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Full Paper

Genomic and epigenomic immunity in common bean: the unusual features of NB-LRR gene family

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Abstract

In plants, a key class of genes comprising most of disease resistance (R) genes encodes Nucleotide-binding leucine-rich repeat (NL) proteins. Access to common bean (*Phaseolus vulgaris*) genome sequence provides unparalleled insight into the organization and evolution of this large gene family (~400 NL) in this important crop. As observed in other plant species, most common bean NL are organized in cluster of genes. However, a particularity of common bean is that these clusters are often located in subtelomeric regions close to terminal knobs containing the satellite DNA *khpu*. Phylogenetically related NL are spread between different chromosome ends, suggesting frequent exchanges between non-homologous chromosomes. NL peculiar location, in proximity to heterochromatic regions, led us to study their DNA methylation status using a whole-genome cytosine methylation map. In common bean, NL genes displayed an unusual body methylation pattern since half of them are methylated in the three contexts, reminiscent of the DNA methylation pattern of repeated sequences. Moreover, 90 NL were also abundantly targeted by 24 nt siRNA, with 90% corresponding to methylated NL genes. This suggests the existence of a transcriptional gene silencing mechanism of NL through the RdDM (RNA-directed DNA methylation) pathway in common bean that has not been described in other plant species.

Key words: NB-LRR, DNA methylation, small RNAs, *Phaseolus vulgaris*, satellite DNA

1. Introduction

Plants have evolved a multi-layered defense system to detect and counter pathogen infection. As a first layer, plants can perceive relatively conserved small molecules, proteins and protein fragments, produced externally to the cell by microbes or host cell degradation products, and collectively referred to as Pathogen Associated Molecular Patterns (PAMPs). This recognition through plasma membrane pattern-recognition receptors (PRR) initiate a resistance response known as PAMP-triggered immunity (PTI).¹ However, successful pathogens have developed proteins or small molecules termed effectors that can strike down PTI, resulting in Effector Triggered Susceptibility (ETS). As a second layer, plants have evolved the ability to recognize either directly or indirectly pathogen effectors using proteins encoded by resistance (*R*) genes. Genes encoding effectors that are recognized by *R* gene products, leading to effective plant resistance called Effector Triggered Immunity (ETI), are genetically defined as avirulence (*Avr*) genes. ETI drives a powerful immune response, epistatic to effector mediated immune suppression and sufficient to limit pathogen spread.²

R genes have been implicated in resistance against diverse and taxonomically unrelated pathogens including bacteria, viruses, nematodes, insects, filamentous fungi and oomycetes. Strikingly, regardless of the plant or the pathogen considered and despite the diversity of pathogen *Avr* proteins, the majority of cloned *R* genes encode intracellular proteins with a conserved central Nucleotide-Binding domain (NB), also known as NB-ARC (Nucleotide-Binding adaptor shared by Apaf1, certain *R* genes and CED4) and a more variable C-terminal Leucine-Rich Repeat (LRR) domain.^{3–5} With regard to their N-termini, two phylogenetically distinct major groups can be distinguished within the NB-LRR or NL proteins.⁶ The first group contains an N-terminal domain with homology to the *Drosophila* Toll and human Interleukin-1 Receptor (TIR), referred to as TIR-NB-LRR or TNL. The second group, corresponding to non-TNL group is usually known as CNL (for CC-NB-LRR), since many members of this group are predicted to form a coiled-coil (CC) structure in the N-terminus. Despite an overall lack of sequence similarity, most of characterized CC domains possess a small 'EDVID' motif.^{7,8} However, a less abundant subclass of CC domain has been described in which EDVID motif is not present and which presents closest sequence similarity to RPW8, a non-NL *R* protein from *Arabidopsis thaliana* that confers broad-spectrum resistance against powdery mildew (*Erysiphe spp.*).^{9,10}

NL encoding *R* genes are present in all sequenced plant genomes in variable number, from less than 100 genes in papaya, cucumber, watermelon and melon^{11,12} to more than one thousand in apple.¹³ Variation in NL number is not necessarily proportional to the genome size and if NL-encoding genes often exhibit spectacular lineage-specific expansions, dramatic contractions have also been reported.¹⁴ This suggests that a limitation in the expansion of NL encoding gene number exists in a plant genome. This limitation possibly reflects fitness costs associated with resistance expression.^{15,16} Genome-wide investigation of NL gene family in various plant species reveal that NL encoding genes tend to be clustered in genomes. For instance, 66% of *Arabidopsis thaliana* NL genes, 76% of the rice NL genes, 73% of potato NL genes, 64% of cucumber NL genes, 81% of melon NL genes, 69% of watermelon NL genes, 81% of apple NL genes, and 70% of cassava NL genes are organized in clusters.^{12,13,17–20} These clusters vary in size and complexity and fall into two types based on the phylogenetic relationship of their NL sequences: homogeneous clusters containing phylogenetically related

sequences that may have undergone frequent sequence exchanges and heterogeneous clusters containing phylogenetically distantly related NL and even both TNL and non-TNL encoding sequences.¹⁴ Coexistence of these two types of clusters suggests that different mechanisms are responsible of NL encoding genes evolution.

Cytosine methylation is an epigenetic modification that affects chromatin packaging and transcription and has been shown to be involved in various biological processes including biotic stress responses.²¹ Whereas in animals, methylation at CG dinucleotides predominates, in plant, cytosine methylation occurs in three sequence contexts controlled by distinct pathways: the symmetric CG and CHG contexts, as well as the asymmetric CHH context (where H = A, C, or T).²² DNA methylation is established in all three contexts through RNA-directed DNA methylation (RdDM) pathway, whereby 24-nucleotide (nt) small interfering RNAs (siRNAs) guide the DNA methyltransferase to the corresponding genomic DNA.^{22–24} Whereas methylation in symmetric CG and CHG contexts can be maintained through DNA replication by context-specific DNA methyltransferases, maintenance of asymmetric CHH methylation requires either CMT2 (at long Transposable Element -TE-) or RdDM (at short TE or genes), depending on the loci that are targeted.^{22,25,26} Different *Arabidopsis* hypomethylated mutants defective in the RdDM pathway showed a modified response to disease after pathogen infection,^{27–29} providing evidence that this pathway modulates immune responses against pathogen. The pattern and the role of DNA methylation differ depending on the targeted genomic features. For instance, methylation of repetitive sequences, such as transposable elements (TEs), generally occurs in all three contexts and acts as a genomic immune system, by suppressing transcription and proliferation of invading DNA elements, thereby maintaining genome integrity.^{30,31} In contrast, cytosines within the transcribed-region of protein coding genes are typically methylated at CG sites, referred to as CG gene-body methylation. Although the function of gene-body methylation remains poorly understood, it seems to modulate gene expression and is generally positively correlated with moderate and/or constitutive expression.^{32–35}

