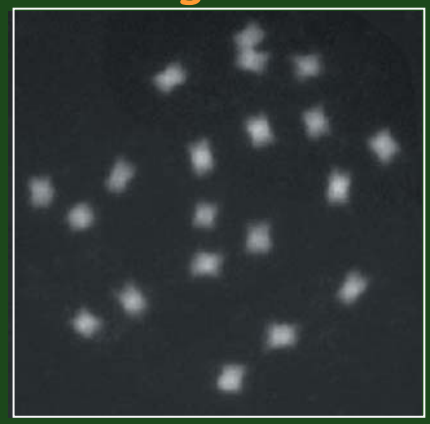
Unlocking the genetic diversity in groundnut's wild relatives

GLIP
Grain Legumes Integrated Project
FOOD-CT-2004-506223

Peanut's genetic bottle-neck

Diploid species with "AA" genome

Diploid species with "BB" genome

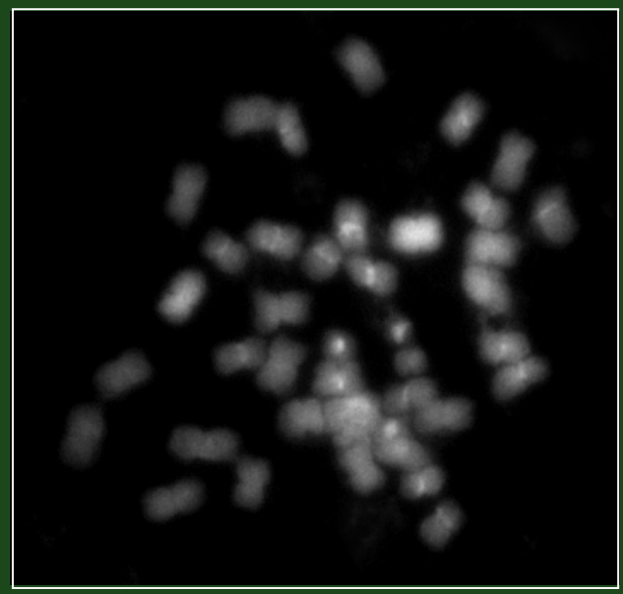


n = 10 x n = 10

Sterile AB hybrid 2n = 20

Genetic bottle-neck !

Spontaneous duplication



Arachis hypogaea

AABB

Project Rationale

A. hypogaea

Few alleles

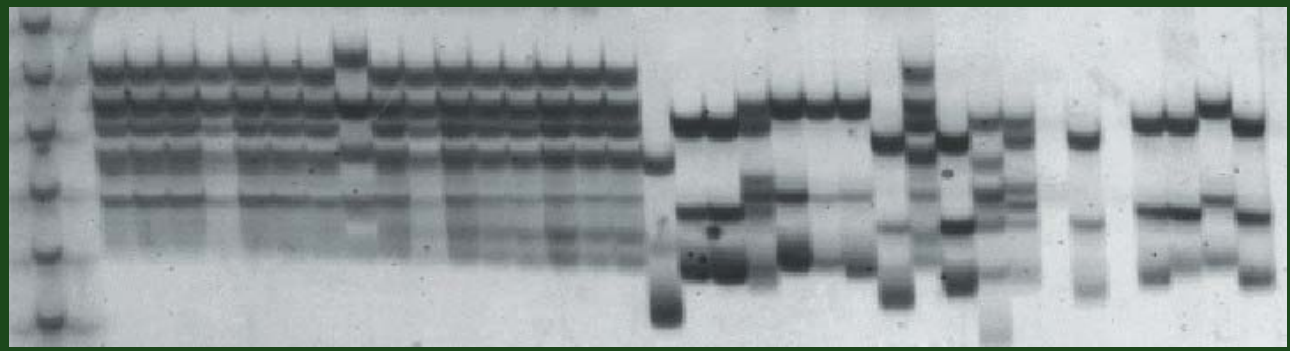
Tetraploid

Wild species:

