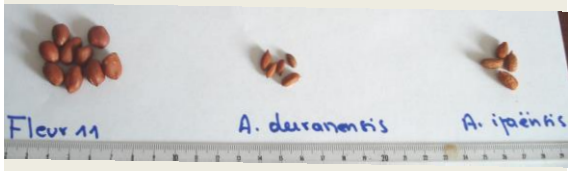
Could small-seeded wild relatives of cultivated peanut be used to increase the size of peanut seeds?

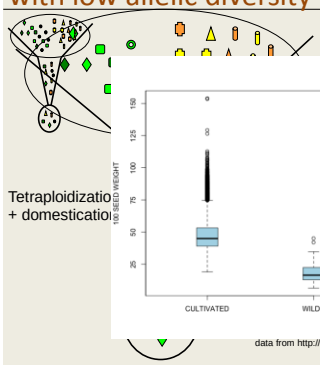


Fonceka D., Tossim H-A, Nguepjop J.R., Bertioli D., Leal-Bertioli S., Jackson S., Rami J.F., Ozias-Akins P.,
PAG– Junuary 2018

Peanut: important food and cash crop

- Peanut (*Arachis hypogaea* L.) is cultivated in about 120 countries in the world
- Peanut is mainly used to produce edible oil and for human and animal consumption.

Cultivated peanut: Allotetraploid (AABB) with low allelic diversity

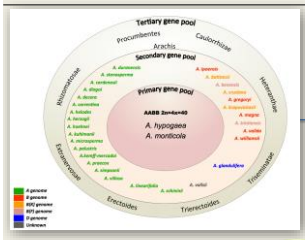


Tetraploidizatio
+ domesticatio

data from http://www.ars-grin.gov

- Genome duplication
- Domestication
- Genetic improvement
- How about the allelic diversity that remains in wild species?

Exploiting the wide diversity within peanut wild relatives



- Synthetic tetraploids from different wild diploid species genomes
- Molecular markers
- Peanut breeding using wild relatives

Widening the genepool of cultivated peanut

A. duranensis

A. ipaensis

A. valida

ISATGR 278-18

X

A. hypogaea
Var Fleur11

F_1 between ISATGR 528 x Fleur11

ICRISAT

Widening the genepool of cultivated peanut

A. ipaensis

A. correntina

A. villosa

X

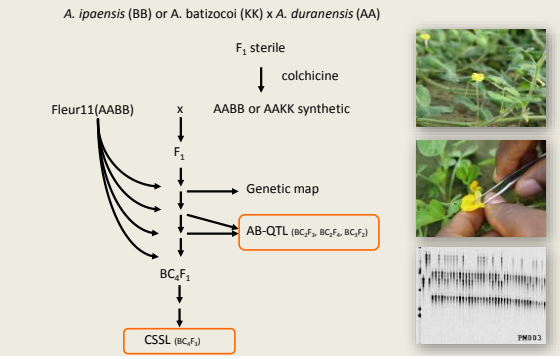
A. hypogaea
Var Fleur11

X

A. batizocoi *A. stenosperma*

The University of Georgia

Population development using (*A. ipaensis* x *A. duranensis*)^{4x} and (*A. batizocoi* x *A. duranensis*)^{4x}

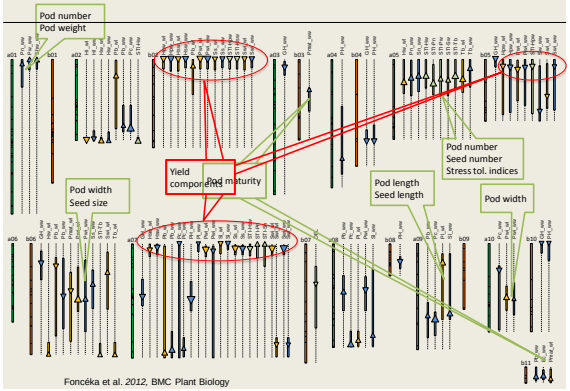


AB-QTLs phenotyping in Senegal

AB-QTLs

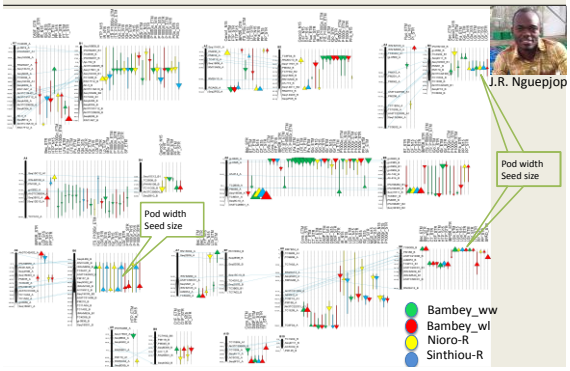
- 2 years, three locations under rainfed or off-season environnements
- Several traits including
  - Biomass
  - Plant, pod and seed morphology
  - Yield components
- Alpha-lattice design
  - 3 replication per location

