PIGEONPEA BREEDING: CHALLENGES AND OPPORTUNITIES

Isabel Vales & ICRISAT Pigeonpea Team
OUTLINE

- Pigeonpea production
- Priority setting
- Breeding goals
- Main constraints in pigeonpea production
- Combining conventional and molecular breeding
- Ensure success of pigeonpea hybrids
- Data management
- Funding
- Outputs
### Pigeonpea production

<table>
<thead>
<tr>
<th></th>
<th>World</th>
<th>India</th>
</tr>
</thead>
<tbody>
<tr>
<td>Area</td>
<td>4.8 mill. ha</td>
<td>3.5 mill. ha</td>
</tr>
<tr>
<td>Production</td>
<td>3.7 mill. t</td>
<td>2.5 mill. t</td>
</tr>
<tr>
<td>Productivity</td>
<td>744 kg ha(^{-1})</td>
<td>697 kg ha(^{-1})</td>
</tr>
</tbody>
</table>

**2010**

- **World area**: 4.8 mill. ha
- **World production**: 3.7 mill. t
- **World productivity**: 744 kg ha\(^{-1}\)
- **India area**: 3.5 mill. ha
- **India production**: 2.5 mill. t
- **India productivity**: 697 kg ha\(^{-1}\)

FAOSTAT 2010

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**Graph:**
- **Area**
- **Production**
- **Yield**

**Legend:**
- Area Harvasted (ha)
- Production (t)
- Yield (kg ha\(^{-1}\))

**Time Frame:**
- 1961 to 2009

**Axes:**
- **X-axis**: Years (1961-2009)
- **Y-axis (left)**: Area (ha)
- **Y-axis (right)**: Production (t), Yield (kg ha\(^{-1}\))
Priority setting – Breeding program

Situation analysis
- Groups, environments
- Production systems
- Seed management
- Farmers, processors and consumer needs & preferences

Priority setting considerations
- Target area and environments
- Germplasm base
- Selection criteria
- Types of cultivars
- Roles and responsibilities

Desired Outcomes
- Productivity
- Health, nutrition
- Diversification
- Environment
- Markets
- Drudgery
- Empowerment
- Policies

Modified from Weltzien 2005
Breeding goals

To develop **high yielding** lines with acceptable **grain quality** and **stability** to be released as **varieties** or used as **hybrid parental lines**

Aspects to prioritize specific objectives and **selection criteria**:
- Agro-ecological zones
- Maturity groups and phenology
- Final use: processing (dal), vegetable, feed, fodder, fuel, etc.
Pigeonpea agro-ecological zones

Central Zone (CZ)
South Zone (SZ)
North East Plain Zone (NEPZ)
North West Plain Zone (NWPZ)

Soil type
Temperature
Precipitation
Evapo-transpiration
Altitude
Latitude
Photoperiod

Cropping systems
Intercrop
Sole crop
Crop windows
Region specific constraints
Pests
Diseases
Abiotic stresses
# Maturity groups in pigeonpea

<table>
<thead>
<tr>
<th>ICRISAT maturity group</th>
<th>Maturity group</th>
<th>Days to 50% flowering (DAP)</th>
<th>Reference cultivars</th>
</tr>
</thead>
<tbody>
<tr>
<td>00</td>
<td>Super-early</td>
<td>&lt; 50</td>
<td>MN 5</td>
</tr>
<tr>
<td>0</td>
<td>Extra-short</td>
<td>51 – 60</td>
<td>ICPL 88039</td>
</tr>
<tr>
<td>I</td>
<td>Extra-short</td>
<td>61 – 70</td>
<td>Prabhat</td>
</tr>
<tr>
<td>II</td>
<td>Short</td>
<td>71 – 80</td>
<td>UPAS 120, ICPL 87</td>
</tr>
<tr>
<td>III</td>
<td>Short</td>
<td>81 – 90</td>
<td>Pusa Ageti, T 21</td>
</tr>
<tr>
<td>IV</td>
<td>Short</td>
<td>91 – 100</td>
<td>ICP 6</td>
</tr>
<tr>
<td>V</td>
<td>Short-medium</td>
<td>101 – 110</td>
<td>BDN 1, Maruti</td>
</tr>
<tr>
<td>VI</td>
<td>Medium</td>
<td>111 – 130</td>
<td>Asha</td>
</tr>
<tr>
<td>VII</td>
<td>Medium</td>
<td>131 – 140</td>
<td>ICP 7035</td>
</tr>
<tr>
<td>VIII</td>
<td>Medium-long</td>
<td>141 – 160</td>
<td>ICP 7065, Bahar</td>
</tr>
<tr>
<td>IX</td>
<td>Long</td>
<td>&gt;160</td>
<td>NP (WR) 15, MAL 13</td>
</tr>
</tbody>
</table>

