CIMMYT

Genetic Resources Program

2005 Highlights

March 2006

Establishment of the Genetic Resources Program

Logframe Priority Summaries – September 2004

The following summary tables present the latest logframe and priorities for the Genetic Resource Program. The major priority setting exercise was conducted during the GRP meeting held at La Mansion del Quixote, Xocotlán, México on 9-10 September 2004. The GRP staff used the logframe developed for the MTP as a starting point, made revisions where necessary (mostly to rephrase and/or combine activities) and established priorities for each for 2005 and 2009. The group did not establish prioirities for 2009 Activities as it was felt these would change significantly in the future given advances in technology. Activity priorities would be set at least a year in advance.

The staff also developed a staffing priority that started with current GRP staff and then indicated needs for 2005 and 2009. The groups decided not to discuss in detail individual staff allocations, but elected to do this electronically following the August meeting.

Tables 1, 2, and 3 are organized by Purpose, Result and Activity. Each table lists the program priority (for 2005 and 2009, except for Activities) and staff allocations (in Full Time Equivalents, FTE). The overall percentage represents the priority across the entire program, whereas the within Purpose and within Result is the priority within the respective single Purpose or Result. Each table, except Table 1, is sorted by decreasing 2005 overall priority. For Table 2 (Results), the ranking for 2005 and 2009 (based on the overall percentage) is indicated to provided a better comparison across years.

Table 4 (Staffing Requirements) provides details on current staffing in the GRP, and projected needs for 2005 and 2009. As indicated, many of the staff requirements for 2005 are available in other CIMMYT programs/areas. These do not necessarily need/should be assign to the GRP, but the group felt it important to indicate the amount to time required to meet GRP needs.

As with any planning process, these are still works-in-progress and will be modified as further planning takes place.

Goal. Enhance the productivity and nutritional quality of maize and wheat varieties used for food and feed through the targeted use of global genetic resources

Table 1. Purpose Priorities	**2005**		
	Overall	**FTE**	**2009**
Purpose 1. Global custodianship, characterization, evaluation and management of the genetic resources of maize, wheat and related species	**50%**	**5.47**	**40%**
Purpose 2. Effective approaches identified in genetic resources and transferred to useful maize and wheat germplasm for improving critical traits as prioritized by CIMMYT and its partners	**40%**	**10.54**	**45%**
Purpose 3. Capacity in genetic resource management, maintenance and use enhanced globally	**10%**	**1.19**	**15%**

Table 2. Result Priorities (sorted by ’05 Rank	**Rank**		**2005**			**2009**	
	‘05	**‘09**	**w/in Purpose**	**Overall**	**FTE**	**w/in Purpose**	**Overall**
Result 1.4. Web-based genebank information, management and distribution system	**1**	**3**	**45%**	**22.5%**	**1.45**	**30%**	**12.0%**
Result 2.3. Bioinformatics platform for handling and analyzing genomic data	**2**	**4**	**35%**	**14.0%**	**0.94**	**20%**	**9.0%**
Result 1.3. Characterized maize and wheat genetic resources	**3**	**1**	**25%**	**12.5%**	**2.25**	**35%**	**14.0%**
Result 2.6. Useful maize and wheat germplasm with enhanced tolerance to abiotic and biotic stresses and enhanced grain quality	**4**	**2**	**25%**	**10.0%**	**3.46**	**30%**	**13.5%**
Result 2.2. Identification of genes, alleles and biological pathways involved in tolerance to abiotic and biotic stresses, enhanced grain quality, and asexual reproduction (apomixis)	**5**	**4**	**15%**	**6.0%**	**2.95**	**20%**	**9.0%**
Result 3.1. Improved capacity for storage and management of genetic resources by CIMMYT’s partners	**5**	**5**	**60%**	**6.0%**	**0.58**	**40%**	**6.0%**
Result 1.1. Enhanced global collection of maize and related species resources, including key genetic materials	**6**	**7**	**10%**	**5.0%**	**0.44**	**10%**	**4.0%**
Result 1.2. Inventoried wheat and related species collection, including key genetic and cytogenetic materials	**6**	**7**	**10%**	**5.0%**	**0.17**	**10%**	**4.0%**
Result 2.1. Maize and wheat consensus maps for tolerance/resistance to abiotic and biotic stresses, and enhanced grain nutrition	**7**	**6**	**10%**	**4.0%**	**1.46**	**10%**	**4.5%**
Result 2.4. Improved marker-assisted selection strategies and use by CIMMYT and its partners	**7**	**6**	**10%**	**4.0%**	**0.99**	**10%**	**4.5%**
Result 3.2. Increased use of genomic approaches by CIMMYT and its partners	**7**	**4**	**40%**	**4.0%**	**0.62**	**60%**	**9.0%**
Result 1.5. Statistical and simulation models for efficient maintenance and use of maize and wheat genetic resources	**8**	**7**	**5%**	**2.5%**	**0.94**	**10%**	**4.0%**
Result 1.6. Strategies for on-farm management of genetic resources	**8**	**8**	**5%**	**2.5%**	**0.21**	**5%**	**2.0%**
Result 2.5. Genetic engineered event of key genes for ultimate deployment to CIMMYT partners	**9**	**6**	**5%**	**2.0%**	**0.74**	**10%**	**4.5%**

Table 3. Activity Priorities (sorted by Overall priority)	**w/in Result**	**Overall**	**Staffing FTE**
Activity 1.4.1. Develop an updated, web-accessible genebank management and information system	**75%**	**13.5%**	**1.00**
Activity 2.3.1. Implement central data repository for CIMMYT-derived genomic data	**70%**	**11.0%**	**0.54**
Activity 1.3.1. Phenotype maize and wheat accessions for key traits	**60%**	**6.0%**	**1.50**
Activity 2.6.3. Characterize at the phenotypic and molecular levels key maize and/or wheat genetic resources under abiotic and biotic stresses, and for nutritional quality	**50%**	**5.6%**	**1.44**
Activity 2.2.1. Identify and validate candidate genes and biological pathways involved in tolerance to abiotic and biotic stresses, enhanced nutritional quality, and asexual reproduction (apomixis) in maize and wheat using functional genomics, allele mining and association genetics	**70%**	**4.8%**	**1.96**
Activity 2.3.2. Identify and adopt key bioinformatics packages for analyzing genomic data	**30%**	**4.7%**	**0.40**
Activity 1.4.2. Incorporate existing genebank data into the new system, improving data quantity and quality	**25%**	**4.5%**	**0.45**
Activity 3.1.4. Increase awareness of usefulness of genetic resources	**60%**	**4.5%**	**0.15**
Activity 3.2.4. Increase awareness of usefulness of genomics approaches	**50%**	**3.8%**	**0.11**
Activity 2.6.4. Incorporate novel sources into useful maize and wheat germplasm using conventional, molecular-marker and/or genetic engineering strategies for further use by breeding programs of CIMMYT and its partners	**30%**	**3.4%**	**1.49**
Activity 1.1.1. Improve and maintain the Latin American, African and Asian maize germplasm collections	**70%**	**2.8%**	**0.37**
Activity 2.4.2. Increase the number and efficiency of marker systems for use by CIMMYT and its partners	**60%**	**2.7%**	**0.35**
Activity 1.3.2. Fingerprint using molecular markers key maize and wheat accessions and related species	**25%**	**2.5%**	**0.63**
Activity 1.2.1. Inventory and maintain entire wheat collection checking quantity, viability and data quality	**60%**	**2.4%**	**0.09**
Activity 3.1.3. Help NARS and CIMMYT partners develop or improve and network genebank facilities	**30%**	**2.3%**	**0.25**
Activity 3.2.2. Conduct workshops and/or host visiting scientists/students in the application of genomics (QTL/gene discovery, MAS) in maize and wheat breeding	**30%**	**2.3%**	**0.32**
Activity 2.2.2. Screen candidate genes from cereals and other species for improved tolerance to abiotic and biotic stresses, enhanced nutritional quality, and asexual reproduction (apomixis) using genetic engineering	**30%**	**2.0%**	**0.99**
Activity 2.1.3. Link genomic regions of interest identified on maize and wheat consensus maps with other species (and vice versa)	**40%**	**1.8%**	**0.24**
Activity 1.2.2. Ensure access to key genetic and cytogenetic materials of wheat into the collection	**40%**	**1.6%**	**0.07**
Activity 2.1.2. Assemble consensus maps for maize and wheat and display multiple traits across environments and populations	**35%**	**1.6%**	**0.27**

Table 3. Activity Priorities (sorted by Overall priority)	w/in Result	Overall	Staffing FTE
Activity 2.5.2. Develop source lines containing these events along with required regulatory information	70%	1.6%	0.31
Activity 1.3.3. Evaluate the usefulness, needs and costs of DNA banking	15%	1.5%	0.12
Activity 3.2.3. Provide appropriate software tools to CIMMYT partners	20%	1.5%	0.10
Activity 2.4.1. Model use of molecular markers in breeding programs to identify optimal application	30%	1.4%	0.53
Activity 1.1.2. Access key related species and genetic materials of maize into the collection	30%	1.2%	0.07
Activity 1.5.2. Evaluate and/or develop population genetic models for efficient regeneration and collection of genetic resources.	60%	1.2%	0.46
Activity 1.6.1. Study the factors affecting diversity (e.g., gene flow, farmer's management, transgenes, improved varieties) within and between farmer grown varieties	60%	1.2%	0.21
Activity 2.1.1. Develop and analyze maize and wheat genetic populations to identify QTL for tolerances to abiotic and biotic stresses, and grain nutitional quality components	25%	1.1%	0.95
Activity 2.6.1. Develop novel 'synthetic' or 'bridge' wheats using wild A, B and D genome donors	10%	1.1%	0.30
Activity 2.6.2. Produce doubled haploid populations of wheat for mapping projects and pre-breeding purposes	10%	1.1%	0.23
Activity 1.5.1. Evaluate and use statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets.	40%	0.8%	0.49
Activity 1.6.2. Determine incentives required for *in-situ* conservation of genetic resources	40%	0.8%	0.00
Activity 3.1.2. Conduct workshops and/or host visiting scientists/students on genebank management (*ex-situ* and *in-situ*)	10%	0.8%	0.10
Activity 2.5.1. Produce low-copy and selectable marker free events of most effective genes	30%	0.7%	0.44
Activity 2.4.3. Establish regional marker laboratories backstopped by a central facility	10%	0.5%	0.11
Activity 3.1.1. Develop user-friendly, portable genetic resource information system	0%	0.0%	0.08
Activity 3.2.1. Develop user-friendly bioinformatics tools	0%	0.0%	0.09
TOTALS		100.3%	17.21

Table 4. Projected staffing needs - note that many of these positions already exist within CIMMYT, and some are already providing support to the GRP

Discipline/Position	Current			2005			2009
Biochemist	0.00			0.50			0.50
Bioinformatics Specialist	2.60	G Davenport, J Riis, J Wang (0.6)		3.00	G Davenport, J Riis, J Wang		2.00
Biometrician	1.00	J Crossa		2.00	J Crossa		2.00
Breeder	4.30	T Ban (0.5), M Lillemo, S McLean (0.8), SJ Suh S Taba (0.5), M vanGinkel (0.5)		4.30	T Ban (0.5), S McLean (0.8), SJ Suh S Taba (0.5), M vanGinkel (0.5) New PDF		4.00
Cell Biologist	0.70	A Pellegrineschi (0.7)		0.70	A Pelegrineschi (0.7)		2.00
Communications Specialist	0.50	D Poland (0.5)		1.00	D Poland		1.00
Cytogeneticist	2.00	M Kazi, M Kishii		1.00	M Kishii		1.00
Entomologist	0.00			0.25	D Bergvinson (0.25)		0.25
Genebank Curator	1.00	S Taba (0.5) M vanGinkel (0.5)		1.00	S Taba (0.5) M vanGinkel (0.5)		1.00
GIS Specialist	0.00			0.30	D Hodson (0.3)		0.30
Molecular Biologist/Geneticist	5.10	T Ban (0.5), L George (0.3), E Perotti, JM Ribaut (0.5), G Rosewarne (0.3), M Sawkins (0.7), A Serratos (0.6) M Warburton (0.8), M William (0.4)		5.10	T Ban (0.5), L George (0.3), E Perotti, JM Ribaut (0.5), G Rosewarne (0.3), M Sawkins (0.7), A Serratos (0.6) M Warburton (0.8), M William (0.4)		5.10
Pathologist	0.00			0.25	D Jeffers (0.25)		0.25
Physiologist	0.50	P Monneveux (0.3) JM Ribaut (0.2)		1.00	P Monneveux (0.3) JM Ribaut (0.2)		1.00
Population Geneticist	0.00			0.25			0.25
Regulatory Specialist	0.00			0.25	S Sullivan (0.25)		0.25
Socio-economist	0.00			0.25	M Bellon (0.25)		0.25
Training Coordinator	0.00			0.40	P Lusani (?)		0.40
TOTALS	**17.70**			**22.40**			**21.95**

Genetic Resources

Narrative Summary	Verifiable Indicators	Means of Verification	Assumptions
Goal. Enhance the productivity and nutritional quality of maize and wheat varieties through the targeted use of genetic resources	At least 25% of the new maize and wheat varieties produced by CIMMYT and its partners containing novel gene combinations derived from elite or untapped genetic resources (e.g., landraces and wild relatives)	Ability to access genetic resource information and seeds via the web Database reports New useful germplasm incorporated into breeding programs Scientific articles and reports	Access to global genetic resources Sufficient variation for a trait in available genetic resources Suitable phenotypic screening methodology for target traits/environments A genetic basis of trait phenotypes Ability to negotiate necessary freedom-to-operate for any required intellectual property
Purpose 1. Global custodianship, characterization and management of the genetic resources of maize, wheat and related species	Genetic resource information available for at least 25000 maize and 75000 wheat accessions Global maize and wheat genetic resource network involving at least 75% of the maize and wheat genebanks	Database reports Scientific articles and reports Feedback from partners	Access to global genetic resources Willingness to establish global network
Result 1.1. Enhanced global collection of maize and related species resources, including key genetic materials	By 2007, a 5-10% increase in the number and type of maize and related species accessions available in the gene bank By 2007, a 5% increase in the number of requests for seed	Database reports Genebank seed requests	Access to global genetic resources
Activity 1.1.1. Improve the Latin American, African and Asian maize germplasm collections			
Activity 1.1.2. Access key related species and genetic materials of maize into the collection			
Result 1.2. Inventoried wheat and related species collection, including key genetic and cytogenetic materials	By 2007, a database with data for at least 75000 wheat and related species	Database reports	
Activity 1.2.1. Inventory entire wheat collection checking quantity, viability and data quality	Complete inventory by end of 2006	Database reports	
Activity 1.2.2. Access key genetic and cytogenetic materials of wheat into the collection	A 25% increase in the number of genetic and cytogenetic stocks by 2006	Database reports	
Result 1.3. Characterized maize and wheat genetic resources	At least 25% of the gene bank accessions characterized at the phenotypic and/or molecular levels by end of 2006	Database reports Scientific articles and reports	Suitable phenotypic screening methodology for target traits A genetic basis of traits
Activity 1.3.1. Phenotype maize and wheat accessions for key traits	5-10% of the maize and wheat accessions phenotyped for at least 1 trait each year	Scientific articles and reports Database reports	
Activity 1.3.2. Fingerprint using molecular markers key maize and wheat accessions and related species	5-10% of the maize and wheat accessions fingerprinted each year	Scientific articles and reports Database reports	
Result 1.4. Web-based genebank information, management and distribution system	A global web-accessible maize and wheat genetic resource information system	Ability to access genebank information globally	
Activity 1.4.1. Develop an updated, web-accessible genebank management and information system	Beta-version available by end of 2005 Operational version by 2006	Available software User reports	

Narrative Summary	**Verifiable Indicators**	**Means of Verification**	**Assumptions**
Activity 1.4.2. Incorporate existing genebank data into the new system, improving data quantity and quality	Data entered by end of 2005	Database reports	
Result 1.5. Statistical and simulation models for efficient maintenance and use of maize and wheat genetic resources	Computer-based models for regeneration of genebank accessions Strategies for efficient genebank management	Scientific articles and reports Computer software Genebank operating manual	
Activity 1.5.1. Evaluate statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets.	Initial models available by 2005 Testing of models in 2006+	Scientific articles and reports	
Activity 1.5.2. Develop population genetic models for efficient regeneration and collection of genetic resources.	Initial models available by 2005 Testing of models in 2006+	Scientific articles and reports	
Result 1.6. Strategies for on-farm management of genetic resources	Knowledge of geneflow in farmers fields At least 1 strategy to improve conservation of farmer varieties At least 50 farmers participating in the on-farm management of genetic resources	Scientific articles and reports Farmer interviews	Willingness of farmers to participate
Activity 1.6.1. Study the effects of gene flow within and between farmer grown varieties			
Activity 1.6.2. Determine incentives required for *in-situ* conservation of genetic resources			
Purpose 2. Effective approaches identified in genetic resources and transferred to useful maize and wheat germplasm for improving critical traits as prioritized by CIMMYT and its partners	At least 1 genetic solution in maize for improved tolerance to abiotic stresses (drought, low nitrogen and acid soil), biotic stresses (storage insect pests and pathogens) and grain nutritional quality (QPM, vitamin A, iron and zinc) At least 1 genetic solution in wheat for improved tolerance to abiotic stresses (drought, low nitrogen, heat and salt), biotic stresses (fusarium, septoria and powdery mildew diseases) and grain nutritional quality (vitamin A, iron and zinc)	Improved sources identified Novel genetic diversity transferred through pre-breeding into adapted genetic backgrounds Useful diversity being incorporated into breeding programs directly or through use of pre-breeding products Scientific articles and reports	Sufficient variation for a trait in available genetic resources A genetic basis of trait phenotypes Ability to negotiate necessary freedom-to-operate for any required intellectual property
Result 2.1. Maize and wheat consensus maps for tolerance/resistance to abiotic and biotic stresses, and enhanced grain nutrition	Consensus maps for drought tolerance and insect resistance in maize by 2005 Consensus maps for drought tolerance and fusarium resistance in wheat by 2006	Scientific articles and reports	Traits are controlled by key consensus genomic regions
Activity 2.1.1. Develop and analyze maize and wheat genetic populations to identify QTL for tolerances to abiotic and biotic stresses, and grain nutritional quality components	At least 1 mapping population analyzed per year	Scientific articles and reports	
Activity 2.1.2. Assemble consensus maps for maize and wheat and display multiple traits across environments and populations			
Activity 2.1.3. Link genomic regions of interest identified on maize and wheat consensus maps with other species (and vice versa)			

