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A gene-based map of the Nod factor-independent *Aeschynomene evenia* sheds new light on the evolution of nodulation and legume genomes

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Abstract

*Aeschynomene evenia* has emerged as a new model legume for the deciphering of the molecular mechanisms of an alternative symbiotic process that is independent of the Nod factors. Whereas most of the research on nitrogen-fixing symbiosis, legume genetics and genomics has so far focused on Galegoid and Phaseolid legumes, *A. evenia* falls in the more basal and understudied Dalbergioid clade along with peanut (*Arachis hypogaea*). To provide insights into the symbiotic genes content and the structure of the *A. evenia* genome, we established a gene-based genetic map for this species. Firstly, an RNAseq analysis was performed on the two parental lines selected to generate a F₂ mapping population. The transcriptomic data were used to develop molecular markers and they allowed the identification of most symbiotic genes. The resulting map comprised 364 markers arranged in 10 linkage groups (2n = 20). A comparative analysis with the sequenced genomes of *Arachis duranensis* and *A. ipaensis*, the diploid ancestors of peanut, indicated blocks of conserved macrosynteny. Altogether, these results provided important clues regarding the evolution of symbiotic genes in a Nod factor-independent context. They provide a
basis for a genome sequencing project and pave the way for forward genetic analysis of symbiosis in *A. evenia*.

**Key words:** *Aeschynomene evenia,* symbiosis; legume; genetic map; comparative genomics

### 1. Introduction

Fabaceae, or legumes, account for ~27% of the world’s primary crop production. The capacity of most legumes to form nitrogen fixing nodules with rhizobia underlies their importance as a source of protein for human and animal diet and of nitrogen in both natural and agricultural ecosystems. Among the 20,000 legume species, around 14,000 fall into the Papilionoideae subfamily that is divided into four main clades Genistoids, Dalbergioids, Phaseoloids and Galegoids (Fig. 1). To advance in the understanding of how legumes have evolved to form nitrogen-fixing symbiosis with rhizobia, two model species belonging to the Galegoid clade and with favorable genetic attributes, *Medicago truncatula* and *Lotus japonicus*, have been extensively studied. This study has revealed a sophisticated symbiotic process that is triggered by the recognition of rhizobial signal molecules called Nod factors (NF) and that involves both the formation of an infection thread guiding the bacteria inside the root and a distant induction of a nodule primordium. Furthermore, the genetic dissection of the nodulation process has allowed the identification and elucidation of the role of many genes that are essential for the different steps of the nodulation process (Fig. 1). Unravelling the molecular mechanisms of this NF-independent process would bring important insights on the evolution of rhizobium-legume symbiosis. Conversely, the Genistoid and the Dalbergioid clades, which are more basal in their divergence within the Papilionoideae, have lagged far behind, even though they contain important crop legumes such as the genistoid lupine (*Lupinus angustifolius*) and the dalbergioid peanut (*Arachis hypogaea*). This is partly due to the large and complex nature of their genomes that makes their study challenging. Hence, in the case of peanut, which is a recent allotetraploid species, the choice was made to sequence first the genomes of its two diploid progenitors, *Arachis duranensis* and *A. ipaensis*. Similarly, genistoid and dalbergioid legumes have been understudied for their symbiotic properties although they display a distinct infection process that is initiated in an intercellular fashion and by the formation of nodules that originate directly from dividing infected cells (Fig. 1). But most surprisingly, in some *Aeschynomene* species, which are phylogenetically related to *Arachis*, an unconventional symbiotic process has also been described where some *Bradyrhizobium* strains are able to form nodules in the absence of NF synthesis (Fig. 1). Unravelling the molecular mechanisms of this NF-independent process would bring important insights on the evolution of rhizobium-legume symbiosis. For this purpose, *Aeschynomene evenia* was proposed as a new model legume because of its advantageous genetic and developmental characteristics for molecular genetics.

To provide insights into the symbiotic gene content and on the structure of the NF-independent *A. evenia* genome, we undertook the development of a gene-based genetic map. RNAseq data obtained for each parental line were mined for symbiotic gene discovery and marker development. These markers were used to

![Figure 1. Phylogeny of the Papilionoid lineage and evolution of the symbiotic infection process.](https://academic.oup.com/dnaresearch/article-abstract/23/4/365/2469965)