Fleur11 x AiAd:95 QTLs for 28 traits in 2 env.



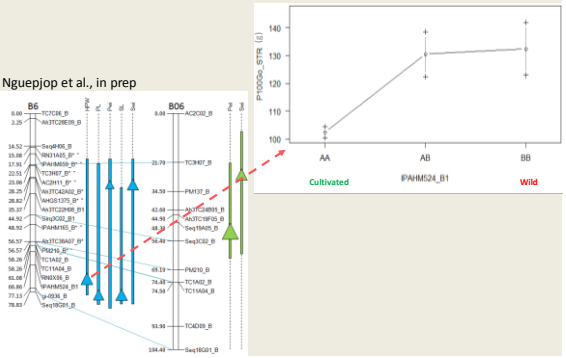
Foncéka et al. *2012*, BMC Plant Biology

Fleur11 x AbAd:232 QTLs for 37 traits in 4 env.

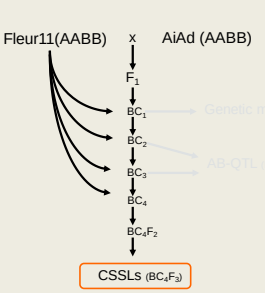


B6 chromosome contributed favorable alleles for seed size

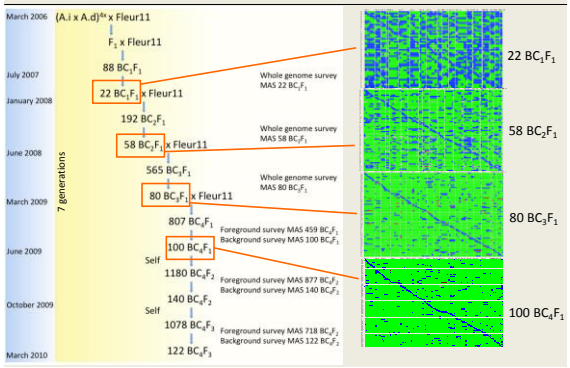
Nguepjop et al., in prep



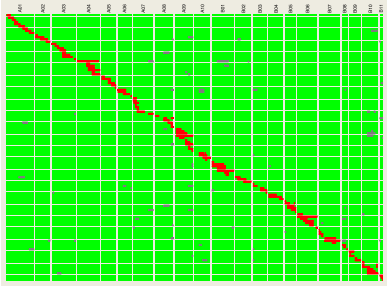
CSSLs development



CSSLs development: breeding scheme



The CSSL Population

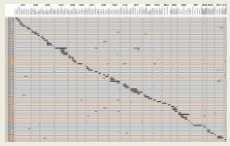


- ✓ 122 CSSLs
- ✓ 92% coverage of the map
- ✓ 39.5 cM on average
- ✓ 72 lines have an unique segment

