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Soybean (*Glycine max*) NF-Y (Nuclear Factor of Y Box) gene family and its potential role under stress conditions and nodulation

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Abstract

The Nuclear Factor of Y box (*NF-Y*) is a transcription factor composed of three subunits (*NF-YA, NF-YB,* and *NF-YC*) involved in the regulation of genes related to physiological processes. In plants, NF-Y genes act in development, in addition to biotic and abiotic stresses response. Regarding *Glycine max* (*Gm*), the *NF-Y* genes are poorly investigated. In this important crop, the characterization of genes related to stresses represents an important material for improvement of cultivars. In this study, *GmNF-Y* genes were investigated through an extensive data mining using several bioinformatics approaches. We identify a total of 21 genes of *GmNF-YA*, 23 to *GmNF-YB*, and 24 to *GmNF-YC* subunits. Results showed that during evolution, *GmNF-Y* genes arose by block duplication and subfuctionalization processes could be occurring in this family. *In silico* expression analyses indicate that *GmNF-Y* genes are not ubiquitously expressed in organs; their expression are instead organ-dependent. In several biotic and abiotic stresses, the majority of *GmNF-Y* genes are modulated, especially during *Phakopsora pachyrhizi* infection, representing a new characterization for these genes. In addition, in root hair inoculated with *Bradyrhizobium japonicum* (nitrogen-fixing bacteria) some genes are modulated. Our study provides an overview of the subtle genetic diversification of the NF-Y family in soybean, through the characterization of genes considering their evolution and structure, and analysis of expression pattern. We highlight a putative involvement of *GmNF-Y* genes under multivariate environmental conditions related to plant defense responses, providing data to be explored further for the generation of stress tolerant/resistant plants.

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Introduction

The Nuclear Factor of Y box (*NF-Y*) is a eukaryotic conserved oligotrimeric transcription factor involved in regulation of genes related to different physiological processes. NF-Y is composed of three subunits: NF-YA, NF-YB, and NF-YC. Each subunit is required for DNA binding, subunit association, and transcriptional regulation [1]. The three NF-Y subunits interact, forming a heterocomplex in plants [2] that can bind CCAAT DNA motifs, controlling the expression of target genes. NF-YA performs specific recognition and binding to the CCAAT-box sequence in the promoter of target genes. NF-YB and NF-YC promote chromatin accessibility to NF-YA and to additional transcription factors involved with the transcriptional regulation process [2-4].

It has been previously showed that NF-Y genes are involved with the transcriptional control of gametogenesis [5], embryogenesis [5,6], nodule development and rhizobia symbiosis [2,7], seed germination [8], hormonal signaling and flowering time [9-11], root architecture and elongation [12], fruit ripening [8], photosynthesis [13,14], endoplasmic reticulum stress response [15], drought response [16-18], grain yield [19], salinity and ABA treatments [18] and cell proliferation in endosperm development [20]. These results clarify that NF-Y genes are involved in several important networks. Their characterization in several species could contribute to the understanding of their wide role in diverse plant mechanisms.

While most eukaryotic genomes possess only one or two genes encoding each NF-Y subunit, in vascular plants each subunit is encoded by gene families [21]. In *Physcomitrella patens*, 2 NF-YA, 9 NF-B, and 12 NF-YC proteins were identified [22]. In the emerging monocot model plant *Brachypodium distachyon*, there are 7 NF-YA, 17 NF-YB, and 12 NF-YC proteins [23]. In rice, there are at least 10 NF-YA, 11 NF-YB, and 7 NF-YC genes [24], while in *Arabidopsis thaliana* there are 10 genes coding for each NF-Y subunit [25].

Soybean (*Glycine max*) is one of the most important crops in the world. Different types of stresses severely restrict soybean productivity. The identification of genes related to stresses regulation is a fundamental issue, representing the raw material for improvement of soybean cultivars. Regarding the NF-Y family, it is poorly investigate in soybean. Here, we carried out an extensive data mining to identify *NF-Y* genes (*GmNF-Y*) in soybean genome. We characterized gene structures, duplication and evolution. *In silico* expression analyses of *GmNF-Y* in organs and stresses conditions were investigated. Our results contribute to the knowledge about the *GmNF-Y* and lay a foundation for deep characterization of this gene family in soybean.

Material and methods

NF-Y gene annotation and domains characterization

The nucleotide and protein sequences of the *A. thaliana* genes available on Phytozome [26] were used as queries to BLAST searches against soybean genome in this database, NCBI and Gramene [27]. The exon-intron of each *GmNF-Y* gene was investigated using GSDS [28].

