Seeds of Discovery (SeeD)

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SAGARPA



SECRETARÍA DE AGRICULTURA, Ganadería, desarrollo rural, Pesca y alimentación



research program Maize





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**



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 \rightarrow 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 of accession → allele frequencies
 within accessions from SNPs
 - Genetic distances among accessions from PAVs
 - 30-fold reduction in costs!



Individual samples

Prioritization of traits

Breeding-oriented Upstream

Seek

collaborations

to mine

data

for basic research

Genetically complex traits

[heat/drought tolerance]

Main emphasis:

Mobilize novel alleles for **complex traits** into **breeding** programs

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)







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

Web portal & data warehouse (Germinate):

Database & interfaces for primary data to manage experiments



(Collaboration with James Hutton Inst. and DArT)

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

Components

from the first

funded by SeeD to be Open-Sourced

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





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