Narrative Summary	Verifiable Indicators	Means of Verification	Assumptions
Result 2.2. Identification of genes, alleles and biological pathways involved in tolerance to abiotic and biotic stresses, enhanced grain quality, and asexual reproduction (apomixis)	Genes, alleles and/or pathways identified for improving abiotic stress tolerance by 2005 Genes, alleles and/or pathways identified for improving biotic stress resistance by 2006 Genes, alleles and/or pathways identified for asexual reproduction by 2007+	Scientific articles and reports	Sufficient variation for a trait in available genetic resources Ability to produce apomictic seed in diploid species Ability to negotiate necessary freedom-to-operate for any required intellectual property
Activity 2.2.1. Identify and validate candidate genes and biological pathways involved in tolerances to abiotic, biotic stresses and grain quality in maize and wheat using functional genomics, allele mining and association genetics			
Activity 2.2.2 Identify gene systems for conditioning asexual reproduction (apomixis) in cereals	Nucellar/ovule-specific and inducible promoters identified by 2005 Embryogenesis genes identified by 2006 Cell differentiation genes identified by 2007	Scientific articles and reports	Ability to negotiate necessary freedom-to-operate for any required intellectual property
Activity 2.2.3. Screen candidate genes from cereals and other species in maize and wheat for improved tolerances to abiotic and biotic stresses, and nutritional quality using genetic engineering	Screen 10 genes for abiotic stress tolerance in wheat by 2006 Screen 10 genes for biotic stress tolerance in wheat by 2007 Screen 5 genes for grain nutritional quality in wheat by 2007+	Scientific articles and reports	Ability to negotiate necessary freedom-to-operate for any required intellectual property
Result 2.3. Bioinformatics platform for handling and analyzing genomic data	Bioinformatics platform established and functioning by end of 2005	Scientific articles and reports Bioinformatic tools User feedback	
Activity 2.3.1. Implement central data repository for CIMMYT-derived genomic data	Data repository available by end of 2005		
Activity 2.3.2. Identify and adopt key bioinformatics packages for analyzing genomic data	Packages available in 2005+		
Result 2.4. Useful maize and wheat germplasm with enhanced tolerance to abiotic and biotic stresses and enhanced grain quality	At least 10 maize and wheat lines as sources for improved tolerance and/or nutritional quality produced per year	Scientific articles and reports Germplasm requests	Sufficient variation for a trait in available genetic resources Ability to negotiate necessary freedom-to-operate for any required intellectual property
Activity 2.4.1. Develop novel 'synthetic' or 'bridge' wheats using wild A, B and D genome donors	At least 50 new 'synthetic' or 'bridge' wheats produced	Scientific articles and reports	
Activity 2.4.2. Produce doubled haploid populations of wheat for mapping projects and pre-breeding purposes	At least 10000 doubled haploid individuals per year	Scientific articles and reports	
Activity 2.4.3. Characterize at the phenotypic and molecular levels key maize and/or wheat genetic resources under water-stress, low nitrogen, and/or acid soils conditions and for resistance to fusarium, septoria and powdery mildew to identify novel sources of tolerance	At least 1000 accessions evaluated for key traits each year	Scientific articles and reports	

Narrative Summary	**Verifiable Indicators**	**Means of Verification**	**Assumptions**
Activity 2.4.4. Incorporate novel sources of tolerance into useful maize and wheat germplasm using conventional, molecular-marker and/or genetic engineering strategies for further use by breeding programs of CIMMYT and its partners	Drought tolerant maize lines by 2005+ Acid soil and drought tolerant wheat lines by 2006+ Fusarium and septoria resistant wheat lines by 2006+	Scientific articles and reports	
Activity 2.4.5. Screen maize and wheat genetic resources for elevated levels of iron, zinc and pro-vitamin A in the grain	Maize and wheat lines screened by 2005+	Scientific articles and reports	
Activity 2.4.6. Incorporate novel sources of elevated levels of micronutrients into useful maize and wheat germplasm using conventional, molecular-marker and/or genetic engineering strategies for further use by breeding programs of CIMMYT and its partners	Increased iron and zinc wheat lines by 2007+	Scientific articles and reports	
Result 2.5. Improved marker-assisted selection strategies and use by CIMMYT and its partners	At least a 10% increase in the number of MAS assays per year At least 1 new effective MAS strategy proposed by 2006	MAS use reports Scientific articles and reports Improved germplasm	Good knowledge of gene networking and interaction Continued demand for MAS
Activity 2.5.1. Model use of molecular markers in breeding programs to identify optimal application	At least 1 new strategy by 2006		
Activity 2.5.2. Increase the number and efficiency of marker systems for use by CIMMYT and its partners	At least 2 new marker systems adopted per year		
Activity 2.5.3. Establish regional marker laboratories backstopped by a central facility	At least 1 regional marker lab established by 2005 At least 4 regional marker labs established by 2007	MAS use reports	Continued demand for MAS in the regions
Result 2.6. Genetic engineered event of key genes for ultimate deployment to CIMMYT partners	Maize and wheat germplasm containing at least 10 transgenic events each for at least 2 genes by 2007	Scientific articles and reports Improved germplasm	Ability to negotiate necessary freedom-to-operate for any required intellectual property NARS and public interest in transgenic varieties Simple gene solutions for critical traits
Activity 2.6.1. Produce low-copy and selectable marker free events of most effective genes	*Agrobacterium* transformation system for wheat by 2005 Gene excision/recombination system for maize and wheat by 2007	Scientific articles and reports	Ability to negotiate necessary freedom-to-operate for any required intellectual property
Activity 2.6.2. Develop source lines containing these events along with required regulatory information	At least 6 events in extended field trials by 2007	Scientific articles and reports Biosafety applications and approvals	Appropriate biosafety regulations for field trials in target countries
Purpose 3. Capacity in genetic resource management, maintenance and use enhanced globally	At least 50 NARS staff trained per year	Workshop and training reports NARS and farmer feedback	
Result 3.1. Improved capacity for storage and management of genetic resources by CIMMYT's partners	Quality of maize and wheat global genetic resources increased in at least 5 NARS each year	NARS feedback	
Activity 3.1.1. Develop user-friendly, portable genetic resource information system	System available by 2006	Software reports User feedback	

Narrative Summary	**Verifiable Indicators**	**Means of Verification**	**Assumptions**
Activity 3.1.2. Conduct workshops and/or host visiting scientists/students on genebank management (*ex-situ* and *in-situ*)	At least 1 workshop held each year At least 2 scientists/students hosted each year	Workshop and training reports	
Activity 3.1.3. Help NARS and CIMMYT partners develop or improve genebank facilities	At least 5 NARS or partners helped each year	NARS feedback	
Result 3.2. Increased use of genomic approaches by CIMMYT and its partners	At least 5 NARS scientists trained in genomic approaches each year	NARS reports Scientific articles and reports	
Activity 3.2.1. Develop user-friendly bioinformatics tools			
Activity 3.2.2. Conduct workshops and/or host visiting scientists/students in the application of genomics (QTL/gene discovery, MAS) in maize and wheat breeding	At least 1 workshop held each year At least 2 scientists/students hosted each year	Workshop and training reports	
Activity 3.2.3. Provide appropriate software tools to CIMMYT partners			

	CIMMYT Internal High Priority Areas	**Where CIMMYT Will Work With Partners,: Partners to Perform the Work**	**CIMMYT Will Not Carry Out This Work; Or only if Specific Funding & Agreements Permit**
Institution	• Genetic conservation through use in genetically enhanced pools • Gene discovery and allele mining combining phenomics and genomics • Breeding of maize, wheat and triticale pops. and lines (NOT cultivars) [and in collaboration with ICARDA, barley for Latin America] • Establish resource conservation technology options (RCTs) that fit into conservation agriculture • Capacity building using information management systems, knowledge sharing and learning-by-doing approach		• Work on livestock • Work on legumes (other than as part of Conservation Agriculture rotations) • Macroeconomic studies • Genetic Transformation other than on drought and insect resistance • Breeding of cultivars/varieties

	CIMMYT Internal High Priority Areas	**Where CIMMYT Will Work With Partners,: Partners to Perform the Work**	**CIMMYT Will Not Carry Out This Work; Or only if Specific Funding & Agreements Permit**
Program 1 ***Genetic Resources***	• Collection and conservation of crop-related bio-diversity • Methodologies for and products from, trait and gene-based identification of useful crop-related bio-diversity *[demand driven by regional programs]* • Development of fully integrated public-access germplasm characterization and enhancement information resources • Methodologies for and products from, improved efficiency of germplasm enhancement *[demand driven by regional programs]* • Development of holistic knowledge-led solutions for drought tolerance and resistance to Fusarium head blight and rust in wheat *[in collaboration with regional programs]*	• *In situ* conservation/farm management • Untargeted pre-breeding activities (elimination ongoing in wheat) • Untargeted in-house up-stream research (for example, apomixis) • Low breeder priority trait mapping (yet to be identified) • Low breeder priority transgenics	• On-farm management of maize and wheat genetic diversity • [systematic] Characterization of genebank entries • Alternatives for communities to grow unique genetic resources • Analysis of policies related to genetic resources and genetic diversity • Economic assessment of the value of genetic resources

Initial Priorities for Creating a Genetic Resources and Enhancement Unit

Generate knowledge, tools and germplasm to assist wheat and maize breeding

- Genetic understanding
- Genomics tools
- Computational tools

> Improve efficiency and precision of accessing biodiversity
> Better understand underlying genetics of target traits
> Develop genomics tools to help genebank mining and selection in breeding programs
> Generate computation tools to assist all of the above

MAIZE	WHEAT
Genomics Tools for Mining Biodiversity	
Drought (genomics)	**Drought** (synthetics and transgenics)
Disease Resistance (MSV) (marker-assisted selection)	**Rusts** (MAS and transgenics)
Pest Resistance (transgenics)	**Fusarium** (holistic approach)
Quality Traits (QPM) (marker-assisted selection and transgenics)	**Quality traits** (marker-assisted selection
Computational Tools for Molecular Breeding	

Defining a Key Set of Priority Products for the Basis of the Business Plan

Primary Product Description	Important Subsidiary Elements	Primary Partner Initiatives
Stress Tolerant maize for enhanced food security and crop diversification	Quality	Generation Challenge Program
Wheat with enhanced water productivity and appropriate quality profiles	Quality	Generation Challenge Program
Rust resistant wheat	Fusarium resistance	Global Rust Initiative Global FHB Initiative
Bio-fortified maize and wheat for improved nutrition and health		HarvestPlus Challenge Program
New traits using technologies to release the value of global crop biodiversity		
Improved tools and methodologies for genetic improvement		MPB-CRC MNC breeding companies IRRI-CIMMYT CRIL
Capacity building in NARS and SME breeding programs		GCP Molecular Breeding Communities of Practice NIAB plant breeding training
Resource conservation technologies for maize and wheat cropping systems		
Speciality maize for income generation		

Establishing Projects as the Operational Unit for Product Development

Project # [Short Title]	Formal Title	Associated Flagship Products
Project 1 Discovery	Conservation and characterization of and targeted access to maize and wheat related biodiversity	#5 and #6: New Traits through Allele Mining and Improved Methodologies for Genetic Improvement
Project 2 Tools	Trait enhancement: tools, methodologies, and germplasm	#5 and #6: New Traits through Allele Mining and Improved Methodologies for Genetic Improvement
Project 3 Stress	Stress tolerant maize	#1: Stress Tolerant Maize
Project 4 Added Value	Nutritional and specialty traits for maize	#4 and #9: Biofortified Maize and Special Trait Maize for Income Generation
Project 5 Africa	African livelihoods	#1: Stress Tolerant Maize; # 4 and #9: Biofortified Maize and Special Trait Maize for Income Generation
Project 6 LAA	Maize for Latin America and Asia	#1: Stress Tolerant Maize; # 4 and #9: Biofortified Maize and Special Trait Maize for Income Generation
Project 7 Drought	Water productive wheat with appropriate quality profiles	#2: Wheat with Enhanced Water Productivity
Project 8 Diseases	Enhanced wheat for more durable resistance to diseases and enhanced production potential	#3: Rust Resistant Wheat
Project 9	Wheat grain enriched for health and profitability	#5: New Traits through Allele and Gene Mining of Global Crop Genetic Resources
Project 10 RCT	Conservation agriculture for maize and wheat cropping systems: Safeguarding soils while increasing water productivity and resource use efficiency	#8: Resource Conservation Technologies
Project 11 KTSA	Knowledge, targeting, and strategic assessment of maize and wheat farming systems	#7: Capacity Building

Project Descriptions

CIMMYT's flagship products that are described in part one of the business plan will be embedded as outputs from a carefully focused project portfolio. The individual projects are described below.

Project 1: Conservation and characterization of and targeted access to maize and wheat related biodiversity [Discovery]

Background
Crop-related biodiversity is the founding asset of the CGIAR and the basic raw material for the international breeding programs of CIMMYT. The emerging niche of the CGIAR in the new millennium builds on this foundation but now with greater emphasis on bioscience-assisted methodologies and intermediate products associated with the efficient identification of target added value traits and their rapid introgression into elite breeding material.

Why CIMMYT?
Structured and well characterized germplasm such as introgression lines, enhanced gene pools, advanced lines, cultivars, genetic mapping populations and mutant stocks are becoming an increasingly critical asset for the global plant research and breeding community. Targeted development, intensive characterization and extensive evaluation (under diverse field conditions) of this germplasm is increasingly seen as the rate limiting factor for translation of outputs from the genomics and information technology revolutions into tangible products for developing country farmers.

Application and translation of upstream research outputs for the development of intermediate products with multi-disciplinary added value will be increasingly dependent upon effective data management systems. Thus, a major new strategic focus in the program is the creation of a fully integrated web-based support system for partners involved with conservation, utilization, evaluation and enhancement of genetic resources, whereby all types of data can be integrated, compared and collectively analyzed and/or queried by anyone anywhere.

Products

- Methodologies for[*] trait and gene-based identification of useful crop-related biodiversity [demand driven by regional programs in combination with new opportunities arising from advances in biosciences]
- Capacity building and technological backstopping to assist NARS, SMEs and CIMMYT breeders to make best use of maize and wheat-related biodiversity (through adoption of new methodologies and uptake of newly targeted germplasm)
- Development of fully integrated, public-access, germplasm characterization information resources [entirely demand driven by end-users][developing resources for integrating all available data within germplasm enhancement pipeline better fits in P2]

- Generation and/or characterization of near-isogenic, introgression and substitution lines, enhanced gene pools, synthetic polyploidy genotypes, genetic mapping populations and mutant stocks for trait-targeted genetic investigations [entirely driven by trait focus priorities]
- Targeted collection, conservation, characterization and distribution of crop-related bio-diversity [increasingly demand driven by end-user trait priorities]

[*this converted to additional statement in next bullet as in new vision GREU products will be methodologies while application for a specific trait target will be in maize and wheat breeding programs supported by GREU]

With whom do we do it?
Conservation and management of genetic resources: IPGRI, FAO, NARS and ARI's together with organizations involved in all relevant international agreements.

Targeted access to valuable genetic variation: ARI's, NARS, IARCs and the private sector particularly through consortia such as the Molecular Plant Breeding CRC and the Generation Challenge Program, the IRRI-CIMMYT alliance and through bilateral arrangements with ARIs and the private sector in OECD countries and strong NARS in China, India, South Africa, Brazil and Argentina.

Where do we do it?
CIMMYT locations: in Mexico but increasingly also in Turkey and Morocco (CWANA), China, India and the Philippines (Asia), and, Kenya and Zimbabwe (East and Southern Africa).

NARS locations: collaborating countries of the Latin American Maize Program (LAMP), and [parallel statement for wheat]. Systemic collaboration with strong NARS in Africa, Asia and Latin America will become an increasingly important component of our operational strategy in many cases extended to include the breeding communities of USA, Europe and Australia.

Who benefits?
NARS and SME maize and wheat breeding programs with spillovers for their clients: resource-poor farmers, processors, consumers and families, with spillovers and synergies with ARIs and multi-national companies in the plant science research community.

Who are the clients?
NARS, SME and IARC breeding programs

Project 2: Tools and Methodologies for Genetic Improvement [Tools]

Background

The overall objective of this project is to develop and validate new methodologies for more efficient and targeted identification and manipulation of new alleles and genes for traits prioritized by end-users in CIMMYT's regional programs, and, in NARS and SME breeding programs. The primary goal of these efforts is to enhance the resilience (to abiotic stresses), yield stability (under biotic stress), nutritional quality (for human and animal consumption) and the profitability of maize and wheat varieties through the targeted use of genetic resources.

Why CIMMYT?

Molecular breeding application facilities at CIMMYT and our partners urgently need to evolve to a new paradigm which is able to take maximum advantage of genotyping out-sourcing enterprises now emerging all over the world. Similarly, the identification of new marker associations is very often better achieved in ARIs. Nevertheless, CIMMYT has a primary niche in developing central information resources and coordinated analysis and representation initiatives. Similarly, it is CIMMYT's role to translate, validate and/or refine appropriate outputs from ARI research to facilitate robust and efficient routine application in plant breeding programs. In particular, applying quantitative knowledge-led phenotyping systems, analyzing environmental and genetic background effects, developing improved methodologies through retrospective analysis of current breeding systems, and devising new selection systems based on holistic indices and computation decision support tools.

The project will generate methodologies for, intermediate products from, and capacity building around, improved efficiency of targeted germplasm enhancement through development of holistic knowledge-led solutions for genetic improvement of trait targets defined by CIMMYT, NARS and SME breeding programs. Thus, the current priorities have been arranged into four trait groups in each crop as follows:

WHEAT – Primary Trait Focus	**Secondary Trait Focus**	**Comments**
Drought tolerance	Root health factors*	
Resistance to rusts	Resistance to other foliar diseases* such as FHB	
Quality traits for human* consumption	Quality traits* for animal consumption	
Improved productivity under resource conservation technologies* (RCTs)		
MAIZE – Primary Trait Focus	**Secondary Trait Focus**	**Comments**
Drought and heat tolerance	Low soil fertility tolerance*	
Pest resistance*	Disease resistance* (including mycotoxins)	
Quality traits*	QPM and other biofortification* (including protein content) for human and animal consumption	Increasingly also for animal consumption and industrial use quality parameters
Improved productivity under resource conservation technologies* (RCTs)		

Products

- Web-enabled integrated data management and analysis systems linking genetic resources, biotechnology, breeding and variety release
- Biotechnology and/or computationally-assisted germplasm enhancement tools and strategies (including molecular breeding decision-support systems)
- Capacity building and technological backstopping to assist NARS, SME and CIMMYT wheat and maize breeders to make best use of new germplasm enhancement tools, methodologies and genetic resources
- *Ex ante* or cost-benefit analysis of impact from GREU outputs (germplasm, tools and methodologies) in flagship projects
- New genetic engineering methodologies and GMC-breeding systems
- New maize and wheat molecular breeding tools through translational genomics from rice and other model systems
- New maize and wheat molecular breeding tools through functional genomics analysis of metabolic pathways important for agronomic traits such as drought tolerance and developmental biology
- [included in previous draft as discussions were at that point still on-going regarding the split of activities between GREU and commodity programs but now this output sits squared in the wheat program]
- Genetically enhanced high quality maize populations with drought tolerance and resistance to biotic stresses [included in previous draft as discussions were at that point still on-going regarding the split of activities between GREU and commodity programs but now this output sits squared in the maize program]

With whom do we do it?
ARI's, NARS, IARCs and the private sector particularly through consortia (G-CP, MPB-CRC) and the IRRI-CIMMYT alliance and through bilateral arrangements with ARIs and the private sector in OECD countries and strong NARS in China, India, South Africa, Brazil and Argentina.

Where do we do it?
Increasingly in the regional locations that offer best proximity to partners and end-users and greatest operational efficiency. CIMMYT locations include Mexico, but increasingly also in Turkey, Morocco (CWANA), China, India and the Philippines (Asia), and, Kenya and Zimbabwe (East and Southern Africa). Strong partnerships are envisaged at NARS locations in Africa, Asia and Latin America.

Who benefits?
NARS and SMEs maize and wheat breeding programs with spillovers for their clients:

resource-poor farmers, processors, consumers and families, with spillovers and synergies with ARIs and multi-national companies in the plant science research community.

Who are the clients?
NARS, SME and IARC breeding programs.