**Figure 1.** Phylogeny of the Papilionoid lineage and evolution of the symbiotic infection process. The tree is a simplified representation with triangle representing the major clades and the two subclades of the Galegoids: the Robinoids and the plastid DNA inverted repeat-lacking clade (IRLC). Known divergence times are indicated in MYA (million years ago) for some nodes (circles) and notable species are listed for each clade. Symbiotic infection processes encountered in the different clades are reported, excepted for the basal clades for which occurrence of nodulation is restricted to few understudied species. Note that *Aeschynomene* is the only legume genus where a Nod-independent symbiotic infection process (*NI*) has been reported for several species, including *A. evenia*. Phylogeny and drawings are adaptations, date estimates and nodulation properties come from previous publications.
2. Materials and methods

2.1. Plant material, culture, crossing and observation
Seed germination, plant culture and hybridizations were performed as described. To develop the mapping population, individual seeds of the A. evenia accessions CIAT8232 (Brazil) and CIAT22838 (Malawi) obtained from CIAT (Colombia) were selfed three times to generate inbred lines and then crossed manually. The hybrid nature of the F1 plants was confirmed with molecular markers as described. Two F1 plants obtained by bi-directional hybridizations were selfed to develop the F2 mapping population in greenhouse. For pollen viability analysis, buds were fixed in Carnoy’s fixative prior to anthesis, when pollen was mature but anthers non-dehiscent, and then stained using a simplified method of the Alexander’s stain as detailed. Pollen viability was scored under the light microscope for at least three flowers per plant by counting aborted pollen grains, which stained pale turquoise blue and nonaborted pollen grains, which stained dark blue or purple.

2.2 DNA and RNA isolation
Genomic DNA was extracted from young leaves using the CTAB method with the addition of β-mercaptoethanol 2% and PVPP 2% to the CTAB solution in order to limit polysaccharides and polyphenols co-extraction. DNA quality and quantity were evaluated in 1% agarose gel electrophoresis and by spectrophotometer before DNA normalization to a concentration of 10 ng/μl.

For RNA extractions, tissue samples were collected from in vitro cultured plants: roots and leaves on 7-days old un-inoculated plants, nodules at 4, 7 and 14-days after inoculation with the Bradyrhizobium strain ORS278. Total RNA was extracted using the SV total RNA Isolation System (Promega) excepted for leaves for which RNA was extracted using a CTAB protocol. RNA was quantified using a NanoDrop ND-1000 spectrophotometer and its quality verified using a 2100 Bioanalyzer RNA Nanochip (Agilent, Santa Clara, CA, USA). For each parental line, a total of 12 μg of RNA was pooled equally from the five tissues for Illumina library construction.

2.3 Development of Illumina transcriptomes
Two mRNA libraries were built and sequenced in one lane as described. The Illumina paired-end sequencing technology generated 2×100 bp independent reads from the 200 bp insert libraries. RNA-seq data were processed for the de novo transcriptome assemblies using the Velvet 1.2.07 and CAP3 08/06/13 softwares and orthologous relationships between contigs of the two transcriptome assemblies were identified by best reciprocal hit search. To evaluate the quality of the assembly, all usable reads were realigned to the contigs using BWA-MEM 0.7.12-r1039 and SAMtools ixdists 1.1. To assess the depth of gene coverage through comparative genome analysis, ORFs were searched in A. evenia transcripts with TransDecoder_r20140704 and used for BLASTX alignment (E value < 10^{-20}) with Blastall 2.2.26 onto the protein database of A. duranensis (Araip. V14167.1.M1.peptide.fa file downloaded from www.peanut.org). Raw Illumina sequence data have been deposited in the NCBI Sequence Read Archive (SRA) under the accession numbers SRR3276128 and SRR3285082, for the CIAT8232 and CIAT22838 lines respectively.

2.4 Sequence search and comparison
Symbiotic gene sequences were obtained from M. truncatula and L. japonicus by searching in the NCBI database. These sequences were used to find orthologous unigenes in an A. evenia local database developed with a Galaxy work bench (INRA, Toulouse, France) (https://bbrc-pipelines.toulouse.inra.fr/galaxy/) and containing the CIAT8232 and CIAT22838 transcriptome data (Supplementary Tables S1, S3; Files S1, S2).

For estimation of divergence time, single-copy genes identified in the CIAT8232 and CIAT22838 transcriptomes were used to obtain orthologous sequences for A. evenia IRLFL6945 from its transcriptome database (http://esttk.cirad.fr) and for A. duranensis and A. ipaensis from their genome sequence database (http://peanutbase.org/) (Supplementary Table S5). Coding sequences were cropped, aligned and used to calculate Ks values with the DnaSP 5.10 software (Supplementary Fig. S1). Divergence times were obtained based on a simple molecular clock assumption and by using the previously known ~49 MYA divergence time estimate between Aeschynomene and Arachis.