Three phenological classes: long-season, full-season and short-season
Flowering patterns

Determinate (DT)

Indeterminant (NDT)
Use-specific traits

**Processed dal**
- Milling quality
- Seed size
- Seed color

**Feed**
- Protein

**Fresh/canned Vegetable**
- Seed size
- Seed color
- Pod color
- Pod length

**Fodder**
- Ratoonability
- Biomass
Basic approach

• Identify lines containing the traits of interest
  Elite germplasm, landraces and wild relatives

• Make crosses to combine traits of interest

• Generate segregating populations: Use appropriate breeding method

• Apply selection. Conventional and marker-assisted (MAS) multi-trait recurrent selection

• Agronomic, quality and disease/pest resistance trials
Genetic resources

Cultivated accessions: 13,077

Crop wild relatives: 555

Cytoplasmic nuclear male-sterility (CMS) system
\((A_1, A_2, A_3, A_4, A_5, A_6, A_7)\)

Mutants
# Pigeonpea germplasm holdings at ICRISAT

<table>
<thead>
<tr>
<th>Material</th>
<th>Number of accessions</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Active collection</strong></td>
<td>13,632</td>
</tr>
<tr>
<td>Landraces</td>
<td>8,215</td>
</tr>
<tr>
<td>Breeding material</td>
<td>4,795</td>
</tr>
<tr>
<td>Wild relatives</td>
<td>555</td>
</tr>
<tr>
<td>Advance cultivars</td>
<td>67</td>
</tr>
<tr>
<td><strong>Core collection</strong></td>
<td>1,290</td>
</tr>
<tr>
<td>Breeding material</td>
<td>466</td>
</tr>
<tr>
<td>Landraces</td>
<td>810</td>
</tr>
<tr>
<td>Advance cultivars</td>
<td>9</td>
</tr>
<tr>
<td>Others</td>
<td>5</td>
</tr>
<tr>
<td><strong>Mini core collection</strong></td>
<td>146</td>
</tr>
<tr>
<td><strong>Base collection</strong></td>
<td>11,794</td>
</tr>
</tbody>
</table>

- **a** Available for distribution to plant breeder;
- **b** 10% of active; **c** 10% of core or 1% of active; **d** Long term storage

Bohra et al., 2011
Examples of important traits harbored by wild relatives

<table>
<thead>
<tr>
<th>Name of wild species</th>
<th>Important trait</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>C. acutifolius</em></td>
<td>Pod borer &amp; pod fly resistance</td>
</tr>
<tr>
<td></td>
<td>Salinity tolerance</td>
</tr>
<tr>
<td><em>C. lineatus</em></td>
<td>SMD resistance</td>
</tr>
<tr>
<td></td>
<td>Pod fly resistance</td>
</tr>
<tr>
<td></td>
<td>High protein content</td>
</tr>
<tr>
<td></td>
<td>Drought tolerance</td>
</tr>
<tr>
<td><em>C. scarabaeoides</em></td>
<td>Pod borer &amp; pod fly resistance</td>
</tr>
<tr>
<td></td>
<td>High protein content</td>
</tr>
<tr>
<td></td>
<td>Salinity &amp; drought tolerance</td>
</tr>
<tr>
<td><em>C. sericeus</em></td>
<td>SMD resistance</td>
</tr>
<tr>
<td></td>
<td>Pod borer &amp; pod fly resistance</td>
</tr>
<tr>
<td></td>
<td>Phytophthora blight</td>
</tr>
<tr>
<td></td>
<td>High protein content</td>
</tr>
<tr>
<td></td>
<td>Salinity &amp; drought tolerance</td>
</tr>
<tr>
<td></td>
<td>High fruit set</td>
</tr>
</tbody>
</table>