Common bean (*Phaseolus vulgaris*) is the most important grain legume for direct human consumption in the world.³⁶ As a major source of dietary protein, minerals and certain vitamins, common bean plays a significant role in human nutrition particularly in developing countries.³⁷ Several diseases caused by diverse pathogens including, fungi, bacteria and viruses, threaten common bean productivity. Many *R* genes effective against these diseases have been genetically described in common bean.^{38,39} The use of resistant genotypes is the most economic and ecologically safe management strategy.⁴⁰ As observed in other plant species, these resistance specificities effective against various types of pathogens are often organized in large gene clusters that co-locate with NL cluster. However, the specificity of common bean genome is that these large clusters are often located at the ends (rather than in the center) of linkage groups (LG).^{38,39} Molecular analysis of BAC clone sequences corresponding to two of these *R* clusters, *B4* and *Co-2* clusters, located at the end of linkage groups *B4* and *B11*, respectively, revealed that these two complex *R* clusters consist of a tandem array of more than 40 CNL sequences.^{41,42} Fluorescence *in situ* hybridization (FISH) analysis revealed that these clusters are located in subtelomeric regions of chromosomes 4 and 11, in the vicinity to terminal knobs.⁴¹ Moreover, phylogenetic and comparative genomics analysis strongly suggest that the CNL present at the *B4* *R* gene cluster derived from CNL of *Co-2* *R* gene cluster, through an ectopic recombination event.

A 528-bp satellite, named *kipu*, has been identified in B4 cluster closely intertwined to NL sequences.⁴¹ *Khipu* is specific to the *Phaseolus* genus, displays a subtelomeric distribution in 17 out of 22 chromosome ends and is a component of the terminal knobs.⁴¹ Recently, the study of *kipu* sequences at the scale of the common bean genome reveals the existence of frequent sequence exchanges between non-homologous chromosomes in subtelomeric regions suggesting that the case reported for B4 and Co-2 clusters is not isolated.⁴³

The genome sequence of common bean, G19833 Andean landrace, has recently been assembled.⁴⁴ Among the 27, 197 annotated protein coding genes, 376 NL genes were predicted. Moreover, recently, a genome-wide analysis of DNA methylation using MethylC-seq has been performed in *P. vulgaris* G19833 genome.⁴⁵ CG-gene body methylation, which is found both in plants and animals, and hypermethylation of TEs in all the three sequence contexts were observed in *P. vulgaris*. Significantly, the satellite repeats *kipu* were found highly methylated throughout the genome. However, the detailed analysis of the methylation pattern of the NL genes has not yet been investigated.

In this study, we present the classification of NL encoding gene family in common bean, their phylogenetic and positional relationships, and their physical organization as well as *kipu* satellite locations on the 11 chromosomes of *P. vulgaris*. As NL encoding genes are often present in close proximity to the methylated *kipu* repeated sequence, we investigated the methylation status of NL encoding genes using the MethylC-seq data that were previously published,⁴⁵ as well as the 24-nt small RNA targeting and the expression level of NL. Our results provide significant insight into the evolution of NL and suggest a new regulation mechanism of NL transcription that has not been described in other plant species.

2. Materials and methods

2.1. Common bean genome resources and NL and *kipu* sequence datasets

This study was performed using the whole v 1.0 genome sequence of G19833 genotype downloaded from Phytozome (<http://www.phytozome.net/>). The complete set of common bean NL sequences used in this study was the initial set of 376 NL sequences annotated in common bean genome in Schmutz et al.,⁴⁴ plus one additional NL gene identified after manual inspection and named Phvul.004G015950 (Supplementary Table S1). Among these 377 NL, 364 were on pseudomolecules and 13 on scaffolds. The *kipu* dataset used in this study is composed of 2,766 *kipu* sequences annotated in Richard et al.⁴³

2.2. Phylogenetic analysis of NL encoding genes

NL genes were subdivided into two subsets, TNL (106 sequences) and non-TNL (271 sequences) subsets and distinct phylogenetic analyses were performed for each subset. The region spanning from the P-loop to the MHD conserved protein motifs was used to construct the phylogenetic trees. Nucleic sequences were initially aligned using ClustalW with default parameters⁴⁶ and then optimized by manual editing using Seaview⁴⁷ (Supplementary Figs S1 and S2). Twenty non-TNL sequences, lacking a P-loop or MHD domains or presenting a highly divergent sequence were discarded from the alignment (Supplementary Table S1). We then checked for evidence of recombination among NL using a suite of programs implemented in RDP version 4,⁴⁸ using parameters described in the literature.⁴⁹ Sequences showing significant evidence of recombination were eliminated from

further analysis (Supplementary Table S1). Submitting the full alignments to Modelgenerator⁵⁰ allowed to identify GTR + I + G and GTR + G models as the bests phylogenetic models to use for TNL and non-TNL, respectively. Maximum-likelihood trees were generated with PhyML.⁵¹ Bootstrap values were computed with the consensus of 1,000 trees generated with PhyML from alignments obtained with PHYLIP's seqboot program.⁵² The resulting phylogenetic trees were displayed using MEGA version 5.⁵³

2.3. Methylation analysis of NL encoding genes

NL methylation analysis was performed on the methylome data of G19833 leaves developed by Kim et al.⁴⁵ For each gene, analyses were performed on the genomic region delimited by the coordinates presented in Supplementary Table S2. For genes not supported by RNA sequencing data (RNAseq), it corresponds to the region from Start to Stop, including introns, while for genes supported by RNAseq data, upstream and downstream untranslated region (UTR) were also included.⁴⁴ Weighted methylation levels⁵⁴ of the 364 NL, 498 PPR and 116 Homeobox genes present in *Phaseolus vulgaris* G19833 pseudomolecules were calculated for CG, CHG and CHH sequence contexts, where H refers to A, C and T. For each gene and cytosine context, probability (one-tailed *P-value*) for the methylation difference from genome-wide average was calculated using the binomial distribution as described by Takuno and Gaut.⁵⁵ Genes were classified into three categories based on the *P-value*: C methylated gene ($P_{CHG} < 0.05$ or $P_{CHH} < 0.05$), CG methylated gene ($P_{CG} < 0.05$ and not C methylated gene), unmethylated gene ($P_{CG} > 0.95$ and not C methylated gene). Integrative Genomics Viewer (IGV) was used to visualize methylome data on G19833 genome.⁵⁶

2.4. Small RNA library construction, sequencing and analysis

RNA samples enriched for small fractions of G19833 young leaves were obtained with miRNeasy Mini Kit (#217004, QIAGEN®) and checked for their integrity on RNANano chip, using Agilent 2100 bioanalyzer (Agilent Technologies, Waldbroon, Germany). Small RNA-seq library was performed according to NEBNext® Multiplex Small RNA Library Prep Set for Illumina instructions (#E7300S, New England Biolabs, Inc.). Small RNA-seq libraries were checked for their quality on DNA1000 chip using Agilent 2100 bioanalyzer (Waldbroon, Germany) before Illumina sequencing (Illumina® California, U.S.A.). The SmallRNA-seq samples have been sequenced in Single-End (SE) with a read length of 100 bases on one lane of HiSeq2000 machine to obtained around 25 million reads. After adaptor trimming and t- and r-RNA removing, using Cutadapt⁵⁷ and SortMeRNA,⁵⁸ respectively, small RNAs of 24-nt length were selected using Prinseq v0.20.4.⁵⁹ Redundant and non-redundant (NR) data sets of 24-nt sRNAs were then mapped on G19833 genome sequence including *kipu*, NL, PPR and homeobox gene family genomic sequences using Bowtie2 (v2.2.6) with '-l 24' and '-n 0' parameters⁶⁰ and mapped reads were counted on each locus (as described for DNA methylation) and expressed in RPKM. A threshold of RPKM > 5 in both redundant and non-redundant data sets was used to consider a sequence as mapped by small 24-nt RNA.