2.5 SSR and INDEL genotyping
Detection of microsatellites in the transcriptome data were performed using the SPUTNIK software by searching for di- to hexanucleotide SSRs with a minimum of three to six repetitions depending on the motifs. Orthologous sequences in the two transcriptome assemblies comprising different lengths of the same SSR motif, with a contig length over 500 nt and with at least 50 nt surrounding the SSR motifs were selected as in silico polymorphic SSRs (Supplementary Table S1). For specific gene mapping, SSR and INDELS were searched by sequence comparison from the two transcriptomes. Primer pairs were designed using Primer3 with tree parameters: (i) a primer length of 20 bp with an annealing temperature of 55 °C, (ii) two ranges of PCR product size of 90–120, 150–180 and 220–250 bp, (iii) the addition of a 5′-end M13 tail (5′-CACGACGTCTTAAACGAC-3′) on the forward primer (Supplementary Table S2). SSR markers were checked for PCR-amplification and co-dominant behavior, organized in 12-SSR multiplexes by combining both the three ranges of fragment sizes and the four fluorochromes (FAM, VIC, NED and PET), and then used to genotype the F2 mapping population as described.

2.6 SNP genotyping
To detect single nucleotide polymorphisms for a set of target genes, sequences of orthologous contigs identified in the two transcriptome datasets were aligned with the MUSCLE program (Supplementary Table S3). Positions of the SNPs were determined by examining the intron/exon structure of orthologous genes in Arachis (http://peanutbase.org/). Whenever necessary, additional SNPs were searched by intron sequencing. Up to three SNPs were selected for each target gene and flanking sequences 50 bp both upstream and downstream each target SNP were sent to KBioscience for primer design (Supplementary Table S4). Genotyping of the F2 mapping population was performed with the KASP genotyping chemistry (KBioscience Ltd., Hoddesdon, UK) on Fluidigm 96.96 Dynamic Arrays using the BioMark HD system (Fluidigm Corp, San Francisco, CA). On the basis of obtained fluorescence, allele call data were viewed.
2.7 Genetic map construction

Linkage analysis was performed on segregated genotypic data from the F2 mapping population using JoinMap® version 4 (Plant Research International BV, Wageningen, Netherlands). The marker loci were attributed to linkage groups using the JoinMap® grouping module with a logarithm of odds (LOD) scores of 6.0. Marker order and genetic distance (in cM) were calculated using a regression mapping algorithm with the following parameters: Kosambi’s mapping function, recombination frequency ≤0.40, and LOD threshold of 1.0 (Supplementary Table S6). The segregation data were tested for deviation from the expected Mendelian ratio using a Chi-square test. LG numbering and orientation were attributed to best fit the A. duranensis and A. ipaensis chromosomes.

2.8 Comparative genomics

Gene sequences underlying the molecular marker loci assigned to the linkage map were blasted against the A. duranensis and A. ipaensis genome sequences (http://peanutbase.org/) to detect significant matches at minimum threshold E values < 10^-60 (Supplementary Table S6). For the purpose of graphic preparation, cM distance on the A. evenia linkage groups were scaled by factors calculated on the basis of the genome size of A. ipaensis, to provide matching chromosomal lengths in base pairs. The graphical comparative maps were drawn using the Circos program (http://circos.ca/) and the SpiderMap software (JF Rami, unpublished).

3. Results and discussion

3.1 Selection of parental genotypes to develop a mapping population

3.1.1 Choice of the reference line

The A. evenia species was proposed as a new model legume to investigate the evolution of the nitrogen-fixing symbiosis because it possesses a number of interesting characteristics for both classical and molecular genetics.21,22 Key attributes of A. evenia include diploidy (2n = 2x = 20), self-pollination, a small genome for a legume, a short growth cycle and a high level of diversity. In addition it is efficiently nodulated by the well-characterized strains Bradyrhizobium ORS278 and ORS285 and it can be transformed using the hairy root system. First nodulation studies were performed on the cultivar IRFL6945 belonging to the A. evenia ssp. serrulata.21 But subsequent analysis of the intra-specific diversity revealed that A. evenia ssp. evenia is more appropriate due to a smaller genome size (415 vs 463 Mb) and the presence of genotypes with a more rapid reproductive cycle and a non-branching habit that facilitate plant management (Fig. 2A,B).22 We made use of this knowledge to select from within the subspecies evenia var. evenia the genotype Mbao CIAT22838, which displays these advantageous characteristics, as the reference genotype. Its nodulation properties were previously shown to be predominantly homozygous, a single seed from the reference genotype was selfed three times to ensure high homozygosity.