Duplication events, synteny, and *Ka*/*Ks* substitution rate analysis

We have analyzed the mechanisms involved with the evolution of *GmNF-Y* genes using the WGmapping tool in the PLAZA v 3.0 database [29]. The physical co-localization of *NF-Y* genes in soybean genome was analyzed in the Genome Duplication Database (PGDD) [30], considering 100 kb syntenic region between paralogous *GmNF-Y*. This analysis uses the BLASTP tool to search for potential anchors (*E* <1e−5, top 5 matches) among every possible chromosome pair in multiple genomes. The homolog pairs identified are used as the input in the multiple collinearity scan (MCsan) program, and an *E* value <1e−10 is considered a significant cut-off. The putative classification of the genes identified in the syntenic regions was accessed using Phytozome and the PLAZA databases.

The ratio of the number of nonsynonymous substitutions per nonsynonymous site (*Ka*) to the number of synonymous substitutions per synonymous site (*Ks*) in paralogous *GmNF-Y* genes was analyzed using the PGDD database.

NF-Y domains characterization

Proteins with at least 25% of homology with the queries were examined to the presence of the NF-Y domains [1] using SMART [31] and InterProScan Signature [32]. GmNF-Y domain conservation was investigated using MEME [33].

Expression analysis of *GmNF-Y* genes

The expression pattern of *GmNF-Y* genes was analyzed using BAR (The Botany Array Resource, [34,35], considering leaves, flowers, green pods, SAM (Shoot Apical Meristem), roots, root tips, nodules and roots inoculated with *Bradyrhizobium japonicum* in different hours after inoculation (HAI). Additionally, Genevestigator database [26] was used to investigate the expression of *GmNF-Y* genes in soybean tissues (inflorescence, roots, seedling and shoots), under stress conditions and perturbations (biotic, chemical, temperature and stress).

Results

GmNF-Y gene annotation and protein *in silico* characterization

Using BLAST approaches, a total of 21 genes encoding *GmNF-YA*, 23 *GmNF-YB*, and 24 *GmNF-YC* subunits were identified (Figure 1, and ESM Table 1 - Electronic Supplementary Material 1). These genes were distributed in several loci, among 2 and 20 chromosomes. A wide difference in the length of *GmNF-Y* genes was observed, ranging to 500 bp up to 6000 bp. Analysis of structure showed that the number of exons was ranged between 4 to 6 exons in *GmNF-YA* genes, while 1 to 5 exons in *GmNF-YB* and 1 to 6 exons in *GmNF-YC* genes. Larges 5´UTR compared to the total gene length were observed in some sequences, as *GmNF-YA9*, *GmNF-YA10*, *GmNF-YA11*, *GmNF-YA14*, *GmNF-YB15*, *GmNF-YC8*, *GmNF-YC9*, *GmNF-YC11*, *GmNF-YC12*, *GmNF-YC13* and *GmNF-YC15*. In addition, wide 3´UTR were also observed in *GmNF-YB14*, *GmNF-YB19* and *GmNF-YC21*. The consensus analyses of the *GmNF-Y* domains showed a high degree of amino acid conservation, especially for *GmNF-YA* and *GmNF-YC* subunits (Figure 1).

NF-Y genes are located in a duplicated region

Figure 2 exemplify the results found considering the analysis of syntenic regions containing the duplicated *NF-Y* genes (ESM Table 2 shows the complete results). Block duplication processes generated all *GmNF-Y* genes encoding subunits A and B (ESM Table 1). Regarding subunit C, *GmNF-YC13*, *GmNF-YC15,* and *GmNF-YC24* were originated by tandem duplication, and *GmNF-YC18* by tandem and block duplication.

To analyze the processes that have driven the changes at the

molecular level, the *Ka/Ks* values between *GmNF-Y* syntenic genes were evaluated. The results showed that all *Ka/Ks* values were <1, indicating that a subfuctionalization process could be acting on these paralogous sequences (ESM Table 2).

