

IN SILICO ANALYSIS OF GENES FAR-RED ELONGATED HYPOCOTYL 3 (FHY3) AND FAR-RED IMPAIRED RESPONSE 1 (FAR1)

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ABSTRACT:

In this study, the protein structure of the representatives of the Far-Red Elongated Hypocotyl 3 (FHY3) and Far-Red Impaired Response 1 (FAR1) gene family present in the Gossypium generation genome, as well as differences and similarities between them, were briefly described.

KEYWORDS: FHY3, FAR1, FRS, domain, gene.

INTRODUCTION:

Light plays an important role in the germination of plant seeds and the onset of biochemical processes that occur in the development of germination. The mutant forms obtained in plants over the last twenty years have shown that they respond differently to a wide spectrum of different light. Thus, when plant mutants were examined in a different spectrum of light, the plants demonstrated hypocothelia under a long-red light, unlike other spectral rays of Light [1]. From this they were given such names as far-red elongated hypocotyls1 (fhy1), fhy2, fhy3. Although the above genes respond to a spectrum of light, they manage different functions in the growth and development of the plant. The fhy1 gene is a homologue of the FHL (FHY1-LIKE), interacting with the phytochrome a (PhyA)

gene and allowing the PhyA gene to enter the nucleus from the cytoplasm under the influence of long-red light [2,3,4]. And FHY2 encodes the PhyA gene and responds directly to the long-red light [1].

Fhy3 is a homologous far1 gene that encodes the gene transposon from the transgressor gene [5,6,7]. Although the fhy3 and FAR1 genes are derived from the genesozozones, evolutionary development is heterogeneous. Scientific research conducted on these genes showed that fhy3 and FAR1 genes play a key role in many processes of cell development, and in the plant, in the formation of chloroplast, in the biosynthesis of chlorophyll, in the development of apical meristema and flowering, in the formation of the immune system of the plant, and in many other processes. From these processes, it is known that the role of fhy3 and FAR1 genes in the growth and development of plants is great. In addition, 12 FAR1-RELATED SEQUENCE (FRS) and 4 FRS-related factor (FRF) proteins were detected in the Arabidopsis thaliana model plant [8,9]. Currently, in addition to the fhy3 and FAR1 genes, the role and the functions that the remaining FRS and FRF family proteins hold in plants remains unclear.

Fhy3 and FAR1 genes are well studied at thaliana. But its function in the hemp plant is

not yet known to us. The data collected in this direction showed that these genes make in the early flowering and harvest of plants [10]. Proceeding from this information, we decided to see the function of this gene through the technology of RNA interference in the hemp plant. First of all, the genome FHY3 and FAR1 genes we harvested through the protein structure literature and the NCBI gene database.

FHY3 and FAR1 transposons are representatives of the FRS family, originating from the mutator-like element (mole) transposon. Transposons are usually coded by autonomous elements. Their function in the cell is to transfer from the location of transposon elements in the chromosome to another location [11]. Transposon as a result of the study of the construction of the free protein, it became known that it is a domain connecting two strands namely N-terminal DNA and C-terminal catalytic domain. N-terminal is a domain linked to DNA, which recognizes the reverse replication of terminal genes in special DNA motifs, and C-terminal catalytic domains divide the two-chain DNA into two strands and introduce transposon elements into the genome [12,13].

Members of the FRS family of kopecks are the N-terminal C2H2 zinc-finger domain (also referred to as the FAR1 DNA binding domain), similar to the Central MULE transposon, as well as the C-terminal SWIM (SWI2/SNF2 and Mudrtransposes) zinc-finger domains. These two domains play an important role in the activity of transcripts [8,7]. The specific motive, which signals the location in the nucleus, was also detected in other members of the family, such as FHY3 and FAR1. But these representatives of the FRS1, FRS8, FRS9 family do not have the above motivation [8]. N-terminal is a type of C2H2 zinc-finger domain where FAR1 is the domain WRKY Glial Cell Missing1 (WRKY-GCM1) supercoil that

connects to DNA. It binds genes to different target parts of the Tis-elements in the promoter [13,7].

We L. Gossypium in this article. we decided to make a bioinformatic analysis of the differences between the representatives of the FRS/FHY3 family of genes belonging to the genus FRS / FHY3.

RESEARCH METHODOLOGY:

In this case, we are Gossypium L. representatives of the FAR1 family of genes, which are considered to be homologous of the FRS, FHY1, FHY2, FHY3 and FHY3 genes belonging to the genus FRS <https://ncbi.nlm.nih.gov> database and its <https://blast.ncbi.nlm.nih.gov/Blast.cgi>, <https://www.ncbi.nlm.nih.gov/Structure/cdd> we worked with the help of similar programs.