2.5. Analysis of NB-LRR genes expression

The publicly available leaves RNA-seq data of common bean G19833 was used to analyze the expression level of NL genes.⁴⁴

Table 1. Number and classification of predicted NB-encoding *R* genes in *Phaseolus vulgaris* genome

Predicted domains	#Full length genes	#Pseudogenes	#Total	%
TNL type	82	24	106	28.1
TIR-NB-LRR	73	20	93	
TIR-NB	8	4	12	
TIR-NB-TIR	1	0	1	
non-TNL type	186	85	271	71.9
CC-NB-LRR	85	18	103	
CC-NB	3	1	4	
NB-LRR	86	64	150	
NB	5	2	7	
CC _{RPW8} -NB-LRR	7	0	7	
#Total	268	109	377	

FPKM (Fragments per kilobase of exon model per million fragments mapped) values corresponding to NL genes were extracted from Phytozome to perform a semi-quantitative categorization. Based on the FPKM scale defined in Hansey et al.⁶¹ expressed genes were divided into three classes: genes with a FPKM value below 5 are low expressed, genes with a FPKM value greater or equal to 5 and less than or equal to 200 are medium expressed, and genes with a FPKM value greater than 200 are highly expressed.

3. Results

3.1. Genome-wide annotation of NL in G19833

The present analysis was carried out on 377 NL genes identified in Schmutz et al.,⁴⁴ including 364 NL genes located on the eleven pseudomolecules and 13 NL genes located on unanchored scaffolds. In brief, common bean NB-encoding genes were identified based on HMM search of the predicted protein sequences of *P. vulgaris* (G19833; JGI, version 1.0) to identify sequences containing NB-ARC domain, completed by a tBLASTn of the NB-encoding sequences identified in the first step, on the entire genome of G19833.⁴⁴ HMM search led to the identification of 398 predicted proteins corresponding to 342 annotated genes and tBLASTn procedure identified 35 additional NL genes. On these 35 additional NL genes, 20 were missing in the JGI annotation and consequently a new identifier was created (the last digits are 50). After manual inspection of the 377 NB-encoding *R* genes candidates 268 are predicted as full length genes and 109 as pseudogenes (i.e. genes with a frameshift or a stop codon before the beginning of LRR domain) (Table 1 and Supplementary Table S1).

Analysis of each NL candidate allowed us to classify them into TNL or non-TNL families (Table 1). From the complete set of 377 NL identified in common bean genome, 106 proteins belong to the TNL group including 82 full length and 24 pseudo TNL genes. The 82 full length genes were distributed as follows: 73 TNL, 8 TN, and one TNT gene (Phvul.008G195300). The remaining 271 NB-encoding genes were collectively grouped into the non-TNL type and were distributed as follows: 103 genes encode CNL, including 85 full length and 18 pseudo genes, four genes encode CN, including three full length and one pseudo genes, 150 genes encode NL, including 86 full length and 64 pseudo genes, and finally seven genes encode NB including five full length and two pseudo genes (Table 1). In addition, within the non-TNL type, seven genes have been identified to possess a variant of the CC domain, the CC_{RPW8} domain which

share close sequence similarity with RPW8, a non-NL *R* protein from *Arabidopsis thaliana* conferring broad-spectrum resistance against powdery mildew (*Erysiphe* spp.).¹⁰ Overall more than two-third of the predicted NL-encoding genes are non-TNL genes and less than one third TNL genes.

3.2. NL physical organization

Physical map positions on the eleven pseudomolecules of G19833 genome were established for 364 (96.5%) of the annotated NL genes (Fig. 1). Both TNL and non-TNL are present on each pseudomolecule, in variable amounts. It is clear that the distribution of NL genes is not random among the chromosomes and that they tend to be organized in clusters. To identify NL clusters, we used a previous definition which specify that NL are grouped in clusters when they are not interrupted by more than eight non-NL genes.¹⁸ Using this criterion, we identified 43 clusters, containing 294 genes in total, on common bean pseudomolecules (Supplementary Table S1). Thus, on G19833 pseudomolecules, 80.8% of predicted NL encoding genes are organized in clusters while the remaining 19.2% (70 genes) are singleton genes. The size of the clusters varied across the genome from 2 to 40 NL. Remarkably, NL clusters in common bean tend to be at the end of chromosomes rather than in the center (Fig. 1). Particularly, three 'super' clusters of NL, consisting of several clusters, were located at the end of Pv04S (Pseudomolecule 4, short arm), Pv10S and Pv11L (Pseudomolecule 11, long arm) (Fig. 1 and Supplementary Table S1). The super cluster on Pv10S mainly consists of TNL sequences, while the two super clusters on Pv04S (41 NL) and Pv11L (71 NL) comprise mainly non-TNL sequences and correspond to the previously identified resistance cluster 'B4' and 'Co-2', respectively.^{39,41,62–64}

3.3. NL phylogenetical and physical relationships

To study the evolutionary relationships among the predicted NL genes, two phylogenetic trees were estimated from the nucleic alignment of NB-ARC domains of non-TNL and TNL genes. The resulting two phylogenetic trees are composed of 243 and 100 non-TNL and TNL sequences, respectively (Fig. 2 and Supplementary Fig. S3). Non-TNL and TNL phylogenetic trees can be divided into nine and four major clades, respectively (Fig. 2 and Supplementary Fig. S3). In both trees, these clades are composed of NL sequences coming from different physical locations (Figs 1 and 2 and Supplementary Fig. S3). For example, the clade CNL-H is composed of 80 NL sequences that map, to two different chromosome ends Pv04S or the end of Pv11L and corresponding to resistance clusters B4 and Co-2, respectively. Consequently, the CNL present at the B4 cluster (B4-CNL) are more similar to the Co-2-CNL than to any other CNL in the bean genome. More heterogeneous clades are also observed. Clade CNL-C is one such example as it is composed of 16 NL sequences from seven different chromosome arms (Pv02S, Pv05S, Pv06L, Pv08S, Pv09L and Pv011S) (Figs 1 and 2). As expected the seven predicted CC_{RPW8}-NL were gathered within the same clade (CNL-R). However, CC_{RPW8}-NL reside on four different locations, end of Pv01S, end of Pv02S, Pv03L and Pv06L. The same observation holds true for many different CNL and TNL clades where phylogenetically close NL sequences can be spread on different chromosome arms, suggesting sequence exchange between non-homologous chromosomes. On the other hand, both non-TNL and TNL phylogenetic trees show that most subclades are composed of NL sequences from the same chromosome arm (Fig. 2 and Supplementary Fig. S3). For example, CNL-A clade is mostly