3.1.2 Choice of a mapping parent

The establishment of a mapping population required the identification of a second parent that has favorable polymorphism while the resulting F2 population should not have developmental and genetic abnormalities. Characterization of the diversity in A. evenia had previously revealed that the genetic polymorphism was the highest between the subspecies evenia and serrulata but that inter-subspecies crosses led to sterile F1 hybrids. Conversely, intra-subspecific hybridizations were shown to generate fully fertile F2 progenies.22 Therefore, to maximize genetic polymorphism, the genotype Bahia CIAT8232 that belongs to the subspecies evenia var. pauciciliata and that presents a distinct geographic origin (African for Mbao versus American for Bahia) was developed as an inbred line and used as the second mapping parent (Fig. 2A). The Mbao and Bahia genotypes present a similar DNA content (415 and 405 Mb, respectively) but they were shown to display a 32% SSR polymorphism.22 This situation is similar to the one observed in Medicago truncatula with the two mapping parents Jemalong and DZA315.16 and between three ecotypes of Arabidopsis thaliana, indicating it is convenient for generating genetic maps.25 In addition, the two genotypes display phenotypic differences making them readily distinguishable such as the branching habit, the timing of flower openings and the presence of a dark throat on the upper petal (Fig. 2B).

3.1.3 Development of an F2 mapping population

Artificial hybridizations were performed using the genotype Mbao CIAT22838 as female and male alternatively and producing F1A and F1B progenies respectively. These F1 plants showed hybrid vigor, intermediate flower characteristics (opening time and shape) and were self-fertile (Fig. 2B). In particular, they displayed equivalent pod set (Bahia: 8.6 ± 0.9, Mbao: 8.2 ± 1, F1: 8.8 ± 1.1 seeds/pod). The resulting F2A and F2B offsprings had no albino or dwarf individuals. Altogether, this suggested that Bahia CIAT8232 was a suitable crossing partner to Mbao CIAT22838 and that the obtained F2 offsprings could be used as mapping population to develop a genetic map.

3.2 Transcriptome sequencing for identification of symbiotic genes and genetic markers

3.2.1 Illumina paired-end sequencing and de novo transcriptome assembly

High-throughput transcriptomic sequencing allows generating a large transcript sequence dataset for gene discovery and development of molecular markers that serve for gene-based map construction. To be able to achieve a broad survey of genes associated with symbiosis, RNA was extracted and pooled from various organs: roots, leaves and nodules at 4, 7 and 14-dpi. In addition, to increase the efficiency of molecular marker development by prior in silico polymorphic analysis, a RNA library was developed for each parental genotype.

Using Illumina paired-end sequencing and after stringent quality check of the raw data, ~72 million reads were kept for the Mbao genotype and ~66 million for the Bahia genotype. Based on these high-quality reads, a total of 51,763 and 52,648 contigs were assembled respectively, with a common N50 of 1,800 bp and a consistent contig size distribution (Table 1). This indicated that a similar transcript content was obtained for both mapping parents. Furthermore,
realignment of all the usable reads to the contigs revealed that ~35,000 contigs were remapped by more than 100 reads and, among them, ~24,500 contigs were realigned with more than 500 reads, suggesting the contigs were well overlapped by the sequencing reads (Fig. 3A). A. evenia being a member of the Dalbergioid clade along with the recently sequenced A. duranensis and A. ipaensis, their genomic data could be also used to assess the quality and coverage of the assembled transcriptomes.22 Since A. duranensis has not experienced the local gene duplications evidenced for A. ipaensis, the former species was better suited for this purpose. Thus, comparative analysis revealed that 60% of total contigs (~31,850) and 83% of contigs over 500 bp in length (~26,378) had BLAST matches (E-value < 10^-5) onto the ~36,700 predicted genes in the A. duranensis genome (Fig. 3B). In addition, plotting the contigs onto top-hit homologous coding sequences of A. duranensis (E-value < 10^-30) indicated a high proportion of genes with complete coding sequence (Fig. 3C). Altogether, these data suggested that a comprehensive gene capture was achieved for A. evenia.