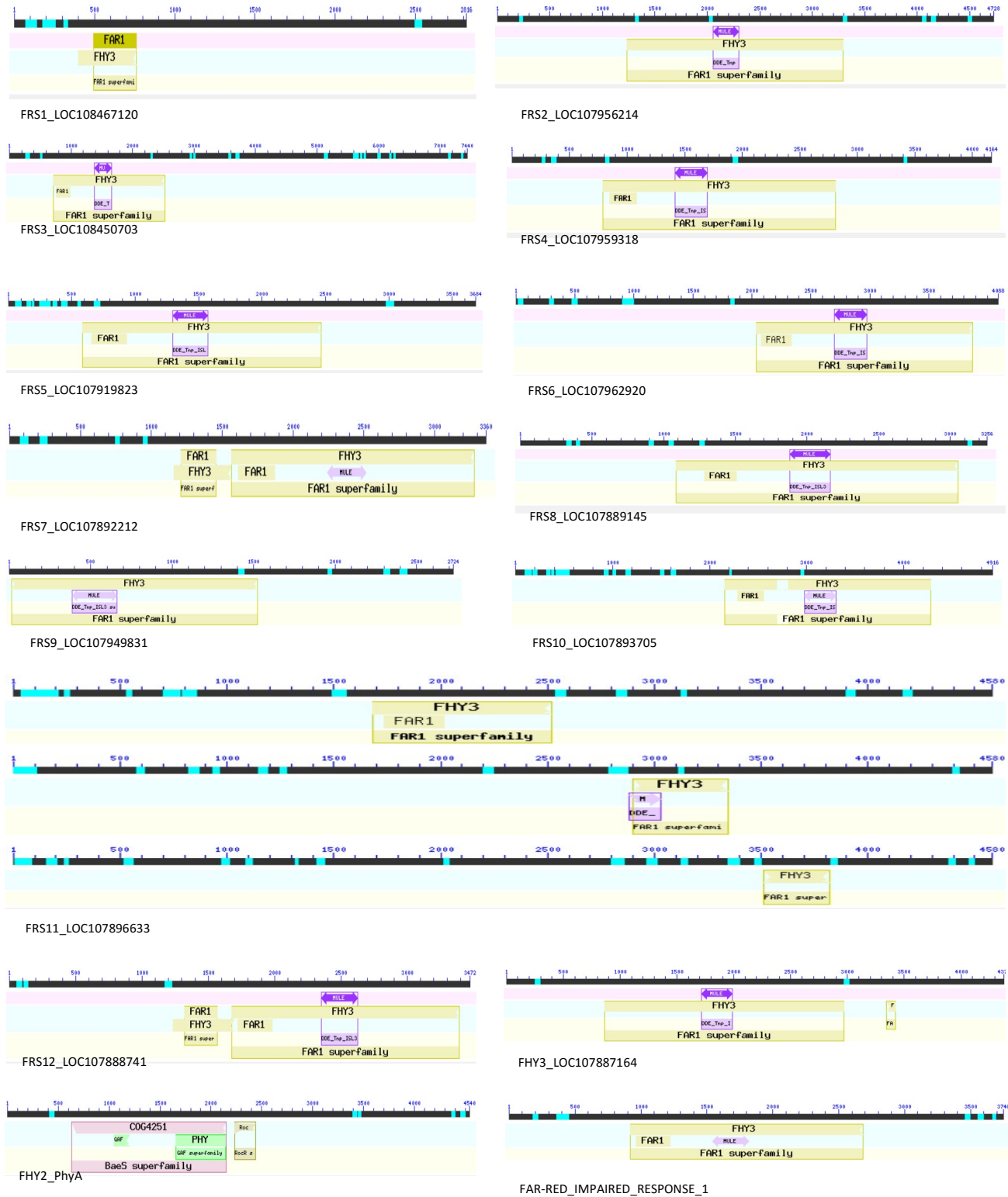
RESULTS OF THE STUDY:

According to the results of the analysis, the generation of Gossypium L. is also A. it became known that thaliana has 12 units of FRS, 3 units of FHY, as well as 1 unit of FAR1. Then, the similarities and differences between these <https://blast.ncbi.nlm.nih.gov/Blast.cgi> we have identified through blastX function of online software. According to this, in the FRS 1,3,4,5,6,7,8,10,11,12 representative offices of the FRS family and in the N-terminal part of the FAR1 gene, the FAR1 domain linked to DNA was identified. The remaining FRS2, frs9 representatives and fhy1, FHY2, FHY3 genes of FRS showed that they do not have this domain. It was also found that frs1 and FHY1, other than the fhy2 genes, also have a MULE transposon domain in the N-terminal part of the FRS gene family representatives.

By scientists A. when the FRS/FHY3 family of genes of the thaliana plant was studied, the same thing became known that these genes were found to have SWIM domain together with the fhy3 gene in the C-terminal

portion. In our analysis, it was found that in the C-terminal part of the FRS/FHY3 gene family

belonging to the Gossypium L generation, the gene coding fhy3 protein is located (Figure 1).



1-picture. FRS / FHY3 representatives of the family of genes. NCBI database used.

CONCLUSION

According to the above literature and the results of the in silico analysis, the fact that the FRS gene family has a MULE transposon domain has shown them to be of great Origin. In addition, it was found that the domain linked to FAR3 DNA, located in the N-terminal part of the FRS/FHY1 gene family, plays a central role in the management of other target genes.

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