Many alleles

Diploid

Wild alleles bring many new traits
and provide polymorphism for genetics

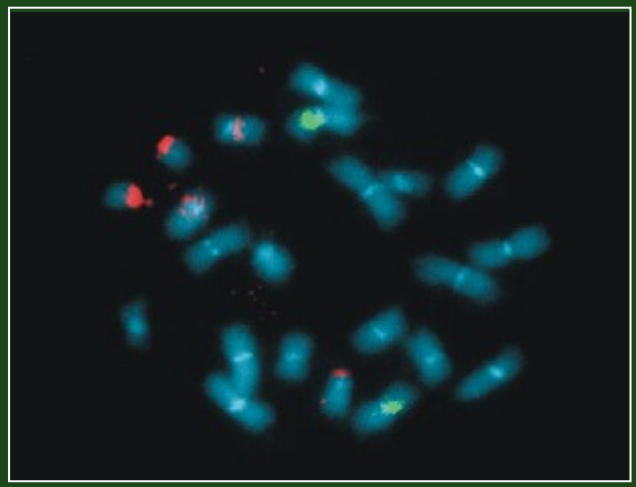


Project Rationale

Resynthesis is a way to introduce variability to cultivated peanut

"A" genome

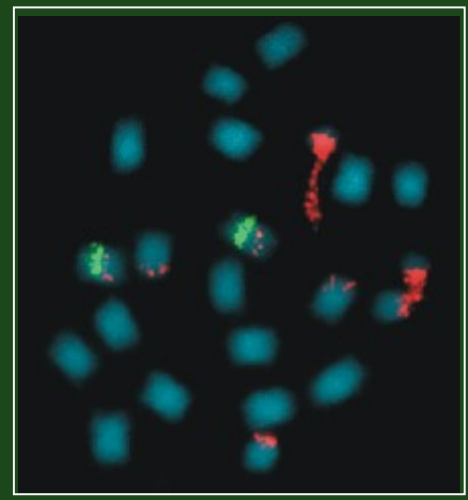
A.duranensis



X

"B" genome

A. ipaensis



Sterile AB F1 hybrid

colchicine

AABB Tetraploid (Synthetic amphidiplo

crossing/backcrossing with *A.hypogaea*

Project Rationale

At Project start

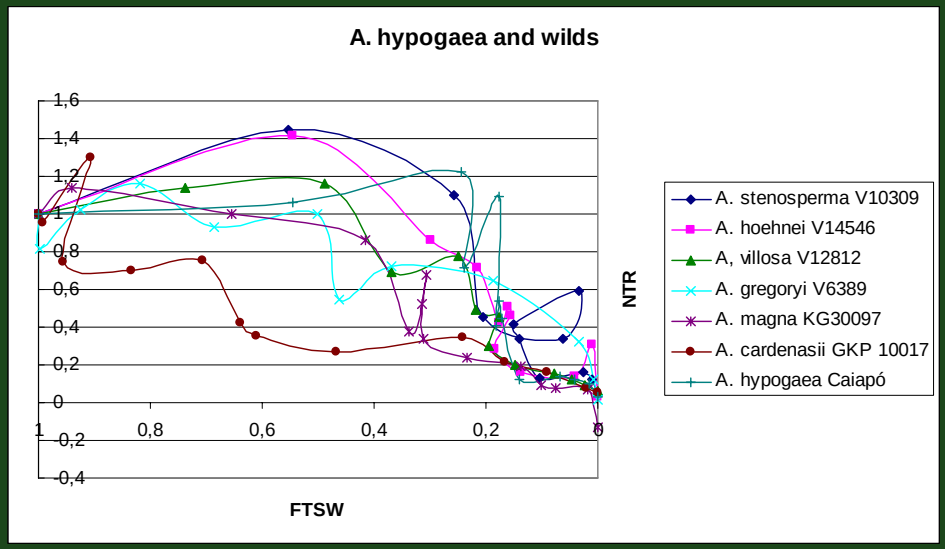
- Only two RFLP maps
- 6 SSR markers published
- Only one case of wild introgression – Charles Simpson

Project aimed for

- Characterization of wild genomes and traits
- Genetic maps and Genomic resources for Molecular breeding
- Introduction of wild genes into breeding programs

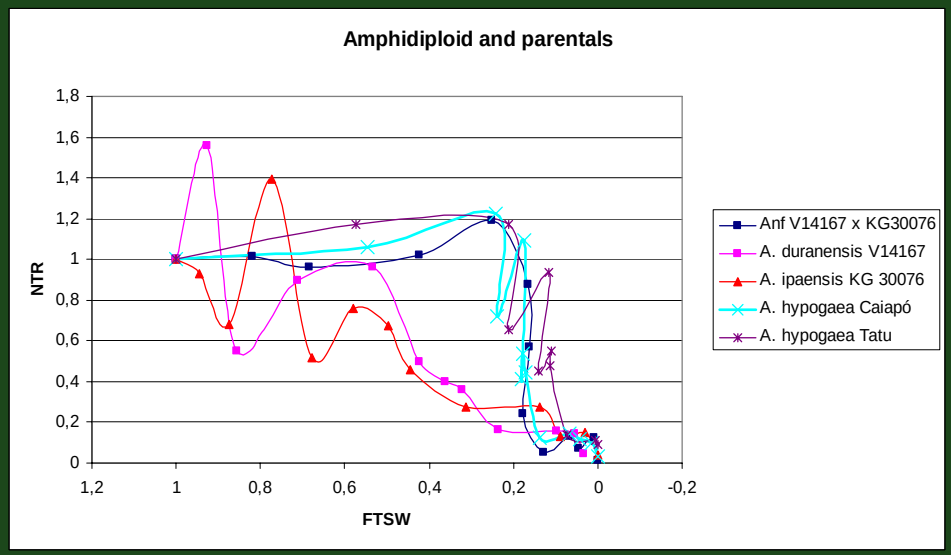
Activities and Results

Wild, synthetic and cultivated drought responses better characterized



Range of transpiration responses

Very high – wilds
Surprisingly high - cultivated

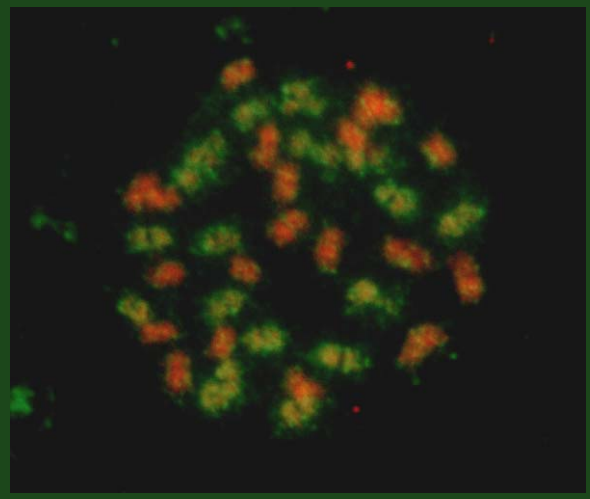


Sythetic amphiploids
are completely different from
parental species

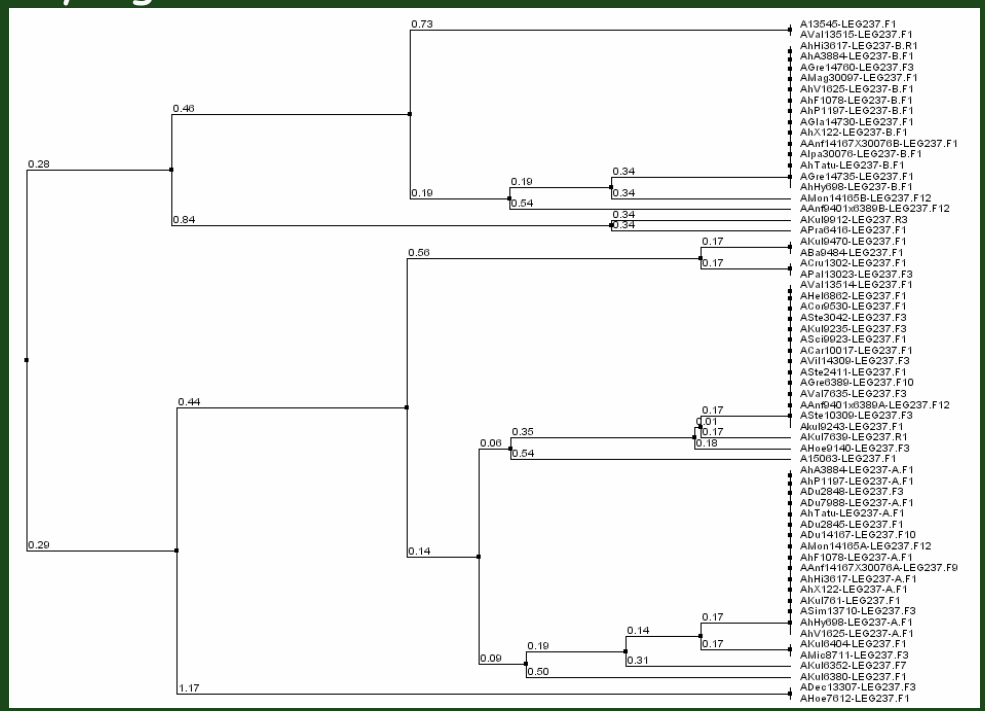
- large effect of ploidy

Activities and Results

Characterization of wild genomes to guide resynthesis



Cytogenetics – FISH and GISH



Wild genomes better characterised

eg.
New potential BB donors
A. williamsii
A. gregoryi
A. valida

New species being used for amphidiploid producion

Single copy gene intron phylogenies

To make maps – we needed markers:

