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**G'O'ZA (*G.HIRSUTUM* L.) *GHFHY3/FAR1* GENLAR OILASI VAKILLARINI TAVSIFLASH.****ХАРАКТЕРИСТИКА ПРЕДСТАВИТЕЛЕЙ СЕМЕЙСТВА ГЕНОВ *GHFHY3/FAR1* У ХЛОПЧАТНИКА (*G.HIRSUTUM* L.)****CHARACTERIZATION OF *GHFHY3/FAR1* GENE FAMILY MEMBERS IN UPLAND COTTON (*G.HIRSUTUM* L.)****Usmanov Dilshod Erkinbaevich<sup>1</sup>** <sup>1</sup>O'zbekiston Respublikasi fanlar akademiyasi, Genomika va bioinformatika markazi PhD**Abdulkarimov Sharofiddin Sayfidinovich<sup>2</sup>** <sup>2</sup>O'zbekiston Respublikasi fanlar akademiyasi, Genomika va bioinformatika markazi, kichik ilmiy xodim**Sobirov Botirjon Masharif o'g'li<sup>3</sup>** <sup>3</sup>O'zbekiston Respublikasi fanlar akademiyasi, Genomika va bioinformatika markazi, kichik ilmiy xodim**Azimov Avazxon Abbasovich<sup>4</sup>** <sup>4</sup>O'zbekiston Respublikasi fanlar akademiyasi, Genomika va bioinformatika markazi, kichik ilmiy xodim**Abdug'afforov Azamat Tojiboy o'g'li<sup>5</sup>** <sup>5</sup>O'zbekiston Respublikasi fanlar akademiyasi, Genomika va bioinformatika markazi, kichik ilmiy xodim**Juraqulov Durbekjon Saydulla o'g'li<sup>6</sup>** <sup>6</sup>O'zbekiston Respublikasi fanlar akademiyasi, Genomika va bioinformatika markazi, stajyor-tadqiqotchi**Buriev Zabardast Tojiboevich<sup>7</sup>** <sup>7</sup>O'zbekiston Respublikasi fanlar akademiyasi, Genomika va bioinformatika markazi. b.f.d. prof.**Annotatsiya**

Yorug'lik o'simliklarning o'sishi uchun muhim omillardan biri bo'lib, o'simliklarda yorug'likka javob reaksiyasi asosan fitoxrom, kriptoxrom va ultrabinafsha nurlar (UV-B) kabi uch turdagi fotoretseptor genlar tomonidan boshqariladi. Ushbu uch guruh fotoretseptorlar ichida fitoxromlar alohida o'rin tutadi. Ushbu guruh vakillari yorug'likning qizil va uzoq qizil nurdan ta'sirlanishi sabab to'g'ridan-to'g'ri yoki bilvosita ko'plab quyi oqim transkripsiya omillarini tartibga soladi va urug'larning unib chiqishiga, poyaning uzayishiga, barglarning kengayishiga hamda gullash, erta pishish jarayonlariga ta'sir ko'rsatadi. Quyi oqim transkripsiya omillari transposazalardan kelib chiqqan FAR1-RELATED SEQUENCE1 (FAR1) va FAR-RED ELONGATED HYPOCOTYL3 (FHY3) (FHY3/FAR1) genlar oilasi hisoblanadi. FHY3/FAR1 genlar oilasi vakillari ko'pgina ekin turlarida o'rganilgan bo'lib, ulardagi amino kislotalar ketma-ketliklari xususiyatlari ochib berilgan. Biz g'o'za (*G.hirsutum* L.) turi genomida mavjud FHY3/FAR1 genlar oilasi vakillari aminokislotlar ketma-ketliklarini tahlil qildik. Ularning individual xususiyatlari, jumladan, oqsil kodlovchi DNK ketma-ketligi (CDS), aminokislotalar ketma-ketliklari, hujayrada joylashuvi, fiziologik va biokimyoviy xossalari aniqlandi.

**Аннотация**

Свет является одним из ключевых факторов, определяющих рост растений. У растений реакция на свет в основном регулируется тремя типами фоторецепторных генов: фитохромами, криптохромами и рецепторами ультрафиолетового света (UV-B). Среди этих трёх групп фоторецепторов особое место занимают фитохромы. Эти гены реагируют на красный и дальний красный свет, регулируя напрямую или косвенно многочисленные нисходящие транскрипционные факторы, тем самым влияя на прорастание семян, удлинение стебля, расширение листьев, цветение и раннее созревание.

Нисходящие транскрипционные факторы включают семейство генов FAR1-RELATED SEQUENCE1 (FAR1) и FAR-RED ELONGATED HYPOCOTYL3 (FHY3), происходящие от транспозаз. Члены семейства генов FHY3/FAR1 были исследованы у многих сельскохозяйственных культур, и их аминокислотные последовательности были подробно охарактеризованы.

В данной работе мы провели анализ аминокислотных последовательностей представителей семейства генов FHY3/FAR1, присутствующих в геноме хлопчатника (*Gossypium hirsutum* L.). Были охарактеризованы их индивидуальные особенности, включая кодирующие ДНК-последовательности (CDS), аминокислотные последовательности, клеточную локализацию, а также физиологические и биохимические свойства.

**Abstract**

Light is one of the critical environmental factors influencing plant growth. In plants, light response is mainly regulated by three types of photoreceptor genes: phytochromes, cryptochromes, and UV-B photoreceptors. Among these groups, phytochromes play a particularly important role. These receptors perceive red and far-red light and subsequently regulate numerous downstream transcription factors either directly or indirectly, thereby influencing seed germination, stem elongation, leaf expansion, flowering, and early maturation processes.

The downstream transcription factors include members of the FAR1-RELATED SEQUENCE1 (FAR1) and FAR-RED ELONGATED HYPOCOTYL3 (FHY3) gene family (FHY3/FAR1), which are believed to have originated from transposases. Members of the FHY3/FAR1 gene family have been studied in various crop species, and their amino acid sequences have been characterized in detail.

In this study, we analyzed the amino acid sequences of FHY3/FAR1 gene family members present in the genome of upland cotton (*Gossypium hirsutum* L.). Their individual characteristics—including coding DNA sequences (CDS), amino acid sequences, subcellular localization, and physiological and biochemical properties—were identified and described.

**Kalit so'zlar:** *G. hirsutum*, FAR, oqsil, FHY3/FAR1, PhyA, gen, genom.

**Ключевые слова:** *G. hirsutum*, FAR, белок, FHY3/FAR1, PhyA, ген, геном

**Key words:** *G. hirsutum*, FAR, protein, FHY3/FAR1, PhyA, gene, genome

**KIRISH**

Yorug'lik o'simliklarning o'sishi va rivojlanishiga ta'sir qiluvchi muhim omillardan biridir. O'simliklarning yorug'likka javob reaksiyasi asosan fitoxrom, kriptoxrom va ultrabinafsha nurlar (UV-B) kabi uch turdagi fotoretseptor genlar oilasi vakillari tomonidan boshariladi. Kriptoxromlar va fototropinlar genlar oilasi vakillari yorug'lik spektrining ko'k/UV-A to'lqin uzunligiga, fitoxromlar genlar oilasi vakillari esa yorug'likning qizil va uzoq-qizil to'lqin uzunliklariga javob beradi [1,2]. Ushbu uch guruh fotoretseptorlar ichida fitoxromlar alohida o'rin tutadi. Ushbu guruh vakillari yorug'likning qizil va uzoq qizil nuridan ta'sirlanishi sabab to'g'ridan-to'g'ri yoki bilvosita ko'plab quyi oqim transkripsiya omillarini tartibga soladi va o'simliklarda morfobiologik o'zgarishlar urug'larning unib chiqishi, poyaning uzayishi, barglarning kengayishi hamda gullash, erta pishish jarayonlariga ta'sir ko'rsatadi [3]. So'nggi o'n yillikda fitoxrom oilasi vakillari xususan fitoxrom A (phyA) geni ustida olib borilgan chuqur tadqiqotlar natijasida ushbu gen yadroda ekspressiyalanishida FHY3/FAR1 genlar oilasi vakillarining roli katta ekanligini ko'rsatdi. FHY3/FAR1 genlar oilasi vakillarining gen va oqsillar tuzilishiga ko'ra transpozazalardan kelib chiqqan degan taxminlar sabab dastlab ularga transkripsiya omil elementlari sifatida qaralagan [4]. *A.thaliana*da fitoxrom A geni ekspressiyasini o'rganish natijasida ushbu gomologik oqsillar guruhi yorug'likning uzoq qizil nuriga javob reaksiyasida fitoxrom A genining muhim tarkibiy qismi sifatida aniqlangan [5].

