
Conserving and mining plant genetic resources using knowledge of the genome

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Conserving and mining PGR

- introduction
 - PGR management
 - new approaches and tools
- molecular marker applications in PGR management
 - detailed case study (apple)
 - brief snapshots of selected CGN research
- Generation Challenge Programme
 - genomic approaches to mining PGR
- conclusions

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Conserving and mining PGR

- plant genetic resources (PGR) conservation evolved from classical taxonomy: qualitative approach
 - number of accessions rather than diversity captured
 - 'having it' more important than 'knowing it'
- State of the World (FAO 1996)
 - 6.1 million accessions in 1308 collections
 - major crops
 - wheat 774 500 accessions
 - barley 485 000 accessions
 - rice 408 500 accessions
 - maize 277 000 accessions

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- current trend *ex situ* PGR management
 - from qualitative
 - collecting, documenting, evaluating individual accessions
 - to quantitative
 - optimising genebank management strategies by approaching the collection as a whole
 - screening large parts of the collections with genomics based techniques

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■ new approaches

- improving genebank efficiency and quality
 - genebank economy
 - genebank quality management
 - accession management
- stimulating use
 - web interfaces
 - search strategies
 - identifying new alleles

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■ new tools

- molecular genetics
 - marker technology
 - allele mining techniques
- information and communication technology
 - Internet
 - bioinformatics

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- application molecular markers in PGR management
 - acquisition
 - improving sampling strategies
 - identifying gaps and improving composition
 - maintenance
 - measuring and reducing genetic drift/shift
 - observing contamination
 - characterization
 - fingerprinting / diversity studies
 - utilization
 - creation of core collections
 - allele mining

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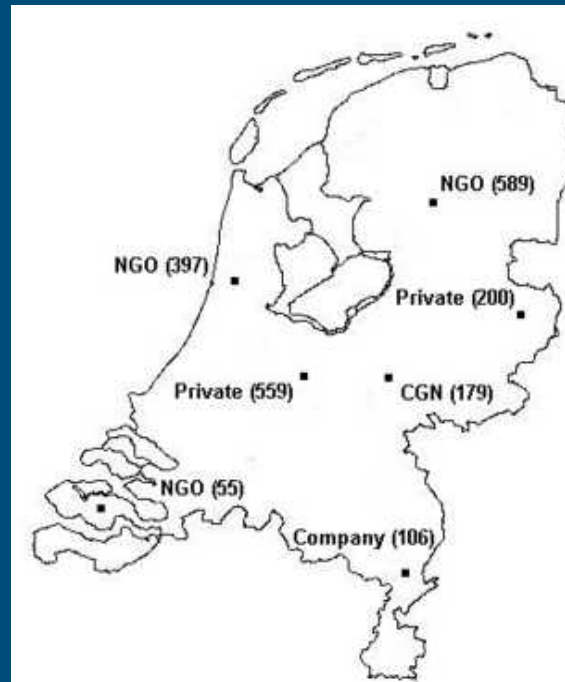
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- examples use molecular markers at CGN
 - support Dutch apple NGO's
 - detailed description
 - various other examples CGN studies using molecular markers to improve PGR management
 - lettuce
 - potato
 - white cabbage
 - barley
 - ryegrass
 - flax
 - Dutch grasslands
 - enset

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- molecular study of Dutch apple collections
 - total ~2000 accessions



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■ molecular study of Dutch apple collections

● interest CGN

- to improve knowledge of diversity in genetic resources of apple in the Netherlands
- to determine the degree of representation of CGNs collection
- to improve efficiency of conservation by supporting actors

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- molecular study of Dutch apple collections
 - study material for microsatellite analysis
 - entire collection of CGN
 - selection from 8 other collections
 - proper documentation
 - Dutch origin
 - foreign material that has been important for cultivation in the Netherlands
 - total sample size: ~700 trees



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■ molecular study of Dutch apple collections

