

Recent advances in maize research:
What do they portend for the resource
poor?

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As it was, it still is...

“Phenotyping capacity has not kept pace with the exponential increase in genotypic knowledge, and large-scale managed stress environments (MSE) are now considered essential to further progress”

Campos et al., 2004; Field Crops Res 90: 19-34

Recent advances in maize research

- Molecular Markers
 - SSRs (Diversity studies, finger printing)
 - Largest Landrace collection characterized,
 - Commercial fingerprinting for DUS
 - Diversity Array Technology markers (DArT)
 - SNP markers
 - Gene identification, Diversity
 - Functional markers (Gene identification linked to function)

Advances cont'd

- Mapping of traits
 - QTL mapping
 - Coupling QTL mapping and Micro-array hybridization (Extreme array mapping - XAM)
(Werner et al., 2005, PNAS 102: 2460-2465)
 - Association mapping (Based on linkage disequilibrium), identify region of unusual similarity measured using molecular markers and associating them with a phenotype
(Ed Buckler Group, Cornell University)
 - Nested Association Mapping
Combining QTL and Association Mapping to produce a high resolution map
(Ed Buckler, Rebecca Nelson & John Doebley Groups)

Advances cont'd

- Whole Genome Sequencing
 - Maize genome sequencing (almost complete?) with 11,255 annotated BAC clones deposited as of August 1, 2007 (<http://www.maizegdb.org>)
- QTLs and Specific Genes sequencing
 - Leaf Rust resistance *Rp1 D* (Colins et al., 1999; Plant Cell 11: 1365-1376)
 - Flowering time gene *Vgt1* (Salvi et al., 2002; Plant Mol. Biol. 48: 601-613)
 - Drought resistance (roots *ABA1*) QTLs (Tuberosa group)
 - Drought physiology QTLs in maize (Tardieu group)
 - (Cloning would allow for development of perfect markers and transgenic crops)
- Dissection of dQTLs –e.g. GLS, NCLB
 - (Wisser et al., 2005; Phytopathology 96(2): 120-129)

Advances cont'd

- Allele mining
 - GCP Project 13, 866 New SNPS identified associated with drought
- Tilling & Eco-tilling
 - Tilling (Targeting Local Lesions in Genomes) is adapted to natural modifications to identify DNA polymorphisms of interest
(Comai et al., 2004 Plant J. 37: 778-786)

Advance in knowledge

- Organization and variability of the maize genome
(Messing and Dooner, 2006; Current opinion in Plant Biology 9:157-163)
- Modeling in science to improve understanding of population structure and association mapping
(Yu et al., 2006 Nat. Genetics 38(2): 203-207)
- Genetic structure of maize and role of dominance
(Wardyn et al., 2007; Crop Sci47: 467-476)
- Understanding molecular basis of quantitative variation and pleiotropy
(Clark et al., 2006, Nat. Genetics 38(5): 594-596)
- Construction of mini-chromosomes in maize
(Yu et al., 2007; PNAS 104(21): 8924-8929)

Advances in other fronts

- Bio-informatics tools
 - Data bases (GCP databases e.g. Dayhoff, GreenPhyl, Maize databases)
 - Data Generation and analysis platforms
 - Software (iMAS, Tassel, Fieldbook etc)

Inbreeding technology

- Doubled Haploid lines production using inducer lines
 - Hasten the inbreeding phase of inbred line development. Obtain inbred lines in as few as 3 generations

New initiatives in crops research funding

- The Gates Foundation Support on food crops research
 - Support to CG Centres (e.g. the DTMA project)
- Alliance for Green Revolution in Africa
 - Support for Agriculture in Africa (Seed systems, Soil health and Marketing)
- Projects on maize Quality and Associated Traits
 - β -Carotene in maize (HarvestPlus)
 - QPMD in development of Quality Protein Maize

**So how are these technologies
affecting agriculture?**

The current situation

- Production in farmers fields still low, in many cases less than 2 tons/ha
- Old varieties still being grown some for as long as 25 years (e.g. Katumani)
- New varieties entering markets still being developed using conventional breeding in SSA (e.g. Zm 521, Zm 421)

Marker Assisted Breeding

- Marker Assisted Breeding
 - Allows increase in numbers screened, reduces the time needed for +ve identification (e.g. use of half seed in maize vs seedling), reduce number of backcrosses etc
 - Markers are a breeding technology with great potential e.g. (QPM, Drebnar et al., 2000; Yield, Koeber 2004; Drought, Ribaut et al., 2002; Drought Ribaut et al., 2004)
 - Map as you go (MAYG)
Has been proposed for complex traits to overcome epistatic effects (Podlich et al., 2004; Crop Sci 44: 1560-1571)
 - Networks formed e.g. AMMANET but minimum marker use out of labs and universities evident

MAB cont'd

- Food and Feed Safety Research: Aflatoxins
 - Use of markers for resistance to aflatoxin accumulation in maize, in near isogenic lines to understand type of resistance mechanism operating in kernels
- (Project Number: 6435-42000-019-08 IITA lines & ARS New Orleans, 2007)

Soil health

- Aluminum tolerance gene
 - Will greatly help with soils low pH in Africa
(Magalhaes et al., 2007; Nat. Genetics 39:1156)
- Nitrogen use efficient QTLs
 - Identification of quantitative trait loci for nitrogen use efficiency in maize
(Mol Breeding 5(2): 187-195)

QTLs and Gene discovery

- Many studies done, many QTLs identified and Candidate genes identified (e.g. 102 on drought)
 - Limited effects due to QTLxE effects, Lack of validation of identified QTLs and genes
 - Few QTLs cloned, therefore their contribution in breeding limited
- Agricultural biotechnology on Bt and Herbicide resistance increasing (e.g. South Africa, Policies and Laws coming in place (Kenya), Animosity to transgenics easing, their use likely to increase

The new funding sources...

- Accelerate use of new tools and technology in agriculture
 - DH technology in hybrid variety development
 - About 10 varieties/country/year proposed under PASS
- Expansion of seed markets and incomes
 - (PASS (40 seed companies aided); DTMA support on community based seed production)
- Increase capacity of NARS
 - PASS (Training of 80 breeders under PASS, GCP (Small grants in capacity building)
- Improve access to data and information
 - GCP (Bioinformatics in SP4, Out sourcing model for services in GCP)

In a nutshell...

- Biotechnology tools advances in the past have not had a major impact in feeding the hungry in developing countries especially in Africa. This might change with new technologies becoming available
 - Bt technology, Herbicide resistance (Suspicion on transgenics decreasing), New technologies/tools becoming available from GCPs first grants
- Gene discovery, allele mining, cloning and related studies unlikely to have impact on food production in the short term
- Genetic diversity studies likely to have a major contribution to how germplasm is used in crop improvement
(Legesse et al., 2007; Hereditas 144: 10-17).
- Fingerprinting of already released varieties being proposed to describe materials for DUS tests by regulatory agencies

All is not well...

- Apparent disconnect between the lab and the field exists
- Validation of already discovered QTLs and Candidate genes slow, integration limited
- But are breeders/consumers expecting too much too soon?
- Are breeders suspicious of molecular biologists and their products?
- How can we integrate more for the sake of resource poor farmers to justify further technology and information generation?



Thank you