In silico* expression of *GmNF-Y

All *GmNF-Y* genes with expression data available in BAR were analyzed. Figure 3 exemplifies the results and the complete results was showed in ESM (Figures 1-3). Regarding subunit A, we observed that in green pods, *GmNF-YA2* was upregulated, while *GmNF-YA8* and *GmNF-YA12* were downregulated. In nodules, *GmNF-YA4, 5, 6, 9,* and *11* were highly upregulated, while *GmNF-YA1* was downregulated. In roots, *GmNF-YA2* was downregulated. In root tips, *GmNF-YA3, 7, 8, 9, 10, 12,* and *18* were downregulated. *GmNF-YA5* was downregulated in flowers. Regarding the NF-B subunits, *GmNF-YB4* was up- and *GmNF-YB19* downregulated in nodules. In roots, *GmNF-YB4* was up- and *GmNF-YB16* was downregulated. In root tips, *GmNF-YB1, 2, 3, 4, 5,* and *17* were downregulated, while *GmNF-YB21* was upregulated. In leaves, *GmNF-YB16* was up-, while *GmNF-YB17* was downregulated. The expression of genes corresponding to subunit C demonstrated that *GmNF-YC3* was upregulated, while *GmNF-YC9* and *GmNF-YC10* were downregulated in nodules. In roots, *GmNF-YC4* and *GmNF-YC11* were upregulated. In root tips, *GmNF-YC3* and *GmNF-YC7* were downregulated, while *GmNF-YC20* was upregulated. *GmNF-YC3, 20* and *21* were upregulated in SAM.

Figure 3 also presented examples *GmNF-Y* genes expression profile in plants growing in soil colonized with *Bradyrhizobium japonicum* (see all results in ESM Figures 1-3). *GmNF-YA2* (12 HAI) and *GmNF-YA17* were upregulated (12 and 24 HAI). *GmNF-YA6* was downregulated in stripped roots (48 HAI). Regarding subunit B genes, *GmNF-YB17* was highly upregulated in root hairs (12 HAI), and downregulated in stripped roots (48 HAI) and root hairs (48 HAI) (Figure 3). Considering subunit C, *GmNF-YC4, 7, 9, 19,* and *20* were downregulated, while *GmNF-YC11* was highly upregulated in stripped roots (48 HAI). *GmNF-YC11* (48 HAI), *GmNF-YC19* (12 HAI), and *GmNF-YC*20 (24 HAI) were downregulated in root hairs.

The expression profile of *GmNF-Y* genes under several perturbations in diverse organs is shown in Figure 4. For elicitor, nutrient, chemical, and temperature, the majority of *GmNF-Y* genes were typically downregulated in all tissues. Under biotic stress, especially under *P. pachyrhizi* fungi infection. In roots, seedlings, and shoots, the majority of *GmNF-YA* genes were modulated. Regarding the subunit B, *GmNF-YB4* was highly modulated under biotic stress conditions. Considering the the subunit C, *GmNF-YC10* was the gene whose expression was modulated in more conditions.

Discussion

The gene family size reflects the number of duplicated genes. As observed to several gene families, soybean presents a high number of NF-Y genes in comparison with other species, as *Arabidopsis* (30 *AtNF-Y* genes) [25] and rice (28 *OsNF-Y* genes) [24]. In a previous work, Quach and collegues (2015) have found the same number of *GmNF-Y* genes that we have presented in this study (68 genes). However, the distribution in *NF-Y* subunits is slightly different from our analysis, since we have used a more recent version of soybean annotated genome.

Even with variation in length, the structural analysis of *GmNF-Y* genes by exon-intron composition showed that some genes present a very similar structure, as observed in all *GmNF-YA* genes, in which the majority presents five exons. The composition of *GmNF-YA18* suggests an exon gain, since it is the only one with six exons, while the composition of *GmNF-YA6*, 9, 10 and 11 suggests the loss of one exon. In relation to *GmNF-YB* and *GmNF-YC,* the majority genes possess only one exon, maybe representing the ancestral structure in these subunits. As the *GmNF-Y* genes are located in duplicated regions, appointed a common origin of paralogous genes, the acquisition of exons may have occurred during the evolution.

Block duplication events happen frequently in plants, because most of them are polyploids and retain duplicated chromosomal blocks. We found the majority of the *GmNF-Y* genes are located in duplicated blocks (ESM Tables 1 and 2, Figure 2), suggesting that segmental duplication contributed significantly to the family expansion. Similar results were observed in annexin [36] and LSD (Lesion Simulating disease) family in Viridiplantae [37]. Interestingly, genes corresponding to subunit C were not duplicated or the duplicated copy was lost, as observed for *GmNF-YC14*, *GmNF-YC17,* and *GmNF-YC23* (ESM Table 2). In fact, several genes from other families present in the syntenic regions had no correspondent paralogous (Figure 2, white arrows), suggesting that the duplicated genes were lost. Multiple episodes of unequal crossovers might lead to increases/decreases in gene copy. Tandem duplication often results from unequal crossing-over. The occurrence of tandem duplication was observed in some genes encoding subunit C, including *GmNF-YC13*, *GmNF-YC15,* and *GmNF-YC24*. An unequal crossover mechanism should have driven the evolution in this subunit.