1993 yilda Whitelam tomonidan olib borilgan tadqiqotda *A.thaliana* mutantlarini qizil va uzoq qizil nur ostida o'stirilishi gipokoteli uzaygan tizmalarni ajratishga sabab bo'ldi. Ushbu oqsillar far-red elongated hypocotyls1 (fhy1), fhy2 va fhy3 deb nomlandi [6]. FHY1 va uning gomologi FHL (FHY1-LIKE) fitoxrom A (phyA) bilan o'zaro ta'sir qiladi va uzoq qizil nur ta'siridan keyin sitoplazmadan yadroga phyA translokatsiyasi uchun zarur hisoblanadi [7,8,9]. FHY2 uzoq-qizil nurga javob beradigan phyA ni kodlaydi [6].

FHY3 va uning gomologi FAR1 transpozazadan olingan transkripsiya omillarini kodlaydi [10,11,12]. FHY3/FAR1 genlar oilasi transpozazalardan kelib chiqishiga qaramasdan, o'simliklarning turli muhit omillariga moslashishda turli xil va kuchli fiziologik funktsiyalarni boshqarilishida ishtrok etadi. FHY3/FAR1 genlar oilasi vakillari hujayrada kechadigan turli jarayonlarda, jumladan yorug'lik signallarining uzatilishida, foto-

## BIOLOGIYA

morfogeneza [11,12], sirkadiyalik soat va gullash vaqtini tartibga solishda [13], meristema hujayralari va gullarni rivojlanishida [14], xloroplast bo'linishi [15], xlorofill biosintezi [16], kraxmal sintezi [17], absisik kislota javoblari [18], oksidlovchi stressga javoblar [19], o'simlik immuniteti [20] tizimlarining boshqarilishida muhim rol o'ynashini ko'rsatdi. FHY3/FAR1 genlar oilasi vakillari dastlab *A.thaliana*da o'rganilgan bo'lib, ushbu model o'simlikda 531 dan 851 gacha aminokislotalarni kodlaydigan 12 ta FAR1-RELATED SEQUENCE (FRS) va to'rtta FRS-RELATED FACTOR (FRF) oilasi oqsillari aniqlangan [21, 22]. Ushbu genlar oilasini *A.thaliana*da o'rganilishi va ko'pchilik vakillarini funksiyasini ochib berilishi boshqa ekin turlarida o'rganilishiga sabab bo'ldi [23,24,25,26,27,28,29,30,31,32,33].

G'o'za (*G.hirsutum* L.) butun dunyo bo'ylab to'qimachilik sanoatini tabiiy tola va chorvachilikni esa ozuqa bilan ta'minlovchi eng muhim texnik ekinlardan biri hisoblanadi. Ushbu ekin turida fotoretseptro genlarini o'rganilishi tola sifati va agronomik ko'rsatkichlarning yaxshilanishiga olib kelgan [34]. Lekin FHY3/FAR1 genlar oilasi vakillarining funksiyasi to'liq ochib berilmagan. Ushbu maqolada biz g'o'za (*G.hirsutum* L.) turi genomida mavjud FHY3/FAR1 genlar oilasiga tegishli 149 ta transkriptlarni fizik-kimyoviy xossalari, hujayra organoidlaridagi ekspressiyasi tahlil qilinadi.

**MATERIAL VA TADQIQOT USHLUBLARI**

G'o'za (*G.hirsutum* L.) GhFHY3/FAR1 genlar oilasi vakillarini aminokislotalar ketma-ketliklarini fiziologik va biokimyoviy xususiyatlari, jumladan aminokislotalar soni, molekulyar og'irlik (MW), nazariy izoelektrik nuqta (pI), alifatik indeks, gidropatiklikning o'rtacha qiymati (GRAVY) va beqarorlik indeksi – ExPASyProPat online dasturi yordamida amalga oshirildi. (<http://www.expasy.org/tools/protparam.html>). Ushbu GhFHY3/FAR1 genlar oilasining amino kislotalar ketma-ketligini hujayra organoidlardagi taxminiy joylashuvi WoLF PSORT dasturi (<https://wolfsort.hgc.jp/>) dasturi yordamida tahlil qilindi.

**NATIJALAR VA MUHOKAMA**

G'o'za (*G.hirsutum* L.) turi genomida 149 ta FHY3/FAR1 genlar oila a'zolariga tegishli transkriptlar aniqlangan bo'lib, ushbu 149 ta FHY3/FAR1 gen tomonidan kodlangan oqsillarning aminokislotalar 74 ta (GhChrD11G0757.1) dan 1023 ta (GhChrD10G1089.1) aminokislota uzunligini hamda maksimal va minimal molekulyar og'irliklari esa aminokislotalar uzunligiga mos ravishda 8811,05 Da va 112241,41 Da ni tashkil etdi (1-jadval). Aminokislotalar izoelektrik nuqtasi 4,48 pI dan 9,88 pI oralig'ida bo'ldi (1-jadval). Ushbu aminokislotalarning GRAVY ko'rsatkichi eng kichik nuqtasi -0,989, eng baland nuqtasi esa 0,263 ni tashkil etdi (1-jadval). Alifatik indeksi 54,57 dan 109,86 gacha bo'ldi. Beqarorlik indeksi 23,65 dan 65,37 gacha bo'ldi (1-jadval). Ushbu amino kislotalarning hujayra organoidlaridagi taxminiy ekspressiysi tahlil qilinganda asosan yadroda, stoplazma va xloroplastda ekanligi aniqlandi (1-jadval).

G'o'za (*G.hirsutum* L.) turi genomida 149 ta FHY3/FAR1 genlar oila a'zolari aniqlangan bo'lib ularning o'zaro solishtirish natijasida ushbu ko'rsatkich 89 tani tashkil qilgan. Lekin biz ushbu tadqiqotda aniqlangan 149 ta transkriptni har birini alohida tadqiq qildik. Olingan natijalar tahlilari shuni ko'rsatadiki 149 transkriptlarning aminokislotalar uzunliklari va ularning og'irliklarida o'xshashliklar kuzatildi. Lekin ushbu o'xshashliklar ularning boshqa ko'rsatkichlarida ya'ni nazariy izoelektrik nuqta (pI), alifatik indeks, gidropatiklikning o'rtacha qiymati (GRAVY) va beqarorlik indeksilarida kuzatilmadi (1-jadval). Bu esa ushbu transkriptlar FHY3/FAR1 genlar oilasining FRS guruhlarining izoform a'zosi ekanligini ko'rsatadi.