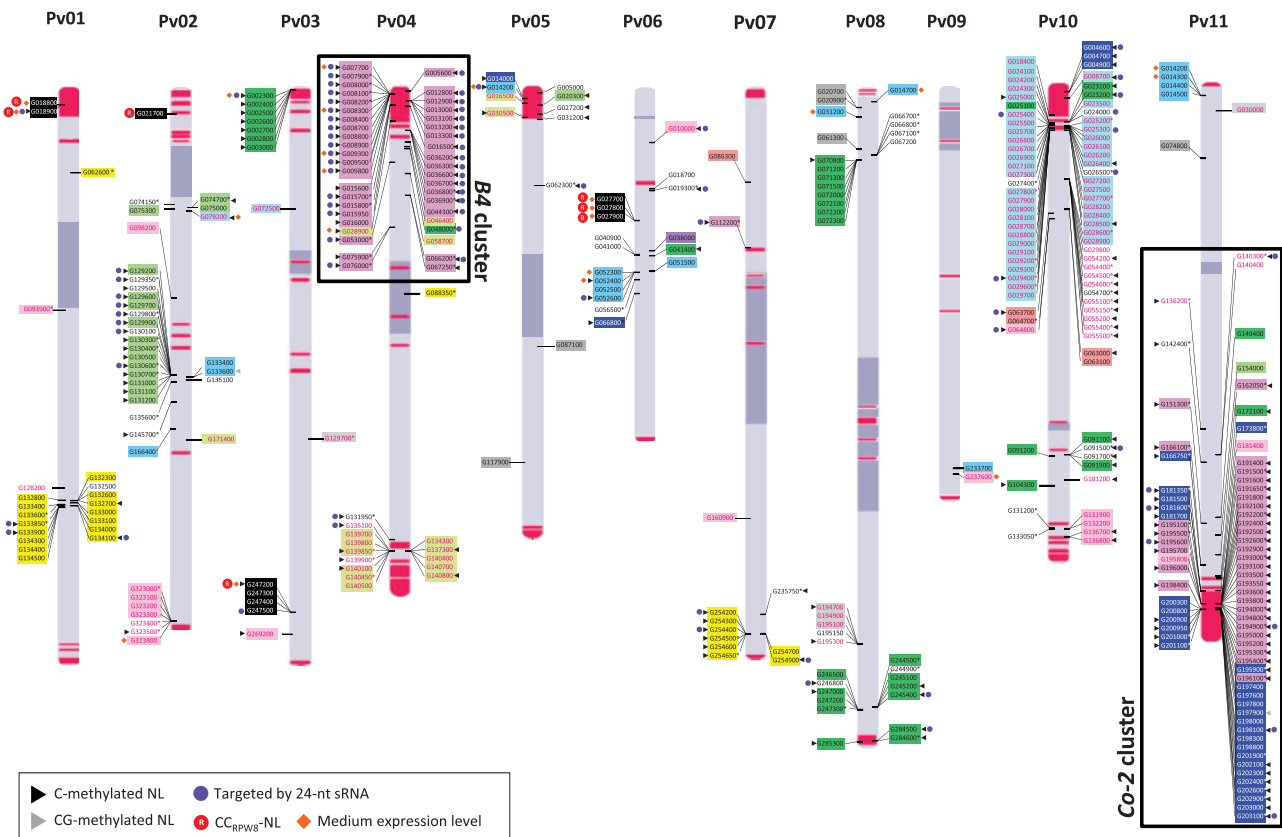


Figure 1. Chromosomal distribution of common bean NL encoding genes and *khipu* satellites. The relative map position of 364 NL encoding genes is shown on the individual pseudomolecules depicting the chromosomes Pv01 to Pv11 as identified in the literature.⁴⁴ Each NL gene has a unique label representing the seven last informative digits from the annotation. For example, G132300 located on pseudomolecule one corresponds to the gene Phvul.001G132300. Genes encoded by the positive and negative DNA strands are depicted on the right and left sides of the chromosome, respectively. TNL sequences are presented in pink font and CNL sequences are presented in black or white font. Colours and background of the genes are identical to the phylogenetic trees (Fig. 2 and Supplementary Fig. S3). NLs corresponding to pseudogenes are denoted by an asterisk (*) after their name. Centromeric positions on individual pseudomolecules were identified using centromere satellite repeats identified in the literature¹⁰³ and are represented by dark blue bars on the pseudomolecules. The arm above centromeric region is designated as 'short' arm while the arm below is designated as the 'long' arm. *Khupu* satellite sequences are indicated with red bars on pseudomolecule structures according to Richard et al.,⁴³ with block sizes proportional to number of *khupu* units. CG methylated genes and genes methylated in the three contexts are depicted by grey and black arrowheads, respectively.

composed of three subclades of NL from Pv03S, Pv08L and Pv08S, CNL-D clade is composed of two subclades of NL from Pv01L and Pv07L, CNL-E clade contains a huge subclade of Pv02L NL and TNL-A contains a subclade of Pv04L NL. If the previous examples clearly illustrate local duplication of NL sequences, clades CNL-G, CNL-H and TNL-D are even more striking (Fig. 2 and Supplementary Fig. S3). These impressive NL amplifications are clearly visible on the physical map, where blocks of NL sequences of the same colors are depicted (pink blocks at Pv04S and Pv11L, light blue block at Pv10S, and dark blue block at Pv11L, Fig. 1). In conclusion, phylogenetic and positional relationships of common bean NL suggest both frequent sequence exchanges between non-homologous chromosomes and local amplification probably resulting from unequal crossing-over.

3.4. NL colocalisation with the subtelomeric satellite DNA *khupu*

Khupu sequences annotated in Richard et al.,⁴³ are depicted in red on the physical map of G19833 (Fig. 1). As previously shown, *khupu* sequences are present on all pseudomolecule ends except on Pv06S and Pv09S (Fig. 1). *Khupu* units are often in close proximity to NL

sequences as noticeable at the end of Pv01S, Pv02S, Pv03S, Pv04S, Pv04L, Pv05S, Pv08L, Pv10S, Pv10L and Pv11L. Strikingly, there are a lot of *khupu* sequences in the three largest NL super clusters, on Pv04S, Pv10S and Pv11L (Fig. 1). However, several NL clusters do not co-locate with *khupu* blocks, such as NL clusters on chromosome 8 or 2 (Fig. 1).