- **Microsatellites - SSRs**

  Co-dominant, transferable between populations

  Useful for plant breeders

  Software and more than 350 SSRs developed ⬅

- **Anchor markers:**

  For comparison of genomes – legume synteny

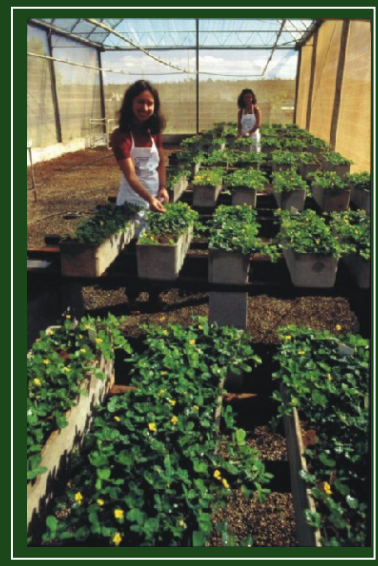
  Software - 450 universal legume anchor primer pairs ⬅

- **Candidate genes:**

  More likely to be linked to traits of interest.

  markers for RGAs and drought response genes ⬅

To make maps - we needed populations



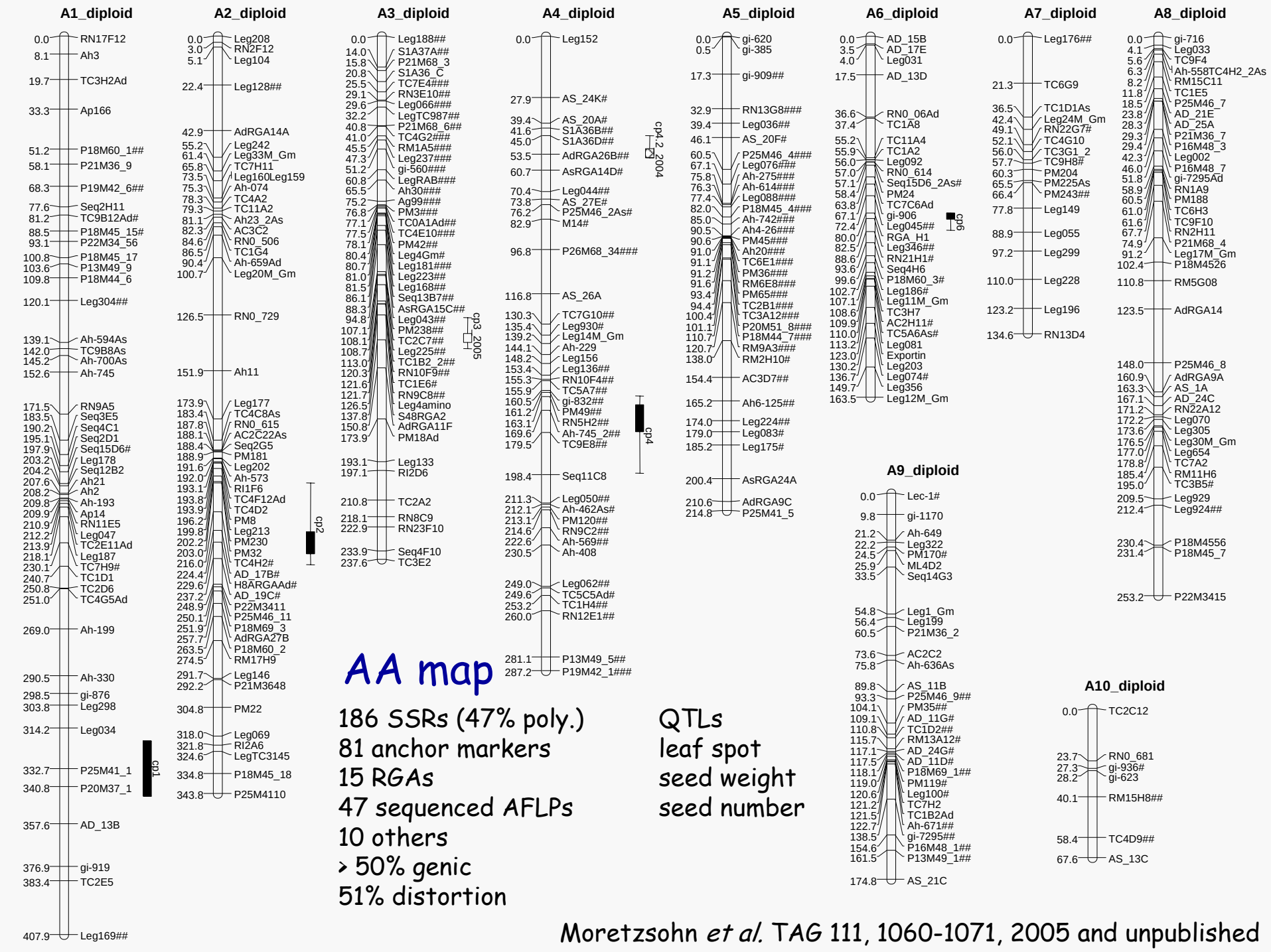
- With wild polymorphism
- To dissect the tetraploid problem
- 2 diploid and one tetraploid population