Ushbu GhFAR1/FHY3 aminokislotalarning izoelektrik nuqtalari butunlay boshqacha bo'lib, ularning kislotaligi va ishqoriyligi boshqacha ekanligini ko'rsatadi. Ko'pchilik FAR1/FHY3 hujayra yadrosi, stoplazmasi va xloroplastida joylashgan. Bir nechta transkriptlar sitoplazma va hujayra membranasida lokalizatsiya qilingan va faqat GhChrA09G1360.1, GhChrD03G0496.1, GhChrA07G2371.1 transkriptlar hujayra yadrosida joylashganligi aniq bo'ldi. Beqarorlik indeksi bo'yicha olingan ko'rsatkichlarda 23.4% transkriptlar barqarorligini, 76.5% esa beqarorligini ko'rsatdi (1-jadval).

**XULOSA**

G'o'za genomida aniqlangan FHY3/FAR1 genlar oilasining vakillarini strukturaviy va funksional jihatdan o'rganilishi, ushbu genlar ishtrokida g'o'zaning biotik va abiotik omillarga chidamli, serhosil va tola sifati yaxshilangan navlarini olishga muhim manba bo'lib xizmat qiladi.

**G'o'za (*G.hirsutum* L.) Gh FHY3/FAR1 genlar oilasi vakillari transkriptlarining tavsifi.**

| No | Gene ID         | Amino<br>Acids | MW (kDa) | pI   | GRAVY  | Instability<br>Index | Aliphatic<br>Index | Subcellular Location                                                        |
|----|-----------------|----------------|----------|------|--------|----------------------|--------------------|-----------------------------------------------------------------------------|
| 1  | GhChrA05G3603,1 | 336            | 39187,43 | 8,69 | -0,719 | 44,88                | 70,21              | nucl: 5, cyto: 5, cysk: 3, pero: 1                                          |
| 2  | GhChrA05G3605,1 | 336            | 39144,41 | 8,69 | -0,699 | 44,87                | 70,21              | nucl: 6, cyto: 5, cysk: 2, pero: 1                                          |
| 3  | GhChrA05G3606,1 | 361            | 42007,34 | 7,00 | -0,7   | 42,03                | 68,86              | nucl: 5, cyto: 5, cysk: 2, vacu: 1, pero: 1                                 |
| 4  | GhChrA06G2180,1 | 693            | 80594,45 | 5,56 | -0,386 | 45,98                | 80,32              | nucl: 6, mito: 3,5, cyto_mito: 2,5, chlo: 2, cysk: 2                        |
| 5  | GhChrD06G2121,1 | 693            | 80601,53 | 5,63 | -0,381 | 45,39                | 79,48              | nucl: 5, chlo: 4, mito: 3,5, cyto_mito: 2,5, cysk: 1                        |
| 6  | GhChrD07G1770,1 | 480            | 55411,88 | 8,18 | -0,651 | 36,49                | 68,79              | nucl: 10,5, cyto_nucl: 7,5, cyto: 3,5                                       |
| 7  | GhChrD11G1767,1 | 842            | 96781,39 | 6,81 | -0,611 | 52,06                | 67,72              | nucl: 12, vacu: 1, mito_plas: 1                                             |
| 8  | GhChrA02G1020,1 | 234            | 26945,41 | 7,75 | -0,821 | 54,9                 | 74,57              | pero: 12, cyto: 2                                                           |
| 9  | GhChrD02G1254,1 | 234            | 26972,48 | 8,35 | -0,834 | 50,56                | 74,57              | pero: 12, cyto: 2                                                           |
| 10 | GhChrA03G2410,1 | 704            | 77182,38 | 8,21 | -0,213 | 44,92                | 85,41              | nucl: 6,5, cyto_nucl: 5,5, cyto: 3,5, cysk: 3, chlo: 1                      |
| 11 | GhChrD02G2399,1 | 705            | 77405,68 | 8,47 | -0,222 | 44,88                | 85,7               | nucl: 7, cyto: 3, cysk: 2,5, cysk_plas: 2, chlo: 1                          |
| 12 | GhChrA07G1989,1 | 258            | 30121,07 | 6,05 | -0,782 | 59,6                 | 77,75              | nucl: 5, cyto: 4, chlo: 3, extr: 1, cysk: 1                                 |
| 13 | GhChrD07G1932,1 | 258            | 30062,02 | 5,9  | -0,785 | 60,16                | 77,4               | nucl: 5, cyto: 5, chlo: 1, extr: 1, vacu: 1, cysk: 1                        |
| 14 | GhChrA08G2982,1 | 593            | 67666,93 | 8,36 | -0,196 | 43,65                | 87,13              | cyto: 6, nucl: 3, cysk: 2, chlo: 1, plas: 1, E,R, vacu: 1                   |
| 15 | GhChrA13G2087,1 | 594            | 67673,18 | 8,65 | -0,185 | 38,26                | 86,85              | cyto: 5, nucl: 3, chlo: 2, cysk_plas: 2, plas: 1,5, cysk: 1,5, E,R, vacu: 1 |
| 16 | GhChrD13G1980,1 | 594            | 67830,33 | 8,65 | -0,207 | 37,95                | 85,22              | cyto: 5, nucl: 4, chlo: 2, plas: 1,5, cysk_plas: 1,5, vacu: 1               |
| 17 | GhChrA13G2387,1 | 758            | 85522,16 | 5,82 | -0,38  | 33,61                | 75,42              | nucl: 7, cyto: 5, vacu: 1, cysk: 1                                          |
| 18 | GhChrD13G2270,1 | 758            | 85460,04 | 5,91 | -0,385 | 33,23                | 74,53              | nucl: 6, cyto: 5, vacu: 2, cysk: 1                                          |
| 19 | GhChrA03G0862,1 | 196            | 21558,45 | 4,48 | -0,65  | 41,47                | 63,78              | nucl: 11, chlo: 1, extr: 1, vacu: 1                                         |
| 20 | GhChrD03G1166,1 | 244            | 27112,86 | 5,32 | -0,732 | 39,58                | 59,63              | nucl: 13, extr: 1                                                           |
| 21 | GhChrA07G2540,1 | 272            | 30909,87 | 8,91 | -0,819 | 56,12                | 65,96              | nucl: 7, chlo: 3, mito: 2, plas: 1,5, golg_plas: 1,5                        |
| 22 | GhChrD07G2425,1 | 225            | 25758,17 | 7,72 | -0,841 | 55,07                | 67,64              | nucl: 8, cyto: 2, plas: 1, pero: 1, cysk: 1, golg: 1                        |
| 23 | GhChrA08G1173,1 | 844            | 94568,91 | 8,83 | -0,398 | 46,45                | 77,35              | cyto: 6, nucl: 4, chlo: 3, vacu: 1                                          |
| 24 | GhChrD08G1130,1 | 844            | 94492,8  | 8,83 | -0,402 | 45,93                | 77,12              | cyto: 7, nucl: 5, chlo: 2                                                   |
| 25 | GhChrA10G0742,1 | 675            | 77947,73 | 8,29 | -0,437 | 44,3                 | 76,39              | nucl: 12,5, cyto_nucl: 7, plas: 1                                           |
| 26 | GhChrD10G0830,1 | 675            | 78003,9  | 8,28 | -0,427 | 43,05                | 76,95              | nucl: 11,5, cyto_nucl: 7, cyto: 1,5, plas: 1                                |
| 27 | GhChrA03G1185,1 | 865            | 99345,62 | 7,32 | -0,544 | 52,48                | 67,29              | nucl: 5, cyto: 2, vacu: 2, chlo: 1, mito: 1, plas: 1, E,R, golg: 1          |
| 28 | GhChrD02G1404,1 | 865            | 99275,34 | 6,94 | -0,562 | 51,5                 | 67,08              | nucl: 5, cyto: 2, vacu: 2, chlo: 1, mito: 1, plas: 1, E,R, golg: 1          |
| 29 | GhChrA05G1169,1 | 745            | 83881,71 | 7,78 | -0,262 | 43,59                | 83,79              | nucl: 5, chlo: 3, mito: 3, cyto: 2, cysk: 1                                 |
| 30 | GhChrD02G1666,1 | 145            | 16366,03 | 7,09 | 0,263  | 23,65                | 102,83             | cyto: 6, nucl: 3, extr: 3, chlo: 1, golg: 1                                 |