3.5. NL DNA methylation

Due to their proximity to repeated and methylated *khupu* satellite sequences⁴⁵ and, at least for B4 and Co-2 CNLs, to their proximity to terminal knobs,⁴¹ we decided to investigate the DNA methylation status of NL genes. Indeed, various examples of methylation spreading from repeated sequence to the neighboring genes have been described.^{65–67} DNA methylation analysis reveals that out of the 364 NL encoding genes present on the pseudomolecules, two (0.6%) are methylated in CG context, 197 (54.1%) are C-methylated genes (i.e. methylated in CHG and CHH contexts), and the remaining 165 genes (45.3%) are unmethylated (Fig. 3, Supplementary Table S1). Among the 104 TNL sequences, 31% are methylated while 64% of the 260 non-TNL sequences are methylated (Supplementary Fig. S4). Approximately, half of the full-length NL are methylated

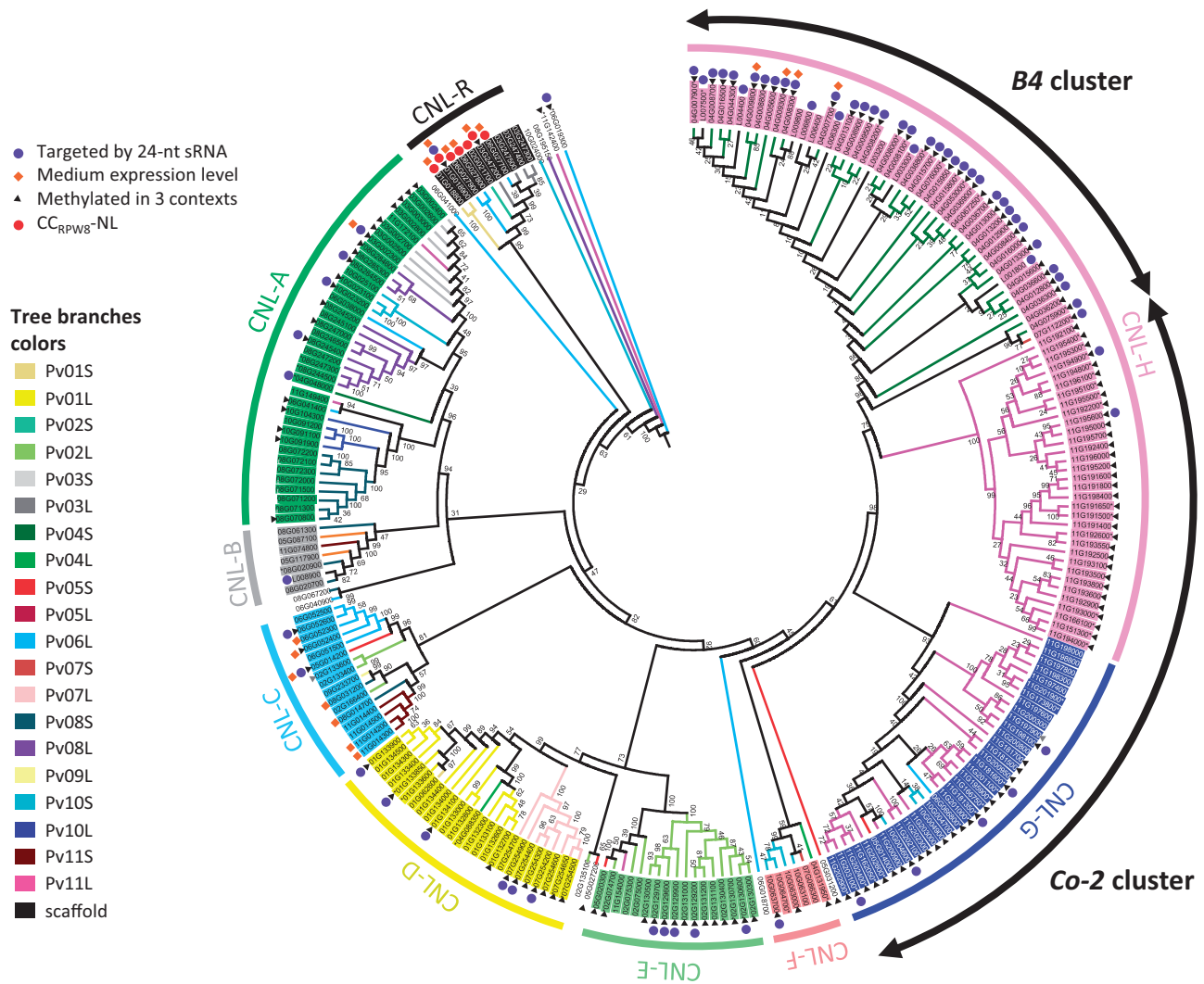


Figure 2. Maximum Likelihood Phylogenetic analysis of the predicted *P. vulgaris* non-TNL genes. Each gene is labeled with its Phytozome identifier without the 'Phvul.' prefix. One color was assigned to each chromosome arm named by a number (from 1 to 11), corresponding to the pseudomolecule number, followed by the letter L (long arm) or S (short arm) and consequently each branch in the tree is colored according to the location of the gene carried by this branch. Pseudogenes are indicated by an asterisk (*) in the beginning or at the end of their name. CG methylated genes and genes methylated in the three contexts are depicted by grey and black arrowheads, respectively.

while almost 70% of the pseudogenes are methylated (Supplementary Fig. S4). This methylation mostly occurs on gene body (Fig. 4). Nearly all the C-methylated NL (89%) were also CG methylated (Supplementary Tables S1 and S3). Consequently, in common bean, ~half of NL sequences are methylated in the three sequence contexts (CG, CHH, CHG), a pattern classically observed for repeated sequences. Manual inspection of each methylated NL genes revealed that out of 197 methylated NL, 34 correspond to NL methylated only in intron with most of these introns containing repeated sequences such as transposable elements (Supplementary Fig. S5). However, the remaining 163 C-methylated NL are methylated on their coding sequence with methylated area ranging from the complete ORF to half of the ORF (Supplementary Figs S5–S7). Inspection of nearby genes of NL genes revealed that they do not present this atypical DNA methylation profile even if located in the same genomic environment (Supplementary Fig. S7). In order to see if this high proportion of methylated genes within NL gene family is specific to this family or a common feature of gene families (that can