A.stenosperma
x
A.duranensis

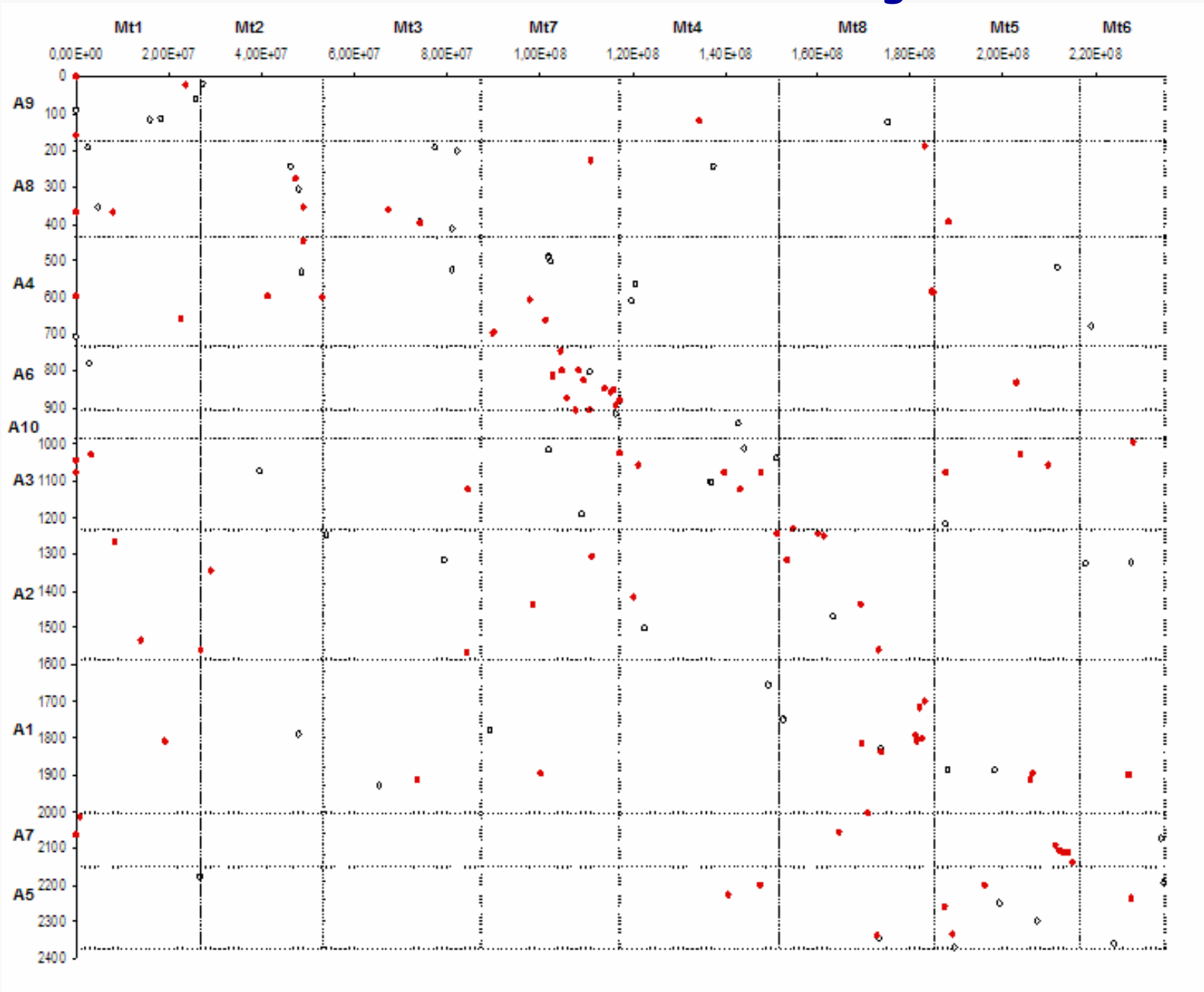
A.magna
x
A.ipaensis

AB
A.hypogaea
x
(*A.duranensis* x *A.ipaënsis*)^{c}

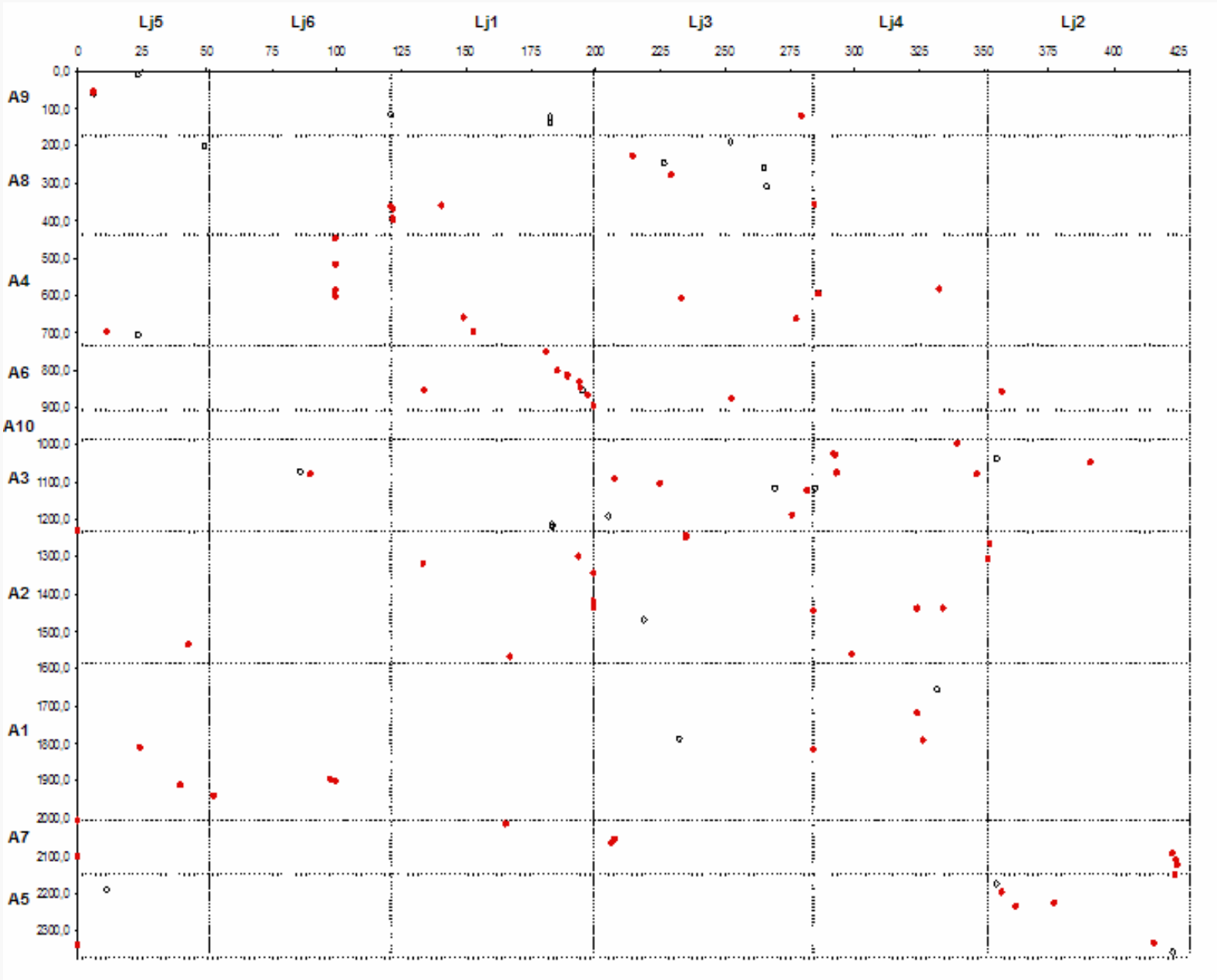
A. hypogaea
x
A. hypogaea


A1_diploid
A2_diploid
A3_diploid
A4_diploid
A5_diploid
A6_diploid
A7_diploid
A8_diploid
A9_diploid
A10_diploid
cp1
cp2
cp3_2005
cp4
cp4.2_2004
cp5
AA map
186 SSRs (47% poly.)
81 anchor markers
15 RGAs
47 sequenced AFLPs
10 others
> 50% genic
51% distortion
QTLs
leaf spot
seed weight
seed number
Moretzsohn et al. TAG 111, 1060-1071, 2005 and unpublished