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|    |                 |      |           |      |        |       |       |                                                             |
|----|-----------------|------|-----------|------|--------|-------|-------|-------------------------------------------------------------|
| 31 | GhChrD05G1160,1 | 428  | 48146,78  | 7,66 | -0,267 | 35,6  | 82,22 | nucl: 6, cyto: 5, cysk: 1,5, cysk_plas: 1,5, vacu: 1        |
| 32 | GhChrD05G1161,1 | 180  | 20493,97  | 9,12 | -0,194 | 59,93 | 85    | nucl: 9, chlo: 3, cyto: 2                                   |
| 33 | GhChrD13G1566,1 | 165  | 18515,37  | 6,13 | 0,25   | 30,76 | 104   | cyto: 8,5, cyto_E,R,: 5, nucl: 2, extr: 1, cysk: 1, golg: 1 |
| 34 | GhChrA10G0952,1 | 1023 | 112233,45 | 8,38 | -0,403 | 48,54 | 77,69 | nucl: 11, cyto: 2, chlo: 1                                  |
| 35 | GhChrD10G1089,1 | 1023 | 112241,41 | 8,58 | -0,414 | 49,82 | 76,55 | nucl: 11, cyto: 2, chlo: 1                                  |
| 36 | GhChrA02G0602,1 | 184  | 21113,51  | 9,44 | -0,516 | 55,58 | 80,43 | nucl: 7, cyto: 4, chlo: 1, plas: 1, extr: 1                 |
| 37 | GhChrA02G0603,1 | 734  | 82418,28  | 5,61 | -0,1   | 36,32 | 86,92 | plas: 10,5, cyto_plas: 6, extr: 1, vacu: 1, E,R,: 1         |
| 38 | GhChrD02G0621,1 | 741  | 83548,41  | 7,91 | -0,332 | 42,39 | 78,72 | nucl: 6, cyto: 4, chlo: 1, mito: 1, plas: 1, cysk: 1        |
| 39 | GhChrA03G1145,1 | 221  | 25595,61  | 8,87 | -0,562 | 51,35 | 80,68 | cyto: 9, nucl: 2, cysk: 2, extr: 1                          |
| 40 | GhChrD02G1268,1 | 221  | 25435,3   | 8,58 | -0,555 | 53,52 | 77,15 | cyto: 8, nucl: 2, extr: 2, cysk: 2                          |
| 41 | GhChrA05G1306,1 | 669  | 77428,31  | 6,24 | -0,38  | 47,16 | 83,12 | pero: 14                                                    |
| 42 | GhChrD05G1286,1 | 669  | 77362,25  | 6,17 | -0,353 | 45,92 | 84,44 | pero: 13, cyto: 1                                           |
| 43 | GhChrA07G1988,1 | 233  | 27013,79  | 8,94 | -0,784 | 59,95 | 72,32 | nucl: 9, cyto: 2, cysk: 2, chlo: 1                          |
| 44 | GhChrD07G1931,1 | 233  | 27008,72  | 8,38 | -0,802 | 62,45 | 72,32 | nucl: 11, cysk: 2, plas: 1                                  |
| 45 | GhChrA09G2866,1 | 751  | 84662,15  | 6,69 | -0,384 | 42,04 | 73,17 | nucl: 10, cyto: 3, plas: 1                                  |
| 46 | GhChrD09G2678,1 | 247  | 28641,22  | 6,09 | -0,758 | 44,66 | 67,57 | nucl: 11, cyto: 2, plas: 1                                  |
| 47 | GhChrA09G1360,1 | 329  | 37905,72  | 6,41 | -0,609 | 45,2  | 66,66 | nucl: 14                                                    |
| 48 | GhChrD09G1249,1 | 481  | 55580,13  | 6,87 | -0,414 | 42,64 | 73,22 | nucl: 11, chlo: 2, vacu: 1                                  |
| 49 | GhChrA09G1160,1 | 735  | 84734,5   | 5,39 | -0,467 | 50,1  | 76,37 | nucl: 8, cyto: 4, vacu: 1, cysk: 1                          |
| 50 | GhChrD09G1069,1 | 735  | 84807,69  | 5,27 | -0,445 | 48,67 | 77,16 | nucl: 8, cyto: 3, cysk: 1,5, cysk_plas: 1,5, vacu: 1        |
| 51 | GhChrA10G1713,1 | 248  | 28615,35  | 6,38 | -0,686 | 44,21 | 72,02 | cysk: 10, nucl: 1, cyto: 1, plas: 1, golg: 1                |
| 52 | GhChrD10G1418,1 | 247  | 28641,22  | 6,09 | -0,758 | 44,66 | 67,57 | nucl: 7, cysk: 6, plas: 1                                   |
| 53 | GhChrA11G0812,1 | 409  | 47013,72  | 6,44 | -0,312 | 51,96 | 80,64 | chlo: 5, cyto: 3, nucl: 2, cysk: 2, mito: 1, plas: 1        |
| 54 | GhChrA11G0813,1 | 237  | 26875,25  | 8,98 | -0,677 | 40,22 | 64,98 | cyto: 12, chlo: 1, mito: 1                                  |
| 55 | GhChrD11G0814,1 | 568  | 65089,18  | 7,58 | -0,339 | 45,67 | 80,86 | cyto: 12, nucl: 1, mito: 1                                  |
| 56 | GhChrA05G2646,1 | 171  | 19849,54  | 8,17 | -0,88  | 41,08 | 62,75 | cyto: 11, chlo: 1, mito: 1, golg: 1                         |
| 57 | GhChrD05G2597,1 | 171  | 19881,42  | 7,65 | -0,989 | 43,62 | 59,82 | cyto: 10, mito: 2, nucl: 1, extr: 1                         |
| 58 | GhChrA09G0553,1 | 882  | 102197,23 | 6,13 | -0,693 | 48,02 | 72,17 | nucl: 13, vacu: 1                                           |
| 59 | GhChrD09G0509,1 | 600  | 69831,89  | 5,76 | -0,501 | 47,03 | 77,37 | nucl: 6, mito: 4,5, cyto_mito: 3, chlo: 2, cysk: 1          |
| 60 | GhChrA10G1714,1 | 207  | 23822,82  | 6,01 | -0,769 | 48,33 | 83,29 | cyto: 6, nucl: 4, chlo: 2, extr: 2                          |
| 61 | GhChrD10G1417,1 | 221  | 25442,63  | 6,19 | -0,723 | 48,82 | 78,91 | nucl: 10, cyto: 2, cysk: 2                                  |
| 62 | GhChrA09G2749,1 | 760  | 87766,51  | 8,73 | -0,525 | 49,84 | 71,12 | nucl: 5, extr: 4, chlo: 2, cyto: 1, vacu: 1, E,R,: 1        |
| 63 | GhChrD09G2571,1 | 760  | 87860,63  | 8,89 | -0,546 | 49,75 | 69,46 | nucl: 6, extr: 5, chlo: 2, E,R,: 1                          |
| 64 | GhChrA06G1499,1 | 207  | 23686,41  | 6,82 | -0,846 | 41,35 | 57,92 | nucl: 6, cyto: 4, chlo: 1, plas: 1, extr: 1, pero: 1        |
| 65 | GhChrD06G1411,1 | 184  | 21021,28  | 7,72 | -0,946 | 39,89 | 54,57 | nucl: 8, extr: 2, chlo: 1, cyto: 1, plas: 1, vacu: 1        |
| 66 | GhChrA09G0411,1 | 821  | 94354,79  | 6,26 | -0,495 | 47,18 | 74,77 | pero: 11, cyto_nucl: 2, nucl: 1,5, cyto: 1,5                |