be considered as a kind of repeated sequences), we looked at methylation pattern of two other gene families. We examined the methylation status of the 498 genes encoding PPR (pentatricopeptide repeat) protein family and the 116 genes encoding Homeobox transcription factor family in common bean genome. Three and two genes in the PPR and Homeobox family, respectively, present an intermediate level of CG methylation and were thus excluded from the following analysis. For the PPR and Homeobox gene family, only 13.6% (7.7% CG body and 5.9% C-methylated) and 13.3% (5.3% in CG body and 7% C-methylated) of the genes are methylated, respectively (Figs 3 and 4, Supplementary Table S2). Consequently, there is a much higher proportion of C-methylated genes in the NL family specifically. Moreover, NL genes present higher levels of DNA methylation when compared with Homeobox and PPR genes, whatever the sequence context (% CG: 53.43 versus 29.27 and 38.17, Wilcoxon test, all $P > 0.05$; % CHG: 39.44 versus 3.47 and 10.97, Wilcoxon test, all $P > 0.05$; % CHH: 2.72 versus 1.17 and 1.02, Wilcoxon test, all $P > 0.05$, for NL genes compared to Homeobox

and PPR genes, respectively) (Table 2). In particular, level of CHG methylation is much higher for NL genes compared to other genes ('all genes', PPR and homeobox genes), although lower than what is observed for TEs (Fig. 4). In conclusion, compared to other gene families, NL gene family presents both a higher proportion of methylated genes and a higher methylation level.

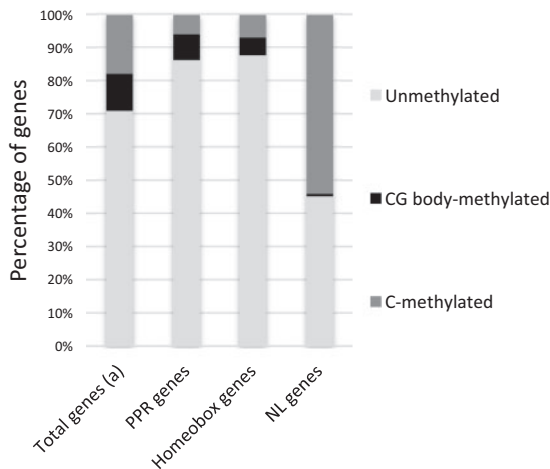


Figure 3. Distribution of the methylated status of the PPR, Homeobox and NL genes in *P. vulgaris*.

^aTotal genes analysis was described in Kim et al.⁴⁵ and correspond to the 27,082 genes annotated in G19833 genome. Among the 498 studied PPR genes, three were found CG-methylated with an intermediate value and were then excluded from this analysis. Among the 116 studied Homeobox Transcription Factor genes, two were found CG-methylated with an intermediate value and were then excluded from this analysis. For the NL genes, the analysis was performed in the 364 NL genes mapped on the G19833 pseudomolecules.

Phylogenetic and positional relationships of methylated NL genes have been studied and methylated NL are depicted by black arrow-heads (Figs 1 and 2 and Supplementary Fig. S3). Concerning the three largest distal NL super clusters, contrasting patterns of methylation were observed since most NL sequences from the clusters on Pv04S (B4 cluster) and Pv11L (Co-2 cluster) are methylated, while few NL sequences of the cluster located on Pv10S are methylated (Figs 1 and 2 and Supplementary Fig. S3). The majority of methylated NL genes from Pv04S and Pv11L clusters belong to CNL-H clade (pink, Figs 1 and 2). Pv11L cluster is also composed of sequences located in clade CNL-G (dark blue, Figs 1 and 2) that are also methylated. Interestingly, this latter clade is also composed of the scarce methylated

Table 2. Average percentage of DNA methylation in the different sequence contexts in repeated elements and various gene families

Genes	%CG	%CHG	%CHH
Total genes ^a	14.65	6.48	0.58
Transposable elements ^a	71.67	61.52	8.05
<i>Khipu</i> satellite repeats ^b	93.29	72.06	5.89
PPR genes ^c	38.17	10.97	1.02
Homeobox genes ^c	29.27	3.47	1.17
NL genes ^c	53.43	39.44	2.72

^aThe average percentage of methylation (see Methods) in the different sequence contexts were calculated for all genes and transposable elements annotated in *Phaseolus vulgaris* G19833 (in this study).

^bThe average DNA methylation levels of *khipu* repeats were determined in Kim et al.⁴⁵

^cThe average percentage of methylation in NL, Homeobox and PPR genes were calculated only for the significantly methylated genes (C- and CG-methylated genes).

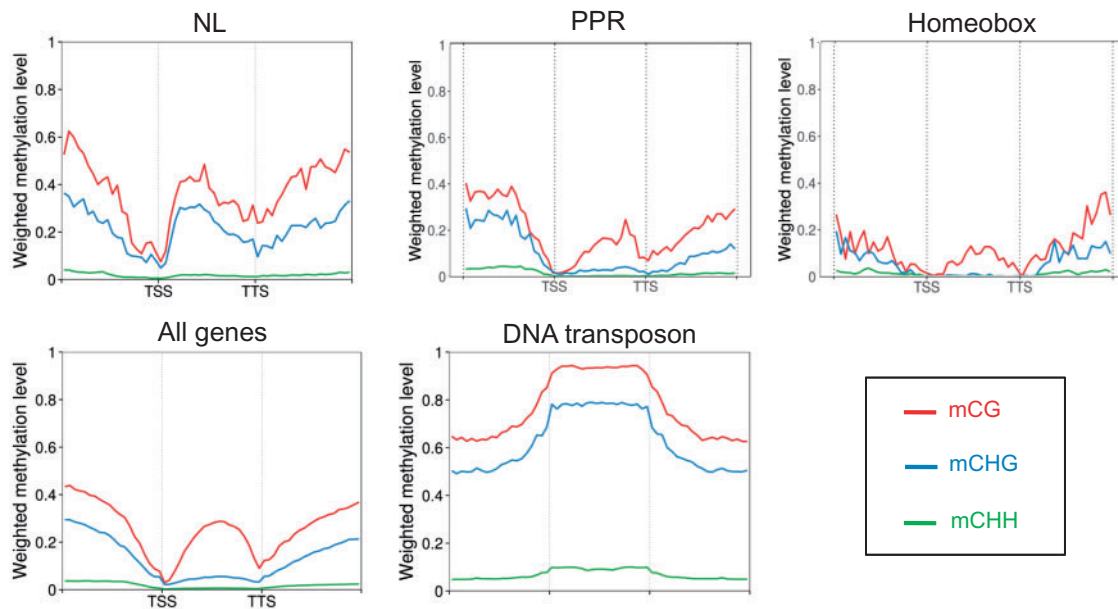


Figure 4. Average distribution of DNA methylation (for the three sequence contexts) of *P. vulgaris* NL, Homeobox and PPR gene families and their flanking regions. Flanking regions are 1 kb. TSS: Transcription Start Site. TTS: Transcription Termination Site. The metaplots for the 364 NL, 116 Homeobox and 498 PPR of G19833 pseudomolecules were performed in this study, using the methylome data of Kim et al.⁴⁵ The metaplots corresponding to the DNA transposons and all genes were previously described in Kim et al.⁴⁵