Soybean experienced whole genome duplication during their evolution. The high *Ks* values observed in the majority of the syntenic regions indicate that the duplicated blocks are a result of ancient polyploidy events [38]. During evolution, duplicated genes can undergo pseudogenization, neofunctionalization or subfunctionalization [39]. A *Ka/Ks* ratio >1 indicates a neofunctionalization process (through positive selection), and a *Ka/Ks* ratio <1 suggests a subfunctionalization process (through negative selection) [40]. In this study, the *Ka/Ks* ratio <1 suggests a subfunctionalization process can be acting in *GmNF-Y* sequences. In soybean, it has been shown that several paralogous genes are undergoing subfunctionalization [40]. The different expression patterns of *GmNF-Y* genes in different tissues and stresses, associated with the *Ka/Ks* ratio, reinforce the occurrence of subfunctionalization.

It is known that members of plant NF-Y family are involved with several processes, as development and biotic stress [25]. *NF-YB2* confers drought tolerance and leads to improved corn yields in transgenic *Z. mays* [16,41,42]. In *A. thaliana*, the overexpression of *NF-YA5* and *NF-YB1* reduces water loss in leaves and improves drought tolerance. In addition, ectopic expression of an *NF-YC* from *Amaranthus hypochondriacus* and *NF-YB* from *Picea wilsonii* confers resistance to water deficiency in *Arabidopsis* [43,44]. In foxtail millet, *NF-YA1* and *NF-YB8* were highly activated in leaves and/or roots by drought and salt stresses and were induced under abscisic acid and H_2O_2 treatments [45]. In rice, the overexpression of *OsNF-YA7* improved drought tolerance [46]. In addition, the overexpression of an *NF-YA* gene (*HAP2E/*Heme-associated protein 2E*)* confers resistance to pathogens, salinity, and drought [47]. Therefore, the involvement of *NF-Y* genes in several networks has been reported, although the precise mechanism of its action is not clear.

It was previously described that *GmNF-YA3* of soybean is in-

duced by various stress treatments, and their overexpression in *Arabidopsis* reduced leaf water loss and enhanced drought tolerance [48]. Otherwise, the GmNF-Y family is poorly explored. Our study characterized for the first time that *GmNF-Y* genes are not ubiquitously expressed in soybean organs; their expression are instead organ-dependent. Our results demonstrate for the first time that *GmNF-Y* genes were modulated under *P. pachyrhizi* fungi, representing a new characterization for these genes (Figure 4). *P. pachyrhizi* is one of the most important pathogens that affect soybean production, responsible for the development of Asian Soybean Rust (ASR) disease. The pathogen attacks leaves, stems, and pods and may defoliate soybean plants in a few days, leading to drastic crop losses. Identifying genes involved in susceptible or resistant response and characterizing their individual roles are key steps for engineering soybean resistant soybean plants. Thus, additional experiments are necessary to better understand the function of these genes in response to ASR.

An interaction between soybean plant and symbiotic soil bacteria, started by the infection of the plant root hair cells by symbiont, results in the nodulation process. In this study, especially after soil bacteria inoculation, the expression of some genes was induced (Figure 3), indicating these genes could play an important role in soybean nodule association besides plant/pathogen interaction. Recently, a phylogenetically conserved group of NF-Y, which interacts to control nodulation, was described [2]. *Medicago truncatula* genes *MtNF-YB16* and *MtNF-YC1/MtNF-YC2* interact with *MtNF-YA1* and *MtNF-YA2* to form *NF-Y* trimers in yeast and in planta. Moreover, a similar trimer was formed in common bean [2]. A number of independent *NF-Y* subunits had been reported to participate in nitrogen-fixing rhizobia symbiosis. This includes the *MtNF-YA1* and *MtNF-YA2* [49-51], *NF-YA1* and *NF-YB1* from *Lotus japonicus* [12], and *NF-YC1* from common bean [7]. In soybean, nodulation and nodule activity are strongly reduced under stress conditions [52]. Thus, it is important to note that the modulation of *NF-Y* genes in both conditions (stresses and nodulation) is an interestingly characteristic to be deep explored, clarifying the importance of this family to soybean improvement.