CIMMYT
Genetic Resources
Program

2005 Highlights

Progress report of outputs and against 2005 MTP milestones

Project	Project output	Output target 2005	Category output target	Level of Achievement
Genetic Resources	Global custodianship, characterization and management of the genetic resources of maize, wheat and related species (MTP Purpose 1)	Genetic resources information available for at least 25,000 maize and 75,000 wheat accessions.	Databases	Partially [on target to exceed 2007 milestone now that CRIL established]
		A 5-10% increase in the number and type of maize and related species accessions available in the gene bank	Inventories	Exceeded 2007 target
		A global web-accessible maize and wheat genetic resource information system – beta-version available by end of 2005. Incorporate existing genebank data into the new system, improving data quantity and quality	Software and databases	Partially [basic system created]
		Evaluate statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets. Develop population genetic models for efficient regeneration and collection of genetic resources	Journal publications	Yes
Genetic Resources	Effective approaches identified in genetic resources and transferred to useful maize and wheat germplasm for improving critical traits as prioritized by CIMMYT and partners (MTP Purpose 2)	Consensus maps for drought tolerance and insect resistance in maize by 2005. Genes, alleles and/or pathways identified for improving abiotic stress tolerance by 2005.	Publications and on-line resources	Partially [delayed due to departing staff]
		Identify gene systems for conditioning asexual reproduction (apomixis) in cereals. Nucellar/ovule-specific and inducible promoters identified by 2005	Genomic materials	Yes
		Bioinformatics platform established and functioning by end of 2005.	Infrastructure	Exceeded target
		Implement central data repository for CIMMYT-derived genomic data by end of 2005. Identify and adopt key bioinformatics packages for analyzing genomic data in 2005.	Database infrastructure and research practices	Partially [delayed due to establishment of CRIL]

Project	Project output	Output target 2005	Category output target	Level of Achievement
Genetic Resources	Global custodianship, characterization and management of the genetic resources of maize, wheat and related species (MTP Purpose 1)	Genetic resources information available for at least 25,000 maize and 75,000 wheat accessions.	Databases	Partially [on target to exceed 2007 milestone now that CRIL established]
		A 5-10% increase in the number and type of maize and related species accessions available in the gene bank	Inventories	Exceeded 2007 target
		A global web-accessible maize and wheat genetic resource information system – beta-version available by end of 2005. Incorporate existing genebank data into the new system, improving data quantity and quality	Software and databases	Partially [basic system created]
		Evaluate statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets. Develop population genetic models for efficient regeneration and collection of genetic resources	Journal publications	Yes
		Incorporate novel sources of tolerance into useful maize and wheat germplasm using conventional, molecular-marker and/or genetic engineering strategies for further use by breeding programs of CIMMYT and its partners. Drought tolerance maize lines by 2005.	Advanced materials	Partially [delayed due to departing staff]
		Screen maize and wheat genetic resources for elevated levels for iron, zinc and pro-vitamin A in the grain	Selected materials	Yes
		Establish regional marker laboratories backstopped by a central facility – at least one regional marker lab established by 2005	Infrastructure	No [due to change of strategic emphasis]
		Agrobacterium transformation system for wheat by 2005	Protocol publication or patent	Yes [patent submitted]
Genetic Resources	Capacity in genetic resource management, maintenance and use enhanced globally (MTP	Improved capacity for storage and management of genetic resources by CIMMYT's partners. Quality of maize and wheat global genetic resources increased in at least 5 NARS each year. At least 5 NARS or partners helped each year.	NARS feedback	No [awaiting ICIS implementation & training of NARS]

Project	Project output	Output target 2005	Category output target	Level of Achievement
Genetic Resources	Global custodianship, characterization and management of the genetic resources of maize, wheat and related species (MTP Purpose 1)	Genetic resources information available for at least 25,000 maize and 75,000 wheat accessions.	Databases	Partially [on target to exceed 2007 milestone now that CRIL established]
		A 5-10% increase in the number and type of maize and related species accessions available in the gene bank	Inventories	Exceeded 2007 target
		A global web-accessible maize and wheat genetic resource information system – beta-version available by end of 2005. Incorporate existing genebank data into the new system, improving data quantity and quality	Software and databases	Partially [basic system created]
		Evaluate statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets. Develop population genetic models for efficient regeneration and collection of genetic resources	Journal publications	Yes
	Purpose 3)	Conduct workshops and/or host visiting scientists/students on genebank management (ex-situ and in-situ). At least one workshop held each year. At least two scientists/students hosted each year.	Workshop and training reports	No [due to other priorities]
		Increase use of genomic approaches by CIMMYT and its partners. At least five NARS scientists trained in genomics approaches each year.	NARS reports	Yes
		Conduct workshops and/or host visiting scientists/students in the application of genomics (QTL/gene discovery, MAS) in maize and wheat breeding. At least one workshop held each year. At least two scientists/students hosted each year	Workshop and training reports	Yes

GRP 2005 Output Highlights

[A] GRP OUTPUT 1 [GENETIC RESOURCES] activities within GREU PROJECT 1: DISCOVERY (P1)

#1	**Expansion of maize germplasm collection**	Suketoshi Taba [Victor H. Chavez-Tovar, Marcial Rivas, and Martín A. Rodríguez]

The cooperative effort of conserving Latin American maize landrace collections

CIMMYT and its cooperator national maize banks began the initiative of rescuing Latin American maize landrace collections in 1992 with the support of USAID and USDA, and the later stage from the World Bank Upgrading project and other donors to CIMMYT. Thirteen national maize banks participated in the projects to start with with an agreement to regenerate the accessions at risk and safety-duplicate them at CIMMYT and NCGRP (National Center for Genetic resources Preservation, Fort Collins Colorado, USA; formerly NSSL). This cooperative network of conservation and regeneration has continued during 2005. We regenerated 1,223 accessions of CIMMYT back-log and Latin American introductions in 2005. We have repeated regeneration for some accessions to avoid genetic drift as we harvested small numbers of ears in the first regeneration. We also received 512 new introductions from the cooperators that were also added to the maize collection. As a result, CIMMYT collection has now 25,377 accessions in total. Further cooperation among CIMMYT and its cooperator institutions in this region is envisioned for safeguarding maize genetic resources.

Outcome of the cooperative project to date

The numbers of the regenerated accessions received at CIMMYT are summarized in Table 1. Only unique accessions became accessed in CIMMYT maize bank. Duplicate accessions identified by the passport data and previous shipment records to CIMMYT were added to the corresponding seed accessions in the CIMMYT collection. We compared the passport data and inventory data between CIMMYT and NCGRP germplasm accessions, and also with the cooperating national banks in order not to duplicate the work of regeneration and to set priority for regeneration.

Numbers of accessions received from the cooperating countries and new introductions to the CIMMYT maize collection, 1993-2005

Country	No. of samples received 1993 – 2005	CIMMYT New Accessions 1993 – 2005
Argentina	896	758
Bolivia	579	473
Brazil	658	569
Chile	713	469
Colombia	1491	1001
Cuba	101	101
Ecuador	1065	252
Guatemala	751	544
Honduras	42	42
Mexico	9831	5092
Paraguay	440	439
Peru	1224	887
Venezuela	184	151
TOTAL	17975	10778

Figure 1. Indicates the results of the new introductions to CIMMYT maize collection from Latin America through the cooperative project, 1993-2005. The results indicated more than 11,000 accessions of Latin American maize germplasm have been introduced at CIMMYT.

Figure 1. The increase of Latin American maize germplasm accessions at CIMMYT through the cooperative project, 1993-2005

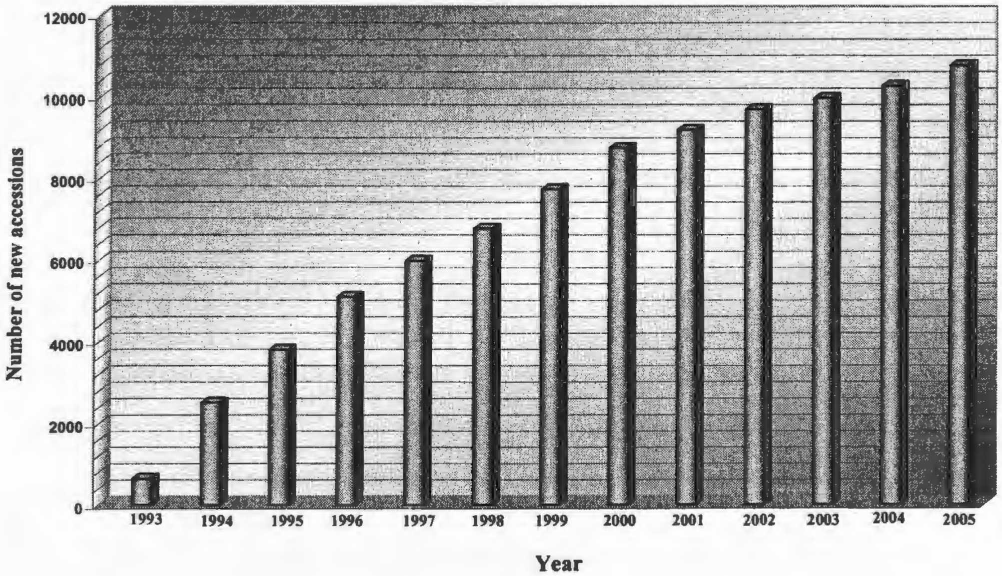

Figure 2. Shows annual increase of CIMMYT maize bank holdings, 1992-2005.

#2	**CRISCO-led maize and wheat germplasm and breeding data migration**	Tom Payne & Jens Riis

The efforts over the last couple of years to upgrade the information system used for maize breeding are now paying off. The full breeding process is now covered by a very user-friendly system made up of:

- Fieldbook, for experiment design and data analysis,
- FieldLog for data collection on PocketPC, and
- MaizeFinder as the data base for storing and accessing all the data

The first version of MaizeFinder with 3000 trials is ready for release.

The future: The system still has inadequate genealogy management, and the possibility to use the ICIS GMS for genealogy management is being evaluated. Likewise, a system for data integration with genomics data is missing, but ICIS is expected to be used for this. The Fieldbook application have also been discussed with the wheat breeders and they are quite interested in a lot of the practical functions e.g. for design of trials, field layout, printing of labels, and analysis of trial data.

The technical issues related to migrating from IWIS to ICIS are being investigated, and some have already been resolved. The IWIS DMS data (i.e. trial data) has been fully converted to the ICIS DMS. Likewise, a script exists for converting the IWIS PMS data to the ICIS GMS (i.e. the genealogy data). However, IWIS contains a series of functions e.g. for international shipments, and bulk field book production, which does not exist in ICIS. To overcome this limitation the possibility is being investigated of IWIS PMS data structure to work with the ICIS GMS. If this can done, then the remaining IWIS components could be kept in place and CIMMYT regional offices e.g. in Turkey and also partners could start to use ICIS without the current problems of parallel genealogy systems in wheat.

The current vision for the future plant breeding (both maize and wheat) and genebank IS is:

- Fieldbook, for experiment design and data analysis
- FieldLog for data collection on PocketPC
- ICIS GMS for genealogy management
- ICIS DMS for storage of trial and nursery data including gene bank data
- ICIS for integration with genomics data
- CropFinder for querying of plant breeding or genebank data online or in PC version

GenbankManager for managing seed stocks and passport data

Maize

- In 2005 3000 trials were imported from individual excel files into a database, MaizeFinder
- A new version of Fieldbook, the tool used for field trials in maize was developed, which has much improved functionality in relation to trial design, data analysis, and export of data to database.

Wheat

- Tools have been developed for converting both IWIS DMS (trial data) and IWIS PMS (genealogy data) to ICIS format, and a full conversion has been done.
- Possibility for substituting IWIS PMS with ICIS GMS is being investigated. It appears feasible, and doing this would solve a major problem in the migration, as some IWIS functionality is not present in ICIS, and the two genealogy systems creates problems with other wheat breeding institutes.

#3 Genebank management system

Jens Riis

Testing of the GenebankManagement system will be carried out during March and April 2006. The data from the maize collection have already been converted, and the testing will be initiated with this data. Initial attempts to incorporate the seed health data have been problematic due to the lack of common identifiers in the current maize genebank and the seed health data. The Genebank system also includes an Internet data mart, CropFinder, for accessing all the data related to the accessions including passport, characterization and evaluation data. CropFinder is designed so that it may also be used to present maize and wheat trial data on the Internet. The functionality developed so far is described below:

FieldLog, pocketPC data collection tool

- Has been used over the last year to collect field data for both maize and wheat.

GenebankManager, the tool for managing seed and passport data internally in genebank

- Security module working
- Query engine and interface for database working
- Workflow for taking seed out working, though reports missing
- Workflow for entering seed works 50 % of steps
- Workflow engine still needs to be linked to other modules
- Maize data has been migrated to new structure, and testing of functionality with users initiated.

CropFinder, internet tool for accessing genebank and plant breeding data, and submitting seed requests.

- Data structure developed and filled with maize collection data
- Query engine and pilot user interface for data queries working
- "Shopping cart" for seed requests missing

Opportunities:

- CropFinder will provide unprecedented access to CIMMYT genebank and plant breeding data, and as such has enormous potential.
- Both FieldLog, GenebankManager, and CropFinder are all developed as generic applications, which can be used both in wheat and maize, and FieldLog and CropFinder also for plant breeding purposes. All can be shared with national partners and other interested institutions.

#4 Overview of seed inspection and distribution

Monica Mezzalama

The SIDU covers three areas of activities:

- Seed Inspection
- Seed Preparation and Distribution
- Data Management

The SIDU receives seed requests of wheat international nurseries, of maize international trials, CIMMYT maize lines, of maize and wheat accessions from the germplasm bank through CIMMYT website, by fax, e-mail or ordinary mail. The SIDU receives also the seed introductions from abroad.

Seed Inspection: The Seed Inspection area functions as the port of entry for seed introductions and as the seed health analyses point for the seed that is leaving CIMMYT. It is responsible for following the quarantine procedure.

Activities for 2005 are summarized in the following table.

		Total no. of nurseries or trials analyzed	**No. of entries tested**	**No. of analysis carried on**
TOTAL FOR OUTGOING MAIZE	International Trials, CMLs, Miscellaneous bank accessions	162	21028	21234
TOTAL FOR OUTGOING SGC	International Nurseries, Miscellaneous, bank accessions	198	76088	28246
TOTAL INCOMING	Maize	19	7759	640
TOTAL INCOMING	SGC	34	9048	1170

Germplasm introduction is facilitated by maintaining valid import permits permanently, keeping close contact with collaborators, receiving the material and making sure that priorities are set (planting dates, special cases, laboratory analyses etc.). The quarantine procedure involves field visits that occur during winter cycles in Toluca, Tlaltizapan, Obregon and summer cycle in Toluca, Tlaltizapan, and Batan. The SHL's average time for delivering results of seed testing has been 20 working days. During 2005 no phytosanitary problem raised from maize and wheat seed introductions.

Phytosanitary management of outgoing germplasm involves the organization of the laboratory and greenhouse testing of international wheat nurseries, maize trials and miscellaneous nurseries. It involves also field visits to the multiplication plots in Mexicali, Batan, Taltizapan and Agua Fria, both in winter and summer cycles.

Seed Preparation and Distribution

Activities for 2005 are summarized in the following tables.

Wheat 2005

Total by program	International Nurseries sets prepared and distributed in 2005	%	Miscellaneous sets prepared	%
Intensive Agrosystems Program	1055	48.12	38	22.49
Rainfed Wheat	870	39.72	46	27.22
Genetic Resources	265	12.1	85	50.30
total	**2190**		**169**	

Maize 2005

Total by program	Trials sets prepared and distributed in 2005	%	Miscellaneous sets prepared	%
Intensive Agrosystems Program	130	20.63	22	6.92
Tropical Ecosystem	500	79.37	211	66.35
Genetic Resources			47	14.78
SIDU (shipments of CMLs)			38	11.95
Total	**630**		**318**	

Seed preparation of wheat, barley and triticale requires the washing procedure in chlorine as prophylaxis against karnal bunt (*Tilletia indica*), chemical treatment and packing. For maize the seed washing procedure is not required.

International Nurseries and trials are defined by the breeders every year and offered through CIMMYT website. Miscellaneous shipments includes bank accessions, CIMMYT maize lines and other materials produced by the breeders in the frame of special projects

Data Management: During 2005 536 sets of wheat international nurseries data and 200 sets of international maize trials data have been received for capture, analyses and loading on CIMMYT website for public access and consultation.

#5	**Optimization and analysis of international nurseries**	Tom/Monica/Tom/Richard/Karim John/Pancho/JHC

Overview of Countries Receiving International Nurseries and Elite Breeding Material

Morgan Stanley Index	WHEAT Kg	MAIZE Kg
Developing	8,559.54	2,879.89
Developed	1,185.88	102.26
Grand Total	9,745.43	2,982.15

WB Income	Kg	Kg
Low	2,380.32	1,078.44
Middle	3,395.96	609.97
Upper middle	2,186.77	1,189.53
High	1,782.38	104.22
Grand Total	9,745.43	2,982.15

WB Indebt	Kg	Kg
Severely	2,289.96	451.46
Moderately	1,580.63	525.29
Less	3,454.96	1,856.23
Not classified	2,419.88	149.16
Grand Total	9,745.43	2,982.15

OECD	Kg	Kg
Not belonging	6,729.62	1,890.75
Belonging	3,015.80	1,091.40
Grand Total	9,745.43	2,982.15

Type of Economy	Kg	Kg
Developing	5,215.90	2,274.56
Emerging	2,868.15	603.38
Developed	1,661.38	104.22
Grand Total	9,745.43	2,982.15

Raw Shipping Data	Production, Yield and Import Data
Microsoft Office Excel Worksheet	Microsoft Office Excel Worksheet

Outputs of Analysis of Wheat International Nurseries

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#6	Global profile for wheat synthetics	Jonathan Crouch, Richard Trethowan, Wayne Powell and David Mowbray

Diversity for Breeding Symposium

14–15th Dec. 2005, NIAB, Cambridge, UK

RE-DOMESTICATION OF THE WHEAT CROP: IMPACT ON GLOBAL WHEAT BREEDING

Jonathan Crouch[1,2], Richard Trethowan[1], Masahiro Kishii[1] and Mujeeb Kazi[1]

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[2]Generation Challenge Program: www.generationcp.org & j.crouch@cgiar.org

Introduction to International Wheat Breeding: The foundation of international wheat breeding that became CIMMYT, contributed to the green revolution in a sufficiently dramatic manner as to be recognized by the Noble Prize committee. This paradigm shift centred on the introduction of a small number of simply inherited traits that transformed wheat architecture and phenology and hence, productivity, in low latitude environments. These breeding programs were also largely focused on increasing productivity in high input cropping systems. Today the global community is demanding similar levels of progress from us yet this time focused on resource-poor cropping systems. This will require an equally dramatic paradigm shift, one that is centred on molecular-enhanced knowledge-led evolutionary-based improvement of complex traits with high epistasis and high genotype-by-environment interaction. Clearly, this will require an intensive multidisciplinary approach based on systemic collaboration between interdisciplinary scientists bridging molecular biology, informatics, biometrics and evolutionary biology with plant breeders, physiologists, pathologist, entomologists and grain quality specialists. CIMMYT believes it has the necessary framework and network to provide a major contribution to this endeavour. However, alliances with advanced research organizations and plant breeding programs in USA, Europe and Australia will be a fundamentally important component of this. Fortunately, by adopting a trait-based approach to our germplasm enhancement activities at CIMMYT, we believe we can also offer substantial contributions to wheat research and breeding for high input cropping systems.

Molecularization of Wheat Breeding: Over the past decade, the wheat breeding program at CIMMYT has been going through a number of quiet revolutions, many of which have been driven by capturing opportunities provided by new technologies. Spirally costs in the 1990's had forced a shift from pedigree breeding to modified pedigree and more recently, selected bulk methods. However, the reduced population size required when applying marker-assisted selection (MAS) has now allowed a dramatic return to pedigree and modified pedigree breeding which allows a more knowledge-led, product design orientated breeding system to evolve as well as the ability to evaluate material from more crosses. Many molecular markers for traits relevant to CIMMYT's client countries are being generated by CIMMYT's collaborators. Currently, the unit costs of MAS and lack of automation are the rate limiting factors for impacts of CIMMYT's molecular breeding efforts. Fortunately, the Molecular Plant Breeding Cooperative Research Centre (CIMMYT is a founding member of the MPB-CRC) has developed methodologies that may ultimately reduce the unit costs of MAS ten-fold. As a result, wheat breeding programs at CIMMYT are preparing for a ten-fold scale-up and scale-out of their molecular breeding operations. The molecularization of wheat breeding at CIMMYT is also an important foundation for improved utilization of genetic resources (see 'Utilization of Synthetic Wheats' section below).

