wider adoption