Conclusion

Altogether, the results presented here have demonstrated that segmental duplication contributed significantly to the expansion of this gene family, and the subfuctionalization process can drive the evolution of duplicated genes. Several *GmNF-Y* members are modulated in soybean nodules and under different stresses. The modulation of *GmNF-Y* expression, especially in response to ASR, suggested their involved in the plant stress response. Future experiments might be important to clarify the relationship between *GmNF-Y* and the transcription regulation of physiological processes that culminate with the resistance/tolerance of soybean plants to biotic/abiotic stress conditions.

Figures

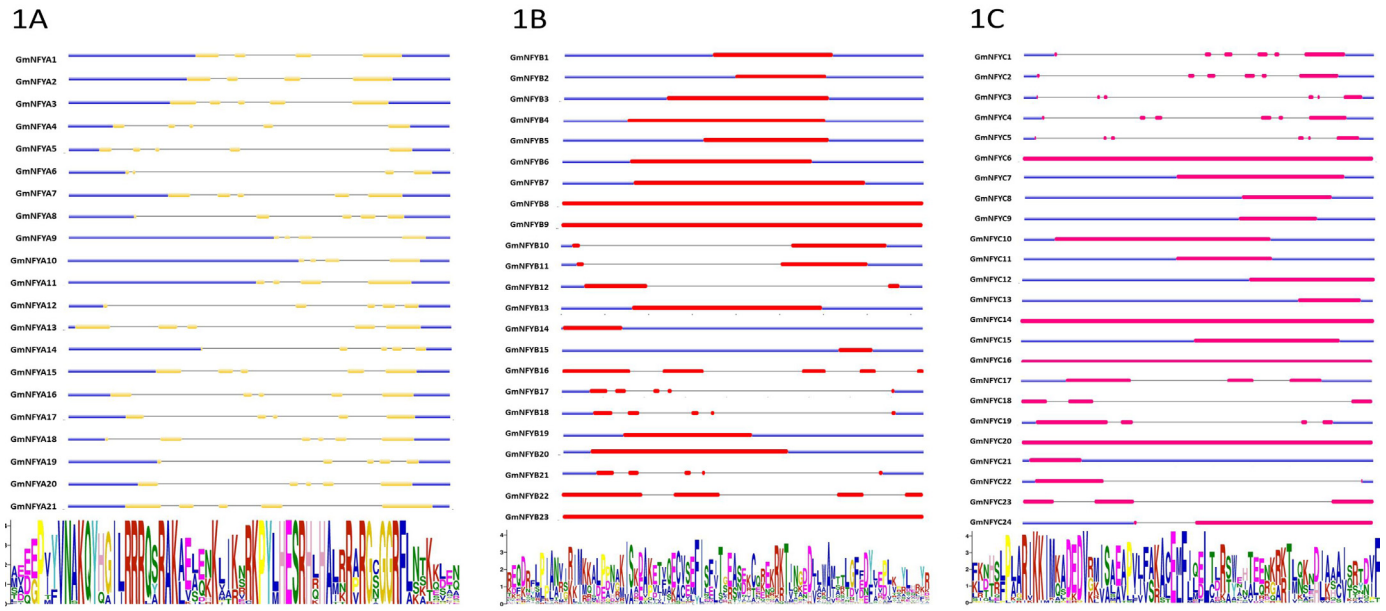


Figure 1: Gene structure and domain conservation of A) *GmNF-YA*, B) *GmNF-YB* and C) *GmNF-YC*. The blue lines indicate the 5`and 3`UTR, the yellow (1A), red (1B) and pink (1C) lines indicate exons and the black lines show intron region. Considering the domain conservation, the total height of each cell indicates the conserved sequence at each position. The height of each letter is proportional to the corresponding relative frequency. The amino acids are colored according to their chemical properties.