Globalization of Wheat Breeding: Perhaps the most dramatic recent change in the wheat breeding program has been facilitated by the increased capability of key NARS partners. The traditional shuttle breeding between two diverse environments in Mexico has served many of CIMMYT's clients very well. However, this approach is not adequate for breeding resistance to certain pests and diseases that are not found in Mexico nor effective for breeding adaptation to certain target environments such as those at high latitudes. Fortunately the capability of some NARS in Asia, Latin America and the newly independent Central Asian republics has greatly improved since the Green Revolution. On this basis, CIMMYT wheat breeders are rapidly decentralizing their shuttle breeding program by joining forces with those NARS, each one specializing in a different pest or disease or unique environmental profile. This partnership mode of operation has also released funds for the modernization of the field breeding operation in Mexico.

Utilization of Synthetic Wheats: With climate change and our increasing focus on resource-poor farmers in marginal cropping systems, drought tolerance has become an over-arching priority. Significant progress is being made in generating wheat varieties with better levels of drought tolerance by incorporating natural variation available in widely adapted diploid progenitors. This is being achieved using wide cross technology which is allowing wheat breeders to recreate the polyploidization step that occurred in evolutionary time prior to the domestication of bread wheat. However, instead of the relatively narrow range of diversity captured in those evolutionary crosses, plant breeders now have available to them the full taxonomic diversity available in the wild relatives of cultivated wheat. As with most crops, the wild relatives are a rich source of pest and disease resistances and tolerances to environmental stresses. However, genome differentiation between wild and cultivated species usually confounds attempts to effectively capture such useful variation in their breeding programs. However, the resynthesis of wheat does not suffer such problems allowing breeders to rapidly incorporate synthetic derivatives into their mainstream programs. This provides CIMMYT with a unique niche for capturing the extensive genetic variation available in its enormous genebank (of over 160,000 accessions) and introgressing it into elite breeding lines. In the case of drought tolerance, this approach has been outstandingly successful. Based on this success, wheat breeders are now applying the same approach to pest and disease resistance, and nutritional quality traits.

The Role of Global Alliances: As bioscience research and plant breeding become increasingly complex and expensive, there is an increasing need for more complex inter-disciplinary, inter-sector and inter-national alliances to retain the cost effectiveness, agility and velocity of our progress. Two recent international initiatives go a long way to setting the scene for such alliances. First the Generation Challenge Program, a $15M a year global program focused on using genomics to release the value of global biodiversity for breeding abiotic stress tolerance traits, particularly drought resistance. Second, the IRRI-CIMMYT Alliance creating the Crop Research Informatics Lab centred on the application of informatics, biometrics and modelling to evolve new knowledge-led methodologies for harnessing the bioscience investment in model species and major crops for improving the pace and scope of breeding progress in cereal crops.

This paper will provide an overview of CIMMYT's wheat research and breeding programs and alliances with particularly emphasis on the role of synthetic germplasm on wheat breeding, past, present and future.

NIAB Symposium Program	Nature Article	New Scientist Article
Microsoft Word Document	Adobe Acrobat Document	Adobe Acrobat Document

#7	Molecular Fingerprinting of Maize and Wheat Composite Collections	Marilyn Warburton and Susanne Dreisigacker

In 2004, the Generation Challenge Program asked CIMMYT to coordinate the genetic characterization of a "core genotype set" of maize and wheat lines encompassing the diversity of each crop in the world. In maize, a set of ~1000 inbred lines and ~500 populations were fingerprinted with 50 SSR markers. The work was done in four different labs (CIMMYT; INRA, France; CAAS, China; and IITA, Nigeria). Optimized and standardized protocols were developed and run in each lab for data integration. In addition, 200 more maize landrace populations were collected and are being genotyped in a separate grant from the GCP. The data have all been collected and are now being deposited in the GCP central repository. An initial data analysis has been run on the maize germplasm to extract a "mini-core" that contains the same amount of diversity as the original set; this mini-core contains only 384 individuals and is ideal for intensive phenotyping, genotyping, and in depth studies such as association mapping studies. In wheat, ~2600 accessions were fingerprinted with 50 SSR markers by CIMMYT; Agropolis, France; ICARDA, Syria, and CAAS, China. Optimized and standardized protocols were developed and run in each lab for data integration. In addition, 400 more accessions are currently being fingerprinted with the same markers by CIMMYT and ICARDA, to bring the total to 3000. The data will soon be finished and put into the GCP central repository, and the mini-core of wheat will be developed soon after. More in depth analyses of these data are possible with this unusually large data set, and partner institutes are working together to fully exploit this data resource. Finally, a resource has been created by identifying all alleles identified at all SSR loci in each set (maize and wheat) and a catalog published that identifies the SSR, primers, allele sizes, and a reference genotype that will amplify this allele.

#8	Major advances in maize trait-enhancement	Suketoshi Taba

Enhancement of gene pools and breeding crosses

For highland gene pools, we evaluated the first cycle S2 progenies in reciprocal recurrent selection scheme (RRS) between pool 5 (highland late white flint "B" hetrotic pattern) x pool 6 (highland late white dent "A" heterotic pattern), pool 7 (highland late yellow flint "B") x pool 8 (highland late yellow dent "A"), and pool 9 (Intermediate white flint "B") x pool 10 (Intermediate white dent "A"). In addition, Intermediate yellow flint "B" (pool 11) and Intermediate late yellow dent "A" (Pool 12) were advanced to S2. The numbers of the testcrosses in RRS varied from 96-255 among the trials. The S2 progenies of the pools 9 and 10 were also sent to Dr. Afriyie Twumasi, Ethiopia for his making the testcrosses with tester lines he uses. Lines from pool 5 and pool 6 are evaluated in Ecuador. The results of the testcross trials are being analyzed

For subtropical gene pools, new germplasm sources were introgressed in the pools: 31 (late white flint "B" heterotic pattern), 32 (late white dent "A" heterotic pattern), 33 (late yellow flint "B"), 34 (late yellow dent "A") to increase yield potential and to enhance agronomic traits such as combining ability, grain texture and color. Breeding crosses between Brazilian core accessions x CMLs were excellent sources of diversity for the subtropical gene pools.

Tropical gene pools of 19 (intermediate maturity white flint "B" heterotic pattern), 20 (intermediate maturity white dent "A" heterotic pattern), 21 (intermediate maturity yellow flint "B"), 22 (intermediate maturity yellow dent "A"), 23 (late white flint "B"), 24 (late white dent "A"), 25 (late yellow flint "B"), and 26 (late yellow dent "A") were advanced to new cycle of reciprocal recurrent selection (RRS-inbred tester or RRS-partner pool) at Agua Fria Station. Breeding crosses and development of new source germplasm from Bank core (Caribbean accessions) x CML testers were also advanced.

Enhancement of Core accessions with line testers

Breeding crosses having 25% of the germplasm from the core accession and 75% from elite line sources were made using several Caribbean core accessions and CML tester lines. Several S2 lines were developed by direct inbreeding and visual selection scheme at TL and AF stations in the breeding crosses of Cuba 124 and Cuba 94 accessions for the heterotic pattern B, and in those of Cuba 91, Trinidad Gp 1, and San Luis Potosi (Snlp) 105 accessions for the heterotic pattern A. In 2003 A, the selected S2 lines from them and those from pool 25 and 26 were testcossed with four opposite testers. The testcrosses were evaluated at six locations during two years from 2003B through 2004B. The results were analyzed in 2005. Several lines of breeding crosses showed good grain yields and agronomic traits as compared with hybrid checks (Table 1 and 2). The breeding procedure was effective to extract new sources of diversity from the landrace core accessions for line development. The superior lines can be used for making enhanced core accessions as well as for enhancing the gene pool 25 and 26.

Table 1. The testcross performance of best 20% of the entries of the trial G25 with CML 479 as a tester at six Mexican locations in 2003-2004. The trial included S2 lines developed from the breeding crosses of Caribbean landrace accessions and Pool 25C$_{31}$, and single crosses among CML lines as checks.

Testcrosses and single crosses	**YLD (Mg ha^{-1})**	**AN (Days)**	**SI (Days)**	**PH (cm)**	**EH (cm)**	**MO (%)**	**EL (cm)**	**ED (cm)**	**KL (cm)**	**KWD (mm)**	**KRN**	**EQ (1-5*)**
G25 C31 HS83-2-1 x CML 479	8.2	69	69	244	125	16.6	17.4	4.7	1.2	87.7	14.2	2.7
[(Cuba124xCML413)xCML 451]53-2-1 x CML 479	8.0	68	69	242	125	16.9	17.7	4.7	1.2	88.5	14.1	2.6
CML 479 x CML 451	8.0	69	70	236	114	17.8	17.5	4.7	1.2	88.4	14.4	2.5
[(Cuba94xCML413)/CML 451]32-1-2 x CML 479	7.9	69	70	239	117	17.4	17.8	4.6	1.2	88.5	14.0	2.5
G25 C31 HS244-1-2 x CML 479	7.8	69	69	247	124	17.3	17.6	4.6	1.3	87.9	14.4	2.7
G25 C31 HS87-2-1 x CML 479	7.7	68	69	245	122	17.4	18.3	4.7	1.2	88.5	14.3	2.5
G25 C31 HS284-2-1 x CML 479	7.7	69	70	250	130	17.2	17.6	4.6	1.2	88.3	14.2	2.5
CML 479 x CML 454	7.5	69	69	241	123	16.4	17.9	4.5	1.2	88.6	13.7	2.6
CML 479 x CML 413	5.8	70	72	243	130	17.2	16.8	4.5	1.2	88.2	13.8	2.7
Trial Mean	**7.1**	**69**	**70**	**244**	**123**	**17.2**	**17.5**	**4.6**	**1.2**	**88.4**	**14.0**	**2.7**
LSD (0.05)	**0.77**	**1.15**	**1.24**	**9.88**	**7.91**	**0.99**	**0.77**	**0.14**	**0.05**	**0.02**	**0.53**	**0.29**
CV (%)	**5.57**	**0.85**	**0.91**	**2.07**	**3.28**	**2.93**	**2.24**	**1.50**	**2.04**	**1.35**	**1.93**	**5.56**

*** 1 for the best - 5 for the poor**

Least significant difference for comparisons between entry means for each trait.

Coefficient of variation

YLD-yield, AN-anthesis, SI-silking, PH-plant height, EH-ear height, MO-moisture, EL-ear length, ED-ear diameter

KL-kernel length, KWD-kernel width, KRN-kernel row number and EQ-ear quality.

Table 2. The testcross performance of best 20% of the entries of the trial G26 with CML451 as a tester at six Mexican locations in 2003-2004. The trial included S2 lines developed from the breeding crosses of Caribbean landrace accessions and Pool 26C_{31}, and single crosses among CML lines as checks.

Testcrosses and single crosses	**YLD** (ton/ha)	**AN** (Days)	**SI** (Days)	**PH** (cm)	**EH** (cm)	**MO** (%)	**EL** (cm)	**ED** (cm)	**KL** (cm)	**KWD** (mm)	**KRN**	**EQ** (1-5*)
(TrinGp1/G26C_{31}/G26C_{31}) -146-3-2-3 x CML 451	8.4	71	71	235	122	17.2	18.1	4.8	1.3	92.2	14.5	2.5
[(Snlp105xCML287)xCL-02450]-55-1-1 x CML 451	8.4	72	73	244	122	17.8	18.5	4.8	1.2	91.0	14.7	2.5
[(Snlp105xCML287)/CL-02450]-68-1-2 x CML 451	8.3	71	71	241	126	17.2	18.3	4.8	1.2	91.3	14.5	2.5
CML 287 x CML 451	8.3	71	71	243	122	18.0	18.2	4.7	1.2	90.7	14.4	2.5
[(Cuba91xCML287)/CL-02450]-87-1-2 x CML 451	8.2	70	71	234	120	18.1	17.0	4.9	1.2	92.1	14.4	2.5
G26 C_{31} HS61-1-1 x CML 451	8.2	70	71	243	119	17.5	17.7	4.8	1.3	93.3	14.4	2.5
(Puer1/G26C_{31}/G26C_{31}) -141-2-1-1 x CML 451	8.2	69	70	240	122	17.0	18.2	4.8	1.2	91.8	14.3	2.5
CL-02450 x CML 451	8.1	70	72	230	117	18.0	17.1	4.9	1.2	90.7	14.8	2.5
CML 479 x CML 451	7.9	69	70	231	113	17.6	17.7	4.7	1.2	89.7	14.5	2.5
Trial Mean	**8.0**	**70**	**71**	**238**	**119**	**17.6**	**17.7**	**4.8**	**1.2**	**91.2**	**14.5**	**2.5**
LSD (0.05) □	**0.61**	**1.17**	**1.26**	**9.05**	**7.56**	**1.05**	**0.79**	**0.15**	**0.04**	**0.03**	**0.63**	**0.19**
CV (%) □	**3.84**	**0.85**	**0.90**	**1.94**	**3.24**	**3.04**	**2.29**	**1.56**	**1.64**	**1.66**	**2.22**	**3.80**

*** 1 for the best - 5 for the poor**

□□ Least significant difference for comparisons between entry means for each trait.

□□ Coefficient of variation

Agronomic traits: YLD-yield, AN-anthesis, SI-silking, PH-plant height, EH-ear height, MO-moisture, EL-ear length, ED-ear diameter KL-kernel length, KWD-kernel width, KRN-kernel row number and EQ-ear quality.

[B] CRIL activities within
GREU PROJECT 1: DISCOVERY (P1) [INFORMATICS]

Establishment of the Crop Research Informatics Lab	**Jonathan Crouch, Graham McLaren, Guy Davenport, Jose Crossa, Jens Riis, Jiankang Wang**

Highlights and Plans

1. Inauguration of the IRRI-CIMMYT Alliance Program on Crop Research Informatics and opening of then CIMMYT CRIL Laboratory
2. Development and signature of the MOA between IRRI and CIMMYT establishing the CRIL Alliance Program
3. Appointment of the Head of the CRIL Alliance Program
4. Collaboration on development of methodology for analysis of GxE in crop multi-environment trials.
5. Investigation of transfer of Wheat information from IWIS to an ICIS based system. Historical evaluation data from International wheat Nurseries was successfully transferred and a new program is being developed to update wheat genealogy information and ultimately merge the IWIS pedigree management system with the ICSI genealogy management system.
6. Review of features of the Maize breeders' workbook system. Test transfer of genealogy information from the maize workbook to ICIS GMS and development of a strategy to merge the workbook with an ICIS local database.
7. On-going collaboration on commissioned work for the Generation Challenge Program especially in the areas of Domain Modeling and Platform Implementation. Prototype platform components ready for demonstration at the GCP meetings in Pretoria in March.
8. Progress on defining the project for institutional management of primary research data for secondary use. Dr Thomas Metz has been identified to lead this project from IRRI and staff will need to be identified to initiate activities in CIMMYT programs.
9. Development of a project proposal on *An Integrated Approach to Identifying New Genetic variation for Breeding Durable Resistance to Rusts in Wheat* by Guy Davenport for possible funding through the CGIAR-Canada Linkage Fund for 2005-2006.

GCP Bioinformatics and Genomic Database Tools

Guy Davenport

We have developed version 2 of the finger-printing database that includes new data from the GCP funding projects and a number of new features. These new features include

- Generate Error Report for and between studies
- Query data by allele, genotype, marker and study
- Export a study into the GCP Template format
- Merge two studies
- Delete a study, which is useful for maintaining subsets of the data in different databases

Future development and integration with other CIMMYT and CRIL database systems in hampered by the use of Microsoft Access DBMS as the underlying database and user interface. We have just started in the context of the GCP informatics platform and the CRIL to develop a new version of this database that will allow the following improvements by separating the user interface from underlying database

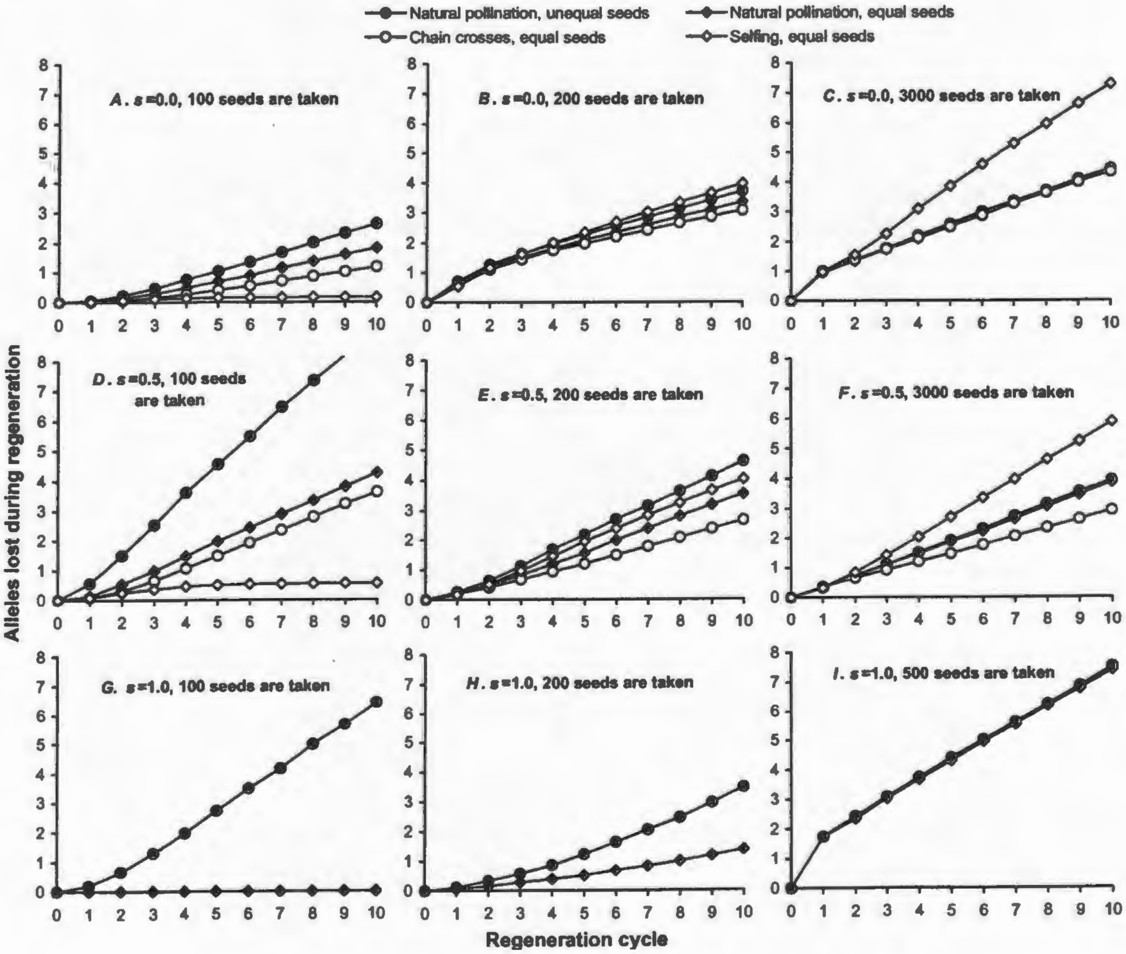
a. This will allow several DBMS to be used with the exactly the same user interface.
b. Provide scalability from single user desktop to multiple user server versions
c. Integration with other systems, e.g. Genebank management system, ICIS, microarray databases, LIMS, CMTV and other data sources, analysis and visualization tools being developed within the GCP

Development of new models for core germplasm selection

Jose Crossa and Jiankang Wang

Computational models were developed for efficient regeneration strategies. Alleles lost during several regenerations were quantified. Article published in Crop Science received an award in 2005.