|     |                 |     |          |      |        |       |       |                                                                          |
|-----|-----------------|-----|----------|------|--------|-------|-------|--------------------------------------------------------------------------|
| 67  | GhChrD09G0385,1 | 821 | 94230,86 | 6,28 | -0,479 | 47,22 | 73,48 | pero: 10, nucl: 2,5, cyto_nucl: 2,5, cyto: 1,5                           |
| 68  | GhChrA04G1493,1 | 549 | 63242,35 | 6,24 | -0,491 | 44,98 | 74,28 | pero: 5, cyto: 3, mito: 2, chlo: 1, nucl: 1, E,R,: 1, cysk: 1            |
| 69  | GhChrD04G1966,1 | 505 | 57924,12 | 6,26 | -0,465 | 49,96 | 69,21 | pero: 6, nucl: 3, chlo: 1, cyto: 1, mito: 1, E,R,: 1, cysk: 1            |
| 70  | GhChrA05G2881,1 | 226 | 25969,11 | 7,62 | -0,262 | 41,54 | 84,25 | cyto: 7, nucl: 4, chlo: 2, mito: 1                                       |
| 71  | GhChrA10G2249,1 | 573 | 66391,23 | 9,57 | -0,482 | 41,15 | 81,52 | cyto: 8, nucl: 4, plas: 1, vacu: 1                                       |
| 72  | GhChrD01G2274,1 | 163 | 19268,06 | 9,23 | -0,762 | 58,21 | 72,88 | cyto: 5, nucl: 4, mito: 3, chlo: 1, extr: 1                              |
| 73  | GhChrD10G1394,1 | 226 | 26458,22 | 9,11 | -0,579 | 57,4  | 77,12 | cyto: 8, nucl: 2, extr: 2, chlo: 1, golg: 1                              |
| 74  | GhChrA02G0115,1 | 589 | 65706,36 | 6,25 | -0,244 | 34,6  | 87,89 | cyto: 10, chlo: 1, nucl: 1, cysk: 1, E,R, vacu: 1                        |
| 75  | GhChrD02G0121,1 | 246 | 28053,89 | 7,71 | -0,608 | 42,18 | 80,04 | cysk: 9, cyto: 4, nucl: 1                                                |
| 76  | GhChrA01G2174,1 | 105 | 12762,81 | 6,73 | -0,176 | 44,75 | 80,95 | pero: 11, nucl: 2, cyto: 1                                               |
| 77  | GhChrA06G0967,1 | 136 | 15969,31 | 6,58 | -0,234 | 52,6  | 76,76 | nucl: 7,5, cyto_nucl: 5, chlo: 3, cyto: 1,5, mito: 1, extr: 1            |
| 78  | GhChrA10G1746,1 | 174 | 20422,33 | 7,67 | -0,457 | 55,71 | 74,6  | nucl: 7,5, cyto_nucl: 5,5, cyto: 2,5, chlo: 1, mito: 1, extr: 1, cysk: 1 |
| 79  | GhChrD01G2104,1 | 296 | 34765,82 | 8,59 | -0,431 | 45,39 | 73,45 | cyto: 8, nucl: 3, pero: 2, mito: 1                                       |
| 80  | GhChrA03G1680,1 | 332 | 38669,69 | 9,48 | -0,782 | 51,21 | 60,54 | nucl: 7, cyto: 6, plas: 1                                                |
| 81  | GhChrA11G3724,1 | 702 | 80478,74 | 8,85 | -0,703 | 43,48 | 65,58 | nucl: 12, cyto: 1, plas: 1                                               |
| 82  | GhChrA05G4627,1 | 858 | 97037,66 | 6,6  | -0,457 | 43,54 | 70,24 | nucl: 12, cyto: 1, vacu: 1                                               |
| 83  | GhChrA10G2453,1 | 858 | 96780,53 | 6,6  | -0,377 | 43,69 | 75,54 | nucl: 10,5, cyto_nucl: 7,5, cyto: 3,5                                    |
| 84  | GhChrD01G2273,1 | 291 | 33534,05 | 8,83 | -0,047 | 35,9  | 85,4  | cyto: 7, nucl: 5, mito: 2                                                |
| 85  | GhChrD04G1174,1 | 584 | 67013,38 | 5,26 | -0,324 | 43,04 | 79,42 | cyto: 13, cysk: 1                                                        |
| 86  | GhChrA11G1671,1 | 322 | 37407,01 | 5,77 | -0,298 | 65,37 | 80,5  | nucl: 5, cyto: 5, cysk: 2, chlo: 1, mito: 1                              |
| 87  | GhChrD05G3176,1 | 230 | 27052,73 | 4,98 | -0,395 | 56,62 | 81,7  | cyto: 6, nucl: 4, chlo: 1, mito: 1, extr: 1, cysk: 1                     |
| 88  | GhChrD07G2331,1 | 463 | 53706,59 | 6,52 | -0,356 | 56,98 | 83,13 | nucl: 5, cysk: 3,5, cyto: 3, cysk_plas: 3, plas: 1,5, mito: 1            |
| 89  | GhChrA08G2390,1 | 589 | 67164,72 | 9,23 | -0,662 | 45,47 | 73,65 | nucl: 6, cyto: 4, chlo: 2, E,R,: 1, pero: 1                              |
| 90  | GhChrA09G0337,1 | 260 | 29217,83 | 4,78 | -0,368 | 34,32 | 84,04 | chlo: 6, extr: 5, cyto: 2, nucl: 1                                       |
| 91  | GhChrD01G1715,1 | 200 | 23580,87 | 7,75 | -0,429 | 46,58 | 75,45 | cyto: 4, chlo: 3, nucl: 2, mito: 2, plas: 1, extr: 1, pero: 1            |
| 92  | GhChrD11G0875,1 | 236 | 27508,51 | 9,88 | -0,54  | 56,24 | 77,58 | nucl: 10, chlo: 1, cyto: 1, extr: 1, cysk: 1                             |
| 93  | GhChrA10G1715,1 | 193 | 22638,39 | 6,08 | -0,95  | 36,71 | 69,22 | nucl: 6, chlo: 2, cyto: 2, mito: 1, plas: 1, extr: 1, pero: 1            |
| 94  | GhChrD10G1416,1 | 241 | 28403,91 | 6,28 | -0,929 | 37,75 | 65,56 | nucl: 6, cyto: 2, mito: 2, chlo: 1, plas: 1, extr: 1, cysk: 1            |
| 95  | GhChrA05G0713,1 | 509 | 58511,85 | 8,36 | -0,638 | 49,96 | 70,31 | nucl: 13, chlo: 1                                                        |
| 96  | GhChrD05G0715,1 | 752 | 87279,15 | 7,39 | -0,498 | 46,81 | 75,07 | nucl: 11, plas: 1, vacu: 1, cysk: 1                                      |
| 97  | GhChrA03G0863,1 | 693 | 79220,27 | 8,33 | -0,423 | 44,63 | 79,09 | nucl: 9, cyto: 4, vacu: 1                                                |
| 98  | GhChrD03G1167,1 | 666 | 76313,94 | 8,53 | -0,461 | 44,6  | 79,65 | nucl: 5, mito: 4, cyto_mito: 3,5, chlo: 1, cyto: 1, plas: 1, cysk: 1     |
| 99  | GhChrA10G2155,1 | 628 | 71639,8  | 5,76 | -0,301 | 48,84 | 82,6  | nucl: 7, cyto: 5, chlo: 1, plas: 1                                       |
| 100 | GhChrD10G2065,1 | 756 | 86267,3  | 6,05 | -0,337 | 50,5  | 78,8  | nucl: 12, plas: 1, vacu: 1                                               |
| 101 | GhChrA01G1653,1 | 710 | 81774,7  | 7,15 | -0,601 | 55,33 | 69,9  | nucl: 10, chlo: 1, cyto: 1, plas: 1, cysk: 1                             |
| 102 | GhChrD01G1635,1 | 819 | 93701,19 | 7,97 | -0,576 | 53,33 | 69,77 | nucl: 12, cyto: 1, vacu: 1                                               |
| 103 | GhChrA03G1247,1 | 752 | 87732,76 | 6,91 | -0,372 | 47,38 | 78,7  | chlo: 8, nucl: 3, cyto_mito: 2,5, mito: 2                                |