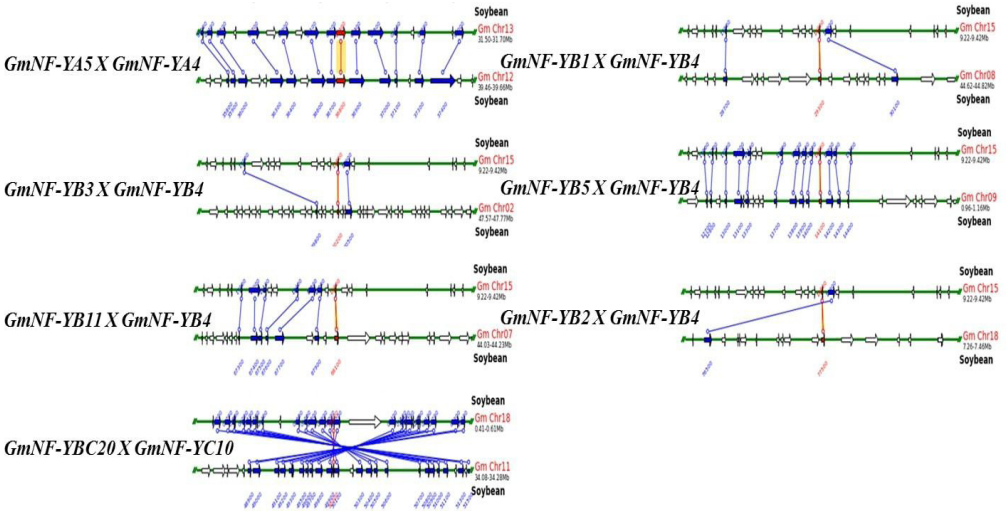


Figure 2: Expression profile of *GmNF-Y* genes under different stress conditions. Red color indicates up- and green indicates downregulated genes (Log 2 ratio).

3A

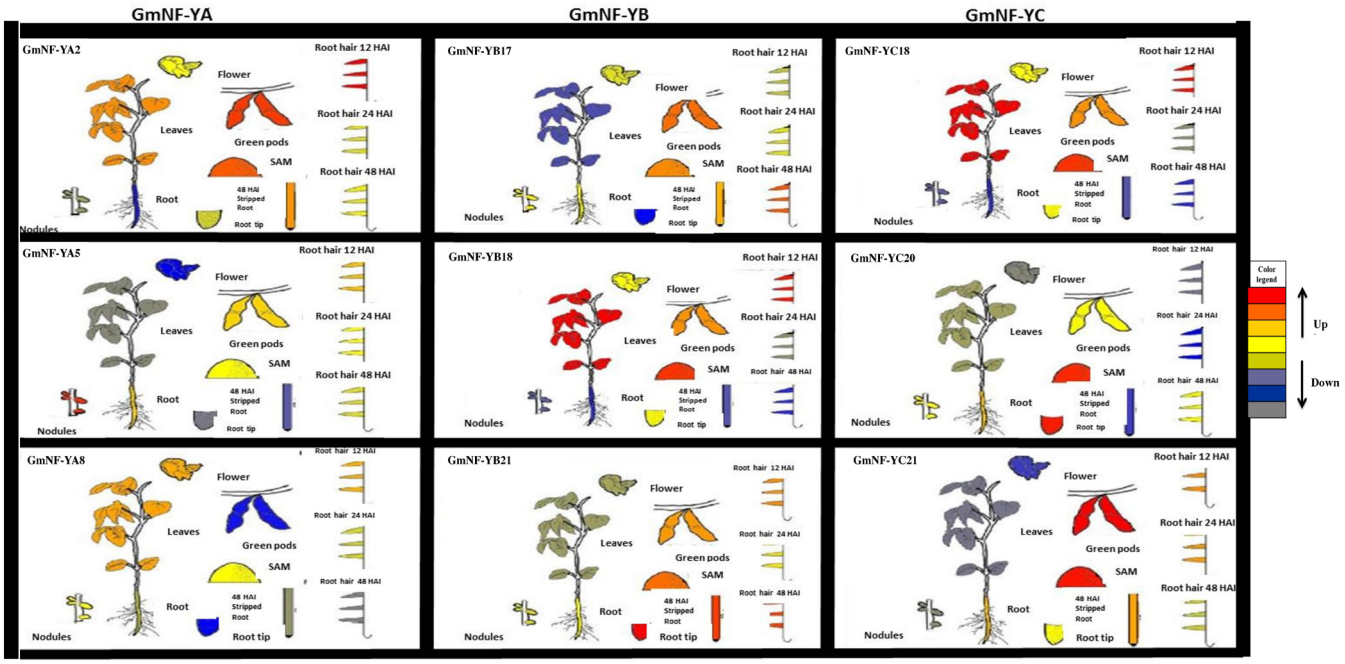


Figure 3: Expression profile of *GmNF-YA, GmNF-YB and GmNF-YC* genes in leaves, flowers, green pods, SAM (Shoot Apical Meristem), roots, root tips and nodules, and roots inoculated with *Bradyrhizobium japonicum*. Red color indicates up- and blue indicates downregulated genes (Log 2 ratio). HAI: Hours After Inoculation. Data were generated using BAR database (Libault et al. 2010a; Libault et al. 2010b).