Different regeneration strategies in maize depending if the crop is 100 allogamous s=0.00 of 100% self pollinated s=1 (Vertical axis – alleles lost. Horizontal axis – regeneration cycles).



Develop population genetic models for efficient regeneration and collection of genetic resources

Jose Crossa

[C] GRP OUTPUT 3 activities within GREU PROJECT 1: DISCOVERY (P1) [TRAINING AND CAPACITY BUILDING]

GCP Training Courses and Visiting Scientists	Marilyn Warburton and Susanne Dreisigacker

The diversity group organized two training courses this year within the GCP project "Characterization of genetic diversity of maize populations: Documenting global maize migration from the center of origin". The first workshop was the introductory meeting, held in Nairobi, Kenya, April 4 – 6, 2005. Here, participants learned about the characterization of heterogenous populations via bulked samples, and an introduction to association analyses. Hands on work include DNA extraction and computer demonstrations. The second workshop was held in Beijing, China, December 5 – 9, 2005. Participants practiced PCR, gel loading and running, and data analyses of the bulked samples. In addition, participants learned about collections and factors affecting diversity of maize in each participating country, and advanced statistical analyses of genetic diversity. The diversity project also hosted several NARs scientists in the GCP project to learn laboratory techniques. Dr. Chaba Jampatong from the National Corn and Sorghum Research Center, Nakhon Ratchasima, Ms. Genying Li from CAAS, and Dr. Chuan-Xiao Xie from CAAS spent between 1 and 5 months at CIMMYT in Mexico. Finally, a workshop was organized for the GCP on October, 3 – 21, 2005 in Santiago de Chile. The goal of this workshop is to provide both conceptual and hands-on training in the use of plant genetic diversity and molecular marker assisted breeding. Emphasis will be on practical applied usage and improving the links between plant breeding, germplasm management and utilization, and molecular biology methods, with a particular focus on the use of microsatellite markers. There were 25 students from 8 countries and 8 presenters. Course reviews were very favorable.

Overview of GRP 2005 Training and Capacity Building

Genetic Resources IRS staff - Conferences, Workshops, Symposiums and Courses during 2005

Name	Title	Dates	Place
Bencivenni, Christelle	Interdrought II Conference	Sep 22 - Oct 3	Rome, Italy
Ban, Tomohiro	4th Canadian Workshop on FHB	Oct 31 - 4	Canada
	7th International Wheat Conference	Nov 24 - Dec 2	Mar de Plata, Argentina
	2005 National Fusarium Head Blight Forum in Winsconsin USA	Dec 10 - 13	Winsconsin USA
Crossa, Jose	ECP/GR Workshop on conservation, management and regeneration of Grain Legume.	Sep 20 -24	Valladolid, Spain
Crouch, Jonathan	US-EC Task Force Workshop	June 19 -23	Washington, D.C.
	Interdrought II Conference	Sep 24 - 28	Rome, Italy
	Science Council meeting: Genomics Research in the CGIAR	Oct 03 - 04	Rome, Italy
	NIAB - Diversity for Breeding Symposium	Dec 12 - 16	Cambridge, UK
Davenport, Guy	Plant and Animal Genome XIII Conference	Jan 15 -19	San Diego, CA
	GCP SP4 Workshop	Feb 14- 18	Wageningen, Netherlands
	ICIS 2005 Developers Workshop	Feb 21 - 25	Roermund, Netherlands
	GCP SP4 Workshop	May 11 - 20	IRRI, Philippines
	Eclipse RCP Software training course	Jun 22 - 13	CIP, Peru
	GCP SP4 Workshop	Aug 13 - 20	Vancouver, Canada
	Interdrought II Conference	Sep 24 - 28	Rome, Italy
	GCP ARM	Sep 29 - Oct 1	Rome, Italy
	1st International Biocurator Meeting	Dec 07 - 14	San Francisco, CA
Dreisigacker, Susanne	Maize Population Diversity Workshop	Dec 02 - 14	Beijing, China
Kishii, Masahiro	5th International Triticeae Symposium	Jun 05 - 10	Prague, Czech Rep.
	2005 National Fusarium Head Blight Forum	Dec 10 - 13	Winsconsin, USA
Lewis, Janet	7th International Wheat Conference	Nov 24 - Dec 2	Mar de Plata, Argentina
	2005 National Fusarium Head Blight Forum in Winsconsin, USA	Dec 10 - 13	Winsconsin USA

Genetic Resources IRS staff - Conferences, Workshops, Symposiums and Courses during 2005

Name	Title	Dates	Place
Bencivenni, Christelle	Interdrought II Conference	Sep 22 - Oct 3	Rome, Italy
Murakami, Jiro	2005 National Fusarium Head Blight Forum in Winsconsin, USA	Dec 10 - 13	Winsconsin USA
Payne, Thomas	European Wheat Aneuploid Conference	Jun 28 - Jul 02	Prague, Czech Rep.
	Iranian National Cereal Meeting	Set 11- Set 18	Iran
	GRIN genebank management software	Set 26-27	USA
	Harvest plus meeting (Tom Payne's attendance was cancelled)	Oct 07- 19	Beijing, China
	7th. Intl. Wheat Meeting	Nov. 25-30	Argentina
Pellegrineschi, Alessandro	VI Simposio Nacional REDBIO 2005 (June 5 - 10)	June 05 - 10	Buenos Aires, Argentina
Ribaut, Jean-Marcel	Interdrought II Conference	Sep 24 - 28	Rome, Italy
Sawkins Mark	Interdrought II Conference	Sep 24 - 28	Rome, Italy
	GCP Workshop	Nov 04 - 14	Nairobi, Kenya
Taba, Suketoshi	Taller de conservación de Recursos Genéticos	Jul 11 - 13	Morelia
	MIG meetings	Oct 09 - 17	Addis Ababa, Ethiopia
	SIRGEALC	Nov 19 - 26	Uruguay
	ASTA	Dec 06 - 10	Chicago, Illinois
Tiessen, Axel	Interdrought II Conference	Sep 24 - 28	Rome, Italy
Warburton, Marilyn	Generation Challenge Program, SP1 Competitive Project Workshop	Mar 30 - Apr 08	Nairobi, Kenya
	Plant Genetic Diversity and Molecular Marker Assisted Breeding	3-22 October	Santiago, Chile
	Maize Population Diversity Workshop	Dec 2 - 12	Beijing, China

GRP 2005 Output Highlights within GREU Project 2 Areas

[D] GRP OUTPUT 2 activities within GREU PROJECT 2: TOOLS (P2)

	Maize drought consensus map	Yunbi Xu [Mark Sawkins, Jean-Marcel Ribaut]

	Association genetics for drought tolerance	Marilyn Warburton [Mark Sawkins, Jean-Marcel Ribaut]

It was agreed that a postdoctoral researcher would be hired as soon as possible to work on the project for two years. Part of that time would be based at Cornell's IGD and part at CIMMYT, Mexico (see attached work plan). Sufficient funds remain in the account for the salary and benefits, but probably a no-cost extension would have to be asked on the project.

A list of 340 possible drought related candidate genes was generated using past drought QTL and expression studies and comparative analyses of drought responsive genes from other organisms (primarily rice and Arabidopsis). This list was narrowed to approximately 40 of the highest priority genes (those most likely to affect a measurable phenotype), from which 50 separate amplicons will be tested to generate SNPs (for very long genes or duplicated genes, two amplicons may be needed to increase the chances of finding a viable association). SNPs will be generated during the summer of 2006.

384 inbred lines from the 400 that are being extensively phenotyped under drought and well watered conditions were chosen and DNA isolated from them. These will be analyzed first with neutral markers to determine their population structure, and then with the 50 candidate gene SNPs. In addition, SNPs from 62 other drought candidates from the list of 340 will be run, as these SNPs have already been discovered at Cornell and released for use in this project. The total of 112 candidate genes is considerably higher than what was originally proposed, and greatly increases the probability of finding genes that significantly affect the performance of maize plants under drought conditions.

Developments in apomixis research

Enrico Perotti

Objective: to engineer adventitious embryony in cereals by over-expressing in ovules genes inducing embryogenesis.

Milestones:

Identify gene systems for conditioning asexual reproduction (apomixis) in cereals.
Nucellar/ovule-specific and inducible promoters identified by 2005.

Achievements: To drive ovule specific expression, the first requirement is the isolation of ovule-specific promoters. A preliminary screen for genes highly expressed in female sexual organs provided us with a promoter driving transcription in the ovules of the model plant *Arabidopsis*. This promoter is being used to ectopically express candidate embryogenesis triggering genes in the ovules. The tissue specific expression of this promoter is presently being tested in rice. Moreover, RNA profiling has permitted the isolation of another rice promoter that appears to be expressed mainly in ovaries. This promoter has been cloned upstream of the GUS marker and the tissue specific expression is currently being monitored in rice.

Some other achievements of the apomixis project in 2005 (CIMMYT, IRD, Limagrain, Pioneer, Syngenta)

A) Characterization of apomixis in a wild relative of maize, *Tripsacum*. Apomixis appears to be the result of a heterochronic deregulation of sexual reproduction.
B) Isolated the *Elongate* 1 gene in maize. Knock out mutants produce unreduced female gametes which is the first step in gametophytic apomixis. The isolation of this gene may be critical for the assembly of gametophytic apomixis in maize.
C) Demonstrated that the induction of embryogenesis in maize does not require *de novo* transcription. As in animals, early embryo development in plants only depends on maternal transcripts present in the egg prior to fertilization.

Establishment of Global FHB Initiative | Tomohiro Ban, Janet Lewis, Jiro Murakami

This effort is led by Tomohiro Ban, adjunct senior scientist from the Japan International Research Center for Agriculture Sciences (JIRCAS) and the FHB team at CIMMYT-Mexico. Useful resistance genes and good cutting-edge methods with DNA markers may be identified and developed during the screening of germplasm. The effects of genotype x environment x *Fusarium* isolate interactions can also be investigated for further understanding and developing integrated pest management approaches.

Sources of resistance to the disease have been elusive. Researchers have never found an accession of wheat, barley, or their wild relatives that is completely immune to FHB. This project aims to acquire potentially novel sources of resistance from global hotspots through our widespread contacts, particularly to control mycotoxin accumulation in wheat grains. We aim to increase FHB resistance using three approaches: (1) acquisition of novel resistance; (2) screening transgressive segregates combining different resistance genes; and (3) evaluation of advanced, adapted materials with multiple-disease resistance.

An alternative way to diversify FHB resistance is to find and utilize resistance source from CIMMYT's gene bank, including wild relatives and ancestral species. We have observed that the FHB spreading resistance of *T. monococcum* ranges from 9.4% to 45.7%, and is higher than that of durum wheat. CIMMYT has produced more than 200 lines of synthetic wheat of the A and B genomes (genome composition: = AAAABB and AABBBB), and there are several resistance candidates where the FHB spreading resistance scores are as low as 9.5%. A total of 7,088 hexaploid wheats (AABBDD)—including 4,532 breeding lines, 1,014 synthetic wheat lines from durum wheat (AABB) x *Aegilops tauschii* (DD) crosses, 571 landraces, and 924 research lines—were screened at CIMMYT's Toluca station using artificial inoculation with 7 *Fusarium* isolates. Of these materials, 1,076 advanced breeding materials and five research populations (666 lines) were screened under natural infection on-farm in Patzcuaro, Mexico. The most promising, resistant lines were assembled the 10th International Scab Resistant Screening Nursery and distributed to 62 participants around the wold.

The challenges and specific activities are based on the new paradigm which arose from the JIRCAS Workshop held in February 2004 in Tsukuba (Ban, 2004). The concept of the Global Fusarium Initiative was proposed and accepted at the 2nd International Symposium on Fusarium Head Blight, incorporating the 8th European Fusarium Seminar, 11-15 December 2004, Florida USA (Van Ginkel and Ban, 2004). A new global collaboration for consensus QTL mapping of FHB resistance in wheat, involving the world's most advanced FHB researchers, will be one of the activities. This initiative will encourage communication and cooperation among individuals, institutions and governments focusing on this disease.

CIMMYT's role in the Global Fusarium Initiative is to provide a platform for international collaboration on *Fusarium* research, and facilitate information exchange, germplasm enhancement and the development of breeding methods and materials globally. This Global Fusarium Initiative will encourage communication and cooperation among individuals, institutions and governments focusing on this disease. Specific activities will be linked using a web site and on-site forums (http://www.fusarium-net.org). Global Genotype x Environmental meta-data compilation, updated global information, and the development of a global crop information system on FHB data will be features of this web site. We are leading a new paradigm for international cooperation and collaborative research to combat the disease, which will contribute to the reduction of poverty and hunger world-wide.

Characterization of slow rusting resistance in wheat | Manilal William and Gary Rosewarne

Wheat molecular breeding (including decentralizing the infrastructure)

Manilal William

CIMMYT's Current capacity for molecular breeding involve the use of approximately 20 markers, of which 8 are being used routinely on large scale marker assisted selection procedures. Most of the markers currently in use extensively are for root related traits such as cereal cyst nematode resistance (Cre1 and Cre3), root lesion nematode (*Rlnn1*), Boron tolerance (*Bo-1*). These are traits for which efficient screening is not possible with existing infrastructure. Having a robust root system is important in wheat, specially in marginal environments where water availability is less than optimum.

Other markers in use are for traits such as fusarium head scab (Sumai 3 derived resistance), barley yellow dwarf virus resistance and rust resistance. These traits are of low heritability with significant environmental influence. In addition, we have validated several markers for Hessian Fly resistance and Russian wheat aphid resistance and have initiated crosses between the sources of resistance and elite germplasm from Morocco in order to introgress these resistances to elite locally adapted cultivars using MAS approaches. Furthermore, several other markers for some quality parameters such as grain hardness (Pin genes), granule bound starch synthase (GBSS-Null), Glu1B over-expression etc. have been validated. In addition, several genes that confer resistance to stem rust have been validated and optimized and crosses initiated with germplasm from Kenya and Morocco. Another set of markers that have been recently validated and optimized are for a set of race specific genes that confer resistance to stem rust. There are genes such as *Sr24, Sr26, Sr38* & *Sr39* that are effective against the new virulent stem rust race. These markers have been optimized and crosses initiated to combine them in CIMMYT wheats as well as in material obtained from Kenya. Segregating populations will be screened with markers to facilitate the advancement of progenies containing the desirable alleles of the genes in question.

In our in-house molecular breeding efforts, early generations such as F2 or F1Top crosses are utilized for MAS assays. This is done with the objective of increasing the frequency of favorable alleles in segregating populations. In order to keep the numbers manageable, we avoid MAS assays for subsequent generations and finally advanced material is screened again to confirm the presence of the markers in fixed lines.

In wheat, the research efforts included characterization of slow rusting genes that confer durable resistance to leaf and stripe rust as well as application of markers in wheat improvement efforts. Bulked segregant analysis and partial linkage mapping continued in several mapping populations in order to identify the genomic regions associated with slow rusting resistance as well as to saturate these regions with markers.

Populations Used:
Avocet x Pavon76 – 146 F6 lines
Avocet x Parula – 141 F6 lines
Avocet x Tonichi – 144 F6 lines

Multiple regions of the wheat genome associated with slow rusting responses have been identified. In Avocet x Pavon76 population, a total of five loci were identified of which three had common effects on leaf and stripe rust jointly. The loci identified are located on chromosomes 1BL (*Lr46/Yr29*), 3BS (*Yr30*), 6BL, 4BL and 6AL. In Avocet x Parula population, a total of four loci have been identified on chromosomes 1BL (*Lr46/Yr29*), 3B (*Yr30*), 7BL and 7DS (*Lr34/Yr18*). Refining the loci identified in Avocet x Tonichi population is underway.

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(Sumai 3 derived resistance), barley yellow dwarf virus resistance and rust resistance. In addition, we have validated several markers for Hessian Fly resistance and Russian wheat aphid resistance and have initiated crosses between the sources of resistance and elite germplasm from Morocco in order to introgress these resistances to elite locally adapted cultivars using MAS approaches. Furthermore, several other markers for some quality parameters such as grain hardness (Pin genes), granule bound starch synthase (GBSS-Null), Glu1B over-expression etc. have been validated. In addition, several genes that confer resistance to stem rust have been validated and optimized and crosses initiated with germplasm from Kenya and Morocco.

In out In-house molecular breeding efforts, early generations such as F2 or F1Top crosses are utilized for MAS assays. This is done with the objective of increasing the frequency of favorable alleles in segregating populations. In order to keep the numbers manageable, we avoid MAS assays for subsequent generations and finally advanced material is screened again to confirm the presence of the markers in fixed lines.

Gene/Trait	**Type of marker**	**Gene**	**Source**	**Routinely Used**	**Optimized**	**Under Optimization**
CCN	STS	Cre1	AUS(MTA)	*		
CCN	STS/SSR	Cre3	AUS (MTA)	*		
BYDV	STS/SSR	BDV2	Public/CIMMYT	*		
Scab	SSR	Sum-3	Public/CIMMYT	*		
Crown rot	SSR	2.49	Mark Sutherland/Aus	*		
Root lesion nem	STS	Rlnn-1	semi-public	*		
Boron tolerance	SSR	Bo-1	Public/AUS	*		
Phairing homolog	STS	ph1b	Public	*		
Multiple rusts	STS	VPM	Public	*		
Quality	SSR	GBSS-null	Public		*	
Quality	SSR	Gardness	Public		*	
Quality	STS	Glu1BX	Public		*	
High Protein	SCAR	HGP	Public			*
Agronomic Traits	STS	Rht1	Public		*	
	STS	Rht2	Public		*	
	SSR	Rht8	Public			*
	SSR	PHS	Public			*
	SSR	LMA	??			*
Insect Resistance	SSR	Dn2	Public		*	
	SSR	Dn4	Public			*
	SSR	H25	Public			*
Rust Resistance	STM/SSR	Sr2	Public			*
	STS	Sr24	Public		*	
	STS/SSR	Sr26	Public		*	
	SSR	Sr38	Public		*	
	SSR	Sr39	Public		*	
	STS	*Lr19*	Public		*	
	STS	*Lr25*	Public			*
	STS	*Lr29*	Public			*
	STS	*Lr37*	Public			*
	STS	*Lr47*	Public			*
	STS	Lr34	CSIRO/AUS		*	
	SSRs	Lr46	CIMMYT			*

[E] CRIL activities within GREU PROJECT 2: TOOLS (P2)

	Molecular breeding simulation tools		**Jiankang Wang**

The genetics and breeding simulation tool QuCim has been maintained and updated properly in 2005. QuCim in the current status can simulate almost all breeding activities in our wheat breeding program, including male master selection, female master selection, parental selection, single cross, backcross, top cross, double cross, doubled haploid, marker-assisted selection etc. QuCim can simulate not only CIMMYT's wheat breeding program but also in principle any other breeding programs for selecting inbred lines, which means all major food cereals in the world, plus basically all leguminous crops. It can also be used when inbred lines are developed that later are to be used in hybrids, such as in the case of maize. Hence its potential to increase breeding effectiveness encompasses all CGIAR mandated crops.

A new functionality called Plug-In has been added to QU-GENE module QuCim so that the physiological model can be implemented through the linkage between QuCim and a crop growth model. We are currently modifying the simulation module QuCim so that the simulation model and physiological model can communicate with each other. A physiological model on leaf elongation rate in maize is under development as an example physiological model.

