

Fresh seed dormancy (FSD) of short duration peanut (*A. hypogaea* L.): latest advances

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Rationale

In peanut, varieties belonging to the subspecies *fastigiata* (Spanish and Valencia) are early-maturing but generally lack FSD.

Only a very few early-maturing varieties and having FSD are available in sub-saharian countries

Consequences of lack of FSD

1. Substantial yield losses (20% of the pod yield) due to field sprouting (Khalifaoui, 1984)
2. Increase of the risk of peanut aflatoxin contamination (Martin, 1999)

Rationale



A harvested plant with germinated pods at the field in a susceptible variety (Fleur 11)



Plants from sprouts after harvest



Rationale

- ▶ a limited number of studies on the inheritance of FSD among Spanish-type peanut
- ▶ there's not yet an attempt to identify molecular markers linked to FSD

Objectives

1. Estimate the number of genes involved in the control of FSD a Spanish x Spanish cross using a population derived from a F1 controlled with SSR markers
2. Identify and map SSR markers linked to FSD

Activities

Development of a F₂ population derived from a controlled F₁ (Fleur 11 x 73-30) with SSR markers

- 76 F₂ seeds were phenotyped at the laboratory along with 100 seeds from each parent
- DNA was extracted from each individual F₂ plant at 15 days after emergence

Parents were prescreened with SSR markers for the genotyping work

- A bulk segregation analysis (BSA) were carried out to find markers linked to FSD
- the markers were placed on a tetraploid peanut map (Foncéka et al., 2009)

RESULTS

- The segregation ratio of the population fit well with a 3:1 (dormant: non-dormant) indicated that **FSD is controlled by one dominant gene.**
- The frequency distribution curve is bimodal, this result corroborates the statement that FSD is under the control of a single gene.
- **No-genetic factors and inadvertent selfed flowers may render ambiguous the phenotyping.**

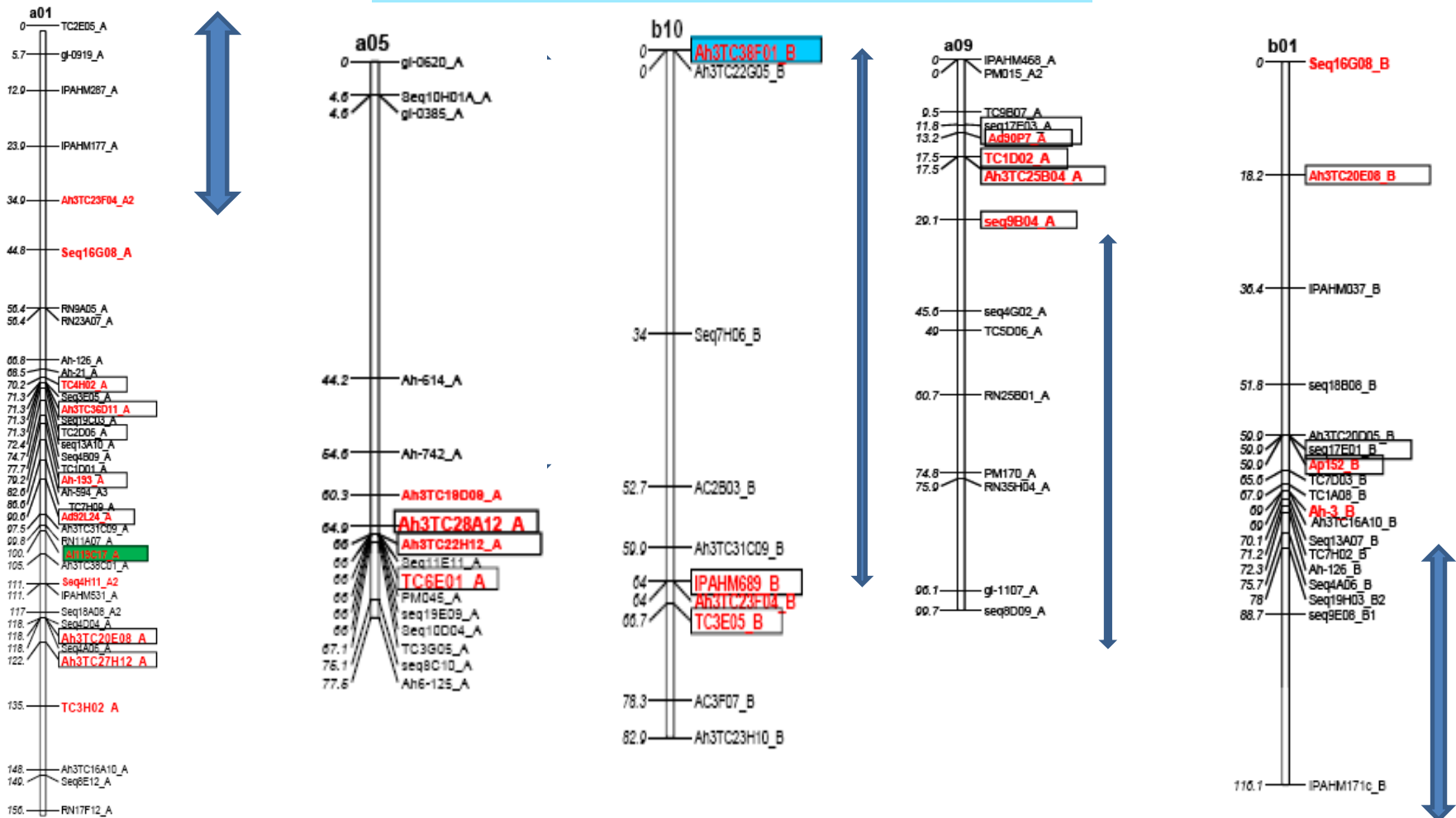
RESULTS

1. Among 558 SSR markers prescreened, 120 SSRs were polymorphic between the parents: (\approx 21% of parental polymorphism) with 107 SSRs giving a clear pattern
2. 86 SSRs were mapped on our tetraploid map (Foncéka, 2009) spanning 101 loci on the whole genome (54 loci of the A genome and 47 loci of the B genome)

RESULTS

Except, the upper arms of **a01, a04, a05, b10** linkage groups (LG) and the lower arms of **b01 and a09** LGs, a quite good satisfactory of the marker density was achieved.

RESULTS



Markers polymorphic between the parents and analyzed in this study are those represented in red color

Linkage groups that are particularly not well covered (arrows indicate the gaps without polymorphic markers)

RESULTS

- Further SSRs screening will allow to find markers linked to fresh seed dormancy in peanut that could be useful for breeding
- Existing peanut maps could be used to ease the screening of other SSR markers that will be mapped on those LGs not yet well covered

Link with other projects

- Earlier project: « Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools »»
- Enhancing groundnut (*Arachis hypogaea* L.) genetic diversity and speeding its utilization in breeding for improving drought tolerance

A photograph of a rural landscape. In the foreground, there is a field of dense green vegetation, possibly a crop field or pasture. In the middle ground, a thatched-roof building is partially visible, surrounded by a fence. The background is filled with a thick line of tall, green trees under a bright sky. The text "Thanks you for your attention" is overlaid in the center of the image.

Thanks you for your attention