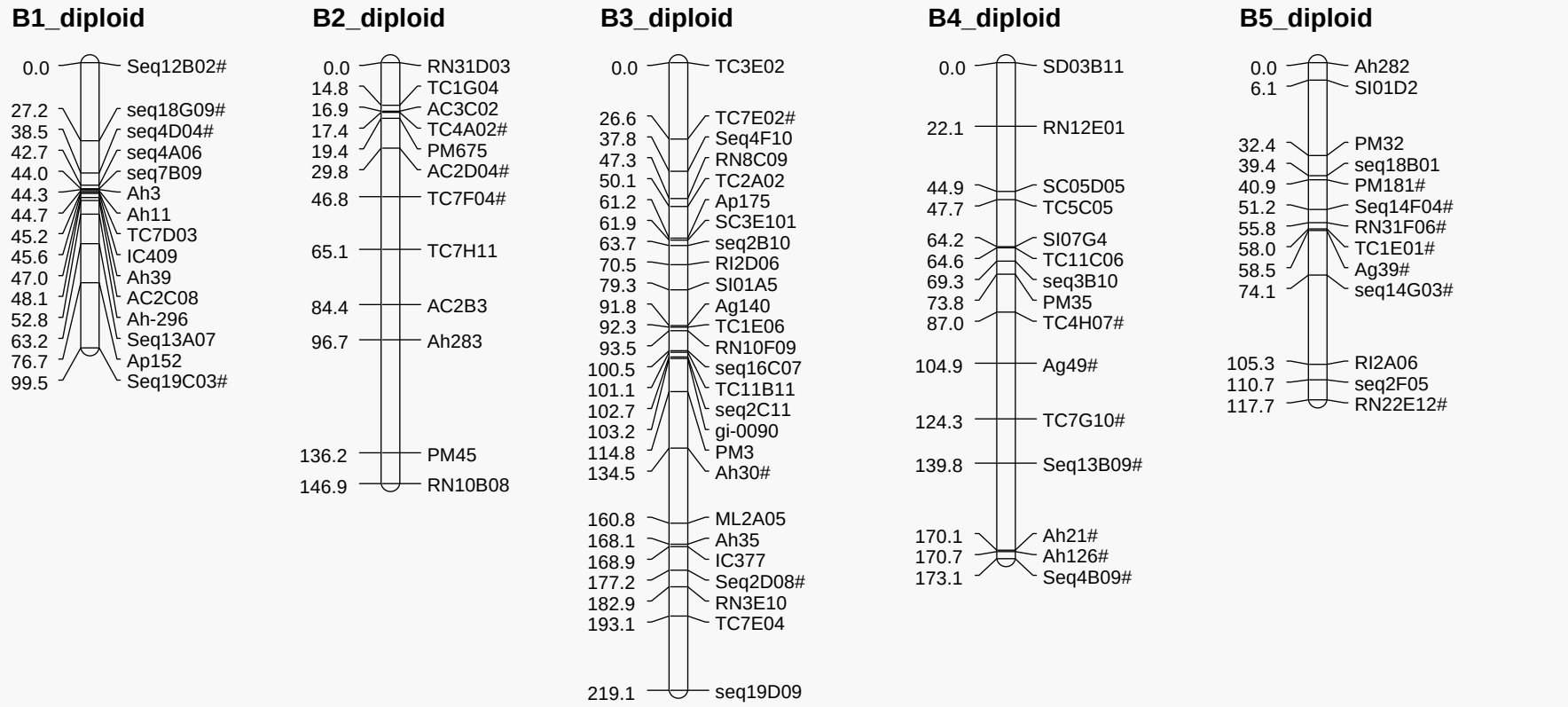
Arachis AA vs Medicago



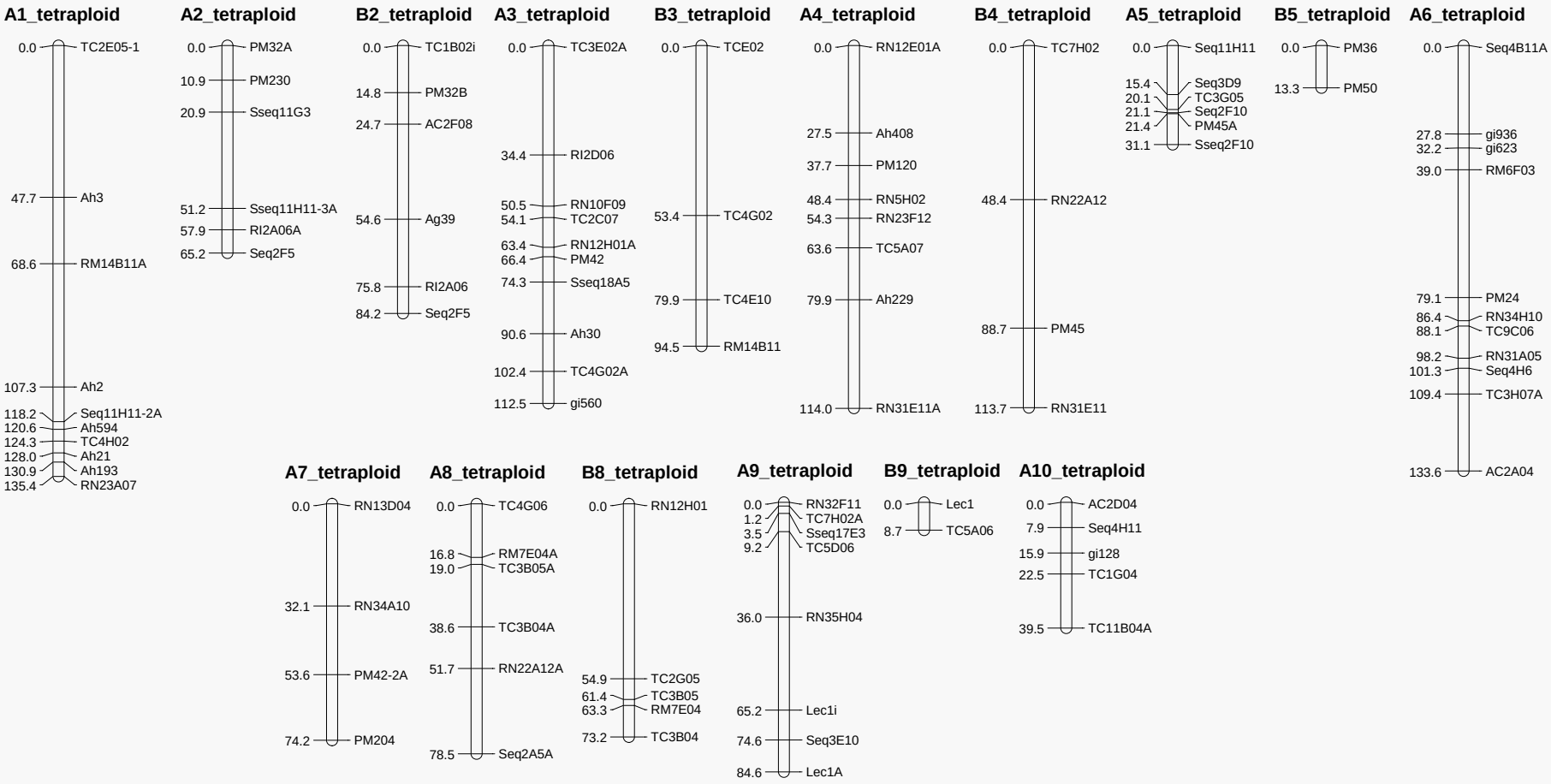
Arachis AA vs Lotus



Activities and Results

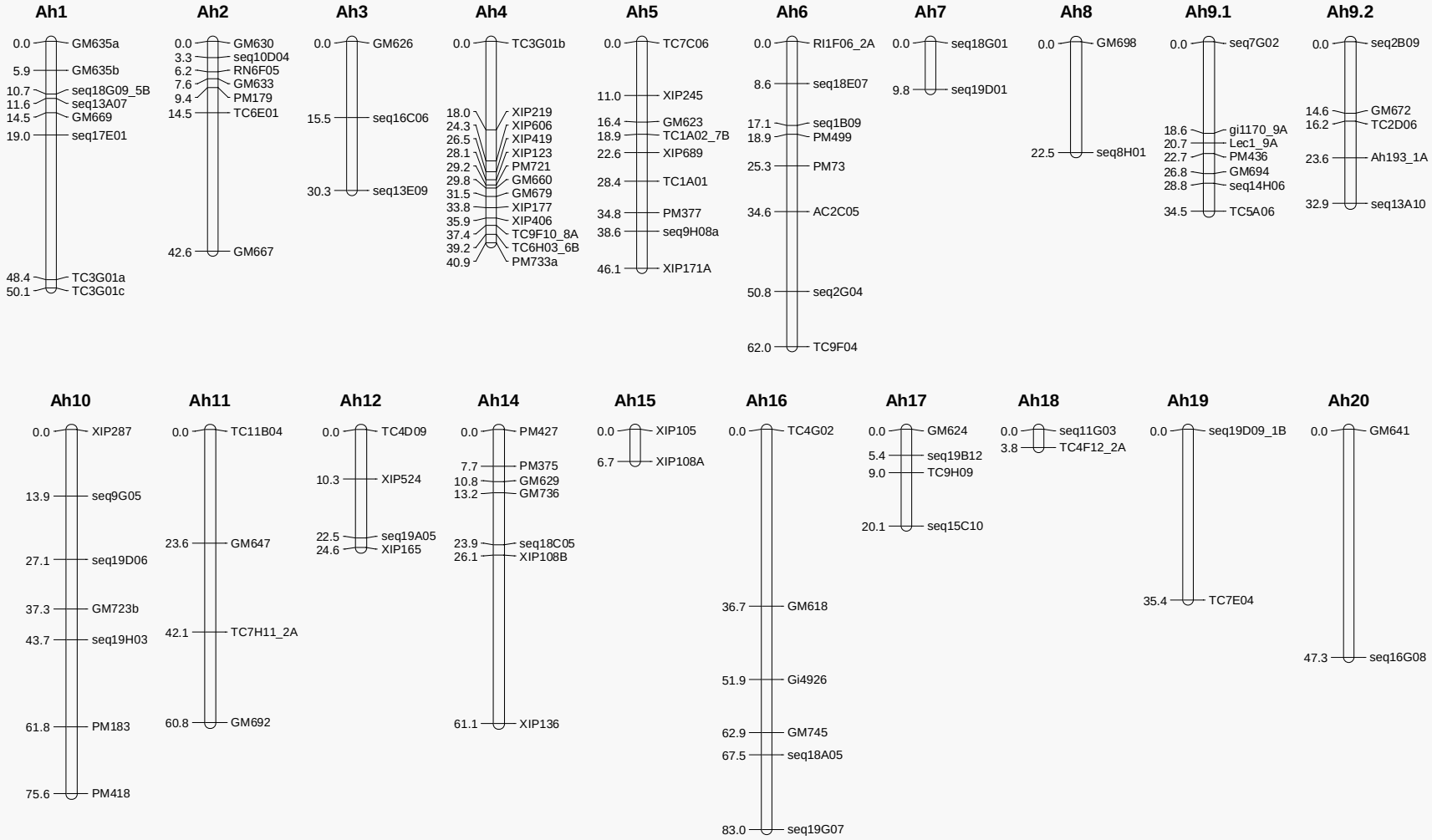


Activities and Results



Synthetic x Cultivated

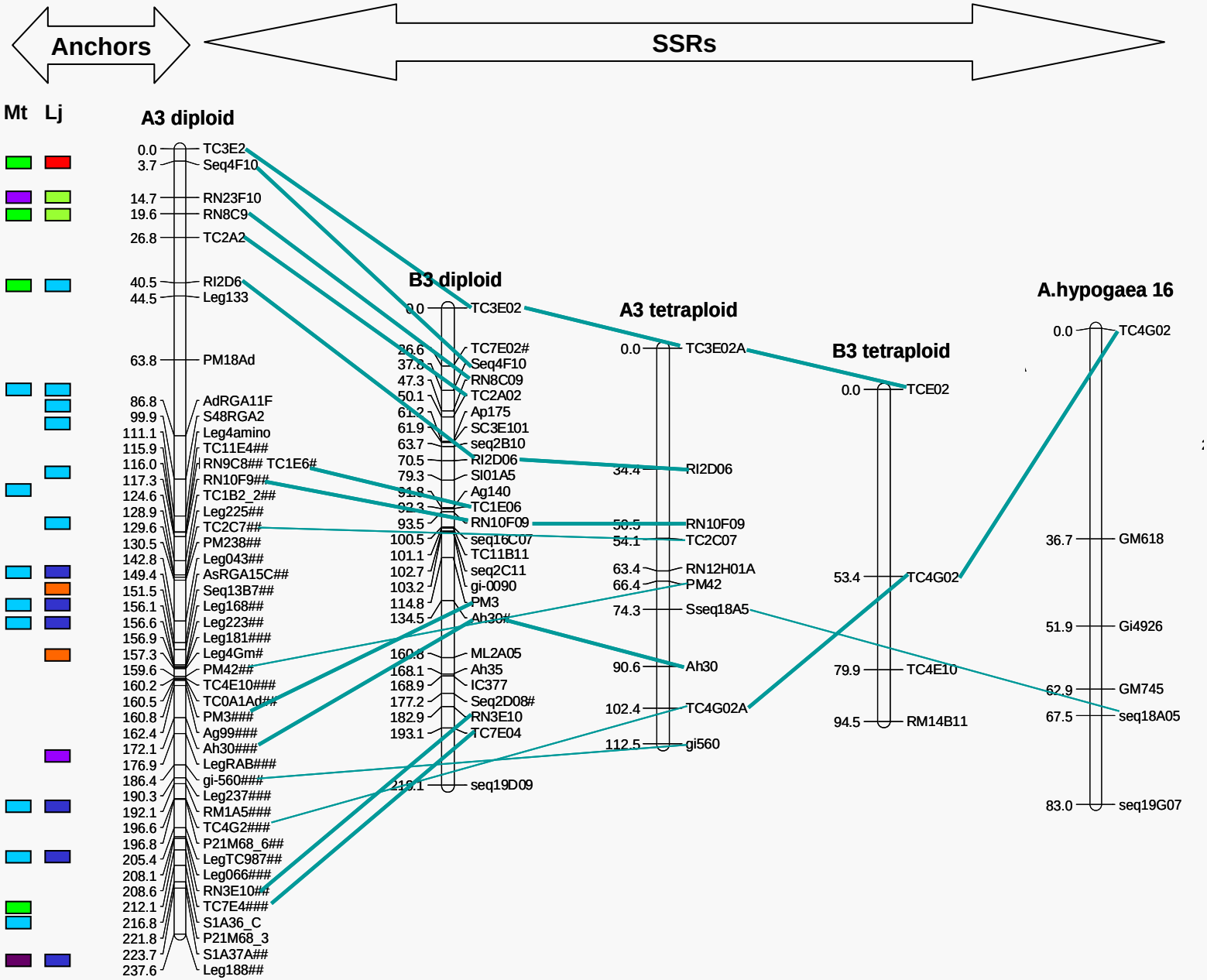
Activities and Results



Cultivated x Cultivated

Activities and Results

Models → Reference diploids → Cultivated



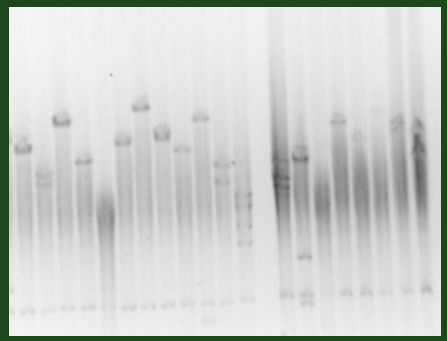
Activities and Results

New Genomic Resources

6,264 ESTs

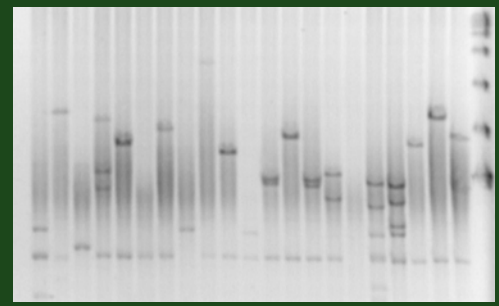
A.stenosperma
x
A.duranensis

BAC (*Hind*III)
c. 80,000 clones
c. 6.5x



A.magna
x
A.ipaensis

BAC (*Hind*III)
c. 80,000 clones
c. 6.5x



AB