● selection of apple microsatellite markers

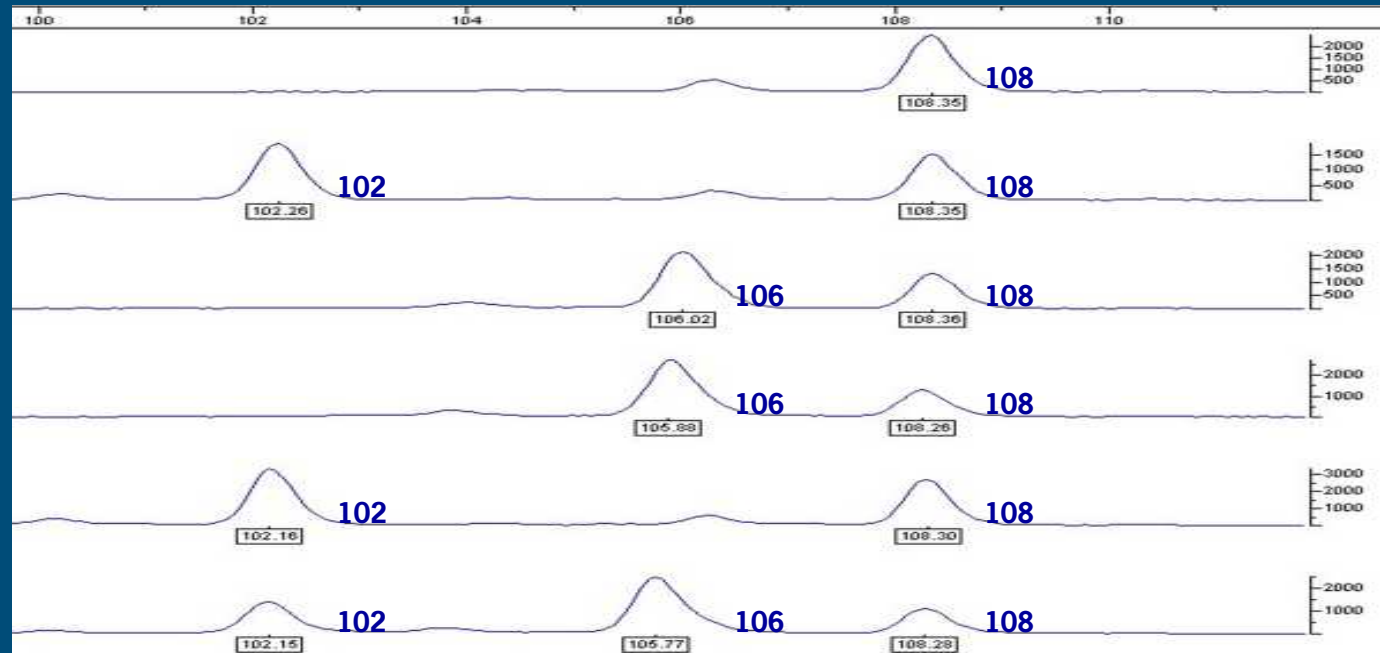
- literature: 150-200 microsatellites
- selection criteria
 - technical qualities
 - degree of variability
 - genome coverage
 - proximity to important genes
 - linkage of data to other studies
- 16 markers selected
 - 11 of the 17 chromosomes covered
 - traits: scab resistance, canker resistance, aphid resistance, firmness, malic acid, allergy genes



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- molecular study of Dutch apple collections
 - identification of microsatellite variation



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- molecular study of Dutch apple collections
 - resolution of the microsatellite markers
 - observed number of alleles
 - 3 - 37 alleles per microsatellite
 - 296 alleles for the total set of 16 microsatellites
 - 18.5 alleles on average per microsatellite
 - probability to find identical genotypes by chance
 - depending on frequencies of the alleles in total sample
 - estimation: $6.4 \times 10^{-20} = 0.0000000000000000000064$

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- molecular study of Dutch apple collections
 - potential duplicates
 - duplication groups based on passport data
 - number of groups: 138
 - total number of trees: 355
 - verification with microsatellite data
 - duplicates confirmed: 147 (41%)
 - duplicates rejected: 202 (57%)
 - to be determined: 6
 - majority of potential duplicates are different despite similarity in accession name