Bohra et al., 2011
Genomic resources

Mapping populations (25)
TILLING population

Molecular markers
  3,072 SSRs
  768 SNPs (GoldenGate assay)
  15,360 DARrT

BAC libraries

Whole genome sequence draft (Asha -ICPL 87119-)

Genetic transformation

Varshney et al., 2010
# Representative pigeonpea mapping populations

<table>
<thead>
<tr>
<th>Mapping populations parental lines</th>
<th>Segregating trait/s</th>
<th>Size of mapping population (generation in 2011)</th>
<th>Polymorphic markers (mapped in F₂ populations)</th>
</tr>
</thead>
<tbody>
<tr>
<td>ICP 28 x ICPW 94</td>
<td>Pod borer</td>
<td>79 (F₅)</td>
<td>254</td>
</tr>
<tr>
<td>ICPB 2049 x ICPL 99050</td>
<td><em>Fusarium</em> wilt</td>
<td>331 (F₅)</td>
<td>400</td>
</tr>
<tr>
<td>ICPL 20096 x ICPL 332</td>
<td><em>Fusarium</em> wilt &amp; sterility mosaic disease</td>
<td>367 (F₅)</td>
<td>40</td>
</tr>
<tr>
<td>ICPL 87119 x ICPL 87091</td>
<td><em>Fusarium</em> wilt &amp; sterility mosaic disease</td>
<td>117 (F₄)</td>
<td>100</td>
</tr>
<tr>
<td>ICPL 20097 x ICP 8863</td>
<td><em>Fusarium</em> wilt &amp; sterility mosaic disease</td>
<td>374 (F₅)</td>
<td>139</td>
</tr>
</tbody>
</table>

Note: SSRs = Simple Sequence Repeat, SNPs = Single Nucleotide Polymorphism
Increasing the genetic diversity at the nuclear level

CWR introgression lines
Landraces
Mutants
Elite lines / parental lines
Varieties

Filter

Pool of materials with traits of interest

Association mapping --- marker-trait association -- filtering for breeding use
Mating and selection schemes

Increase the genetic base of the breeding pool
Enhance recombination
Genetic studies

Bi-parental crosses

$P_1 \times P_2$

$F_1$

$F_2$

$F_3$

RILs

Pedigree-based

→ Backcrossing

BC introgression

→ BC + selfing
Increasing the genetic base of the breeding pool and enhancing recombination

Multi-parent crossing

**PP MAGIC Population** (8 parents: A, B, C, D, E, F, G, H)

- **2-way**
  - AxB
  - AxC
  - AxD
  - AxE
  - AxF
  - BxCAxHAxG
  - BxD
  - BxE
  - BxF
  - BxG
  - CxD
  - CxE
  - CxF
  - CxG
  - CxH
  - DxH

- **4-way**

- **8-way**

- **~1,400**
  - RIL
  - RIL
  - RIL
  - RIL
  - RIL
  - RIL
  - RIL
  - RIL

Increasing the genetic base of the breeding pool and enhancing recombination.
Increasing the genetic base of the breeding pool and enhancing recombination

Multi-parent crossing

PP NAM population

~2,400 RILs
### Diversification of CMS base

<table>
<thead>
<tr>
<th>Cytoplasm</th>
<th>Wild species</th>
</tr>
</thead>
<tbody>
<tr>
<td>A₁</td>
<td>C. sericeus</td>
</tr>
<tr>
<td>A₂</td>
<td>C. scarabaeoides</td>
</tr>
<tr>
<td>A₃</td>
<td>C. volubilis</td>
</tr>
<tr>
<td>A₄</td>
<td>C. cajanifolius*</td>
</tr>
<tr>
<td>A₅</td>
<td>C. acutifolius*</td>
</tr>
<tr>
<td>A₆</td>
<td>C. lineatus</td>
</tr>
<tr>
<td>A₇</td>
<td>C. platycarpus</td>
</tr>
</tbody>
</table>

* C. cajan used as female; In the other CMS systems the wild species was used as female
Stable male-sterility across locations and years
High no. of fertility restorers
High $F_1$ fertility restoration
Genetic basis of traits of interest