3.2.2 Identification of putative orthologs of symbiotic genes

To determine which symbiotic genes can be identified in A. evenia, a BLAST search was performed in the Bahia and Mbao transcriptomes using the sequence of symbiotic genes characterized in the two model legumes M. truncatula and L. japonicus.8,27–33 This allowed the identification of a single sequence in A. evenia for 36 out of 47 symbiotic genes analysed, for which the putative orthology was checked by reciprocal BLAST and sequence alignment (Fig. 4; Files S1, S2). These genes completely covered the different steps of the nodulation process: Nod signaling, activation and regulation of transcription, nodule organogenesis and regulation of nodulation (Fig. 4). This coverage suggested that these steps were conserved in A. evenia, but it could not be excluded that some of these genes were only involved in the arbuscular mycorrhizal symbiosis or in other biological processes. So far, only the A. evenia SYMRK, CCaMK, CRE1 and DNF1 orthologs were effectively demonstrated to play a role in nodulation.34,35

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**Figure 2.** Differentiation within the A. evenia species and its use for genomic and genetic studies. (A) Schematic phylogeny depicting the genetic differentiation within the A. evenia species and the relationships with Arachis sp.18,22 Dash lines connect the tetraploid A. hypogaea to its most probable diploid genome donors A. duranensis and A. ipaensis. Divergence times at certain nodes (circles) were estimated using a relaxed molecular clock (Table 3). (B) Phenotypic patterns which distinguish CIAT22838 and CIAT8232 lines and impact on the F1 hybrid obtained by cross-pollination: plant habit (ramified or not), time of flower opening (early and late), flower shapes (standard shape and dark throat indicated by an arrow), pod production. Bars = 5 mm.
Interestingly, for some other symbiotic genes, transcripts were not detected despite the use of root and nodule materials for the transcriptomes. Missing genes are involved in three symbiotic processes: bacterial recognition (i.e. \textit{LYK3} and \textit{LYR3}), rhizobial infection (i.e. \textit{ANN1}, \textit{EPR3}, \textit{FLOT} and \textit{RPG}) as well as nodule functioning and immunity (i.e. \textit{DNF2}, \textit{FEN1}, \textit{SUNERGOS1}, \textit{SymCRK} and \textit{VAG1}) (Fig. 4). In the absence of genomic data for \textit{A. evenia}, it was not possible to determine whether these genes were absent, not expressed or missed when mining the transcriptome data. But, it is worth noting that the concerned genes are involved in symbiotic processes that present sharp differences between \textit{A. evenia}, \textit{M. truncatula} and \textit{L. japonicus} (Fig. 1).\textsuperscript{2,19} As a consequence, these first observations represented important cues to further investigate the evolution of rhizobial symbiosis.

3.2.3 Development of EST-based molecular markers

To allow the development of molecular markers, the Bahia and Mbao transcriptomes were searched for microsatellites. These were subsequently analysed for \textit{in silico} polymorphism by comparing the orthologous SSR-containing contigs of the two parental genotypes and filtered to allow primer design on flanking sequences. \textit{1,500} microsatellites complying with these criteria were identified, the most abundant type of repeat motif being tri-nucleotides (46.4%), followed by di-nucleotides (35.9%) (Table 2). \textit{500} SSR sites were selected for primer design and used for assessment of the polymorphism between the two parental genotypes and the \textit{F1} progeny by capillary sequencing. Of the 412 successfully amplified SSRs, 335 (81%) were co-dominant, 50 (12%) were dominant and 27 (7%) were not polymorphic. Hence, thanks to the \textit{in silico} analysis, the efficiency of polymorphic SSR development was increased by 2.5-fold compared to previous work with no prior filtering of the genic SSR tested on the same Bahia and Mbao genotypes.\textsuperscript{22} Finally, a set of 318 co-dominant SSR markers was retained for the genotyping of the \textit{F2} mapping population (Supplementary Tables S1, S2).

In order to map the symbiotic genes, polymorphisms were also searched for by comparing the orthologous sequences from the two parental genotypes and were converted into molecular markers. When no polymorphic SSR and no INDEL could be detected, Single Nucleotide Polymorphism (SNP) was used instead for KASP assay design (Supplementary Tables S1–S4). Subsequently, at least one molecular marker could be satisfactorily developed for each identified symbiotic gene, except for two genes, \textit{SEN1} and \textit{RSD}, that lack of polymorphism. A few additional markers were also used, notably to locate the \textit{5S} and \textit{45S} loci that were previously identified on \textit{A. evenia} chromosomes by cytogenetics (Supplementary Tables S1, S2).\textsuperscript{21}