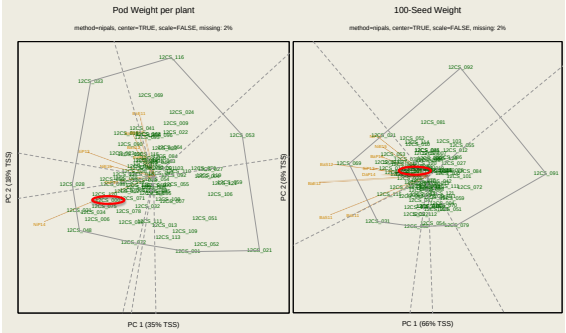
Foncéka et al. *2012* Plos ONE

CSSL analysis: phenotyping in Senegal

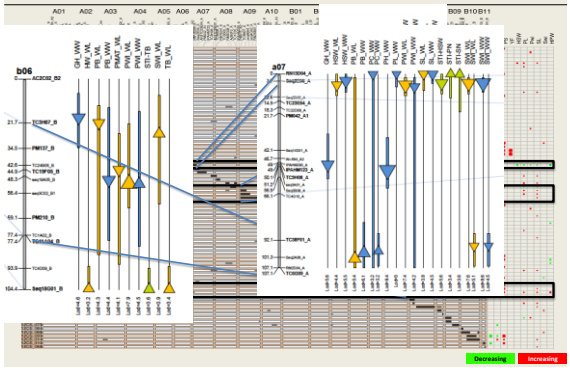
- Subset of 80 CSSLs
- 4 years in 5 locations under rainfed and irrigated conditions totalizing 12 env.
  - Alpha-lattice design
  - 3 replications/location
- Plant architecture
- Yield components



Results from 9 environnements: PW, HSW



Seed size QTL validation using the CSSL

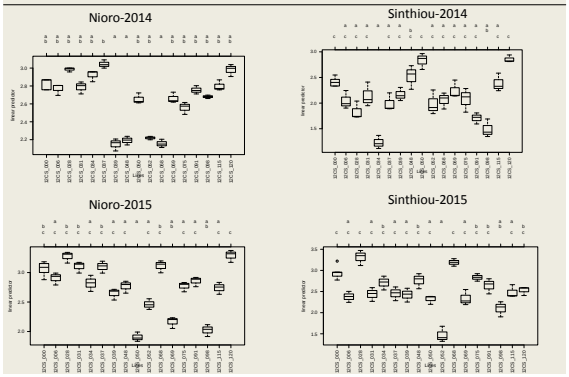


CSSL analysis: phenotyping in Senegal

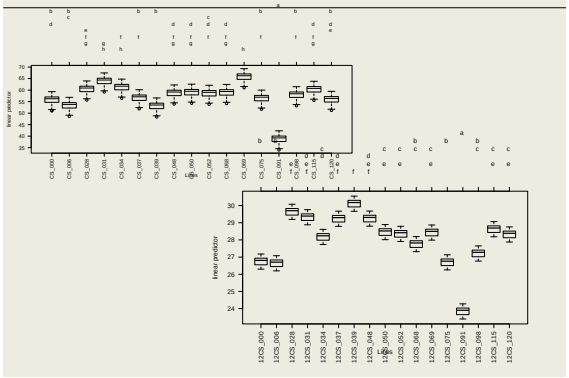
CSSL

- 16 CSSL selected based on yield component traits. 2 years, three locations under rainfed conditions totalizing 6 environnements
- Traits
  - Total Biomass
  - Yield t/ha
  - Hundred pod and seed weight
- Alpha-lattice design
  - 3 replication per location