- No. of genes involved (qualitative vs quantitative)
- Location and position
- Gene action
- Interactions (inter-genic, intra-genic and G x E)
- Heritability
- Phenotypic variance explained
Methods for estimating the number of effective factors

- **Classic methods:**
  e.g., the Castle-Wright estimator (review: Lynch and Walsh, 1998)
  - Assumptions:
    - additive gene effects
    - unlinked loci
    - + alleles in one parent only
    - no transgressive segregation

- The start of **QTL approaches:**
  Association between mendelian factors and quantitative traits
  Sax (1923)
  - “Mendelize” the segregation
  - Correlate segregation of the quantitative trait with that of qualitative trait, i.e., markers
  - QTL = quantitative trait locus = gene/s
Flowering Pattern

• NDT preferred over DT in most areas
• One major gene and several minor genes explain flowering pattern
• NDT is dominant over DT
• Pedigree and backcrossing methods can be used to obtain NDT/DT lines
• DT vs NDT could be used as morphological markers to confirm purity of parental lines and confirm hybridity
• Knowledge of the molecular genetic basis will allow to identify heterozygotes and confirm homozygote NDTs at early generation stages and facilitate selection
Flowering time and photoperiod

- Flowering time preferences are region specific
- Flowering time has high heritability
- **Earliness** is partially dominant
- Earlier flowering genotypes tend to be less photoperiod sensitive
- Two major genes are likely responsible for photoperiod response
- Pedigree-based selection has been effective in developing super-early lines
- Knowledge of the molecular genetics basis will allow to select at early stages and also facilitate introgression of photoperiod insensitivity to medium duration
Fusarium wilt

- Major and minor genes for resistance/tolerance
- **Resistance is dominant** over susceptibility
- Susceptible parents could carry minor tolerant genes
- Major genes can be introgressed via pedigree-based and backcross approaches
- **FW resistant A/B lines will generate FW resistant hybrids**
- Gene/marker-trait association: no of genes, position, effect, interactions
- Pyramiding major and minor genes: durability and stability of FW resistance/tolerance
Sterility Mosaic Disease

• Major and minor genes for resistance/tolerance

• **Resistance** to SMD is **recessive/dominant** over susceptibility

• Resistance is isolate specific

• Major genes can be introgressed via pedigree-based and backcross approaches. Selfing will expose recessive alleles.

• **SMD resistant A/B and R lines are needed to generate SMD resistant hybrids**

• Gene/marker-trait association: no of genes, position, effect, interactions

• Pyramiding major and minor genes: durability and stability of SMD resistance/tolerance
Pod borers

- Host-plant tolerance/resistance is scarce (i.e. 10 out of 10,000 lines)
- **CWR introgression lines**: sources of tolerance/resistance
- Mechanisms of tolerance/resistance: ovipositional nonpreference and recovery capacity
- NDT plants suffer less damage: focus on NDT
- **Transgenic Bt**
- Backcross approaches and MAS to introgress Bt into A/B and/or R lines
- Backcross approaches to introgress Bt into cleistogamous varieties
- Pyramiding natural host-plant tolerance and Bt: durability and stability of pod borer tolerance/resistance
Yield and yield components

• Both additive and non-additive effects for yield and yield components

• Main yield components reported to show significant heterosis:
  Pods per plant
  Pod clusters per plant
  Branches per plant
  seed size
  Seeds per pod
  Plant height

• Improvement of parental lines: A/B and R for yield and yield components

• Development of CMS hybrids: focus on performance *per se*, heterosis and SCA
Abiotic stresses: Water-logging

- **Resistance/tolerance** to water-logging is **dominant** over susceptibility
- Major and minor genes for resistance/tolerance
- Major genes can be introgressed via pedigree-based and backcross approaches.
- **Water-logging resistant/tolerant** A/B lines will generate WL resistant/tolerant hybrids
- Gene/marker-trait association: no of genes, position, effect, interactions
- Pyramiding major and minor genes: durability and stability of WL resistance/tolerance
Combination of multiple desirable traits