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- molecular study of Dutch apple collections
 - example of confirmed duplicates

| Collection | POM-ABD | | | CGN | | | FRU/NPV | | | KRU/BAA | | |
|--------------|------------|-----|-----|--------------|-----|-----|--------------|-----|-----|-----------------|-----|-----|
| Variety name | Notaris Ko | | | Notarisappel | | | Notarisappel | | | Notarisappel WF | | |
| Marker 1 | 151 | 159 | 161 | 151 | 159 | 161 | 151 | 159 | 161 | 151 | 159 | 161 |
| Marker 2 | 156 | 166 | 173 | 156 | 166 | 173 | 156 | 166 | 173 | 156 | 166 | 173 |
| Marker 3 | 242 | 254 | | 242 | 254 | | 242 | 254 | | 242 | 254 | |
| Marker 4 | 145 | 147 | 176 | 145 | 147 | 176 | 145 | 147 | 176 | 145 | 147 | 176 |
| Marker 5 | 160 | 162 | | 160 | 162 | | 160 | 162 | | 160 | 162 | |
| Marker 6 | 153 | 155 | 161 | 153 | 155 | 161 | 153 | 155 | 161 | 153 | 155 | 161 |
| Marker 7 | 164 | 186 | 188 | 164 | 186 | 188 | 164 | 186 | 188 | 164 | 186 | 188 |
| Marker 8 | 95 | 103 | | 95 | 103 | | 95 | 103 | | 95 | 103 | |
| Marker 9 | 170 | 178 | | 170 | 178 | | 170 | 178 | | 170 | 178 | |
| Marker 10 | 123 | 125 | 137 | 123 | 125 | 137 | 123 | 125 | 137 | 123 | 125 | 137 |
| Marker 11 | 218 | 220 | 262 | 218 | 220 | 262 | 218 | 220 | 262 | 218 | 220 | 262 |
| Marker 12 | 178 | 182 | | 178 | 182 | | 178 | 182 | | 178 | 182 | |
| Marker 13 | 220 | 232 | 254 | 220 | 232 | 254 | 220 | 232 | 254 | 220 | 232 | 254 |
| Marker 14 | 207 | 209 | | | | | 207 | 209 | | 207 | 209 | |
| Marker 15 | 210 | | | 210 | | | 210 | | | 210 | | |
| Marker 16 | 120 | | | 120 | | | 120 | | | 120 | | |

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- molecular study of Dutch apple collections
 - potential duplicates based on marker data
 - total sample: 695 trees
 - duplicate groups: 119
 - number of trees involved: 339
 - redundancy: 220 (32%)
 - observed genotypes: 475 (68%)
 - unexpected duplicates
 - 66% of the observed groups
 - majority of identical microsatellite genotypes are not in line with the passport data

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- molecular study of Dutch apple collections
 - example unexpected duplication group
 - CGN Reinette Rouge Etoilée
 - ROSSEL Sterappel
 - POM-JON Paradijszoet
 - KRU/BAA Dubbele ster
 - FRU/NPV Duchesse's Favourite

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- molecular study of Dutch apple collections
 - potential redundancy per collection
 - potential redundancies (220)
 - within collections 73 (33%)
 - between collections 147 (67%)
 - majority of redundancies are between collections

| Collection | FRU/NPV | CGN | KRU/BAA | ROSSEL | POM-BEE | POM-JON | FRIJNS | POM-ABD | Total set |
|-------------------------|---------|------|---------|--------|---------|---------|--------|---------|-----------|
| # Analyzed trees | 241 | 175 | 80 | 78 | 60 | 30 | 16 | 15 | 695 |
| # Internal redundancies | 36 | 19 | 3 | 10 | 0 | 0 | 1 | 4 | 220 |
| % Internal redundancies | 14.9 | 10.9 | 3.8 | 12.8 | 0.0 | 0.0 | 6.3 | 26.7 | 31.7 |

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- molecular study of Dutch apple collections
 - unique diversity within collections
 - each collection consists for about half of unique genotypes
 - majority of the alleles occurs in multiple collections

| Collection | FRU/NPV | CGN | KRU/BAA | ROSSEL | POM-BEE | POM-JON | FRIJNS | POM-ABD | Total set |
|--------------------|---------|-----|---------|--------|---------|---------|--------|---------|-----------|
| # Analyzed trees | 241 | 175 | 80 | 78 | 60 | 30 | 16 | 15 | 695 |
| # Unique genotypes | 125 | 104 | 38 | 38 | 30 | 12 | 8 | 1 | 356 |
| # Observed alleles | 210 | 237 | 203 | 175 | 149 | 134 | 122 | 97 | 296 |
| # Unique alleles | 13 | 37 | 17 | 9 | 0 | 2 | 0 | 0 | 78 |