CSSL analysis: Pod Yield per environment

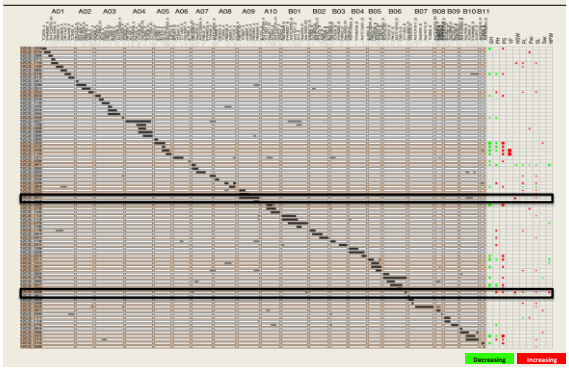


CSSL analysis: 100-seed weight and pod length

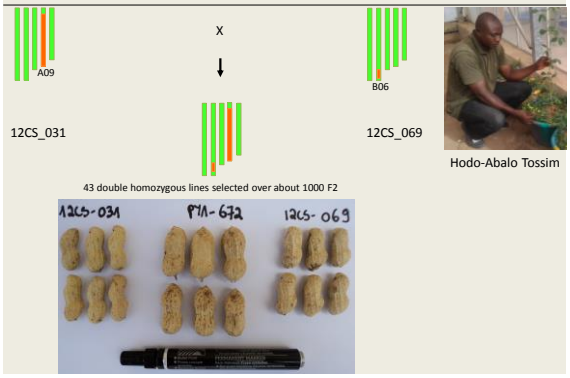


CSSL : Some lines registered as variety in Senegal

Pyramiding of seed size QTLs



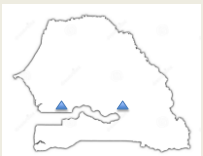
Pyramiding of seed size QTLs



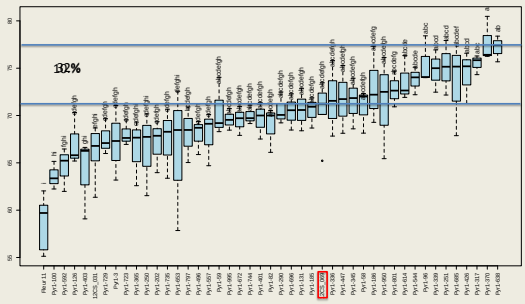
Hodo-Abalo Tossim

Pyramiding of seed size QTLs

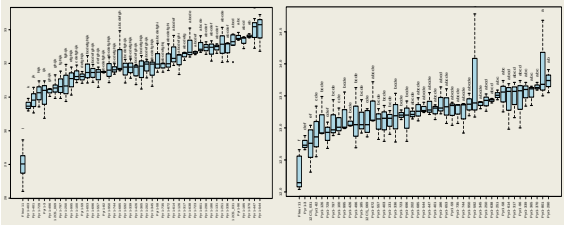
- 42 pyramiding lines plus the 2 CSSL parental lines (12CS_031 and 12CS_069 and Fleur 11. One year, two locations under rainfed conditions
- Traits
  - Total Biomass
  - Yield t/ha
  - Hundred pod and seed weight
  - Pod length and width
- Alpha-lattice design
  - 3 replication per location



Pyramiding of seed size QTLs: 100-seed weight



Pyramiding of seed size QTLs: Pod length and width

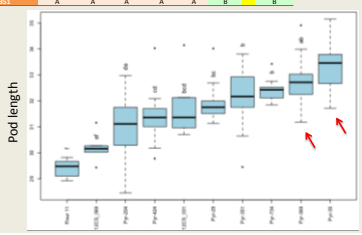


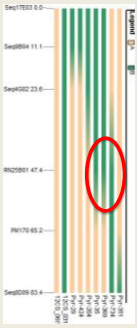
Pod Length

Pod width

Precising the Pod Length QTL(s) position(s) on A09

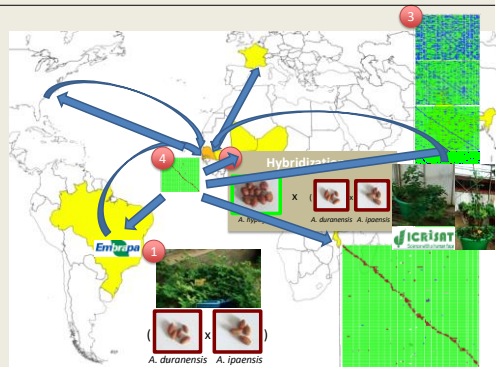
Markers	Seq17E03	Seq9B04	Seq4G02	RN25B01	PM170	Seq8D09	Seq18G01
Chromosome	A09	A09	A09	A09	A09	A09	B06
Pos. (cM)	0	11.1	23.6	47.4	65.2	83.4	104.4
12CS_069	A	A	A	A	A	A	B
12CS_031	B	B	B	B	B	B	A
Pyr29	B	B	A	A	A	A	B
Pyr424	B	B	B	A	A	A	B
Pyr204	B	B	B	A	A	A	B
Pyr35	B	B	B	B	A	A	B
Pyr369	B	B	B	B	A	A	B
Pyr734	A	A	A	B	B	B	B
Pyr351	A	A	A	A	A	B	B





Graphical genotypes of F2

The beautiful story of the partnership



Summary

- We crossed (*A. ipaensis* x *A. duranensis*)^{4x} and (*A. batizocoi* x *A. duranensis*)^{4x} to Fleur11 for developping AB-QTL and CSSL populations
- We phenotyped extensively the AB-QTLs and CSSL populations and found that wild alleles can contribute positive variation to seed size and other agronomic traits
- AB-QTL and CSSL populations are accurate for QTL mapping
- We used the CSSL lines for QTL validation, for pyramiding of seed size QTLs and for refining the QTL position.
- The CSSL population has been distributed to many partners and are being evaluated for various traits

Acknowledgments

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Rajeev Varshney

Embrapa
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Soraya Leal-Bertioli
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AAGB 2018 in Senegal