

Genetic map of *Aeschynomene evenia*

Construction of an SSR-based genetic map of the tropical legume *Aeschynomene evenia*: an essential tool for deciphering the Nod-independent symbiotic process and for improving nodulation efficiency in *Arachis hypogaea*

ABSTRACT

The tropical *Aeschynomene* legumes use a unique Nod-independent infection process that is believed to correspond to an ancestral state of the nitrogen-fixing rhizobium-legume symbiosis. The study of this system should therefore shed new light on the origin and evolution of symbiosis by uncovering the basic underlying the process of nodulation.

To advance in our knowledge of this Nod-independent symbiotic process, we performed a molecular phylogeny of the genus *Aeschynomene* that evidenced the Nod-independent infection process arose in a single clade. Within this lineage, *A. evenia* (2n=20, 430 Mb) appears to be the most appropriate species to constitute a bona fide model legume since it presents all the characteristics required for functional analysis (Arrighi et al., 2012).

Taking advantage of the intraspecific diversity in *A. evenia*, we have developed in the frame of the "AeschyMap" project a genetic map for this species. For this purpose, polymorphic SSR markers were mined in the Illumina transcriptomes of the two mapping parents and used for high-throughput genotyping of the F2 mapping population. This lead to the development of a genetic map comprising ten linkage groups and revealing a high synteny with the crop legume arachid that belongs to the same Dalbergioid clade as *Aeschynomene*.

Most of the symbiotic genes described in model legumes, which use a classical nodulation process, could be identified in the transcriptomes of *A. evenia*. They were mapped thanks to SNP markers and they were found to be localized in syntenic regions with arachid, thus comforting their probable orthology. These results provide the first insights on the genome structure of *A. evenia* and represent a significant tool for the mapping of new symbiotic loci.

Keywords : Microscopic (Gene/cell), Genomics, Genetic mapping, Symbiosis, Bean / Pea

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PERSPECTIVES

This genetic map will support the "AeschyNod" ANR project (2014-2019) which aims at performing a "mutagenesis" strategy to generate and screen plant mutants defective for nodulation. To make successful this strategy, we are also developing a reference genome sequence for *A. evenia*, which will

accelerate the map-based cloning of symbiotic genes.

The acquired knowledge should bring important highlights on the specific determinants of the Nod-independent process and the evolution of the nitrogen-fixing symbiosis in the legume family.