Integration of Genomics in Crop Improvement: Molecular Breeding

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Outline

• Establishing a Common Premise: Operative Terms

• Overview of Current Status of Molecular Breeding --- Private & Public sectors

• Perspectives for Molecular Breeding
Operative Terms

- **Genomics**
  The study of all components of genetic material in a chromosome set

- **Plant Breeding**
  Science of altering the genetic pattern of plants in order to increase their value

Scientific American, Jan. 2009
Classical Plant Breeding

- Relies on hybridization
- (Deliberate) interbreeding of closely or distantly related individuals
- Crossbreeding introduces traits/genes from one variety or line into a new genetic background
- Selection
To Facilitate Plant Breeding

Generating diversity

• Mutagenesis
  - chemical & physical mutagens, transposons

• Enhancing hybridization
  - Cell and tissue culture
    - protoplast fusion, embryo rescue, somaclonal variation
    - doubled haploidy

• Recombinant DNA tools
  - Cloning of useful genes and genetic transformation
Selection is complicated by

• Genotype by environment interaction
• Polygenic inheritance
• Biology of the plant e.g. growth & development cycles
• Expensive assays
• Volume, bulk, etc.
Molecular Breeding

• Integration of molecular biology techniques into breeding is termed molecular breeding

• 2 major components
  
  – Transgenic approaches
  
  – Development of associations between DNA sequence variation and trait phenotypic variation

  • High throughput DNA-based prognostics used as a component of a breeding program
Transgenic approaches

Have worked for traits with a simple gene-to-phenotype relationship

- e.g. Bt for insect resistance and multiple herbicide resistance genes

http://anrcatalog.ucdavis.edu/
Yes, with knowledge of:

- Genes responsible for, or closely linked to, the trait
- Genome location of molecular markers in relation to trait (including quantitative loci – QTL)
- This constitutes Marker-Assisted Breeding (or Marker-Aided Selection, MAS)

http://www.ars.usda.gov/Research/docs.htm?docid=7203
Main considerations for the use of DNA markers in MAS

- Reliability
- Levels of polymorphism
- DNA quantity & quality
- Technical procedure
- Cost
MAS approaches are being applied for:

- simply inherited traits
- quantitative traits

Where:

- marker-trait associations are sufficient
- requisite marker polymorphisms can be identified, and
- a high throughput system for assay is available

Cooper et al. (2004)

Collard and Mackill, 2008
In general, while considering molecular breeding options, are there --

- Reduction in costs?
- Improvements in precision and accuracy?
- Step-change improvements in phenotypes that were previously not accessible?
- The identification of industry game-changing technologies for complex genotype-environment systems?
Marker Assisted Selection

Common applications of MAS in Plant Breeding

- Marker-assisted evaluation of breeding material
- Marker-assisted backcrossing
- Pyramiding
- Early generation selection
- Combined MAS
Successful implementation of molecular marker assisted breeding required

- Modification to Breeding Program Structure
- Molecular Markers
- Genotyping Platform
- Phenotypic Information
- Information Technology systems

Eathington et al. (2007)
Breeding Program Structure

- Molecular marker information increases the complexity of a breeding program (volume of data, frequency of analyses and decisions)

**Breeding Technology**
- Marker Labs
- Statistics
- Pathology
- Winter Nurseries
- Trait Integration
- Breeding Methodology Experimentation

**Line Development Breeding**
- F1 to National Testing
- Technology Optimization
- Breeding Methodology Experimentation

**Commercial Breeding**
- Product Characterization
- Channel Support
- Testing
- Data quality

Partitioned the process into components to enable optimal execution

Eathington *et al.* (2007)
Marker Assisted Selection

Molecular Markers and Genotyping Platform

Evolution through cheaper PCR-based markers e.g. SSRs, - made cheaper by automation - to fully automated molecular marker fingerprinting systems from DNA extraction through allele calling based on SNPs

• Identified and developed assays for thousands of corn SNPs
  • large %age in putative genes
  • all SNPs on a consensus linkage map

• From 2000 to 2006
  • total molecular marker data point production grew over 40X
  • cost per data point decreased over 6X
Marker Assisted Selection

Phenotypic Information

- Rule of thumb: Quality of marker phenotype associations is dependent on the quality of the phenotypic information.
- At Monsanto, combination of specialized breeders and equipment enabled an 80% increase in yield trial plot capacity in the last four to five years.
- Phenomics

http://www.cropdesign.com/prod_planthandling.php

http://www.plantphenomics.org.au/HRPPC
3-tier system at Monsanto

• Global all crop plant breeding system

• Information system for the molecular genotyping laboratories

• An integrated molecular marker decision making system
**MAS:** Public Sector work on important food crops

**Available**

- Molecular markers, genetic maps, QTL
- Use of candidate gene-based and association mapping common
- MAS procedures for improvements of biotic and abiotic stresses tolerances and quality traits for crops e.g. rice, maize, wheat, barley, pearl millet, cassava and common bean

**Still undone**

- Translate and integrate this knowledge into appropriate tools and methodologies for plant breeding programs

Dwivedi *et al.* (2007)
So far with cassava:

ACMV resistance

Akano et al. (2001)
At CIAT --- work on drought tolerance in common bean and aluminum resistance in tropical forage grasses (*Brachiaria* spp.)

Ishitani *et al.* (2004)
Strengths of MAS

- Can save time (up to 50%)
- Compared to GM, biosafety concerns obviated
- Unmasks hidden potentials
- Consistent
- Captures gene and interactions rather than single gene action
- With reducing costs, enhanced accessibility

Cahill & Schmidt (2004)
Weaknesses of MAS

• Scope limited by being gene-centred

• Expensive infrastructure

• Minor crops crowded out

• Corporate control and IP

• Confusion & synergy with GM
MAS: why the low impact

- Still at the early stages of DNA marker technology
- MAS results may not be published
- Reliability and accuracy of quantitative trait loci mapping studies
- Insufficient linkage between marker and gene/quantitative trait locus
- Limited markers, levels of polymorphism
- Effects of genetic background
- QTL X environment effects
- Relatively high cost of MAS
- ‘Application gap’ between research laboratories and plant breeding institutes
- ‘Knowledge gap’ among molecular biologists, plant breeders and other disciplines
• Rapid spread of DNA technology, developments in association studies (QTL, MAS)
• Watershed demonstration of advanced BC QTL
• Suited for transgenesis
• Rapid growth in genomics (candidate genes, SNPs)
• High throughput platforms (DNA extraction to genotyping)
• Publicly available markers and user-friendly databases
In the mean time

• A greater level of integration among conventional breeding, QTL mapping/validation and MAS

• Careful planning and execution of QTL mapping studies (especially for complex quantitative traits) and an emphasis on validating results prior to MAS

• Optimization of methods used in MAS such as DNA extraction and marker genotyping, especially in terms of cost reduction and efficiency, and

• Efficient systems for data storage (from in-house laboratory information management systems [LIMS] to publicly available databases)
In the mean time

Exploit advantages of MAS

• Use markers for
  • Selection of parents in breeding programmes
  • MAS for high-priority traits that are difficult, time consuming or expensive to measure
  • Minimizing linkage drag via recombinant selection
  • Pyramiding -- screening of multiple traits per line (i.e. per unit of DNA), rapidly eliminating unsuitable lines after early generation selection

• Exploit the time savings for line development for accelerated variety release