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|     |                 |     |          |      |        |       |        |                                                                              |
|-----|-----------------|-----|----------|------|--------|-------|--------|------------------------------------------------------------------------------|
| 104 | GhChrD02G1297,1 | 692 | 80404,07 | 6,13 | -0,396 | 46,44 | 79,61  | nucl: 7, mito: 2,5, chlo: 2, cysk: 2, cyto_mito: 2                           |
| 105 | GhChrA06G1242,1 | 669 | 77955,67 | 6,77 | -0,486 | 39,58 | 74,99  | nucl: 8, cysk: 2,5, cyto: 2, cysk_plas: 2, vacu: 1                           |
| 106 | GhChrD06G1208,1 | 671 | 77878,51 | 6,47 | -0,486 | 38,66 | 74,49  | nucl: 7, cysk: 2,5, cyto: 2, cysk_plas: 2, vacu: 1, pero: 1                  |
| 107 | GhChrA07G2371,1 | 852 | 97693,71 | 6,13 | -0,479 | 53,52 | 70,72  | nucl: 14                                                                     |
| 108 | GhChrD07G2281,1 | 745 | 84636,01 | 6,63 | -0,399 | 53,34 | 71,6   | nucl: 13, vacu: 1                                                            |
| 109 | GhChrA11G3512,1 | 775 | 87503,99 | 7,26 | -0,322 | 40,08 | 78,94  | nucl: 6, chlo: 3, cyto: 2, cysk: 2, mito: 1                                  |
| 110 | GhChrD11G3399,1 | 803 | 90852,79 | 7,78 | -0,307 | 39,54 | 80,07  | chlo: 6, mito: 3,5, cyto_mito: 2,5, nucl: 2, cyto: 1, cysk: 1                |
| 111 | GhChrA01G1459,1 | 111 | 12866,7  | 6,69 | -0,248 | 29,63 | 76,49  | cyto: 5, chlo: 3, nucl: 2, mito: 1, plas: 1, extr: 1, golg: 1                |
| 112 | GhChrA01G2175,1 | 203 | 23420,2  | 7,53 | -0,192 | 45,86 | 85,91  | nucl: 8, cyto: 4, chlo: 1, mito: 1                                           |
| 113 | GhChrA02G0116,1 | 260 | 29778,91 | 8,58 | -0,821 | 49,62 | 71,96  | nucl: 6, cyto: 5, extr: 2, chlo: 1                                           |
| 114 | GhChrA03G0469,1 | 883 | 99817,65 | 6,23 | -0,478 | 44,9  | 70,91  | nucl: 12, cyto: 1, plas: 1                                                   |
| 115 | GhChrA03G0946,1 | 130 | 15622,26 | 9,01 | -0,365 | 41,31 | 84     | cyto: 10, nucl: 2, cysk: 2                                                   |
| 116 | GhChrA05G4637,1 | 172 | 20152,13 | 9,24 | -0,594 | 33,73 | 70,29  | pero: 10, nucl: 2, cyto: 2                                                   |
| 117 | GhChrA06G0836,1 | 148 | 17341,7  | 9,59 | 0,164  | 32,51 | 109,86 | mito: 7, chlo_mito: 4,83333, cyto_mito: 4,33333, nucl: 3, cyto: 2, chlo: 1,5 |
| 118 | GhChrA06G1652,1 | 111 | 13029,01 | 8,48 | -0,245 | 30,81 | 90,45  | cyto: 5, chlo: 3, nucl: 2, extr: 2, plas: 1,5, cysk_plas: 1,5                |
| 119 | GhChrA08G2725,1 | 209 | 23777,6  | 6,43 | -0,139 | 39,73 | 93,83  | cyto: 6, nucl: 4, chlo: 2, extr: 1, cysk: 1                                  |
| 120 | GhChrA08G3083,1 | 709 | 80840,93 | 6,49 | -0,409 | 39,27 | 79,72  | nucl: 5, cyto: 3, chlo: 2, cysk: 2, plas: 1,5, mito_plas: 1,5                |
| 121 | GhChrA09G0480,1 | 507 | 58107,16 | 6,29 | -0,63  | 51,43 | 62,52  | nucl: 13, cyto: 1                                                            |
| 122 | GhChrA09G1359,1 | 424 | 49043,78 | 9,16 | -0,068 | 44,11 | 91,37  | nucl: 7, cyto: 7                                                             |
| 123 | GhChrA10G1477,1 | 519 | 59008,98 | 8,08 | -0,615 | 44,67 | 74,99  | nucl: 5, chlo: 4, extr: 2, cyto: 1, E,R,: 1, pero: 1                         |
| 124 | GhChrA10G1915,1 | 165 | 19284,46 | 9,62 | -0,362 | 50,43 | 74,36  | chlo: 13, nucl: 1                                                            |
| 125 | GhChrA10G2154,1 | 264 | 30135,37 | 4,69 | -0,643 | 34,31 | 71,29  | chlo: 9, extr: 3, nucl: 1, cyto: 1                                           |
| 126 | GhChrA10G2406,1 | 274 | 31939,15 | 9,46 | -0,254 | 43,32 | 88,25  | cyto: 12, nucl: 1, mito: 1                                                   |
| 127 | GhChrA11G1770,1 | 843 | 97000,77 | 6,95 | -0,608 | 51,97 | 67,64  | nucl: 13, mito_plas: 1                                                       |
| 128 | GhChrA11G2041,1 | 327 | 37974,71 | 8,7  | -0,241 | 42,01 | 80,15  | cyto: 7, cysk: 3,5, cysk_plas: 2,5, nucl: 1, vacu: 1, golg: 1                |
| 129 | GhChrA11G3026,1 | 204 | 23901,42 | 9,56 | -0,81  | 28,51 | 69,26  | cyto: 6, nucl: 4, plas: 2, extr: 1, cysk: 1                                  |
| 130 | GhChrA12G1454,1 | 641 | 73545,13 | 8,93 | -0,264 | 41,04 | 89,11  | chlo: 4, nucl: 4, cyto: 4, plas: 1, cysk: 1                                  |
| 131 | GhChrD03G0495,1 | 141 | 16471,07 | 9,23 | -0,551 | 50,91 | 74,54  | chlo: 8, cyto: 3, nucl: 1, mito: 1, plas: 1                                  |
| 132 | GhChrD03G0496,1 | 601 | 68093,2  | 6,27 | -0,536 | 43,32 | 66,32  | nucl: 14                                                                     |
| 133 | GhChrD05G3261,1 | 305 | 35648,2  | 9,25 | -0,495 | 30,8  | 78,56  | cyto: 4, cysk: 4, extr: 3, nucl: 2, golg: 1                                  |
| 134 | GhChrD07G1088,1 | 250 | 29246,44 | 9,6  | -0,577 | 50,06 | 70,48  | cyto: 7, nucl: 2, chlo: 1, mito: 1, plas: 1, extr: 1, cysk: 1                |
| 135 | GhChrD07G1730,1 | 620 | 71173,76 | 8,52 | -0,631 | 43,49 | 67,32  | chlo: 8, nucl: 5, cysk: 1                                                    |
| 136 | GhChrD07G2588,1 | 759 | 86623,51 | 6,04 | -0,367 | 45,12 | 80,84  | nucl: 9, cyto: 5                                                             |
| 137 | GhChrD08G1075,1 | 648 | 74278,54 | 8,18 | -0,406 | 48,61 | 76,85  | cyto: 7, cysk: 2,5, chlo: 2, cysk_plas: 2, nucl: 1, pero: 1                  |
| 138 | GhChrD08G1405,1 | 336 | 38992,6  | 9    | -0,296 | 39,82 | 79,26  | cyto: 7, E,R,: 5, mito: 2                                                    |
| 139 | GhChrD09G0554,1 | 200 | 23738,72 | 8,79 | -0,14  | 25    | 94,5   | nucl: 6, cyto_nucl: 6, mito: 2,5, chlo: 2, cyto_mito: 2, plas: 1             |