A.hypogaea
x
(*A.duranensis* x *A.ipaënsis*)^{c}

A. hypogaea
x
A. hypogaea

subtractive library TAG24 and ICGV86031
water stressed -FTSW 0.11
500 non-redundant candidate sequences

Now's the time to move to the field !

Activities and Results

Incorporation of amphiploids to breeding programs

(*A.ipaensis* x *A.duranensis*)^{c} - EMBRAPA
(*A. gregoryii* x *A. linearifolia*)^{c} - EMBRAPA
[(*A.cardenasii* x *A.diogoi*) x *A.batizocoi*]^{c} - Prof. C. Simpson

Activities and Results

Incorporation of amphiploids to breeding programs

Female parent	Male parent	Generation	Number of seed
Fleur11	AixAd	BC1	336
55-437	AixAd	BC1	333
GC8-35	AixAd	BC1	383
GC8-35	TxAG6	F1	65
73-30	TxAG6	F1	24
IAC-Runner	AixAd	BC1	150
Caiapo	AixAd	BC1	120

→ ILs

Data Format and Release

ESTs from a wild *Arachis* species for gene discovery and marker development 2007 BMC Plant Biology, 7:7 doi:10.1186/1471-2229-7-7 *Open Access Journal*
All marker information at:
http://www.biomedcentral.com/content/supplementary/1471-2229-7-7-S1.xls
EST sequences have been submitted to Genbank. (numbers EH041934- EH048197)

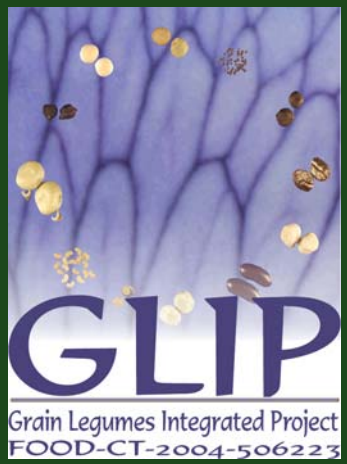
A general pipeline for the development of anchor markers for comparative genomics in plants 2007 BMC Genomics 2006, 7:207 *Open Access Journal*
Table of anchor markers available at:
http://cgi-www.daimi.au.dk/cgi-chili/GeneticMarkers/table

