Seeds of Discovery (SeeD)

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Coordinated by:

CIMMYT
International Maize and Wheat Improvement Center

Funded by:

SAGARPA
SECRETARIA DE AGRICULTURA,
GANADERIA, DESARROLLO RURAL,
PESCA Y ALIMENTACIÓN
Climate change
Soil degradation, falling water tables
Costs of fertilizer and energy
Genetic erosion

Global average yield (tons per hectare)

Year


8 7 6 5 4 3 2 1 0

Wheat Maize

[Source: USDA PDS database]

Anticipated demand by 2050 (FAO)

[Genetic resources for food security]
Potentially valuable genetic variation, the raw material for crop improvement, remains untapped on genebank shelves, at a time when challenges to crop production are unprecedented.

Genebanks should NOT be museums. They should enable breeders worldwide to use high-value genetic diversity to meet tomorrow’s challenges.
Systematically identify & mobilize novel, beneficial genetic variation into breeding programs to accelerate genetic gains.
Beneficial alleles

Diversity atlas

‘Bridging Germplasm’

Capacities

Tools
Genotyping-by-sequencing (GbS)

- **NG sequencing platforms**: 10,000 – 100,000-fold drop in costs
- **RE-based GbS** for big-data-driven, systematic **harvesting of novel, beneficial genetic variation** from genebanks
  
- Simultaneously **discovers** and classifies DNA polymorphisms → minimizes ascertainment bias
- Methylation filtration (PstI) → gene-rich regions
GbS = configurable platform

Adjust No. of markers vs. No. of DNA samples → two GbS ‘flavors’

- **Cornell** University *(ApeKI)*: Lots of markers (~600K markers; SNP only), higher error rates, more missing data, imputation needed → **maize AM**

- **DArTseq** (Diversity Arrays Technology; PstI): Fewer markers (~60K; both SNP & ‘PAV’), lower error rates, less missing data, no imputation → **maize & wheat diversity surveys**
  - Maize: **DNA pools** of 30 plants per accession → allele frequencies within accessions from SNPs
  - Genetic distances among accessions from PAVs
  - **30-fold reduction in costs!**
Prioritization of traits

Breeding-oriented

Main emphasis:
Mobilize novel alleles for complex traits into breeding programs

Upstream

Seek collaborations to mine data for basic research

Genetically complex traits
[heat/drought tolerance]

Genetically simple traits
[some diseases]

‘Low-hanging fruits’ for breeding
WHEAT genetic diversity survey

- One individual per accession
- **40,000 accessions sequenced** to this date
- Positions of sequence tags from new DArTseq consensus map (64K)
- Comprehensive diversity analysis underway (stratification into ploidy levels → allele re-calling within ploidy levels → gene pools → core sets)
WHEAT phenotypic diversity

- Per-se phenotyping easier than in maize
- Screened ~70,000 accessions for at least two of the following characters (1,400,000 data points from 30 trials across 9 locations):
  - Heat tolerance
  - Drought tolerance
  - Low-P tolerance
  - Resistance to spot blotch, tan spot or Karnal bunt
  - Grains: hardness, color, protein, test weight, yellow berry, Fe, Zn
  - Adaptation to different agro-ecological zones in Mexico
WHEAT heat-tolerance screen (70,000)

Number of Mexican landraces with grain yield >150 grams m\(^{-2}\) under heat stress (Cd. Obregón, México)

- Red: heat-tolerant Iranian landraces
- Yellow: Heat-tolerant Mexican landraces
- Blue: ESWYT
- Green: SAWYT
WHEAT ‘bridging germplasm’

Linked topcross panel (LTP)

- TC chains with partly overlapping parents for joint linkage/AM in elite genetic backgrounds
- 200 accessions (synthetics, landraces; FIGS sets from ICARDA and Australia)
- 15 elite lines selected by breeders
Network of inter-operable tools

Database & interfaces for primary data to manage experiments

Web portal & data warehouse (Germinate): Validated genotypic & phenotypic data

Visualization tools (Flapjack, CurlyWhirly, ...)