|     |                 |     |          |      |        |       |       |                                                      |
|-----|-----------------|-----|----------|------|--------|-------|-------|------------------------------------------------------|
| 140 | GhChrD09G0681,1 | 257 | 29880,39 | 8,77 | -0,319 | 42,97 | 88,4  | cyto: 12, mito: 2                                    |
| 141 | GhChrD09G1244,1 | 221 | 25494,3  | 8,94 | -0,283 | 42,94 | 78,46 | cyto: 7, chlo: 4, nucl: 1, mito: 1, plas: 1          |
| 142 | GhChrD10G1532,1 | 362 | 41527,73 | 5,86 | -0,553 | 48,67 | 73,29 | cyto: 6, nucl: 4, chlo: 2, mito: 1, cysk: 1          |
| 143 | GhChrD10G1575,1 | 264 | 30610,43 | 9,3  | -0,376 | 51,18 | 75,38 | cyto: 8, nucl: 3, mito: 1, plas: 1, cysk: 1          |
| 144 | GhChrD10G2448,1 | 372 | 42299,98 | 8,64 | -0,539 | 38,98 | 71,32 | nucl: 7, cyto: 4, chlo: 1, mito: 1, plas: 1          |
| 145 | GhChrD11G0757,1 | 74  | 8811,05  | 6,16 | -0,473 | 30,26 | 67,16 | cyto: 4, extr: 4, chlo: 3, nucl: 1, mito: 1, plas: 1 |
| 146 | GhChrD11G2816,1 | 364 | 39944,86 | 4,59 | -0,736 | 33,62 | 65,33 | cyto: 6, cysk: 5, nucl: 2, extr: 1                   |
| 147 | GhChrD12G0852,1 | 296 | 34004,55 | 9,55 | -0,471 | 44,31 | 83,07 | cyto: 5, nucl: 4, mito: 3, plas: 1,5, golg_plas: 1,5 |
| 148 | GhChrD13G1101,1 | 183 | 20471,79 | 8,68 | -0,007 | 50,73 | 93,01 | cyto: 9, E,R,: 4, extr: 1                            |
| 149 | GhChrD09G1114,1 | 674 | 74624,26 | 6,14 | -0,553 | 55,28 | 65,12 | nucl: 10, chlo: 3, cyto: 1                           |