GeMprospector - Online Design of Cross-Species Genetic Marker Candidates in Legumes and Grasses. Nucleic Acids Research 34 (Web Server issue): W670-W675 *Open Access Journal*
The web program GeMprospector available at:
http://cgi-www.daimi.au.dk/cgi-chili/GeMprospector/main

Microsatellite based, gene-rich linkage map for the AA genome of *Arachis* (Fabaceae). 2005 Theoretical and Applied Genetics. 111:1060-1071.
Genetic map info in paper.
All marker information at:
http://dx.doi.org/10.1007/s00122-005-0028-x

New softwares for automated microsatellite marker development. 2006 Nucleic Acids Research, 34 (Web Server issue): E31. *Open Access Journal*
Software available at:
http://finder.sourceforge.net/

Links with other projects



Generation

GCP - TLI

Improving tropical legume productivity for marginal environments in sub-Saharan Africa

GCP – Capacity building Grant

Application of molecular tools for controlled wild introgression into Peanut cultivated germplasm in Senegal

ICRISAT
India
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Rajeev Varshney
Aruna Rupakula
David Hoisington

UCB, Brazil
David Bertioli
Ana Carolina José
Dione Mendes
Rinaldo Perreira

UCG, Brazil
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Jens Stougaard
Leif Schauser
Birgit Hougaard
Anna Marie Nielsen
Jakob Fredslund
Lene Madsen
Niels Sandal

Kazusa DNA Research Institute
Satoshi Tabata

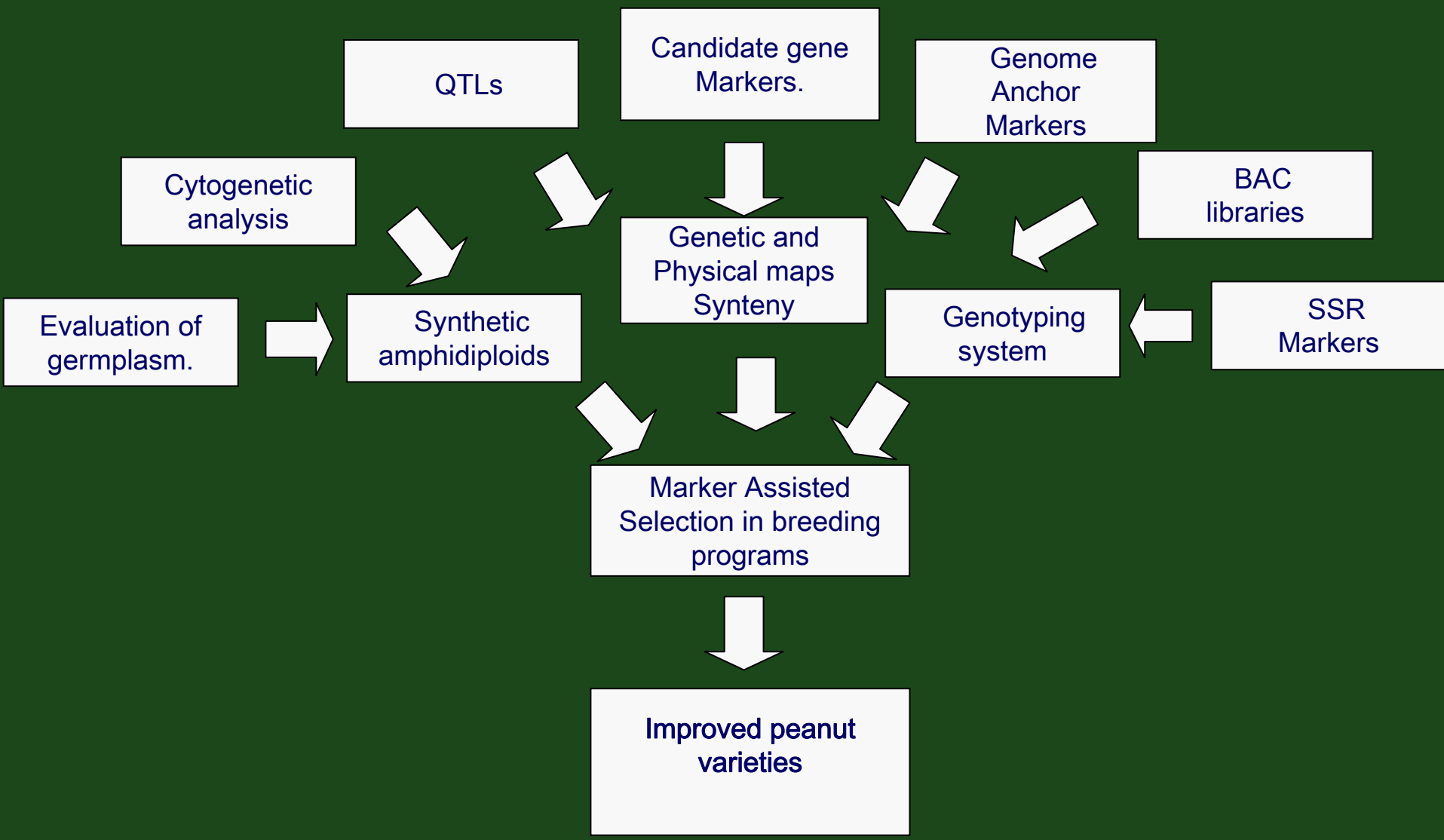
EMBRAPA, Brazil
Soraya Bertioli
Marcio Moretzsohn
Patricia Messenberg
José Valls
Karina Proite
Stephan Nielen
Ana Cristina Brasileira
Simone Ribeiro
Marcos Gimenes
Alessandra Favero
Fernando Campos

CIRAD
France
Angelique d'Hont
Olivier Garsmeur
Jean-Francois Rami

IBONE, Argentina
Guillermo Seijo

CERAAS/ISRA- Senegal
Ousmane Ndoye
Issa Faye

Summary


QTLs
Candidate gene Markers.
Genome Anchor Markers
Cytogenetic analysis
BAC libraries
Genetic and Physical maps Synteny
Evaluation of germplasm.
Synthetic amphidiploids
Genotyping system
SSR Markers
Marker Assisted Selection in breeding programs
Improved peanut varieties