3.3 Construction of the genetic map and mapping of symbiotic genes

3.3.1 Genotyping of the 220 \textit{F2} mapping population

110 \textit{F2A} and the 110 \textit{F2B} individuals, which were obtained by bi-directional crossings of the Bahia and Mbao genotypes, formed the
The resulting genetic map spans 1,036 Kosambi cM, with an average of 400 kb/cM. The 10 linkage groups have different genetic sizes ranging from 82 to 130.8 cM and contained 13–49 markers (Table 3). This leads to average distances between two adjacent markers varying from 2.6 to 7.5 cM but with maximum interval sizes per linkage group ranging from 10.7 to 25.1 cM (Table 3). This situation is reminiscent to what has been already observed in Vignaunguiculata and Lensculinaris for which genetic maps were also developed with gene-based markers. The gaps have been proposed to correspond to gene-poor regions or to recombination hotspots. In addition, mapping of the 5S and 45S rDNA loci further enabled distinguishing two linkage groups. Thus the 5S rDNA locus was found to locate on linkage group AeLG8 with a central position (at 55.6 cM on total 96.2 cM length) that is in accordance with the proximal localization previously observed on metaphase chromosomes by GISH. Conversely, two 45S rDNA loci were shown to locate to in secondary constrictions of satellite chromosomes. Sequence polymorphism for the ITS region allowed mapping only one of the two loci on the upper part of the linkage group AeLG10 (at 19.4 cM on a total 82 cM length) (Fig. 5). Finally, gene-specific markers corresponding to symbiotic genes were found to be distributed in all but one (AeLG2) linkage groups, with AeLG5, AeLG6, AeLG7 and AeLG9 containing the majority of them (Fig. 5).

3.3.3 Regions of segregating distortion (RSD)

Although almost all markers complied with the 1:2:1 expected Mendelian ratio for co-dominant genetic markers, two regions of segregation distortion were observed (Table 3, Fig. 6A). The AeLG2 RSD comprised up to 10 markers covering a map distance of up 70 cM and the AeLG9 RSD contained 11 markers (among which the symbiotic NSP1 and EFD genes) distributed over 45 cM, altogether representing 10% of the genetic map. In both cases, there was a strong overrepresentation of the Bahia allele and a near complete disappearance of the Mbao allele where the distortion culminated.
Figure 5. Genetic map of *Aeschynomene evenia*. The genetic map based on F2 mapping population CIAT2283 × CIAT8232 is comprised of 364 gene based markers including SSR, INDEL and SNP (KASP) markers. The ten linkage groups are designated as AeLG1-AeLG10. The code to the right of the linkage groups refers to the marker or syntenic gene name. The numbers to the left of the linkage groups refer to the genetic distances (Kosambi cM) from the top.

### Table 3. Characteristics of the *Aeschynomene evenia* genetic map

<table>
<thead>
<tr>
<th>LG</th>
<th>Total length of loci (cM)</th>
<th>Number of markers</th>
<th>Number of markers</th>
<th>Average distance (cM)</th>
<th>Min-max distances (cM)</th>
<th>Distorted markers (P &lt; 0.001)</th>
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<tr>
<td>AeLG1</td>
<td>107.1</td>
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<td>13</td>
<td>7.5</td>
<td>0–22.3</td>
<td>10</td>
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<tr>
<td>AeLG3</td>
<td>113.1</td>
<td>44</td>
<td>49</td>
<td>2.6</td>
<td>0–25.1</td>
<td>0</td>
</tr>
<tr>
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<td>46</td>
<td>2.8</td>
<td>0–13.3</td>
<td>0</td>
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<tr>
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<td>48</td>
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<td>0</td>
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<tr>
<td>AeLG6</td>
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<td>0–20.6</td>
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</table>

whereas the proportion of heterozygotes remained unaltered. Judged from these skewed genotypic frequencies, a strong selection in favor of the Bahia alleles occurs at these RSD.

Distortions can be caused by chromosomal structural rearrangements, differences in DNA content, gene incompatibilities or deleterious recessive alleles. Inversion or translocation events have been shown to be the cause of distortions in genetic maps of other legume such as *M. truncatula*, *L. japonicus* and *L. culinaris*. 13,26,38–41 Such events are more likely to occur when performing interspecific crosses than when using related genotypes, but one cannot exclude that a chromosomal rearrangement occurred within the subspecies *evenia* to which both the Bahia and Mbao genotypes belong. In addition, even if they display a similar overall DNA content, this DNA content may not be identical in the two RSD regions. Comparison of the genotypic data for the F2 and F3B mapping populations, revealed similar allele skewing in the two RSD regions, indicating that the observed distortions were independent of maternal and paternal effects. However, pollen viability analysis showed that the F1 progeny contained ~38% aborted pollen in contrast to the Bahia and Mbao parental genotypes that showed more than 99% pollen viability (Fig. 6B,C). This F1 semisterility may account for the observed skewed genotypic frequencies, as it has been reported for some *M. truncatula* crosses. 38 Although, this RSD can alter genetic distances, it does not compromise marker ordering in the SDR regions.