Breeding lines/Cultivars/Landraces/CRW introg./Mutants

- Bi-parental populations
- Pedigree
- Backcross

- Multi-parental populations
- MAGIC
- NAM

Large populations generated

- Phenotyping + Genotyping
- Selections

- Test-crosses/Diallel crosses
- Selections SCA

A lines

BC to CMS lines

B lines/varieties

R lines/varieties

New CMS Hybrids

Sterility mosaic resistance: R, B/A
Fusarium wilt resistance: B/A lines + R
Fertility restoration: R lines
Maturity: R, B/A
Yield and yield components: Based on heterosis
Molecular breeding for variety and hybrid parents development

**Advantages**
- Early selection
- Selection in absence of the disease/trait/restoration testing
- Independent of environmental conditions
- Pyramiding of resistance genes

**Challenges**
- Recombination
- Complex traits
- Crossing barriers
- Linkage drag

☑ Reduce time
☑ Reduce number of lines
☑ Guide selection
## Pigeonpea cultivars

<table>
<thead>
<tr>
<th></th>
<th>Varieties</th>
<th>Hybrids</th>
</tr>
</thead>
<tbody>
<tr>
<td>Seed production</td>
<td>Target environment</td>
<td>Pollinators required</td>
</tr>
<tr>
<td></td>
<td>Pollinators desired, but not essential</td>
<td></td>
</tr>
<tr>
<td>Isolation fields</td>
<td>100-200 m</td>
<td>500 m</td>
</tr>
<tr>
<td>Technical expertise</td>
<td>Low to medium</td>
<td>High</td>
</tr>
<tr>
<td>Cost</td>
<td>Low to medium</td>
<td>Medium to high</td>
</tr>
<tr>
<td>Pure genetic stocks</td>
<td>Important</td>
<td>Very important</td>
</tr>
<tr>
<td>Seed system</td>
<td>Mainly informal</td>
<td>Formal or well trained informal</td>
</tr>
<tr>
<td>Commercial grain</td>
<td>Heterosis</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>&gt; 20%</td>
</tr>
</tbody>
</table>
The promising solution...

High yielding disease tolerant CMS hybrids
Advantages of CMS hybrids

- 30-40% more yield
- More vigor
- 44% greater shoot mass (less seeding rate required)
- 40-50 greater root mass (better drought tolerance)
- Ideal for intercropping
- 30% more fuel wood
ICPH 2671

Maruti group hybrid

### Years
- 2005: 3183
- 2006: 2694
- 2007: 2702
- 2008: 2022
- Mean (n=43): 2650

### Yield kg ha⁻¹
- ICPH 2671:
  - 2005: 1855
  - 2006: 2066
  - 2007: 2140
  - 2008: 1746
- Maruti:
  - 2005: 2005
  - 2006: 2066
  - 2007: 2140
  - 2008: 1746

### Note:
- Total yield difference: 35.8%
ICPH 2433

A Short-duration hybrid

<table>
<thead>
<tr>
<th>Year</th>
<th>ICPH 2433</th>
<th>UPAS120</th>
</tr>
</thead>
<tbody>
<tr>
<td>2005</td>
<td>2416</td>
<td>2093</td>
</tr>
<tr>
<td>2006</td>
<td>1937</td>
<td>1148</td>
</tr>
<tr>
<td>2007</td>
<td>2419</td>
<td>1945</td>
</tr>
<tr>
<td>2008</td>
<td>2176</td>
<td>1608</td>
</tr>
<tr>
<td>Mean (n=33)</td>
<td>2237</td>
<td>1608</td>
</tr>
</tbody>
</table>

31.6%
Success of the CMS hybrid system

- Parental line purity
- Stable male sterility system
- Maximum heterosis
- Professional implementation of the CMS hybrid technology
- Constant training, monitoring and evaluation
- Efficient formal and informal seed systems
- Promotion and marketing efforts
Impurity/changes in parental lines

Outcrossing
Mixtures
Non-stability of male sterility
Damage by pest and diseases
De novo variation
  Mutations
  Epigenetic variation
Un-intended selection
Early release of heterogeneous parental lines/varieties
PURE parental lines