A case study on efficient use of marker-based selection in wheat has been completed. In total, 9 marker-linked genes were considered in the case study and three parents were used, i.e., Sunstate, Silverstar/TIN, and HM14BS. The best strategies using marker based selection in genotype building for a top cross among the three parents have been identified. A draft research paper has been prepared on the work described above.

As the number of published genes and QTL for various traits continues to increase, the challenge for plant breeders is to determine how to best utilize these in the improvement of crop performance. Through a case study with chromosome segment substitution lines, we found QuCim can also use the QTL mapping results and identify the best crossing and selection strategy before conducting field experiment, and therefore can help breeders integrate the knowledge from genomics and molecular biology into their breeding programs. A draft research paper has been prepared on this work.

Statistical model for predicting breeding values with emphasis on genotype x environment interaction

Jose Crossa and Graham McLaren

We have developed statistical models for assessing genotype x environment interaction of multi environments trials using information on the coefficient of parentage matrix. This assesses the additive part of the variability but also understanding the impact of the additive par on the additive x environment interaction component. Results show that the models work very well and more precise estimates of yield performance can be obtained. Breeders must benefit for obtaining precise estimate for selecting parents for crosses.

New selection index for breeding and marker assisted selection (MAS) using molecular marker

Jose Crossa

New selection index based on principal component analysis was developed. The research is a theoretical and it shows the statistical properties of the estimators. The new approach allows to compute the response to selection as well as to predict future selection gains in future selection cycles.

The index does not utilize economics weights which is an advantage because it only relies in objectives estimators.

New statistical and bioinformatics tools for understanding G-by-E in plant breeding

Guy Davenport and Jose Crossa

Agrobacterium transformation system for wheat

[F] GRP OUTPUT 3 activities within GREU PROJECT 2: TOOLS (P2) [TRAINING AND CAPACITY BUILDING]

AMBIONET impact assessment	Luz George

CIMMYT develops key information and inputs – specialized breeding materials and methods –that enable the development of new maize and wheat varieties more rapidly and effectively. These find application in the breeding programs, within CIMMYT and in the national programs in developing countries. Serving as a facilitator for enabling the use of these technologies in national programs, the Asian Maize Biotechnology Network (AMBIONET), a network of maize scientists from six Asian countries (China, India, Indonesia, Philippines, Thailand and Vietnam) was established in 1998 by CIMMYT. The network, funded through two phases (1998-2005) by the Asian Development Bank, aimed to strengthen the national program research capacity in maize molecular breeding. The research/breeding work towards the improvement of locally preferred maize varieties was done in the national programs in collaboration with CIMMYT, which contributes training, information, germplasm, and scientific and technical backstopping.

AMBIONET activities focused on creating markers for those traits where MAS offered greatest advantage but where markers are not yet available. Under AMBIONET collaboration, four QTL maps for downy mildew (DM) resistance were constructed as a region-wide effort and by individual national program in India, the Philippines, and Thailand. QTLs maps for resistance to other diseases– two for sugar cane mosaic virus (SCMV), one for head smut, and one for banded leaf and sheath blight were also made by national programs in China. Disease resistance has been transferred through MAS to local lines in India for DM and in China for SCMV. The network also supported the practical use of diversity information to guide the development of superior crosses as well as the formation of synthetics.

An impact assessment of AMBIONET (Pray, 2006) concludes that maize research in Asia has been strengthened, particularly in China, India and Indonesia. Much of the AMBIONET research is focused on small farmer problems. Although farmers are just starting to benefit from AMBIONET research, the size of the benefits is difficult to predict, although these benefits will probably greatly exceed AMBIONET expenditures. Using numbers from farmer surveys substantiated by expert opinion and experiment station data, the impact study projected the benefits from some technologies in a few countries. As an example, the adoption of downy mildew resistant varieties in Southeast Asia and virus resistant hybrids in China could easily pay for the costs of AMBIONET in a few years and give very high rates of return to the investment in research. CIMMYT has also gained knowledge about Asian maize germplasm, and knowledge and molecular markers for important diseases.

Launch of Cereal Molecular Breeding Communities of Practice

Jonathan Crouch and Luz George

Progress in molecular breeding research has enhanced plant breeding in a number of ways. Not only is the time to develop a new variety significantly reduced, breeders can now more effectively and directly control the alleles to be selected and can improve traits that were not possible using traditional phenotypic screening. Molecular marker analysis is now a relatively routine component of many modern breeding programs, having reached significant efficiencies of scale particularly in the private sector. Most public sector breeding programs, however, have been slow to adopt the use of marker technologies. This is partly due to a dichotomy between plant breeders and molecular biologists in the public sector and the relatively high unit costs of genotyping. The GCP and its Molecular Breeding Communities of Practice (MB-CoP), propose to address both constraints.

Trends in the application of molecular tools and techniques have important implications for molecular plant breeding in the future. Continual improvement in the capability of labs to generate molecular data has come through the development of new types of markers allowing increasing automation. However, this has tended to come with the negative consequence of an increase in the cost of equipment required to achieve high-throughput low-cost genotyping and in turn, the capacity to see molecular genotyping achieve impacts at the scale of modern plant breeding programs. In advanced labs and in animal and human research, this has led to an increased tendency towards centralization and in particular, a shift to an out-sourcing mode of operation. We expect the same trends to follow in public sector plant science and breeding, and in tropical agricultural research and development. Moreover, we believe that "Molecular Breeding Communities of Practice" are an effective mechanism to assist the ultimate clients of the GCP to most rapidly and effectively move to the optimum operational structure for their genotyping needs. Indeed, the increase in commercial enterprises for human diagnostic genotyping services for example, has also been associated with the growing number and strength of associations and consortia focusing on improvements in methodologies, quality control and cooperative research activities. Examples of emerging consortia of this type in plants are the Rice Functional Genomics Consortium (www.iris.irri.org/IRFGC), the Maize Genetics Cooperative (http://w3.ag.uiuc.edu/maize-coop/mgc-info.html), and Promusa (www.promusa.org), among others. In some cases, a large proportion of members are from the private sector, yet they still see good added value from sharing their advances and contributing to cooperating research projects. If well coordinated and properly funded, the MB-CoP can become an equally powerful force for the evolution and impact of plant genomics for tropical crop improvement.

Several crop-specific biotechnology networks have been established in Asia, Africa and Latin America during the 1980's and 1990's (Appendix 1). Many of these covered a wide range of activities including upstream research and capacity building. Unfortunately, in some cases major donors have pulled out from further funding of such networks. However, all these networks still present an excellent basis for the development of GCP MB-CoP that can be used to validate, refine and apply new GCP technologies in national breeding programs. Conversely in other crops, conventional breeding networks have sufficiently matured to become prime candidates for the introduction of marker-assisted selection systems and other molecular breeding approaches. However, many of these breeding programs are not receiving international development assistance or are significantly under-funded, which seriously threatens their long-term impact. Thus, the GCP will provide seed funds for the MB-CoP that will evolve from former crop-specific biotech networks or through the molecularization of strong conventional breeding networks. In so doing, we hope to bring the concept back into the priorities of major donors and thereby leverage substantial funds for scaling the concept up and out. This catalytic role of seed funds from the GCP will be vital part of the strategy; its eventual success is indicated by the fact that cumulative/cooperative fund raising is already a reality (see Appendix 2 for example of funds leveraged by AMBIONET NARS).

Significant investments in infrastructure and human resource development by national programs and international funding agencies have resulted in a skilled cadre of national research scientists, but there is now an urgent need to maintain momentum. Modest support of key players in networks such as the Rockefeller Foundation Rice Biotechnology Program, and the Asia Rice Biotechnology Network (ARBN) and Asian Maize Biotechnology Network (AMBIONET) in Asia, will allow a decade or more of investment to be turned to the benefit of the GCP product development and delivery pipeline. Similarly, this decade of experience with cereal molecular breeding in Asia can be readily translated for the benefit of a range of crops in Latin America and Africa. Thus, it is the intention of the GCP MB-CoP to generate cooperative activities that bridge across crops and regions.

The GCP will impact on future plant breeding by providing the technologies and tools for breeders to utilize DNA markers in their selection strategies and to access new genetic diversity. At its first meeting, the GCP Stakeholder Committee (Minutes of the GCP Stakeholder Committee meeting, 29-30 November 2004, Rome, Italy) called attention to the important role of plant breeders, with an appeal to fully include them in GCP activities to ensure that the outputs and products are relevant, and will benefit farmers and consumers in developing countries. It has been difficult to achieve this through diverse research projects funded by the competitive and commissioned grants processes. Thus, SP3 wishes to approach this in a different way, and prove the concept that this can be achieved through fostering MB-CoP's.

	Establishing regional marker labs	

Progress in the implementation of EPRM and CCER recommendations

Recommendations and suggestions from the text (related to GREU activities)

If the BoT consider the above approach as valuable then a similar process will be followed in 2006 for the 2004 maize and wheat CCERs.

Defining Vision Statement from the Executive Summary

The changes in the external environment include the "gene revolution" in molecular genetics and genomics, the controversy surrounding the development and release of genetically modified organisms (GMOs), the "IT revolution" in information sciences and bioinformatics, growing private investment in plant breeding of non-hybrid crops, the changing intellectual property environment the evolution of the CGIAR including the continuing shift in funding from unrestricted to restricted and introduction of Challenge Programmes. Clearly, CIMMYT is a Centre in transition – reforming and reshaping itself to face a rapidly changing external environment.

Specific Recommendations	GREU-Related Action
The Panel recommends that senior Management and Programme Directors undertake a much more rigorous process to define goals for the new strategy that provide a framework within which to organize projects and activities and against which progress in meeting the goals can be measured. In addition to strengthening the implementation of the new strategy, the process will enable the Programme Directors as a team to identify a set of goals that are congruent across the Centre.	New MTP with time-bound quantitatively verifiable indicators (2005): Pillars of the business plan (2005): (I) HOLISTIC FRAMEWORK (innovation to impact) (II) PRODUCT-DRIVEN (highly focused) (III) TRAIT-BASED TEAMS (inter-disciplinary synergies/added value)
The Panel recommends that the data acquisition, data management and genebank user interface be upgraded in the CIMMYT genebank for both wheat and maize as a matter of urgency.	Implementation of CRISCO workplan (2005) Establishment of IRRI-CIMMYT Informatics Alliance (2005-06)
The Panel recommends that Management review the staff survey results in detail with special attention to staff morale, communication of policies, clarity of goals, performance recognition, and staff evaluation, and take appropriate corrective action as a matter of urgency.	IRS one-on-one [mentoring] discussions NRS group discussions Monthly disciplinary group operations meetings Quarterly program theme meetings Quarterly scientist workplan reviews (QVIs)
The Panel recommends that a full cost recovery/pricing system for support services be implemented to recover the full costs from projects and users of services. This will reduce the pressure on unrestricted funding and make it available for other high priority activities at the Centre, including building the working capital to the required level.	Tlalti field station cost-recovery (2005) Greenhouse cost-recovery (2006) Restructuring of MAS service lab (2005-06) Restructuring the financing of SIDU (2005-06)
The Panel recommends that maize research in CIMMYT identify the high priority Marginal Maize Production Areas (MMPAs) in each mega-environment.	Recruit maize molecular breeder to focus on (2005-06) and develop project proposals in the following areas: Quality traits (including reduced mycotoxins) Non-transgenic host plant insect resistance Fast track breeding techniques (including DH) Management of maize breeding data (with CRIL)

Chapter 1 – Background and Context

Recommendation or Suggestion in the Text	GREU-Related Action
First, the advances in genomics at the more applied end are likely to flow quickly through to crop improvement programmes making greater investment by CIMMYT in areas such as marker assisted selection (MAS), molecular fingerprinting of genebank accessions, transformation technology and gene and trait mapping, a critical priority if CIMMYT is to maintain modern and competitive programmes and assist developing country NARS to access and use these technologies.	Create integrated molecular breeding programs facilitated by the creation of maize and wheat molecular breeder positions Molecular breeding communities of practice (proposal submitted to GCP in 2005)
Second, with respect to gene discovery and more upstream research, CIMMYT is likely to be a very minor player amongst a large field of alternate suppliers in developed countries, especially in maize but increasingly in wheat. Therefore it will need to concentrate its limited resources in those areas that are of priority interest to smallholder farmers and where CIMMYT has a competitive advantage. As a consequence, CIMMYT will need access to the advances made by others to ensure its wheat and maize improvement programmes remain competitive and it will need to develop the relationships and mechanisms that facilitate this access.	Focus on coordination and translation of upstream research through the creation of global trait-based initiatives with an emphasis on rapid progress through alliances and out-sourcing
Third, one of CIMMYT's strong advantages at this time is the maize and wheat genetic resources it holds in trust as these can now be mined much more rapidly than in the past. However, even here there are numerous alternative suppliers, and with synteny, unless CIMMYT moves to make its collections a key asset in the global research effort, it will quickly be replaced by alternatives.	Foster and synergize global networks centered around CIMMYT germplasm – including integrated on-line informatics system – through the creation of core and mini-core collections based on diverse traits, specific trait-targets and molecular fingerprinting (latter already funded by GCP)
Information technology (IT) has also advanced rapidly over the last two decades so that the collection, storage and manipulation of very large data sets are now potentially routine. The capacity to acquire, store and manipulate large bodies of data is critical to cutting edge research in areas such as plant breeding, genetic resources, genomics and geographic information systems (GIS). Hence if CIMMYT is to remain competitive in research in these areas it will need to have up to date capacity in IT.	Use GCP composite and mini-composite germplasm collections as a focus point for global communities. Use CRIL as a focus point for web-enabling genebank to variety selection data

Chapter 1 – Background and Context cont'd

Recommendation or Suggestion in the Text	GREU-Related Action
The Centre as well as the CGIAR System needs to work with developing country institutions to explore new ways of making the technologies poor farmers need available to them.	Create molecular breeding communities of practice including the molecularization of the globally decentralized wheat shuttle breeding systems
Privatization of the breeding of crops that were once exclusively in the public domain is expanding rapidly not only in developed countries but also in a number of the stronger developing countries. With the growth in private investment, public investment is likely to rapidly diminish.	Build alliances with strong developing country NARS – China, India, South Africa, Brazil etc – through molecular breeding communities of practice
Of course, private companies will not invest in variety development for more marginal areas where profits are difficult to generate. In countries and regions that can support a strong seed industry, corporate rather than public breeding programmes are likely to become increasingly important as partners and users of CIMMYT's improved germplasm over the coming decade. In contrast, in marginal areas which cannot support a viable commercial seed industry, government programmes are likely to be replaced by NGOs.	CIMMYT may consider focusing product development on marginal cropping systems CIMMYT needs to give increasing focus to developing improved traits in widely adapted genetic backgrounds GREU needs to focus on developing, validating and implementing new approaches to accessing (from germplasm collections) and manipulating (in breeding programs) targeted genetic variation
It would be expected that a joint gene bank programme would have generated significant efficiencies.	Create a unified genebank (2005) and implement operational efficiencies (2006)
The rationale [of the IRRI-CIMMYT alliance] was the anticipated gains in international agricultural research and development, especially in areas such as genetic resources, genomics, IT, and GIS among others.	Establish CRIL (2005-06), create integrated web-enabled databases and analytical tools (2006-07) and scale-out into a pan-CGIAR informatics unit (2007-08)

Chapter 2 – CIMMYT's New Strategy

Defining Vision Statement
"CIMMYT acts as a catalyst and leader in a global maize and wheat innovation network that serves the poor in developing countries. Drawing on strong science and effective partnerships, we create, share, and use knowledge and technology to increase food security, improve the productivity and profitability of farming systems, and sustain natural resources."

The "mind of the strategy" is described in the plan as a set of initiatives:

- Harnessing maize and wheat genetic diversity for humanity
- Strengthening the global maize and wheat innovation network through policies and institutions, capacity building, and analysis of strategic global issues
- Reducing vulnerability in dryland, stress-prone, food-grain systems by managing risk
- Improving livelihoods and conserving natural resources in tropical agro-ecosystems
- Safeguarding food security in densely populated areas through sustainable intensification
- Increasing food security in Africa through better technology and improved markets

Recommendation or Suggestion in the Text	GREU-Related Action
A particularly acute issue may be assuring staff that the planning process genuinely modelled a change in the organization's culture to a more collaborative and inclusive style of working and was not a one-off exercise. Other problems with the document ...substantial scale and complexity ...rhetorical style ...critical elements difficult to uncover and assess ...jargon and facile language ...substantial gaps ...what was substantively different or new. Absence of goals, priorities, results, leadership and resource allocation.	Annual planning with stakeholders, donors and leading experts Routinely capture of external perspectives through mini-reviews and colloquiums Translate Vision, Strategy and MTP into action plans through the definition of QVIs (translating the business plan into the MTP into the scientist workplans).
Provide a way to target and measure impact.	Impact assessment and cost-benefit analysis of intermediate products (pending)
It appeared to the Panel that for the foreseeable future the new CIMMYT strategy looks like the old strategy with nominally different programmatic "homes."	Increasing focus of core funds on time bound, task force style, flagship programs that are clear pillars of the new vision – for example, CRISCO leading to the establishment of CRIL
There are clear areas within CIMMYT's Programmes where failing to make additional investments quickly will result in the loss of any future strategic value for a Programme or activity.	Focus core investment on primary areas of strategic value and cut losses in other areas

Chapter 3 – Research Accomplishments

Recommendation or Suggestion in the Text	GREU-Related Action
There is a need for a stronger commitment and closer collaboration with the ABC for a steady progress in moving biotechnology into wheat breeding programmes.	Create holistic product-driven trait-based teams and empower maize and wheat molecular breeders plus maize and wheat program breeders to define and review the biotechnology research agenda
The Wheat Programme together with the ABC should make an internal assessment of costs and opportunities of biotechnology for its breeding endeavours, identifying priorities and specifying commitments and timing.	Mini-reviews with Michel Ragot (Syngenta) and Wayne Powell (NIAB) in 2005
More attention has to be devoted to more traditional techniques as production of double haploids in wheat. Based on the use of double haploids that are available and are in use in commercial programmes in developed countries to enhance the rate of production of improved winter wheat cultivars, should be seriously considered for implementation in the IWWIP. Bread wheat haploids should be produced not just for research projects, but at a larger scale for the breeding programmes. Research for production of double haploids in durum wheat is also needed.	Establish a large-scale winter wheat double haploid program in CWANA (pending) Developing proposals for DH research in maize (on-going)
There is no evidence to show whether productivity in the resource poor farming areas of the world has been improved and whether the improvements, if any, could be attributed to the CIMMYT germplasm.	Use molecular fingerprinting in impact assessment to evaluate this critical statement
Most critical is the need for a full-time data manager dedicated to the maize research even under the new programme structure.	Recruit an informatics scientist (with special focus on ICIS migration) under the CRIL initiative (2006)
The ABC was largely supported by special project funds with less than 10% unrestricted funding in recent years.	Establish an institutional strategic commitment to molecular breeding (on-going)
The Biotechnology Group produced some 65 peer reviewed publications during 1999-2004 (Table 3.5), on average 0.6 per researcher annually (1999-2003).	Increase to 2-3 during coming MTP through quantitative targets in all scientist workplans
These include new tools to identify highly heterotic combinations in maize which should improve the efficiency of the breeding process by helping to reduce the number of hybrid combinations that need to be made, and reduce the time taken to identify potential commercial varieties. They also include an increasing number of molecular markers for QTL's controlling stress tolerance, particularly drought tolerance, in both wheat and maize.	Focus on validation, refinement and large-scale application of new technologies to improve germplasm access, utilization and enhancement
It is clear that the demand for marker services in the breeding programmes will quickly exceed the current capacity of the service laboratory. Hence there is an ongoing need to increase the capacity of the laboratory to meet breeders' needs.	Restructure the Service Lab under maize and wheat molecular breeding (research and application) programs (see below for further details)