3.4 Comparative analysis with *Arachis*

3.4.1 Estimate of time divergences

With the aim of fostering genomic and symbiotic comparative analysis, we wanted to further our knowledge of the genetic differentiation in *A. evenia* and of the evolution within the Dalbergioid clade that contains *Aeschynomene* and *Arachis*. A ~49 MYA divergence of *Aeschynomene* and *Arachis* was previously estimated from chloroplast gene phylogenies (Fig 2A). 45 Using this date for calibration and assuming a simple molecular clock, we made a rough estimate for the divergence times between different *A. evenia* genotypes and between the two *Arachis* ancestral species of peanut. The coding reading frame of seven single-copy nuclear genes was obtained from the transcript databases available for *A. evenia* genotypes (CIAT2323), Goias (IRFL6945) and Mbao (CIAT22838) and their *Arachis* orthologs in the genome sequences of *A. duranensis* and *A. ipaensis* (Fig 2A, Table 4, Supplementary Table S5). Synonymous substitution rates (Ks) were calculated for binned values and an
average mutation rate of $5.34 \times 10^{-3}$ substitutions/synonymous site/Mya was obtained by using the 49 MYA value for the *Aeschynomene–Arachis* divergence.6

This enabled an estimate of divergence time between the two mapping parents that belong to *A. evenia* ssp. *evenia* var. *evenia* and var. *pauciflora* at ~0.4 Mya, reflecting both the low difference observed in polymorphism and the cross-compatibility between the two varieties.22 In contrast, a much older divergence time of ~3.3 Mya was deduced for *A. evenia* ssp. *evenia*–*A. evenia* ssp. *serulata*. This is in agreement with the pronounced genetic differentiation of the two *A. evenia* subspecies evidenced by the difficulty of making successful crosses and the almost completely sterile hybrids.22 This divergence time is similar to the ~3.5 Mya obtained for *A. duranensis*–*A. ipaensis*, which are genetically isolated, thus supporting the idea that the two *A. evenia* subspecies are at the final stage of the speciation process. Interestingly, the value calculated for the *Arachis* species couple is in accordance with other estimates (2.1–3.5 Mya).18,42 Therefore, our approach seems to be valid to provide a timeframe for *A. evenia* evolution.

### 3.4.2 Genome conservation and evolution with *Arachis ipaensis*

Several studies have undertaken comparative genomics within the Papilionoids revealing that the degree of synteny is correlated with
phylogenetic distance of the legume species. The first glimpses of genome evolution within the Dalbergioid clade were only recently obtained by the genome sequencing of the two putative genome donors of peanut. This revealed a mostly one-to-one correspondence between the two species, with the genome of A. duranensis, but not of A. ipaensis, having undergone several major rearrangements. To perform the Aeschynomene-Arachis genome comparison, we made use of the gene-based nature of the markers mapped on the genetic map of A. evenia (2n = 20) to locate orthologous sequences on the chromosomes of A. duranensis and A. ipaensis (2n = 20) (Supplementary Table S6). Although all the transcripts used to develop the markers did not necessarily contain predicted coding reading frames, ~97% of them (353 out of 364) showed significant matches to Arachis sequences. To facilitate comparison, the Aeschynomene linkage groups have been numbered and oriented to best match the corresponding Arachis chromosomes (Supplementary Fig. S2A,B).

When the A. evenia linkage groups and the A. ipaensis chromosomes were aligned, extensive stretches of shared colinearity between them were evident (Fig. 7A, Supplementary Fig. S2A). Some linkage groups of A. evenia showed hits mainly with one chromosome of A. ipaensis, notably AeLG1 that matches Araip.A01, AeLG2 with Araip.A02, AeLG3 with Araip.A03, AeLG6 with Araip.A06 and AeLG9 with Araip.A09 (Fig. 7A). However, detailed analysis of macrosynteny between homologous chromosomes evidence internal rearrangements such as translocations and inversions (Fig. 7B). In addition, even though A. evenia and A. ipaensis share the same base chromosome number of 10, one-to-one relationships do not hold true for the remaining A. evenia linkage groups. Instead, they appear to be composed of segmental syntenic blocks matching different chromosomal positions in A. ipaensis as exemplified by AeLG4 that contains three conserved blocks found in the chromosomes Araip. A03, A04 and A10. It is worth noting that some gaps observed within Aeschynomene linkage groups are coincident with syntenic block junctions and thus may correspond to more variable regions prone to genome restructuring as suggested earlier. In addition, Aeschynomene loci mostly match and cover the euchromatic arms of Arachis chromosomes while only few loci map pericentromeric regions (Fig. 7A). This observation is consistent with all the euchromatic regions of the A. evenia genome being captured by the gene-based markers composing the genetic map.