- Trusted seed source
- Genetic purity
- Physical purity: seed quality, seed health, germination
- Location for seed production
  - Isolation: field, cages and/or nets
  - Pollinators
- Roguing
- Spacing: row to row and plant to plant
- Ratios: A:B and A:R
- Field maps and labeling
- Planting time: Stagger plantings, off-season planting
- Harvest: sequential
- Storage: proper segregation
- Crop management: weeding, fertilization, irrigation, disease/pest control
Genetic purity

Visual observation in the field

Morphological uniformity

Height uniformity

Maturity uniformity

Health uniformity

Fertility/sterility considerations

Rogue out off types
Genetic purity
Visual observations in the field using NEPs

A line X R line

Hybrid

New NEPs
Under exploration:
Genetic purity
Using molecular markers

SSR screening of A & R lines

Selection of polymorphic SSR markers between A and R

Hybrid 1
ICPH 2671
298 bp
301 bp
R line
ICPR 2671
301 bp
A line
ICPA 2043
298 bp

Hybrid 2
ICPH 2438
220 bp
228 bp
R line
ICPR 2438
221 bp
A line
ICPA 2039
228 bp

Selected set of SSRs for routine testing ‘Genetic Purity Kit’
Seed production
- B lines
- R lines
- A lines (A x B)
- Hybrids (A x R)

Under net

Isolation (>=500 m from commercial pigeonpea field)
# Pollinators

<table>
<thead>
<tr>
<th>Natural conditions</th>
<th>‘Artificial’ conditions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Field</td>
<td>Field or cages</td>
</tr>
<tr>
<td>Hymenoptera - bees</td>
<td>Honey bees (hives)</td>
</tr>
<tr>
<td>Diptera - Flies</td>
<td>Humans</td>
</tr>
<tr>
<td>Lepidoptera - Butterflies and moths</td>
<td></td>
</tr>
<tr>
<td>Homoptera - Sucking pests</td>
<td></td>
</tr>
</tbody>
</table>

Considerations:
- Insect population
- Water
- Trees
- Weather conditions
Pollination under nets using bees
# Seed Production: Locations

<table>
<thead>
<tr>
<th>State</th>
<th>District</th>
<th>Location</th>
<th>Area (ha)</th>
<th>Prod. (kg ha⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>High-Yielding Locations:</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MP</td>
<td>Indore</td>
<td>Indore</td>
<td>0.15</td>
<td>2,267</td>
</tr>
<tr>
<td>AP</td>
<td>Niz’ bad</td>
<td>Renjal</td>
<td>0.40</td>
<td>1,750</td>
</tr>
<tr>
<td>Gujarat</td>
<td>Ahm’bad</td>
<td>Ahm’ bad</td>
<td>0.80</td>
<td>1,063</td>
</tr>
<tr>
<td><strong>Low-Yielding Locations:</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Karnataka</td>
<td>Raichur</td>
<td>Jawalgera</td>
<td>4.0</td>
<td>158</td>
</tr>
<tr>
<td>AP</td>
<td>Mah’ngr</td>
<td>CS Nagar</td>
<td>1.4</td>
<td>136</td>
</tr>
<tr>
<td>AP</td>
<td>Nandyal</td>
<td>Loc 1</td>
<td>0.6</td>
<td>133</td>
</tr>
</tbody>
</table>
Purity of hybrid parents

- Pure parental lines: A, B, R
- Recommended Isolation distances
- Stager planting of parental lines
- Presence of bee pollinators
- Proper roguing
- Recommended spacing
- Recommended A:B or A:R ratios
- Accurate field maps and labels
- Sequential harvest
- Proper segregation of seed
- Other managements practices

• Incorporation of SSR makers
• Incorporation of phenotypic makers
PLANT BREEDING DATA MANAGEMENT
Trained personnel

Modern equipment

Data management system

Faster and more accurate results

Facilitate decisions for the breeding program

Revolutionizing Science and Engineering Through Cyberinfrastructure" ("Atkins report")

*National Science Foundation* (Atkins et al. 2003; Gold 2007a)
Trained personnel

- Preparation of templates for data collection
- Automatic data collection
- Curation
- Archival
- Data analysis
Modern equipment