Chapter 4 – The New Research Programme

Recommendation or Suggestion in the Text	GREU-Related Action
No economic studies are available to underpin the priority setting process or to identify priority traits for germplasm enhancement and gene discovery projects.	Carry out cost-benefit and *ex ante* analysis focused on intermediate products
Amalgamation of the formerly separate wheat and maize collections into one integrated unit. The benefits of a single programme would not only be financial but also political.	Create a unified genebank
The development of a comprehensive data base management system for the integrated genebank to enable global web-based access. The Panel notes that CIMMYT is formally investigating the adoption and implementation of ICIS which, if it were accepted, would bring CIMMYT in line with several other Centres including IRRI. The Panel strongly supports this decision.	Create the CRIL as an ICIS-based crop informatics system in collaboration with IRRI and GCP offering interaction and linkage with a global community of public and private, north and south, research and breeding organizations
Completion of the inventory of the entire wheat collection held by CIMMYT checking seed quantity and viability, and data quality.	Planned for 2006 in coordination with implementation of a bar-coding system
Greater emphasis on maize pre-breeding through development of a breeder's core subset of tropical and subtropical lowland accessions based on field evaluation data. Pre-breeding will broaden the genetic base of the CIMMYT maize genepools for tropical, subtropical and tropical highland climatic conditions.	Create maize and wheat core collections (done through GCP composite and mini-composite collections in 2005-06) targeted core collections for maize and wheat should be created in 2006
More targeted research in maize on in situ on-farm conservation to enhance farmers' varieties. Such work has started by analyzing the intra-racial diversity of the race complexes that are being cultivated by farmers today. The best accessions representing the racial diversity and characteristics required by farmers should be reconstituted and efficiently used.	Refocus EU ear-marked unrestricted core funds on in situ research and germplasm enhancement
A commitment to molecular characterization of the wheat and maize accessions it holds in trust using molecular markers on a priority basis. However, the Panel was of the view that CIMMYT needed to greatly enhance its capacity in high throughput marker technology, either through investment in new technologies or greatly increased investment in established technologies. Unless it does this in the very near future, it will not be able to meet the demands for these services from the genetic resources and breeding research and hence its own Programmes.	Set QVI for application of marker screening and fingerprinting. The wheat molecular breeder commits to half the cost (through partial out-sourcing) and double the throughput of wheat MAS in 2006. The new maize molecular breeder will set similar targets for 2007 based on establishment of validation programs in 2006 and establishment of an effective new platform for genotyping through out-sourcing

Chapter 4 – The New Research Programme cont'd

Recommendation or Suggestion in the Text	GREU-Related Action
CIMMYT will also have to review its need for capacity in bioinformatics, particularly in terms of operational resources.	Build-up capacity through partnerships and alliances (including CRIL)
The Panel noted that the use of molecular markers in maize breeding is lagging behind that in wheat breeding. This is surprising given the high use of molecular markers in private maize breeding programme. The Panel therefore strongly suggests that CIMMYT should establish a working group composed of researchers from the Biotechnology Group and maize breeding to ensure faster application and efficient use of molecular markers in maize breeding.	April review mission with Michel Ragot (Syngenta) and contribution to Science Council Genomics Task Force set the stage for building an alliance with Pioneer and Cornell University to establish an effective high throughput low cost platform for genotyping through out-sourcing
The Panel also noted CIMMYT's commitment to the prevention of the unintended presence of transgenic materials (GMOs) within its genebank accessions through rigorous gene bank management and congratulates the Centre on its comprehensive efforts in this area.	Scale-up of routine GMO testing (2005-07)
Ex ante impact assessment studies cannot be successfully designed and carried out without the effective contribution of breeders, resource conservation, crop management and others specialists, for instance, in the construction of baselines and the identification and description of technology impact pathways. To facilitate the establishment of a multidisciplinary approach to conducting ex ante impact studies, the Panel recommends that increased integration through time allocation be secured between ITA staff and non-social scientists in the other programmes.	Create team for cost-benefit and ex ante analysis of GRP intermediate products (dedicated session on this topic during the Science Forum led to a subsequent commitment to pursue joint fund raising efforts in this area)
CIMMYT still does not have costings for many of the components of its breeding activities.	Incorporate cost-benefit analysis into ongoing molecular breeding simulation projects

It is clear that the demand for marker services in the breeding programmes will quickly exceed the current capacity of the service laboratory. Hence there is an ongoing need to increase the capacity of the laboratory to meet breeders' needs.	Restructure the Service Lab as an MAS Application Research Group Focus critical mass on methodological development, refinement and facilitiated application Make best use of out-sourcing and alliances Foster hubs for molecular breeding communities of practice in Africa and Asia
Marker assisted selection has a key role to play in the future breeding activities of both wheat and maize. It is clear that CIMMYT needs to upgrade its DNA extraction capability and develop a high throughput marker service laboratory dedicated to meeting the needs of wheat and maize breeding as well as the associated research groups in genetic resources.	
An issue for CIMMYT is whether it should be involved in marker development or access markers developed by the many public and private institutions involved in this area of research. The EPMR Panel feels that CIMMYT should leave the development of markers to others and instead focus on their use in the development of germplasm targeted at smallholder farmers except in those rare instances where markers are not available or under development for a particular trait of high priority to CIMMYT.	
CIMMYT also needs to keep a close watching brief on developments in high throughput marker technology. New technologies are on the horizon which would, if they are commercially successful, offer high throughput, low cost (10-20c/data point against current cost of $1-2/data point) molecular marker applications in wheat improvement. Again CIMMYT's prime interest will be the use, rather than the development, of these technologies to enhance its wheat improvement activities once they have been shown to have application.	

1. New Ideas – (a) Strategic Issues

Trait-based teams

Having created a simplified and less obtrusive institutional structure, it is now critically important to establish and empower multidisciplinary teams that can rapidly focus on their respective outputs and products. In some cases, the newly established projects will already naturally provide this vehicle. However, in other cases sub-divisions may be justified (e.g. the global rust and Fusarium initiatives) or project activities across crops would benefit from closer association (e.g. drought tolerance in maize and wheat). Finally, there are a few cases where disciplinary areas will justify the formation of a team structure (e.g. molecular breeding). These teams should be limited in number, output-driven, time-bound, and flexibly structured.

Increasing emphasis on strategic alliances and out-sourcing partnerships

The CGIAR as a whole is becoming less cost competitive in its core areas, ARIs are experiencing this same effect in many areas of biotechnology. Nevertheless, CIMMYT scientists retain a strong competitive edge for understanding the overall context and coordinating contributors from a variety of different positions in the value chain. In turn, this will lead CIMMYT to seek a new niche in data integration, analysis and interpretation associated with a gradual decrease in genomics data generation capacity. Meanwhile, CIMMYT retains a strong comparative advantage for precision phenotyping. The establishment of the IRRI-CIMMYT Alliance Crop Research Informatics Lab is designed to capture synergies and niches in many of these areas.

IRRI-CIMMYT Alliance **Crop Research Informatics Lab**	Microsoft Word Document	Microsoft Word Document
	Microsoft Word Document	Microsoft Word Document

More systemic alliances with strong NARS to leverage their capacity for south-south collaboration

With the changing profile of NARS strength and economic development of some of our tradition partners, CIMMYT is in a unique position to establish regional centers of excellence with India, China, South Africa and Argentina to serve our weak partners in South Asia, Central Asia, East and Southern Africa, and the Southern Cone in addition to (and modeled on) the ongoing relationship with Turkey for West Asia and North Africa.

Ex ante analysis and/or cost-benefit analysis of intermediate products from GREU

As CIMMYT's portfolio increasingly emphasizes this area, there is a critical need to develop methodologies to track our success.

1. New Ideas – (b) Priorities for Funding Raising in New Niche Areas

New computational approaches synergizing between biometrics and bioinformatics

As we build critical mass in computational systems we must strive to create a justifying niche for CIMMYT-IRRI with respect to lead the way in the development of new approaches to data integration and analysis.

Predicting performance of genotypes in agricultural systems using Artificial Neural Networks	Microsoft Word Document	G. Davenport and J. Crossa
Developing computational methods to harness useful biodiversity for genetic resources conservation and germplasm enhancement in CIMMYT	Microsoft Word Document	J. Crossa and G. Davenport

Helping our partners take over more of our traditional niche areas

As we aspire to focus on more upstream activities we must be careful to provide the necessary backstopping environment to ensure that our traditional partners can quickly and effectively pick-up on the activity areas that we are withdrawing from.

Molecular Breeding Communities of Practice	Microsoft Word Document	Microsoft Word Document	Microsoft Word Document
	Microsoft Word Document	Microsoft Word Document	

New tools and methodologies for molecular breeding of complex traits

	Wheat	**Maize**
GCP Proposals	Large-scale mapping of drought tolerance	Large-scale SNP genotyping for germplasm fingerprinting and molecular breeding
	Trait-target development and molecular breeding and of synthetic derivatives	Development of an efficient double haploid protocol for genetic analysis and breeding

2. New Opportunities

Key alliances and Out-sourcing Partnerships

There are many collaborations and networks associated with GREU activities but the following ones are fundamental to our operation - for rapid progress, substantial fund raising from non-traditional sources and significant impact.

GENETIC RESOURCES (P1)

Partner	***Topic***	***Primary contact point***
Cornell University, USA	Maize diversity analysis	Marilyn Warburton
NIAB, England	Wheat germplasm enhancement	Wayne Powell

MOLECULAR BREEDING (P2)

Partner	***Topic***	***Primary contact point***
Pioneer Hybrid International, USA	Maize molecular breeding	Yunbi Xu
MPB-CRC	Wheat molecular breeding (MAS and GMOs)	Manilal William
NIAB, England	Wheat germplasm enhancement	Wayne Powell
CAAS, China	Molecular breeding modeling	Jiankang Wang

RESEARCH INFORMATICS (CRIL)

Partner	***Topic***	***Primary contact point***
IRRI	Research Informatics Lab	Graham McLaren
Wageningen University The Netherlands	QTL mapping and QTLxEnv inetraction	Fred vanEeuwijk
CAAS, China	Molecular breeding modeling	Jiankang Wang

TRAINING AND CAPACITY BUILDING

Partner	***Topic***	***Primary contact point***
AMBIONET	Maize molecular breeding in Asia	Luz George
AMMANET	Maize molecular breeding in Africa	Jedidah Danson
Wheat International Trial Network		Manilal William
GCP Global Cereal Molecular Breeding Communities of Practice		Luz George

Critical Strategic Alliances for Modernizing Maize and Wheat Breeding at CIMMYT

[1] ***Maize molecular breeding***
Founding partners: CIMMYT-Cornell-Pioneer/Syngenta/Limagrain
Donors: GCP and/or Gates Foundation

[2] ***Wheat molecular breeding***
Founding partners: CIMMYT-NIAB-ACPFG
Donors: GCP and/or EU

[3] ***Computational systems for molecular breeding***
Founding partners: CIMMYT-IRRI-[ARI yet to be identified]
Donors: Nordic opportunities

[4] ***Capacity buidling***
Molecular breeding communities of practice
Alliance with NIAB for training modern plant breeders

[A] Nomenclature: "Molecular breeding" in the broadest sense of "Modern breeding" – merging conventional approaches, DH, transgenics, NIRS and other biochemical assays, MAS and computational systems.

[B] Synergies: In each case creating and leading a community of practice to capture north-south, strategic-applied, south-south, MNC-SME, public-private sector synergies.

GRP-GREU ***Infrastructure Building Activities and Plans***

	2005	2006	2007
ABC	Pilot testing outsourcing	Restructure and upgrade processes	Complete major cultural change
Transgenic lab at El Batan	Initiate restructure and upgrade of processes	Complete transition to 100% focus on wheat	Large-scale high throughput Agro-mediated pipeline
Biotech capacity in the regions	Luz and Jedidah	Build maize transgenics group in BECA	Establish maize and wheat transgenic capacity in Asia
Glasshouses		Initiate cost recovery	Reach complete cost recovery
Tlalti	Initiate cost recovery (50% of > $300K)	Major upgrade	Reach complete cost recovery
Seed Health & Distribution	Debt recovery ($500K)	Reach routine GMO testing targets	
Genebanks		Initiate combined operations for increased efficiency	Complete unification of the genebanks
CRIL	Establish CIMMYT unit	Unify IRRI-CIMMYT units	Expand to include one other institution

3. Emerging concerns

Creating an institutional culture capable of operationalizing the business plan

As with all institutional change initiatives in the CGIAR, we are always in danger of repacking business as usual in a new range of boxes. The institutional structure needs to be sufficiently confident to set the agenda and monitoring system and get out the way and let the scientists get on with the job. Equally the institutional practices/norms need to be reframed in a way that will empower those product-driven teams and not constrain them. To a certain extent the state of the breeding programs and the structure of the projects for wheat are already moving in this direction. The transition will be more complex for maize but once achieved will have greater impact. Probably the greatest challenge in culture change is to facilitate a change from the perception of the enemy within to the enemy outside – the sense that there is more to gain from working together (or more to the point more to lose if we do not do so) – the creation of a common vision of a single product (improved maize or wheat production) remains a substantial challenge.

Initiating a transition away from finished products/towards technology-assisted germplasm enhancement

The business plan calls for a radical new way of working which if successful should leverage additional funds from both restricted and unrestricted sources. This vision is to create the lightest institutional structure, the least obtrusive administrative structure and then empower teams that are focused on products … increasingly traits, tools and methodologies – (i) delivering better alleles and genes in reasonable genetic backgrounds with tools for NARS and SME breeding programs to effectively manage that novel genetic variation in their adaptive breeding programs, and, (ii) at the same time developing, validating and helping apply complete new crop improvement methodologies. For both maize and wheat there is a substantial job to do in order to coerce scientists to walk the talk of the business plan. And most critically, to help them see that this new approach is our comparative advantage niche that will allow us to consolidate a stronger future position – whilst for other historical activities there are increasingly cheaper and/or more politically suitable providers and we must be seen to clearly advocate and support those partners to effectively fulfill those activities. This will have the dual effect of contributing to our capacity building outcomes whilst at the same time freeing up expertise, scientist time and operation funds to focus on our newly defined niche areas.

Modernizing support services

Finance and administration in particular still have a long way to go in order to be a support rather than a constraint to the research. Many activities were decentralized during the 1990's and urgently need to be centralized, computerized and automated where possible to allow greater operational efficiency. Many aspects of human resources and support services also need similar attention. Most critically there is a urgent need to modernize and simplify our policies whilst also giving great attention to ensuring an alignment of policy with practice. The transition to a high level of cost recovery has been forced upon us at the most difficult of financial times. Ensuring a smooth transition with the least negative effects (internally and externally) remains an enormous challenge. With little surplus funds internally to buffer this transition the only alternative is to enter a rapid fund raising drive for large projects that fully fund these cross charges.

Creating a focused fund raising operation with both momentum and responsiveness

We still have a long way to go to convince every scientist that they have a major role and responsibility in fund raising and that they need to get passionate about it – not in an unfocused entrepreneurial way but in a highly targeted way completely aligned to business plan priorities – and not at this stage to bring in new people and activities but rather to reduce our burden of staff costs on unrestricted budgets and release some of those funds for strategic activities.

Actioning a transition away from CIMMYT HQ/Mexico-centric operational structure/towards a globally decentralized structure

It seems clear that Latin America is not our primary target and that maintaining a large workforce in Mexico will become increasingly cost inefficient. We need to take every opportunity to shift activities to appropriate high skill low labour cost areas. However, we need to do this in a way that creates minimum new infrastructural liabilities in the regional locations. We need to develop our operations in locations where physical facilities are under the responsibility of others – this also gives us great flexibility to shift again when appropriate. Equally importantly if gives us an opportunity to build systemic alliances with partners closer to the farmers and consumers whilst at the same time breaking down the ivory towers perception of the CGIAR amongst many of our NARS partners.

Becoming a knowledge-based organization

The CRIL provides a perfect foundation for building the necessary infrastructure for a knowledge-based organization but the functioning of this approach is a much great challenge – particularly to change the culture of data ownership – for scientists to see greater value in sharing their data than hiding it away. CIMMYT has a unique opportunity to capture substantial international profile by placing all our data on the web – this will encourage global communities to work more on our germplasm and will also leverage new unrestricted funding opportunities. This then goes to the core of our future niche – as a trusted convener and exchanger of knowledge, skills, approaches and germplasm for improved maize and wheat product systems. In the value chain context, we will have an increasing role in coordinating the value chains in which we contribute [filling rate limiting gaps ourselves or advocating/assisting others to do so] and an increasingly focused contribution to fewer more specific elements of that value chain. Perhaps our greatest role will be to facilitate the transition from a handover pipeline approach to a value web approach. Our role in generating data should rapidly decrease while our role in managing, organizing, integrating and analyzing data from across global providers should be seen as one of our primary comparative advantage niches. However, there remains a major cultural change challenge to ensure widespread adoption of this perspective. As we do less ourselves while doing more facilitating others to do themselves, naturally our training activities should be rapidly increasing – at the moment, it is unclear that there is a willingness from staff and donors to fund this critical element.

Evolving from responsive to strategic management

It is inevitable at a time of great external pressures (particularly financial) that we have become overally responsive in our management style. Now is the time for us to articulate to the outside world that we have heard their concerns, adapted our structures and strategies, and now we must focus on the tactical and strategic issues that will allow us to achieve great impact from this new vision. This will include articulating internally a newly positive atmosphere about our potential for great success yet at the same time ensuring an internalization amongst each and every staff member that we are on a path of constant change, of continuous searches for greater efficiency. Nevertheless, within this that the overarching goal and vision will remain constant. Most critically everyone must see the huge undertaking facing us in order to convert the rhetoric into tangible outcomes and impacts. Critically, the administrative support systems of the institute must be strengthened to allow management to free-up time for strategic and tactical issues.

Transforming from an e-mail centric to an action orientated culture

There is a clear trend for e-mail technology to make us less efficient we must make a concerted effort to focus more of our time on audiovisual technologies. We must also force ourselves to seek other more efficient means of sharing the right information to the right people – there is a clear need for someone to be assigned the responsibility of internal communication for improved operational efficiency. At the same time it is essential for us to move to a more structured, disciplined and accountable process of linking the strategic vision to activities, workplans, outputs and rewards – there is a clear need for us to establish some institutional norms/best practice processes to guide our operational frameworks. Our reticence to experiment in the area of internal innovation policy must be quickly dissolved – we must be ready to accept that operationally we are all often highly inefficient.

4. Specific Problems – (a) *ISO9000 Application for SIDU Accreditation*

Background

The CIMMYT seed health laboratory has operated since 1998 under the approbation of the Mexican Phytosanitary Direction General (DGSV). This approbation is regulated by the Federal Law of Metrology and Normalization and by the norm NOM-036-FITO-1995 and it is renewed every 2 years. The approbation allows CIMMYT seed health laboratory to carry out internally the quarantine process on imported seed and to carry out the analysis to support the granting of the international phytosanitary certificates that accompany outgoing seed. Due to the fact that we analyze our own material we have also a phytosanitary officer assigned by the DGSV as an external auditor (paid by CIMMYT). This situation is clearly greatly beneficial for the cost and time efficiency of CIMMYT's international operations and our effectiveness to serve our stakeholders globally (see 'Germplasm Distribution' section of 'GRP 2005 Highlights' for specific details).

Current Situation

The last approbation expired on January 30, 2006. The renewal of the approbation under NOM-036-FITO-1995 is conditional on accreditation by the international norm ISO/IEC 17025-1999, adopted by the Mexican norm NMX-EC-17025-IMNC-2000. The process for receiving this accreditation is carried out in Mexico by the Mexican Entity for Accreditation, "asociacion civil" (a private company) (EMA, a.c.). The process consists of 8 phases, each requiring accomplishment of the requirements of the previous phase before being allowed to start on the next phase.