## ADABIYOTLAR RO'YXATI

1. Heijde, M.; Ulm, R. UV-B photoreceptor-mediated signalling in plants. *Trends Plant Sci.* 2012, 17, 230–237.
2. Voitsekhovskaja, O.V. Phytochromes and other (photo)receptors of information in plants. *Russ. J. Plant Physiol.* 2019, 66, 351–364.
3. Li, F.W.; Rothfels, C.J.; Melkonian, M.; Villarreal, J.C.; Stevenson, D.W.; Graham, S.W.; Wong, G.K.; Mathews, S.; Pryer, K.M. The origin and evolution of phototropins. *Front. Plant Sci.* 2015, 6, 637.
4. Ma L and Li G (2018) FAR1-RELATED SEQUENCE (FRS) and FRS-RELATED FACTOR (FRF) Family Proteins in Arabidopsis Growth and Development. *Front. Plant Sci.* 9:692. doi: 10.3389/fpls.2018.00692
5. Wang, H.; Wang, H. Multifaceted roles of FHY3 and FAR1 in light signaling and beyond. *Trends Plant Sci.* 2015, 20, 453–461.
6. Whitelam, G. C., Johnson, E., Peng, J., Carol, P., Anderson, M. L., Cowl, J. S., et al. Phytochrome A null mutants of Arabidopsis display a wild-type phenotype in white light. *Plant Cell* 5,(1993)., 757–768. doi: 10.1105/tpc.5.7.757.
7. Desnos, T., Puente, P., Whitelam, G. C., and Harberd, N. P. FHY1: a phytochrome A-specific signal transducer. *Genes Dev.* (2001). 15, 2980–2990. doi: 10.1101/gad.205401.
8. Hiltbrunner, A., Viczian, A., Bury, E., Tscheuschler, A., Kircher, S., Toth, R., et al. Nuclear accumulation of the phytochrome A photoreceptor requires FHY1. *Curr. Biol.* (2005). 15, 2125–2130. doi: 10.1016/j.cub.2005.10.042.
9. Zhou, Q., Hare, P. D., Yang, S. W., Zeidler, M., Huang, L. F., and Chua, N. H. FHL is required for full phytochrome A signaling and shares overlapping functions with FHY1. *Plant J.* 43, (2005). 356–370. doi: 10.1111/j.1365-3113X.2005.02453.x.
10. Hudson, M., Ringli, C., Boylan, M. T., and Quail, P. H. The FAR1 locus encodes a novel nuclear protein specific to phytochrome A signaling. *Genes Dev.* 13, (1999). 2017–2027. doi: 10.1101/gad.13.15.2017.
11. Wang, H., and Deng, X. W. Arabidopsis FHY3 defines a key phytochrome A signaling component directly interacting with its homologous partner FAR1. *EMBO J.* 21, (2002). 1339–1349. doi: 10.1093/emboj/21.6.1339.
12. Lin, R., Ding, L., Casola, C., Ripoll, D. R., Feschotte, C., and Wang, H. Transposase-derived transcription factors regulate light signaling in Arabidopsis. *Science* 318, (2007). 1302–1305. doi: 10.1126/science.1146281
13. Li, G., Siddiqui, H., Teng, Y., Lin, R., Wan, X. Y., Li, J., et al. Coordinated transcriptional regulation underlying the circadian clock in Arabidopsis. *Nat. Cell Biol.* 13, (2011). 616–622. doi: 10.1038/ncb2219
14. Li, D., Fu, X., Guo, L., Huang, Z., Li, Y., Liu, Y., et al. FAR-RED ELONGATED HYPOCOTYL3 activates SEPALLATA2 but inhibits CLAVATA3 to regulate meristem determinacy and maintenance in Arabidopsis. *Proc. Natl. Acad. Sci. U.S.A.* 113, (2016). 9375–9380. doi: 10.1073/pnas.1602960113
15. Ouyang, X., Li, J., Li, G., Li, B., Chen, B., Shen, H., et al. Genome-wide binding site analysis of FAR-RED ELONGATED HYPOCOTYL3 reveals its novel function in Arabidopsis development. *Plant Cell* 23, (2011). 2514–2535. doi: 10.1105/tpc.111.085126
16. Tang, W., Wang, W., Chen, D., Ji, Q., Jing, Y., Wang, H., et al. Transposase-derived proteins FHY3/FAR1 interact with PHYTOCHROME-INTERACTING FACTOR1 to regulate chlorophyll biosynthesis by modulating HEMB1 during deetiolation in Arabidopsis. *Plant Cell* 24, (2012). 1984–2000. doi: 10.1105/tpc.112.097022
17. Ma, L., Xue, N., Fu, X., Zhang, H., and Li, G. Arabidopsis thaliana FAR-RED ELONGATED HYPOCOTYLS3 (FHY3) and FAR-RED-IMPAIRED RESPONSE1 (FAR1) modulate starch synthesis in response to light and sugar. *New Phytol.* 213, (2017). 1682–1696. doi: 10.1111/nph.14300
18. Tang, W., Ji, Q., Huang, Y., Jiang, Z., Bao, M., Wang, H., et al. (2013). FAR-RED ELONGATED HYPOCOTYL3 and FAR-RED IMPAIRED RESPONSE1 transcription factors integrate light and abscisic acid signaling in Arabidopsis. *Plant Physiol.* 163, 857–866. doi: 10.1104/pp.113.224386
19. Ma, L., Tian, T., Lin, R., Deng, X. W., Wang, H., and Li, G. Arabidopsis FHY3 and FAR1 regulate light-induced myo-inositol biosynthesis and oxidative stress responses by transcriptional activation of MIPS1. *Mol. Plant* 9, (2016). 541–557. doi: 10.1016/j.molp.2015.12.013
20. Wang, W., Tang, W., Ma, T., Niu, D., Jin, J. B., Wang, H., et al. A pair of light signaling factors FHY3 and FAR1 regulates plant immunity by modulating chlorophyll biosynthesis. *J. Integr. Plant Biol.* 58, (2016). 91–103. doi: 10.1111/jipb.12369
21. Lin, R., and Wang, H. Arabidopsis FHY3/FAR1 gene family and distinct roles of its members in light control of Arabidopsis development. *Plant Physiol.* 136, (2004). 4010–4022. doi: 10.1104/pp.104.052191
22. Aguilar-Martinez, J. A., Uchida, N., Townsley, B., West, D. A., Yanez, A., Lynn, N., et al. Transcriptional, posttranscriptional, and posttranslational regulation of SHOOT MERISTEMLESS gene expression in Arabidopsis determines gene function in the shoot apex. *Plant Physiol.* 167, (2015). 424–442. doi: 10.1104/pp.114.248625
23. Chen, Q., Song, Y., Liu, K., Su, C., Yu, R., Li, Y., Yang, Y., Zhou, B., Wang, J., & Hu, G. (2023). Genome-Wide Identification and Functional Characterization of FAR1-RELATED SEQUENCE (FRS) Family Members in Potato (*Solanum tuberosum*). *Plants*, 12(13), 2575. <https://doi.org/10.3390/plants12132575>
24. Wang, F.; Wang, X.; Zhang, Y.; Yan, J.; Ahammed, G.J.; Bu, X.; Sun, X.; Liu, Y.; Xu, T.; Qi, H.; et al. SIFHY3 and SIHY5 act compliantly to enhance cold tolerance through the integration of myo-inositol and light signaling in tomato. *New Phytol.* 2022, 233, 2127–2143.
25. Chen, Y.; Deng, J.; Chen, J.; Zeng, T.; Yu, T.; Huang, Q.; Chen, P.; Liu, Q.; Jian, W.; Yang, X. Genome-wide identification and expression analysis of FAR1/FHY3 transcription factor family in tomato. *Plant Physiol. J.* 2021, 57, 1983–1995.
26. Li, X.; Li, Y.; Qiao, Y.; Lu, S.; Yao, K.; Wang, C.; Liao, W. Genome-Wide Identification and Expression Analysis of FAR1/FHY3 Gene Family in Cucumber (*Cucumis sativus* L.). *Agronomy* 2024, 14, 50. <https://doi.org/10.3390/agronomy14010050>

27. Zhang, S.; Xu, F.; Zhang, Y.; Lin, J.; Song, C.; Fang, X. Fine mapping and candidate gene analysis of a novel PANICLE AND SPIKELET DEGENERATION gene in rice. *Euphytica* 2015, 206, 793–803.
28. Kiseleva, A.A.; Potokina, E.K.; Salina, E.A. Features of Ppd-B1 expression regulation and their impact on the flowering time of wheat near-isogenic lines. *BMC Plant Biol.* 2017, 17, 172.
29. Liu, Z.; An, C.; Zhao, Y.; Xiao, Y.; Bao, L.; Gong, C.; Gao, Y. Genome-Wide Identification and Characterization of the CsFHY3/FAR1 Gene Family and Expression Analysis under Biotic and Abiotic Stresses in Tea Plants (*Camellia sinensis*). *Plants* 2021, 10, 570.
30. Dai, J.; Sun, J.; Peng, W.; Liao, W.; Zhou, Y.; Zhou, X.R.; Qin, Y.; Cheng, Y.; Cao, S. FAR1/FHY3 Transcription Factors Positively Regulate the Salt and Temperature Stress Responses in *Eucalyptus grandis*. *Front. Plant Sci.* 2022, 13, 883654.
31. Zeps, M.; Kondratovičs, T.; Grigžde, E.; Jansons, Ā.; Zeltnš, P.; Samsone, I.; Matisons, R. Plantlet Anatomy of Silver Birch (*Betula pendula* Roth.) and Hybrid Aspen (*Populus tremuloides* Michx. × *Populus tremula* L.) Shows Intra-specific Reactions to Illumination In Vitro. *Plants* 2022, 11, 1097. <https://doi.org/10.3390/plants11081097>.
32. Wang, X.; Liu, S.; Zuo, H.; Zheng, W.; Zhang, S.; Huang, Y.; Pingcuo, G.; Ying, H.; Zhao, F.; Li, Y.; et al. Genomic basis of high-altitude adaptation in Tibetan *Prunus* fruit trees. *Curr. Biol.* 2021, 31, 3848–3860.e8.
32. Du, J.; Zhang, L.; Ge, X.; Xiang, X.; Cao, D.; Yang, H.; Hu, J. Genome-Wide Identification and Characterization of the FAR1/FHY3 Family in *Populus trichocarpa* Torr. & Gray and Expression Analysis in Light Response. *Forests* 2021, 12, 1385. <https://doi.org/10.3390/f12101385>
33. Yuan, N.; Wang, T.; Liu, T.; Yang, Y.; Du, J. Genome-wide analysis of the FAR1/FHY3 gene family in Cotton. *Cott. Sci.* 2018, 14, 1–11.
34. 7. Abdurakhmonov IY, Buriev ZT, Saha S, Jenkins JN, Abdurakimov A, Pepper AE. (2014) Phytochrome RNAi enhances major fibre quality and agronomic traits of the cotton *Gossypium hirsutum* L. *Nat Commun.* 2014;5:3062. doi: 10.1038/ncomms4062. PubMed PMID: 24430163.