sequences present on the globally unmethylated Pv10S cluster. This suggests that methylation of NL encoding genes could be influenced by their sequence, as closely related sequences (e.g. belonging to the same clade) share the same methylation status. However, within the clade CNL-D (yellow, Figs 1 and 2), NL sequences located at the end of Pv07L are mostly methylated in contrast to NL sequences located on Pv01L (Figs 1 and 2). This is also the case for the clade CNL-A (green, Figs 1 and 2) where all the sequences of the end of Pv03S are methylated whereas only half of the NL of the end of Pv08L are methylated and only one sequence is methylated in the cluster of Pv08S. Interestingly, the methylated NL sequences of CNL-A clade that reside in Pv03S are organized in a cluster (cluster 03 A, Supplementary Table S1) tightly linked to *kipu* sequences, as the three methylated NL genes from the extremity of Pv08L in cluster 08 G (Phvul.008G284500, Phvul.008G284600, Phvul.008G285300) (Fig. 1 and Supplementary Table S1). These latest observations suggest that methylation on NL genes could also be influenced by physical location, and especially by the proximity of *kipu* repeats.

3.6. Common bean NL and *kipu* satellite DNA are massively targeted by 24-nt small RNAs

Because 24-nt sRNAs mediates RNA-directed DNA methylation (RdDM) and transcriptional gene silencing (TGS) of transposable elements, we then analyzed the relationship between *kipu* satellites, NL genes and 24-nt sRNA populations. 3, 087, 771 redundant and 1, 895, 583 non-redundant reads of 24-nt sRNAs were sequenced in G19833 young leaf library (Supplementary Tables S1 and S2). *Kipu* sequences were abundantly mapped by 24-nt sRNAs with 2596 out of 2677 *kipu* sequences mapped with the selected criteria (Supplementary Table S2). Ninety out of 377 (24%) NL genes are predicted to be targeted by 24-nt sRNAs. As for DNA methylation, NL gene family seems to have a different profile compared with other gene families since for PPR and Homeobox families only 7 out of 498 (1.4%) and 1 out of 116 (0.9%) are targeted by 24-nt sRNAs, respectively (Supplementary Table S2). The analysis of chromosomal repartition reveals that almost all C-methylated non-TNL sequences of the cluster located at Pv04S (B4 cluster) are also targeted by 24-nt sRNAs (Figs 1 and 2). Strikingly, a different situation is observed for the phylogenetically closely related NL sequences located at the end of Pv11L (Co-2 cluster; Clade G) that are also DNA methylated but are mostly not predicted to be targeted by 24-nt sRNAs (Figs 1 and 2).

3.7. NL expression

We used publicly available RNA-seq data of common bean G19833 to study NL expression level in young trifoliate leaf tissue. Globally, the level of expression of NL was either low (286 NL genes with RPKM < 5) or not detected (48 NL genes with RPKM = 0). Only 22 NL genes can be considered as moderately expressed ('medium', with RPKM comprised between 5 and 200) (Supplementary Table S1). Interestingly, with the exception of Phvul.002G021700, all the CC_{RPW8}-NL genes belong to this 'medium expression gene' category. Another noteworthy element is that almost one third of the 22 moderately expressed NL genes, are from clade CNL-C (seven genes). Within the nine remaining moderately expressed NL genes, five reside on Pv04S, including one TNL and four CNL from clade CNL-H.

4. Discussion

Previously considered as an orphan crop, important genomic resources are now available in common bean thanks to the advent of

next-generation sequencing (NGS) technologies.⁶⁸ Based on multiple omics data from the sequenced common bean genotype G19833,^{44,45} our results indicate that gene movements play a crucial role in NL evolution in common bean genome and that NL present an atypical DNA methylation pattern.

4.1. NL evolution in common bean genome through both local amplification and sequence exchange between non-homologous chromosomes

We identified 377 NL-encoding genes in G19833 genome with approximately one third of TNL- and two thirds of non-TNL-encoding genes. As observed in other plant species, these NL sequences are mostly organized in clusters.^{18,19} In common bean most of the large NL clusters are located at the ends of the chromosomes and present a huge size compared to other species. This peculiar location has also been observed in several other plant species such as potato, tomato and cotton.^{19,69,70} However, this feature of NL clusters is not observed in all plant species and even in all Legume species since it has not been reported in *Arabidopsis*, Rice or *Medicago*.^{17,18,71} With regard to their huge size, it is particularly impressive for the NL clusters located at the end of Pv04S (B4 cluster), Pv11L (Co-2 cluster) and Pv10S, each containing more than 40 NL sequences. FISH analyses have revealed a subtelomeric location for B4 and Co-2 clusters.⁴¹ Distal regions of the chromosomes are highly recombinant compared to pericentromeric regions and are consequently favorable to promote NL amplification through unequal crossing-over.^{44,72,73} In agreement with that, we found that these three large NL clusters are composed of phylogenetically related NL, suggesting local amplifications of NL sequences. Similarly, in other plant species, extensive amplification of a few NL subfamilies have increased NL copy number considerably.^{74,75} On the other hand, some clusters are also composed of phylogenetically distant sequences, suggesting sequence exchange between non-homologous chromosomes. The present genome wide analysis shows that the B4 CNL are more similar to the Co-2 CNL than to any other CNL, confirming that the B4 cluster derives from the Co-2 cluster through an ectopic recombination between non-homologous chromosomes in subtelomeric regions.⁴¹ The same pattern has been observed in the phylogeny of the subtelomeric satellite DNA *kipu*, closely intermingled to NL sequences.⁴³ These NL and *kipu* movement could have taken place in the context of sequence exchange between subtelomeres of non-homologous chromosomes as reported in human genome.⁷⁶ Moreover, this proximity of NL with highly repeated sequences present on most of chromosome ends could promote unequal-crossing. Taking together these observations strongly suggest that in common bean, distal regions of the chromosomes are highly recombinant compared to pericentromeric regions and are consequently favorable to promote NL amplification through unequal crossing-over.

4.2. Common bean NL genes display a transposon-like methylation pattern in their coding region

MethylC-seq performed on G19833 allowed us to sensitively measure cytosine methylation within specific sequence contexts on NL genes. According to current views of DNA methylation patterns in plants, gene body methylation occurs mainly in a CG context whereas non-CG methylation is limited to repeated sequences such as transposable elements and non-protein-coding repeats.^{35,77–81} Contrasting with this view, we observed that more than half of common bean NL genes are methylated in their gene body not only in CG but also in CHG and CHH. Consequently, in common bean, most NL genes are methylated

like transposons in their coding regions but with a lower level (Table 2 and Fig. 4). This non-CG methylation pattern seems specific to the NL gene family since it was not observed for genes belonging to other gene families such as PPR or Homeobox transcription, even if some members were also located in subtelomeric regions (Supplementary Fig. S8). Moreover, NL neighboring genes do not present this atypical DNA methylation profile even if located in the same genomic environment, strongly suggesting that this atypical methylation profile is specific to the NL gene family and is not simply due to their location (Supplementary Fig. S7). This unusual DNA methylation profile and targeting by 24-nt sRNAs of NL gene family have not been described yet in other plant species. Therefore, this analysis should be extended to other gene families in common bean as well as in other plant species to see if this phenomenon is specific of NL genes in common bean. In plants, other atypical genes displaying in their coding region a transposon-like methylation pattern have been reported including *Asr1* gene in tomato⁸² and *CRP* (*Cystein-Rich Peptide*) gene family in *Arabidopsis*.⁸³ Interestingly, a possible retrogene origin has been proposed for CRP genes.