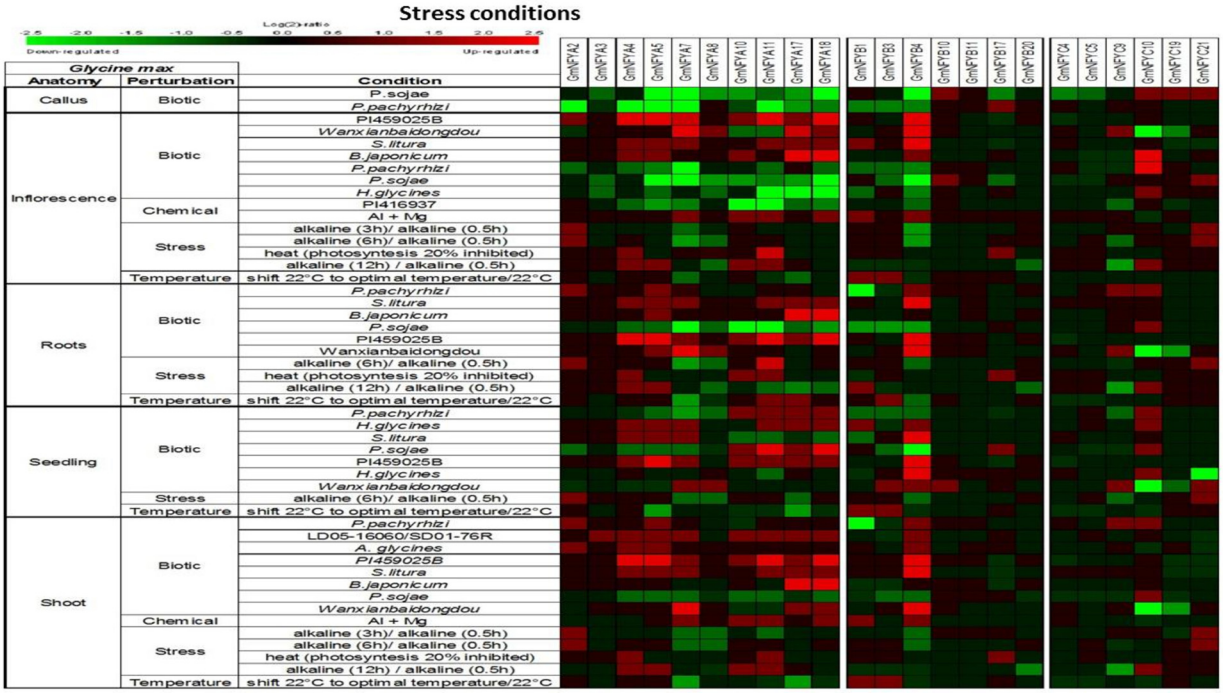
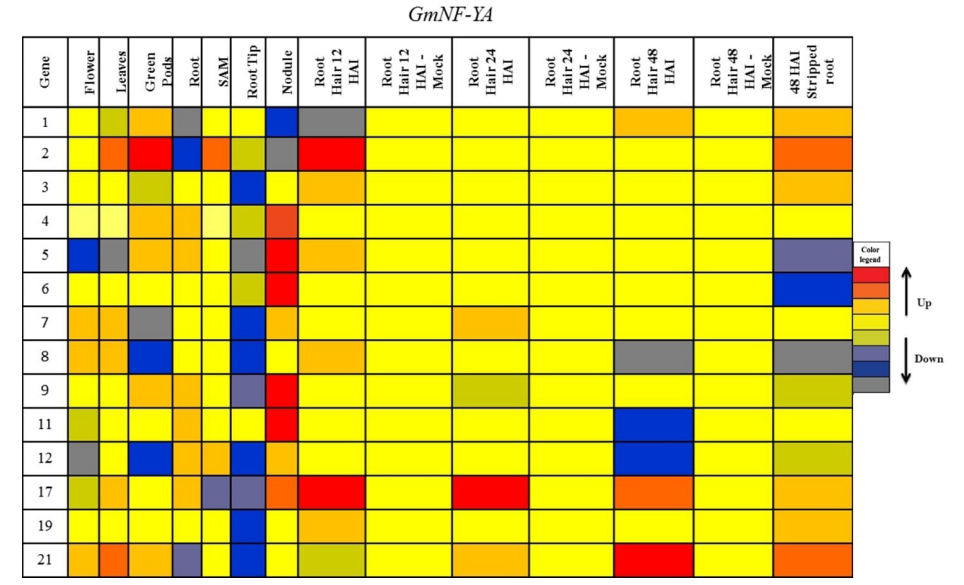
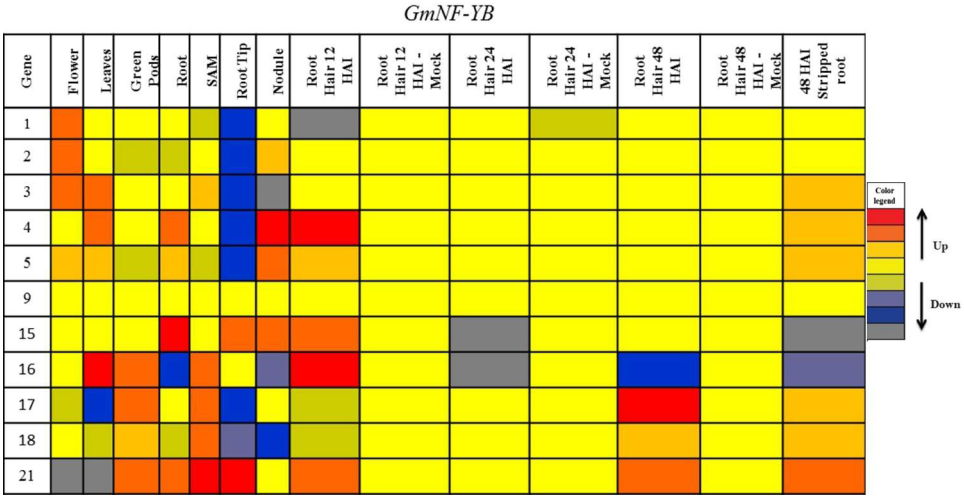
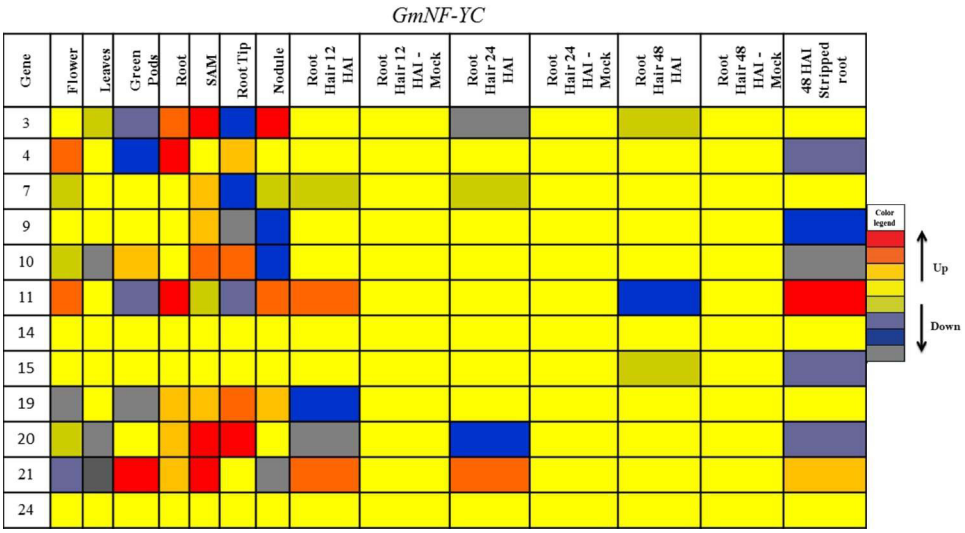


Figure 4: Syntenic regions between *GmNF-Y* genes analyzed using the PGDD database. The green horizontal line represents the chromosome. The blue and red vertical lines and arrows represent the duplicated orthologous; the red line represents the sequence that was used as the search query. The white arrow indicates genes without correspondent paralogous.







ESM Figures 1-3: FExpression profile of *GmNF-YA*, *GmNF-YB* and *GmNF-YC* genes in leaves, flowers, green pods, SAM (Shoot Apical Meristem), roots, root tips, nodules, and roots inoculated with *Bradyrhizobium japonicum*. In order to generate more understandable figures, the expression data were adapted from BAR images. Red color indicates up- and blue indicates down-regulated genes. A direct comparison of each specific gene in each organs/tissues is applicable. However, comparison among different genes is not adequate. Data were generated using BAR database (Libault et al. 2010 (a); Libault et al. 2010 (b).

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