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- molecular study of Dutch apple collections
 - management implications apple study
 - improvement of documentation
 - improvement of variety determination
 - identification of redundancies and removal of internal duplicates
 - identification of unique material (guidelines for safety duplication)
 - formation of a network of co-operating collections

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- optimization of protocol for adding modern lettuce varieties to CGN collection
 - comparison new varieties with CGN collection
 - information from breeders
 - microsatellite study
 - outcome: improved protocol to select varieties with highest added value



Treuren et al. 2008, GRACE 55: 319-330.

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- reduction size CGN's potato collection
 - about 2000 accessions
 - 110 wild species
 - 314 accessions of the series Acaulia
 - AFLP study
 - taxonomic validation
 - sampling strategies
 - outcome: considerable rationalization and optimisation collection strategy



McGregor et al. 2002, TAG 104: 146-156.

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- study of diversity and validation regeneration protocol in CGN cabbage collection
 - comparison drift/shift during regenerations with distances between accessions
 - sampling after 'real' regeneration
 - AFLP study
 - outcome: need to improve regeneration protocol or collection composition

Hintum et al. 2007, TAG 114: 777-786.



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- intra-accession variation in barley
 - improvement of regeneration methods
 - avoidance of genetic drift
 - avoidance of selection
 - case study in barley
 - cultivars, landraces and wild material
 - AFLP study
 - outcome: methodological knowledge and recommendations for splitting accessions

Treuren & Hintum 2001, GRACE 48: 287-295.



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- regeneration of perennial ryegrass
 - variation in pollination
 - loss of genetic integrity
 - paternity analysis
 - microsatellite study
 - outcome: methodological knowledge and recommendations for regeneration protocol improvement

Treuren et al. 2006, Euphytica 147: 367-382.



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- redundancy study in flax
 - CGN collection: ~1000 accessions
 - 317 accessions of breeder's lines
 - many similar accession names
 - poorly documented
 - hardly requested for utilisation
 - AFLP study
 - outcome: recommendations for bulking accessions



Treuren et al. 2001, TAG 103: 144-152.

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- development *in situ* conservation strategy for old Dutch grasslands
 - perennial ryegrass, white clover and Kentucky bluegrass
 - comparison of old grasslands to nature reserves and cultivars
 - AFLPs and morphological variation
 - outcome: support to policy decisions for *in situ* conservation



Treuren et al. 2005, Mol Ecol 14: 39-52.

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- study clonal variation in Ethiopian enset
 - on farm conservation in Ethiopia
 - many synonyms
 - AFLP and morphological study
 - identification of duplicates
 - outcome: rationalisation conservation program

Negash et al. 2002, Crop Science 42: 1105-1111.



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■ Generation Challenge Programme

- an international initiative to use genomic science to mine PGR collections of major crops and use it in poor farmers crops
- initiative of the CGIAR



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■ Generation Challenge Programme

● objectives

- utilize plant genetic diversity for crop improvement
 - develop low cost technologies for germplasm genotyping, allele mining and molecular breeding
 - integrate genomics with plant physiology and/or biology
- capacity building and delivery of products
 - create and enable adoption of mechanisms for products to reach end-users

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■ Generation Challenge Programme

● consortium



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■ Generation Challenge Programme