Genebank management (GrinGlobal)

Database & interfaces for primary data to manage experiments

Web services

High-level data repository (Genesys): Passport & summarized data

Components funded by SeeD to be Open-Sourced from the first production version onwards (2015)

(Collaboration with James Hutton Inst. and DArT)
Capacity building

• Training workshops (120 researchers):
  – Informatics tools
  – GbS data generation & interpretation

• Genetic analysis service in partnership with DArT:
  Mainstream genomics platforms for breeding in Mexico

maize breeders

wheat breeders
Jonás Aguirre (UNAM), Flavio Aragón (INIFAP), Gary Atlin, Odette Avendaño (LANGEBIO), Michael Baum (ICARDA), David Bonnett, Hans Braun, Ed Buckler (Cornell Univ.), Juan Burgueño, Vijay Chaikam, Alain Charcosset (AMAZING), Gabriela Chávez (INIFAP), Jiafa Chen, Charles Chen, Andrés Christen (CIMAT), Angelica Cibrian (LANGEBIO), Héctor M. Corral (AGROVIZION), Moisés Cortés (CNRG), Sergio Cortez (UPFIM), Denise Costich Lino de la Cruz (UdeG), Etienne Duveiller, Marc Ellis, Armando Espinosa (INIFAP), Néstor Espinosa (INIFAP), Gilberto Esquivel (INIFAP), Luis Eguarte (UNAM), Mustapha El-Bouhssini (ICARDA), Gaspar Estrada (UAEM), Juan D. Figueroa (CINVESTAV), Pedro Figueroa (INIFAP), Jorge Franco (UDR), Guillermo Fuentes (INIFAP), Bonnie Furman, Amanda Gálvez (UNAM), Héctor Gálvez (SAGA), Karen García, Silverio García (ITESM), Noel Gómez (INIFAP), Gregor Gorjanc (Roslin Inst.), Sarah Hearne, Carlos Hernández, Juan H. Hernández (INIFAP), Víctor Hernández (INIFAP), Luis Herrera (LANGEBIO), John Hickey (Roslin Inst.), Huntington Hobbs, Puthick Hok (DArT), Javier Ireta (INIFAP), Andrzej Kilian (DArT), Huihui Li, Marta Lopes, George Mahuku, Francisco J. Manjarrez (INIFAP), David Marshall (JHI), César Martínez, Carlos G. Martínez (UAEM), Manuel Martínez (SAGA), Ky Matthews, Iain Milne (JHI), Terrence Molnar, Moisés M. Morales (UdeG), Henry Ngugi, Francis Ogbonnaya (ICARDA), Alejandro Ortega (INIFAP), Iván Ortiz, Leodegario Osorio (INIFAP), Natalia Palacios, José Ron Parra (UdeG), Tom Payne, Javier Peña, Cesar Petrol (SAGA), Kevin Pixley, BM Prasanna, Ernesto Preciado (INIFAP), Matthew Reynolds, Sebastian Raubach (JHI), María Esther Rivas (BIDASEM), Carolina Roa, Alberto Romero (Cornell Univ.), Ariel Ruiz (INIFAP), Carolina Saint-Pierre, Jesús Sánchez (UdeG), Gilberto Salinas, Yolanda Salinas (INIFAP), Carolina Sansaloni (SAGA), Ruairidh Sawers (LANGEBIO), Sergio Serna (ITESM), Paul Shaw (JHI), Rosemary Shrestha, Aleyda Sierra (SAGA), Pawan Singh, Sukhwinder Singh, Giovanni Soca, Ernesto Solís (INIFAP), Kai Sonder, Ken Street (ICARDA), Maria Tattarins, Maud Tenaillon (AMAZING), Fernando de la Torre (CNRG), Heriberto Torres (Pioneer), Samuel Trachsel, Grzegorz Uszynski (DArT), Ciro Valdés (UANL), Griselda Vásquez (INIFAP), Humberto Vallejo (INIFAP), Víctor Vidal (INIFAP), Eduardo Villaseñor (INIFAP), Prashant Vikram, Martha Willcox, Peter Wenzl, Víctor Zamora (UAAAN)