Single plant threshers

Dal processor

Grain counters

Data loggers

Barcode readers

Barcode printer

Balances USB
Data management system/software

• Relational database
• Phenotypic, genotypic data
• Experimental design preparation
• Design crossing blocks
• Field/lab books
• Data collection
• Data sharing
• Data analysis
• Data query
• Decision tools
• User friendly
• Different access control levels
Plant breeding data management software: **AGROBASE**, **PRISM**, **KATMANDOO**
Important aspects for consideration

Standard and Uniform

✓ Pedigree system
✓ Nomenclature of experimental lines, crosses, hybrids, etc.
✓ Experimental design
✓ Data collection
✓ Traits (‘Trait dictionary’)
✓ Treatments (definition, format, units, protocols)
✓ Locations
Archival of data and documents

- Inventories/crossing books
- Inbred lines/varieties
- A, B, R lines
- Segregating populations
- General crossing books
- CMS hybrid books
- Seed availability
- Multi-location, multi-year data
  - Agronomic
  - disease/pests
  - Georeferences
  - Weather
  - Soil
- Publications & reports
Some immediate benefits

Save time and money, improve efficiencies and reduce errors

- Save time in data capture
- No waiting for data entry clerks to capture data
- Data cleaning hardly required
- Automatic data validation and checking
- Possibility of reusing templates
- Save paper, ink

Additional benefits

- Data immediately available for analysis
- Simplified data analysis
- Faster breeding decisions
Outputs of the data management system

- New discoveries based on exploring historical data
- Information for use in new data-driven research
- Preservation of scholarly outputs
- Facilitate data/information queries and sharing
- Meet requirement of funding agencies (data management, retention and access)
Integrated Breeding Workbench

The IBP Configurable Workflow System

Breeding Activities

- Project Planning
  - Open Project
  - Specify objectives
  - Identify team
  - Data resources
  - Define strategy

- Germplasm Management
  - Parental selection
  - Crossing
  - Population development

- Germplasm Evaluation
  - Experimental Design
  - Fieldbook production
  - Data collection
  - Data loading

- Molecular Analysis
  - Marker selection
  - Fingerprinting
  - Genotyping
  - Data loading

- Data Management
  - Data loading
  - Data cleaning
  - Quality Assurance

- Data Analysis
  - Trait analysis
  - Genetic Analysis
  - QTL Analysis
  - Index Analysis

- Breeding Decisions
  - Selected lines
  - Recombinants
  - Recombination plans

Breeding Applications

- Workbench administration & configuration
- Strategic simulation
- Molecular breeding design
- Query applications
- Nursery manager
- Field book application
- Lab book application
- Quality assurance application
- Statistical analysis applications
- Decision support applications: MABC MAS MARS GWS
A Molecular Breeding Information System

Key Information System
- ST: Sample Tracking
- PIM: Pedigree Information
- LIMS: Laboratory Information
- FDM: Field Data
- A&DS: Analysis & Decision Support

Platform Services
- Genetic Resource Service
- Marker Service
- Trait Service

GRSS

Genetic Resources

Parental Material
- Choose parental material based on haplotype values, known genes, traits and adaptation
- Develop crossing scheme based on genotype and phenotype compatibility

Crossing Block
- Pedigree information updated

Nursery 1
- Selection of lines based on QTL analysis / estimation of marker breeding values
- Pedigree information updated

Nursery 2
- n cycles of selection and recombination

Evaluation Trials
- Selection on index of marker values
- Multi-location testing
- Selection of improved lines based on trait improvement and adaptation

Improved Lines
- Pedigree information updated

Public Crop Information

Breeding Information System

High density genotyping
Phenotypic characterization
High density genotyping
Phenotypic evaluation
Marker genotyping
Multi-location testing

Cultivars and breeding lines
Outputs

- Improved pure lines (varieties)
- Improved parental lines
- Identification of best hybrid combinations
- Genetic knowledge of fertility restoration, heterosis, FW, SMD, WL, etc.
- CMS hybrid production technology
- Molecular breeding
- Data management system
- Formal courses in breeding, genetics and seed production
- Training technicians, farmers, graduate students, scientists
- Consultancies
Funding

International sources
- Climate change (drought, water logging)
- Poverty alleviation (tech. transfer)

National (India) sources
- Molecular genetics
- Molecular breeding
- Expansion of hybrids
Thank you!