



Résilience et adaptations des agricultures. Transition agroécologique et souveraineté alimentaire.

4^{ème} édition de la Conférence
Intensification Durable

23 - 25 avril 2024 UCAD (CIGASS), DAKAR, SÉNÉGAL



S3-45

Poster

Deciphering the genetic basis of biological nitrogen fixation in peanut (*Arachis hypogaea* L.) using an interspecific QTL-mapping population

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Peanut (*Arachis hypogaea* L.) is an allotetraploid grain legume crop cultivated in Africa mainly by poor farmers, in nitrogen (N) and phosphorus (P) depleted soils and in low intensification systems. Improving biological nitrogen fixation (BNF) in peanut could be of great interest to increase yield and lift-up soil fertility. We used a subset of 83 chromosome segment substitution lines (CSSLs) derived from the cross between a wild synthetic tetraploid AiAd (*A. ipaensis* × *A. duranensis*)_{4x} and the cultivated variety Fleur11. The population was evaluated in shade-house conditions for traits linked to BNF. Three conditions were tested: - N, + N and - N + inoculated with a known efficient *Bradyrhizobium vignae* strain, ISRA400. Leaf chlorophyll content and total biomass were used as surrogate traits for BNF. We found significant variations for both traits specially linked to BNF, and 04 QTLs (quantitative traits loci) were consistently mapped in two consecutive experimentations. At all QTLs, the wild alleles decreased the value of the trait, indicating a negative contribution of the wild parent on BNF. Additionally, the CSSL population was also evaluated for three consecutive years in farmer fields. Phenotypic variations of traits related to BNF (total nitrogen content), and yield components (pod weight) were recorded. A significant variation was observed for all traits, and several QTLs were identified. Common QTLs between shade-house and farmer field conditions were identified. An in-depth characterization under controlled conditions of specific lines carrying QTL regions that impede BNF, allowed to pin-point the genetic mechanisms underlying the QTLs (i.e. nitrogen fixation effectiveness, nodule colonization and development and genotype/strain compatibility). Our results provide new insights into BNF in peanut in Senegal and will help targeting this trait in peanut breeding programs.

Mots clés : Peanut; Biological nitrogen fixation; interspecific population; QTL