4.3. What is responsible for DNA methylation on NL genes?

Phylogenetic and positional relationships of methylated NL genes in the G19833 pseudomolecules revealed that methylation status of NL genes could be influenced by their nucleotide sequence (as exemplified in clades CNL-G; -H, -R) or physical location. It is noteworthy that physically clustered genes often present the same methylation pattern. For example, genes of clade CNL-A are found mostly methylated in regions containing *kipu* repeats whereas they are mostly unmethylated in other chromosomal regions. What is responsible for DNA methylation of NL genes?

4.3.1. RdDM pathway mediated by 24-nt sRNAs

In plants, *de novo* cytosine methylation in the three sequence contexts and maintenance of methylation on asymmetric methylation sites (CHH) require the RdDM pathway, which involves numerous factors, including 24-nt sRNAs that guide methylation on homologous DNA sequences.^{22,84} While this pathway mainly targets repetitive elements, such as transposable elements, there are few reports of gene body methylation in the three contexts. One example is the CRP genes in *Arabidopsis* where cytosine methylation is partly dependent on the RdDM pathway⁸³ and NL genes in common bean is an additional example. Indeed, in the present study, we showed that 90 NL genes (80/364 total NL genes mapped on G19833 pseudomolecules, 21.9%) are targeted by 24-nt sRNAs in their transcribed region. Strikingly, nearly all of them (76/80, 95%) are also highly gene-body methylated in the three sequence contexts as for example on Pv02L and Pv04S (*B4* cluster) (Fig. 1 and Supplementary Fig. S9). Altogether, this suggests that in common bean, the RdDM pathway could target not only repeated sequences but also NL genes. This hypothesis is supported by the clear correlation between the NL gene body regions targeted by 24-nt sRNA and the methylated regions (Supplementary Figs S6 and S7). However, many C-methylated NL genes (61.4%; 121/197 mapped on G19833 pseudomolecules) are not targeted by 24-nt sRNAs, as for example most of the NL genes from Co-2 cluster (Pv11L), suggesting that another mechanism(s) (spreading of methylation see after), is responsible for cytosine methylation of these NL sequences. The *B4* and *Co-2R* clusters share

many similarities: sequence content, subtelomeric physical location with proximity to *kipu* satellite sequences and high methylation status. However, they present a contrasting pattern regarding 24-nt sRNAs which target most of *B4*-NL but only few *Co-2*-NL (Fig. 1). Since the main difference between these two R clusters is the fact that *B4* NL are young compare to *Co-2* NL,⁴¹ it is tempting to speculate that this contrasting 24-nt pattern is due to their age difference. This is reminiscent of what has been described for retroelements, where RdDM, although targeted to transposons and repeats throughout the genome, is particularly notable at younger retroelements in *Arabidopsis* and in *Gossypium raimondii*.^{80,85–88}

4.3.2. Spreading of DNA methylation from the satellite repeats, *kipu*

Methylated NL clustered on Pv03S, Pv04S, Pv08L and Pv11L present common features. They are all located at chromosome extremities which are enriched in the satellite sequence *kipu*, previously found to be highly methylated in the three sequence contexts (CG, CHG, CHH). Several studies in plants have detailed that DNA methylation can « spread » beyond repetitive elements (TEs or tandem repeats), over 200–1000 bp.^{89,90} Consequently, we propose that the methylation pattern observed on NL genes of these chromosomal regions could result from a methylation spreading originating from the *kipu* sequences, especially on Pv03S, Pv08L and Pv11L (*Co-2* cluster) where methylated NL genes are not targeted by 24-nt sRNAs.

4.4. Biological role of cytosine methylation on NL genes: most of NL genes are expressed at a low level in common bean?

In plants, cytosine DNA methylation is involved in regulation of gene expression during normal development. DNA methylation in the promoter region of genes, whatever the cytosine context, is associated with a transcriptional silencing of the corresponding gene (for example FWA, SDC).^{90,91} Concerning DNA methylation in coding region, its influence on expression depends on the sequence context of methylated cytosine and on the methylation level. Indeed, genome-wide analyses of DNA methylation and gene expression revealed that CG-gene body methylation is positively correlated with gene expression^{34,35,92,93} while CHG or CHH gene body methylation can be negatively associated with gene expression levels.^{82,83,94} In that context, even if the biological role of the transposon-like methylation pattern of the NL gene bodies is not yet clear, we propose that it is likely related to gene silencing. Our results are consistent with these observations since 87.3% of C-methylated NL (172/197 C-methylated NL) are very poorly expressed or even not detected in leave RNA-seq data. Consequently, in addition to the well described post-transcriptional gene silencing mechanisms of NL involving microRNAs targeting NL mRNA,^{95–97} our results suggest the existence of an additional regulation mechanism of NL at the transcriptional level. Together, these mechanisms could be essential to down-regulate resistance expression in plant during normal growth condition, in absence of pathogen attack. Indeed, resistance genes may impose a fitness cost on host plants, and consequently their expression needs a high degree of control.¹⁶ Since increasing data suggest that DNA methylation dynamically responds to biotic stress,^{28,29,98} we propose that this methylation could be withdrawn in the presence of the pathogen allowing NL expression only when needed. Consequently, this peculiar subtelomeric genomic environment may favor the proliferation of large NL gene clusters due

to, not only increased recombination but also to some form of silencing allowing a large amplification of NL sequences without fitness cost, as it has been proposed for F-box superfamily in *Arabidopsis*.⁹⁹

5. Conclusion

In the present report, we have shown that NL sequences can move in the common bean genome and are methylated in the three sequence contexts like transposable elements. Another element that brings NL and transposable elements closer is their ability to damage DNA. Indeed, if this feature is well known for transposable elements that can integrate DNA after cleavage of the insertion site by a transposase or an integrase,^{100,101} a recent study has revealed the potential of NL proteins to bind genomic DNA *in planta*¹⁰² and to induce DNA damage through nicking *in vitro*. Altogether this suggests that NL genes could be considered as retrogenes.

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Conflict of interest

None declared.

Supplementary data

Supplementary data are available at DNARES online.

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