The costs of the process are:

1. $77,084.85 pesos for submitting the applications for the 3 subject areas necessary for the laboratory to operate: mycology, bacteriology and virology.
2. Additional costs (not predictable but likely less than administrative fee cited above); the per diem fees and allowances for the EMA personnel that will be assigned to the lab for the evaluation and validation of the methods, equipment, personnel and infrastructure.
3. Internal costs of adjusting processes, policies and protocols in line with accreditation requirements (not predictable but estimated by those who have passed through this process, to cost up to 10% of the operating cost of the unit, viz. up to US $50,000).

N.B. Failure at any stage can invalidate the entire process irrespective of the up-front payment for the whole process made to EMA.

Implications

1. The importance of being able to carry on in-house the seed testing is well established. Quantity and quality of the testing, speed and efficiency are guaranteed to maintain our seed movement efficiency at the level required for our collaborators. If CIMMYT was no longer allowed to carry out this activity in-house, it would have to rely on an external laboratory throught sub-contracting in order to work through the large amount of material the CIMMYT exchange – the cost effectiveness and timeliness of this option has not been investigated
2. Although the accreditation would allow us to follow a revenue generation stream by accepting contract work, we may not chose to do so in view of our not-for-profit status.
3. It is not clear if the accreditation of the laboratory will be required by any phytosanitary service in the world to recognize the validity of the international phytosanitary certificate
4. CIMMYT prestige at the Mexican and international level would increase considerably.

Action-plan for Fund Raising for SIDU ISO9000 Accreditation Process

[1] BoT assistance with championing proposal to Nordic donors – potential collaborations with KVL, Denmark (for proposals to DANIDA), with the former NLH Ås (the Agric. Univ. of Norway), Norway, with SLU main campus (and Alnarp) in Sweden, with the Nordic Gene Bank, and in Finland for FINIDA. [2] BoT assistance with championing proposal to USA donors (including foundations).

4. Specific Problems – (b) Maintaining momentum on CRIL activities

Completion of CRISCO 2005 activities under CRIL

- CropFinder, Fieldbook, and FieldLog are all complementary to ICIS and will be valuable additions to the ICIS functionality.
- The maize breeding IS still suffers from inadequate genealogy management, but this could be solved by connecting the ICIS GMS for Fieldbook.
- IWIS has both large overlap of functionality with ICIS, but also much additional functionality which is not present in ICIS. This makes migration complex, and this is why the possibility of substituting the IWIS PMS with the ICIS GMS is being investigated.
- With current staffing levels in crop IS it will not be possible both to implement new genebank IS in 2006, maintaining existing crop IS, and also move forward with ICIS migration.
- The lead developer of FieldLog, GenebankManager, and CropFinder is leaving at end of April, and finishing/maintaining the genebank applications is a concern.

Funding of Core CRIL Establishment Activities

Tasks such as data curation, informatics support of other projects and general infrastructural development are being forced off the list of activities to be funded in 2006 due to funding constraints. These issues need long-term commitment to enable a strong strategy to emerge as the foundation of future CRIL activities and impact. It appears that there is no alternative to cross-charging for these services, support and consultancy.

Data Compatibility and Quality

Much of the long-term success of CRIL will depend on the quality and comparability of data coming from diverse sources. We need to be very careful how we plan experiments and store the data afterwards in order to ensure that the data can analysis. To do this properly we need to develop SOPs (standard operating procedures) for the entire process of data collection, management and analysis. This is clearly a substantial undertaking – see section 6 for further details.

4. Specific Problems – (c) Reducing the SIDU budget

Rationalizing the SIDU shipping list

Optimizing GMO testing

4. Specific Problems – (d) Scientific and manage constraints due to private sector and or ARI agreements

4. Specific Problems – (d) Major Problems and Concerns from Project 7

Problems and Concerns from Project 7	Actions by Projects 1 or 2
Up-grading marker-assisted selection versus	No doubt we do not have the level of capital investment to reach the necessary throughput to sufficiently reduce unit costs. Out-sourcing CE separation is an intermediate solution – ultimately we need to move to an array based platform Meanwhile two relevant pilot tests in 2006 will give some insight: - Pilot studies with large-scale SNP genotyping of maize including using array platform - DArT pilot projects
Large-scale DArT genotyping of parental lines	GRDC funding of DArT fingerprinting of international nurseries should give a good insight and perhaps leverage for funding to fingerprint parental genotypes
Environmental characterization of international nurseries	Critical added value for integration of data from genebank to variety selection
NARS version of ICIS	ICIS migration and creation of ICIS-light for wheat and maize NARS is a top priority
Lack of trained NARS and training opportunities	NIAB alliance for training of modern plant breeders
Loss of quality of data	CRIL should have a major role to play here
Lack of CIMMYT internal scientific meetings	Quarterly meetings of trait-based teams
Time constraints to write projects and publications	Focus, focus, focus

5, Staff and Resource Allocation

The year 2005 was a complex one for GRP (as indeed it was for the entire institute). Most critically for GRP, there was a large number staff departures (involving 8 – mostly senior scientist positions - see table below) that although offered opportunities to invest in the new strategy were nonetheless highly disruptive for progress towards agreed MTP milestones. In addition, the change in leadership with associated strategic adjustments was inevitably a high transaction cost event. Finally, it can not be discounted that a 50% director (with other 50% committed to Generation Challenge Program management) could not provide the best operational support during this transition year and this arrangement has been corrected for 2006.

Staff Departures GRP 2005 & GREU 2006

Name	***Position/Activities***	***Reason for Departure***	***Follow-up***
Ranjana Bhattacharjee (January)	Maize genebank post-doc	None-arrival for personal reasons	Position frozen
Scott McLean (April)	Biotech related glasshouse and field experiments	Right-sizing	Not replaced
Maarten van Ginkel (May)	Wheat genebank and germplasm enhancement	Right-sizing	Replaced by Tom Payne
Marilyn Warburton	Maize and wheat diversity analysis	Sabbatical at Cornell University	Returning mid-2006
Philippe Moneveaux (August)	Maize drought physiology consultant	Consultancy position closed	Replaced by Jose Luis Araus (staff position) from mid-2006
Jean-Marcel Ribaut (September)	Head of maize drought genomics group, biotech disciplinary group, Tlalti station	Moved to Director of GCP	Replace by maize molecular breeding (Yunbi Xu from April 2006)
Alessandro Pellegrineschi (October)	Head of genetic engineering group	Moved to Pioneer USA	Replaced by Jonathan Crouch as leader of group and wheat transformation post-doc (from mid-2006)
Mark Sawkins (March)	Maize drought genomics scientists	Moved to Syngenta USA	Position frozen
Jens Riis (April)	Crop informatics specialist	Consultancy position closed	To be replaced under CRIL

Genetic Resources Program 2005 Overview of Major Expenditures

	Expenses	EXPENSES BY		
	2005	SOURCES OF FUNDS		
SALARIES		**Unrestricted**	**EU**	**Restricted**
Salaries & allowances IRS	$1,169,236	$344,381	$158,164	$666,691
Salaries & allowances NRS	$949,413	$221,966	$353,782	$373,665
Consultants	$174,169	$12,015	$0	$162,154
Sub total	$2,292,818	$578,362	$511,946	$1,202,510

STAFF COST SAVINGS 2006		**Unrestricted**	**EU**	**Restricted**
		% cost saving	% cost saving	% cost saving
TOTAL IRS	$137,321	24%		8%
TOTAL NRS	$73,032	33%		

	Expenses	**Unrestricted**	**EU**	**Other restricted**
OPERATIONS	**2005**			
ICT charges	$250,938	$102,114	$27,625	$121,199
Depreciation	$120,915	$102,609	$18,306	
Tlaltizapan	$119,000	$119,000	$0	$0
Biometrics	$29,595	$29,595		
Sub total	$520,448	$353,318	$45,931	$121,199

Staff Administrative Home Changes Related to GRP to GREU Evolution

Name	*2005 Home*	*Proposed 2006 Home Program*	*2006 Primary Project Focus Area*
Global FHB Initiative			
Tomohiro Ban	GRP	Wheat Program	P8 – Diseases
Jiro Murakami	IAP	Wheat Program	P8 – Diseases
Janet Lewis	GRP	Wheat Program	P8 – Diseases
Global Rust Initiative			
Choong-Hyo Yun	GRP	Wheat Program	P8 – Diseases
Hiro Nakamura	GRP	Wheat Program	P9 – Quality
Drought			
Mark Sawkins	GRP	Position frozen	P3 – Stress
Axel Tiessen	GRP	Maize Program	P3 – Stress or P6 - LA & Asia
Eric Nurit	GRP	Contract ends in June so should just lapse under GREU	P3 – Stress
Jose Luis Araus	TES/GRP	Maize Program (50% of salary from GREU)	P3 – Stress
Molecular Biology			
Enrico Perotti	GRP	GREU (create Developmental Biology group and seek funds for wheat activities)	P4 – Added value
Jedidah Danson	ALP	GREU (creating infrastructure and methodologies at BECA)	P6 – Nutrition
Luz George	TES/GRP	Maize Program	P5 - LA & Asia
Molecular Breeding			
Manilal William	RWS	GREU	P2 [Wheat Molecular Breeder]

Final 2006 GREU Staff Portfolio - Administrative homes in GREU*

Genetic Resources (P1)	Tom Payne (wheat)	Masahiro Kishii (wheat wide crosses and genetic stocks) & Mujeeb Kazi
	Suketoshi Taba (maize)	Vacant position (maize population genetics)
	Monica Mezzalama (SIDU)	

Germplasm Mining (P1)	Marilyn Warburton	New GCP PDF (maize)
		Susanne Dreisigacker (wheat)

Molecular Breeding (P2)	Yunbi Xu (maize MAB)	Jedidah Danson (maize transformation in Africa)
	Manilal William (wheat MAB)	Debra Skinner (low cost markers consultant) & Wayne Powell
		CRC PDF (wheat transformation)

Computational Systems CRIL (P1 & 2)	Graham McLaren	Jose Crossa & consultants
		Jens Riis & consultants
		Guy Davenport & consultants
		Jiangkang Wang & consultants

*technological backstopping of GREU-related activities in GMP and GWP will be strengthened

This new structure provides an excellent expertise critical mass but is potentially severely constrained by insufficient junior scientists which urgently needs to be addressed by the recruitment of pending post-doc positions, addition of adjunct [visiting] scientists from strong NARS, creation of seconded scientist positions from public and private sector ARIs.

Relationship between Projects and Products

Project # **[Short Title]**	**Formal Title**	**Associated Flagship Products**
Project 1 Discovery	Conservation and characterization of and targeted access to maize and wheat related biodiversity	#5 and #6: New Traits through Allele Mining and Improved Methodologies for Genetic Improvement
Project 2 Tools	Trait enhancement: tools, methodologies, and germplasm	#5 and #6: New Traits through Allele Mining and Improved Methodologies for Genetic Improvement
Project 3 Stress	Stress tolerant maize	#1: Stress Tolerant Maize
Project 4 Added Value	Nutritional and specialty traits for maize	#4 and #9: Biofortified Maize and Special Trait Maize for Income Generation
Project 5 Africa	African livelihoods	#1: Stress Tolerant Maize; # 4 and #9: Biofortified Maize and Special Trait Maize for Income Generation
Project 6 LAA	Maize for Latin America and Asia	#1: Stress Tolerant Maize; # 4 and #9: Biofortified Maize and Special Trait Maize for Income Generation
Project 7 Drought	Water productive wheat with appropriate quality profiles	#2: Wheat with Enhanced Water Productivity
Project 8 Diseases	Enhanced wheat for more durable resistance to diseases and enhanced production potential	#3: Rust Resistant Wheat
Project 9	Wheat grain enriched for health and profitability	#5: New Traits through Allele and Gene Mining of Global Crop Genetic Resources
Project 10 RCT	Conservation agriculture for maize and wheat cropping systems: Safeguarding soils while increasing water productivity and resource use efficiency	#8: Resource Conservation Technologies
Project 11 KTSA	Knowledge, targeting, and strategic assessment of maize and wheat farming systems	#7: Capacity Building

6. Quality Issues

Data Compatibility and Quality

Much of the long-term success of CRIL will depend on the quality and comparability of data coming from diverse sources. We need to be very careful how we plan experiments and store the data afterwards in order to ensure that the data can analysis. To do this properly we need to develop SOPs (standard operating procedures) for the entire process of data collection, management and analysis.

The lack of SOP goes far beyond biotech data but needs to include all areas. Until we know what and how we do things, we will never be able to have QA or QC, or even know what can be improved. The problem is that most people don't have the time to document their work since they spend most of their time doing it. If the CRIL is to be successful it is essential that we assign some time of informatics specialists

Summary of GRP Outputs and Action Plans Against 2005 MTP Milestones

Project	Project output	Output target 2005	Category output target	Level of 2005 Achievement	2006 Action Plan
Genetic Resources	Global custodianship, characterization and management of the genetic resources of maize, wheat and related species (MTP Purpose 1)	Genetic resources information available for at least 25,000 maize and 75,000 wheat accessions.	Databases	Partially [on target to exceed 2007 milestone now that CRIL established]	Data migration should proceed more rapidly now that CRIL established
		A 5-10% increase in the number and type of maize and related species accessions available in the gene bank	Inventories	Exceeded 2007 target	Move to a more targeted gap filling approach
		A global web-accessible maize and wheat genetic resource information system – beta-version available by end of 2005. Incorporate existing genebank data into the new system, improving data quantity and quality	Software and databases	Partially [basic system created]	Finalizing and implementing the most appropriate genebank management system should now proceed rapidly under CRIL
		Evaluate statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets. Develop population genetic models for efficient regeneration and collection of genetic resources	Journal publications	Yes	Adopt an intensive application and refinement approach
Genetic Resources	Effective approaches identified in genetic resources and transferred to useful maize and wheat germplasm for improving critical traits as prioritized by CIMMYT and partners (MTP	Consensus maps for drought tolerance and insect resistance in maize by 2005. Genes, alleles and/or pathways identified for improving abiotic stress tolerance by 2005.	Publications and on-line resources	Partially [delayed due to departing staff]	Appointment of maize molecular breeder and alliance with Pioneer on molecular breeding of drought tolerance in maize should facilitate a dramatic ramp-up in impact of outputs from the maize drought genomics group

Project	Project output	Output target 2005	Category output target	Level of 2005 Achievement	2006 Action Plan
Genetic Resources	Global custodianship, characterization and management of the genetic resources of maize, wheat and related species (MTP Purpose 1)	Genetic resources information available for at least 25,000 maize and 75,000 wheat accessions.	Databases	Partially [on target to exceed 2007 milestone now that CRIL established]	Data migration should proceed more rapidly now that CRIL established
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		A global web-accessible maize and wheat genetic resource information system – beta-version available by end of 2005. Incorporate existing genebank data into the new system, improving data quantity and quality	Software and databases	Partially [basic system created]	Finalizing and implementing the most appropriate genebank management system should now proceed rapidly under CRIL
		Evaluate statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets. Develop population genetic models for efficient regeneration and collection of genetic resources	Journal publications	Yes	Adopt an intensive application and refinement approach
	Purpose 2)	Identify gene systems for conditioning asexual reproduction (apomixis) in cereals. Nucellar/ovule-specific and inducible promoters identified by 2005	Genomic materials	Yes	Scale-out developmental biology research to include wheat and genomics solutions for increasing yield potential
		Bioinformatics platform established and functioning by end of 2005.	Infrastructure	Exceeded target	Leverage the new critical mass and profile of the IRRI-CIMMYT Alliance CRIL for significant new fund raising opportunities

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		A 5-10% increase in the number and type of maize and related species accessions available in the gene bank	Inventories	Exceeded 2007 target	Move to a more targeted gap filling approach
		A global web-accessible maize and wheat genetic resource information system – beta-version available by end of 2005. Incorporate existing genebank data into the new system, improving data quantity and quality	Software and databases	Partially [basic system created]	Finalizing and implementing the most appropriate genebank management system should now proceed rapidly under CRIL
		Evaluate statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets. Develop population genetic models for efficient regeneration and collection of genetic resources	Journal publications	Yes	Adopt an intensive application and refinement approach
		Implement central data repository for CIMMYT-derived genomic data by end of 2005. Identify and adopt key bioinformatics packages for analyzing genomic data in 2005.	Database infrastructure and research practices	Partially [delayed due to establishment of CRIL]	Should now proceed rapidly under CRIL
		Incorporate novel sources of tolerance into useful maize and wheat germplasm using conventional, molecular-marker and/or genetic engineering strategies for further use by breeding programs of CIMMYT and its partners. Drought tolerance maize lines by 2005.	Advanced materials	Partially [delayed due to departing staff]	New institutional structure, new product-driven framework and new trait-based teams should facilitate a dramatic increase in production of new trait-enhanced

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		Evaluate statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets. Develop population genetic models for efficient regeneration and collection of genetic resources	Journal publications	Yes	Adopt an intensive application and refinement approach
		Screen maize and wheat genetic resources for elevated levels for iron, zinc and pro-vitamin A in the grain	Selected materials	Yes	Develop improved methods for targeted discovery of genetic resources with improved quality traits
		Establish regional marker laboratories backstopped by a central facility – at least one regional marker lab established by 2005	Infrastructure	No [due to change of strategic emphasis]	New Strategy Globally decentralize biotech support of regional programs and partners through alliances and out-sourcing partnerships

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		Evaluate statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets. Develop population genetic models for efficient regeneration and collection of genetic resources	Journal publications	Yes	Adopt an intensive application and refinement approach
		Agrobacterium transformation system for wheat by 2005	Protocol publication or patent	Yes [patent submitted]	Optimize agrobacterium-mediated transformation system in CIMMYT lab and transfer entire pipeline to this protocol and terminate all biolistics activities
Genetic Resources	Capacity in genetic resource management, maintenance and use enhanced globally (MTP Purpose 3)	Improved capacity for storage and management of genetic resources by CIMMYT's partners. Quality of maize and wheat global genetic resources increased in at least 5 NARS each year. At least 5 NARS or partners helped each year.	NARS feedback	No	Launch major fund raising initiative for creating a global community of practice of cereal genebank managers across NARS, LDC-universities, CGIAR and ARIs – including data management on a common ICIS-based platform

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		Evaluate statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets. Develop population genetic models for efficient regeneration and collection of genetic resources	Journal publications	Yes	Adopt an intensive application and refinement approach
		Conduct workshops and/or host visiting scientists/students on genebank management (ex-situ and in-situ). At least one workshop held each year. At least two scientists/students hosted each year.	Workshop and training reports	No [due to other priorities and lack of targeted restricted funds]	Include these activities in cereal germplasm conservation community of practice proposal for potential funding through Global Trust, LAMP and others
		Increase use of genomic approaches by CIMMYT and its partners. At least five NARS scientists trained in genomics approaches each year.	NARS reports	Yes	Maintain level of training courses for use of genomics in managing, utilizing and enhancing genetic resources through funding from GCP and other donors

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		Evaluate statistical genetic models for classifying genetic resources, studying phenotypic and genetic diversity, and forming core subsets. Develop population genetic models for efficient regeneration and collection of genetic resources	Journal publications	Yes	Adopt an intensive application and refinement approach
		Conduct workshops and/or host visiting scientists/students in the application of genomics (QTL/gene discovery, MAS) in maize and wheat breeding. At least one workshop held each year. At least two scientists/students hosted each year	Workshop and training reports	Yes	Maintain level of training courses in development and application of molecular breeding tools and methodologies through funding from GCP and other donors