**3.4.3 Macrosynteny analysis for the symbiotic genes**

Considering the divergence time between Aeschynomene and Arachis (~49 Mya) relative to the isolation time of the Dalbergioid clade from the Phaseoloids and Galegoids (~53 Mya), along with the 3 to 3.3-fold larger genome of A. duranensis and A. ipaensis (1,230 and 1,360 Mb, respectively) compared to A. evenia (415 Mb), the high level of macrosynteny documented here between Arachis and Aeschynomene is remarkable. Much of the expansion in Arachis genomes may be due to retroelements, but it has done little to disrupt macrosynteny that is dominated by large chromosome arms-size rearrangements. Such macrosynteny was found to be maintained for the symbiotic genes mapped onto the A. evenia linkage groups, suggesting that true orthologous relationships were identified (Fig. 7A). One noticeable exception concerns the **CCaMK** gene that is mapped onto AeLG8 and is positioned between two syntenic blocks, while its A. ipaensis ortholog locates on Araip.A01 chromosome within a block that is syntenic to AeLG1 (Fig. 7A,B). Although it is not possible to determine the extent to which macrosynteny relationships identified by genetic mapping are indicative of conserved microsynteny, it is interesting to note that a retrotransposon insertion site was previously identified 364-bp upstream of the **AeCCaMK** gene. Since retrotransposons are known to be involved in genome restructuring and also to induce gene mobility, further studies may help
determining their potential impact on the genomic environment of this key symbiotic gene in A. evenia.

4. Conclusions and perspectives

To advance in our understanding of the NF-independent symbiosis in the model legume A. evenia, we developed a genetic map incorporating expressed genes that are likely to be involved in nodulation. Previous characterization of different genotypes in A. evenia allowed us to select the Mbao genotype as a reference for molecular genetics and the Bahia genotype as a suitable crossing parent to develop a F2 mapping population. Transcriptome in silico analysis for the two parental genotypes enabled an efficient selection of polymorphic molecular markers that were used to genotype the mapping population. The choice of genotyping methods, i.e. multiplexing and capillary sequencing for SSR and INDEL markers along with the KASP assays for SNP markers resulted in 99.4% complete genotyping data. The genetic map was resolved in 10 robust linkage groups that most likely represented the 10 chromosome pairs in A. evenia. The availability of a high-density map containing easy-to-use and cost-effective markers will facilitate gene and QTL mapping work in A. evenia.

Given the gene-based nature of the markers used, this genetic map provided the first insights into the structure of the genome space and, in particular, uncovered the distribution of expressed orthologs of known symbiotic genes. Comparative genomic analysis with Arachis further evidenced that the Aeschynomene genome constituted of macrosyntenic blocks. Therefore, this genetic map of Aeschynomene could form the basis for future efforts in the scaffold anchoring and assembly in an Aeschynomene genome sequencing initiative. The availability of a whole genome sequence is now feasible thanks to the next-generation sequencing technologies. This will allow much better comparison with Arachis to characterize genome evolution within the Dalbergioid clade. In particular, microsynteny analysis will allow investigating if chromosome rearrangements and transposable elements had an impact on certain symbiotic genes as suspected for the AcCCaMK gene and those that could not be found in the transcriptome datasets. Understanding how these symbiotic genes evolved (by changes of gene expression or by gene loss) in a NF-independent context would be an important advance in understanding the evolution of nodulation.

In addition, an a priori identification of symbiotic genes in A. evenia using a mutagenesis approach should be a powerful tool. In this perspective, a strategy combining gene mapping with sequencing at gene or whole genome-level will allow an efficient identification of new alleles and new symbiotic loci among mutant lines, as has been successfully performed in M. truncatula and L. japonicus. New methods, such as SHOREmap and MutMap, now integrate simultaneous mapping and mutation identification in a single step by deep whole-genome resequencing of pooled DNA from a F2 mutant population. This population can be obtained either by crossing the mutant to the mapping parent or to the original WT parental line used for mutagenesis. In the latter case, mapping relies on the detection of mutagenesis-induced polymorphisms. The similar genetic backgrounds present the advantage of both simplifying segregation patterns and suppressing the occurrence of distortions. As a result, applying this strategy to A. evenia, the identification of new symbiotic genes should be straightforward and should facilitate the deciphering of the molecular mechanisms of the NF-independent process.

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Conflict of interest

None declared.

Supplementary data

Supplementary data are available at www.dnaresearch.oxfordjournals.org.

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