● some facts

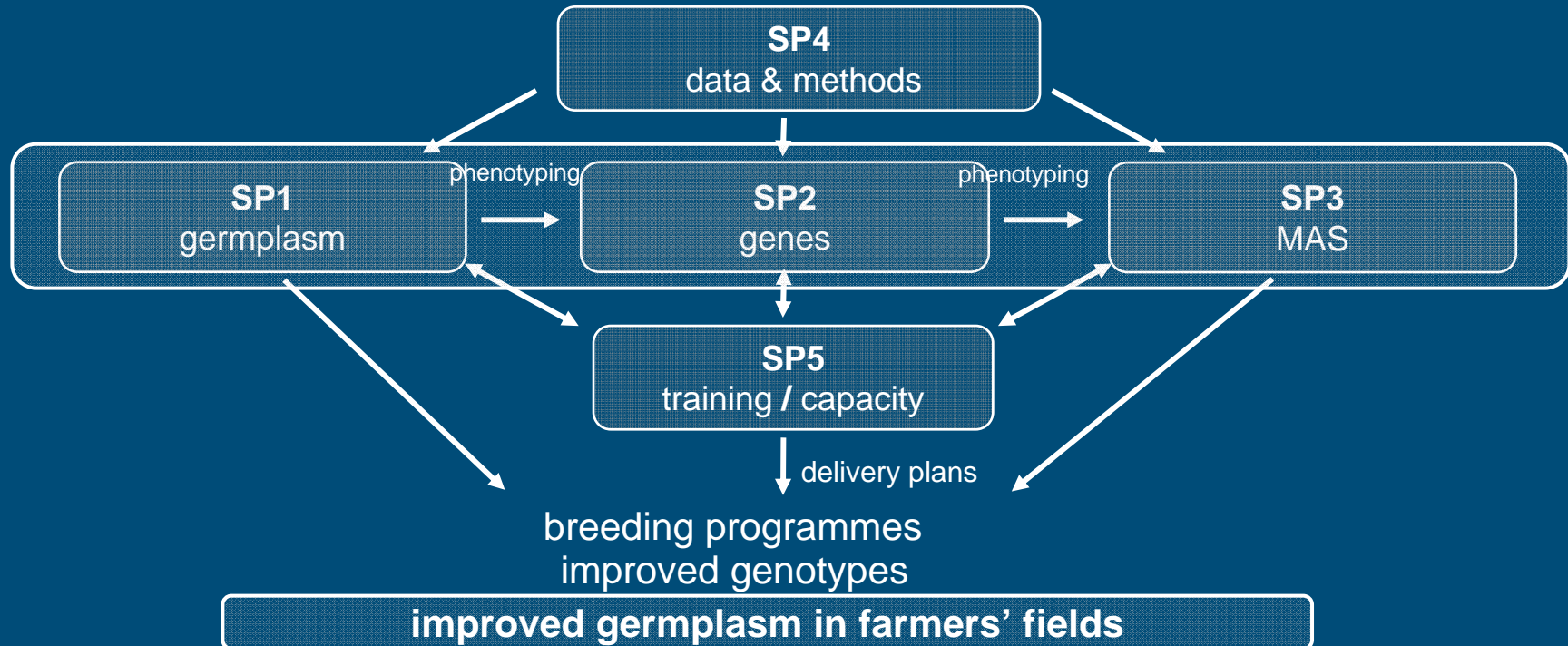
- launched in August 2003 (10 year framework two 5 year periods)
- target areas: marginal environments in Sub-Sahara Africa, Latin America and South East Asia
- mandate crops: all CGIAR crops
- mandate traits: drought tolerance and associated traits
- budget c. \$16M / year of which 70% for research
- major donors
 - European Union
 - UK Department for International Development
 - Bill and Melinda Gates Foundation

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■ Generation Challenge Programme

● research structure



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■ Generation Challenge Programme

- genomics: central component
 - large scale fingerprinting of all crops
 - up to 50 microsatellites x 3000 accessions
 - development hi-throughput technologies / pipelines
 - candidate gene identification
 - forward and reverse genetics
 - QTL analysis
 - allele mining
 - EcoTILLING
 - ‘mining strategies’
 - study of orthologous candidate genes

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■ Generation Challenge Programme

- expected outputs relevant to PGR management
 - knowledge about the diversity in germplasm collections (and methodologies to study this)
 - methods and tools for identifying allelic diversity in germplasm collections based on DNA sequences

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■ conclusions

- molecular marker technology has great potential to improve PGR management
 - but little impact so far
- applications are aimed at specific research questions, not at routine operations
- costs of molecular analysis are still limiting factor in most cases
 - high throughput technology is required

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