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G'O'ZA (*GOSSYPIMUM SPP*) TURLARI *GHFHY3/FAR1* GENLAR OILASI VAKILLARINI SOLISHTIRMA BIOINFORMATIK TAHILLAR YORDAMIDA ANIQLASH

ИДЕНТИФИКАЦИЯ ПРЕДСТАВИТЕЛЕЙ СЕМЕЙСТВА ГЕНОВ *GHFHY3/FAR1* У ВИДОВ ХЛОПЧАТНИКА (*GOSSYPIMUM SPP*) С ИСПОЛЬЗОВАНИЕМ СРАВНИТЕЛЬНОГО БИОИНФОРМАТИЧЕСКОГО АНАЛИЗА

IDENTIFICATION OF *GHFHY3/FAR1* GENE FAMILY MEMBERS IN *GOSSYPIMUM SPP.* USING COMPARATIVE BIOINFORMATIC ANALYSIS

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Annotatsiya

Transposazalardan kelib chiqqan *FAR1-RELATED SEQUENCE1* (*FAR1*) va *FAR-RED ELONGATED HYPOCOTYL3* (*FHY3*) (*FHY3/FAR1*) transkripsiya faktorlari oilasi yorug'lik signallarini uzatishda, turli xil fiziologik va rivojlanish jarayonlarida, jumladan, urug'ning unib chiqishi, fotomorfogenez, gullash va stress reaksiyalarida hal qiluvchi rol o'ynaydi. Hozirgi kunda ushbu gen oilasi vakillari bir qancha sabzavot, texnik va manzarali ekilar turlarida bioinformatik va funksional tavsiflangan. Ushbu maqolada biz *FHY3/FAR1* genlar oilasi gomologlarini g'o'za *G. hirsutum* turiga tegishli Texas Marker1 (*TM1*) model tizmasi genomiga *A. thaliana*, kartoshka (*Solanum tuberosum*), terak (*Populus trichocarpa* Torr. & Gray), choy (*Camellia sinensis*) ekinlarining *FHY3/FAR1* genlar oilasi vakillariga solishtirib o'rgandik. Solishtirma bioinformatik tahlillar asosida g'o'za *FHY3/FAR1* genlari jami 149 ta aniqlandi. Aniqlangan genlar o'rtasida o'tkazilgan solishtirma tahlillar natijasi 89 tani tashkil etdi. Ushbu aniqlangan gomolog genlarning aminokislotalar ketma-ketliklari va oqsil kodlovchi nukleotid ketma-ketliklari (*CDS*) tahlillari natijasida barcha aniqlangan transkriptlarda *FHY3/FAR1* genlar oilasining vakillariga xos bo'lgan *MULE*, *SWIF*, *FAR1/FHY3* DNA binding domenlariga ega ekanligi

aniqlandi. Ushbu tadqiqot natijalari g'ozaning FHY3/FAR1 gen oilasining evolyutsiyasi va funksiyasini o'rganishga hamda bu genlar oilasining g'ozga o'sishi va rivojlanishidagi molekulyar mexanizmi boshqarishni tushunish uchun keyingi tadqiqotlarga asos bo'ladi.

Аннотация

Транскрипционные факторы семейства FAR1-RELATED SEQUENCE1 (FAR1) и FAR-RED ELONGATED HYPOCOTYL3 (FHY3), происходящие от транспозаз, играют ключевую роль в передаче световых сигналов, а также в различных физиологических и морфологических процессах, включая прорастание семян, фотоморфогенез, цветение и реакции на стресс. В настоящее время представители этого семейства генов были описаны с использованием биоинформатических и функциональных методов у ряда овощных, технических и декоративных культур. В данной статье мы исследовали гомологи генов семейства FHY3/FAR1 у хлопчатника *Gossypium hirsutum* на основе модельного генома сорта Texas Marker-1 (TM1) в сравнении с представителями семейства генов FHY3/FAR1 у таких культур, как *Arabidopsis thaliana*, картофель (*Solanum tuberosum*), тополь (*Populus trichocarpa* Torr. & Gray) и чай (*Camellia sinensis*).

В результате сравнительного биоинформатического анализа у хлопчатника было выявлено 149 генов семейства FHY3/FAR1. После углубленного сравнения были подтверждены 89 гомологичных генов. Анализ аминокислотных последовательностей и кодирующих (CDS) нуклеотидных последовательностей показал, что все идентифицированные транскрипты содержат домены, характерные для генов семейства FHY3/FAR1 — MULE, SWIF и FAR1/FHY3 DNA-binding.

Результаты данного исследования служат основой для дальнейшего изучения эволюции и функционального значения генов семейства FHY3/FAR1 у хлопчатника, а также для понимания молекулярных механизмов, регулирующих рост и развитие данного растения.

Abstract

The FAR1-RELATED SEQUENCE1 (FAR1) and FAR-RED ELONGATED HYPOCOTYL3 (FHY3) transcription factor family, which originated from transposases, plays a crucial role in light signal transduction and various physiological and developmental processes, including seed germination, photomorphogenesis, flowering, and stress responses. To date, members of this gene family have been bioinformatically and functionally characterized in several vegetable, industrial, and ornamental crops.

In this study, we identified homologs of the FHY3/FAR1 gene family in *Gossypium hirsutum* using the genome of the Texas Marker-1 (TM1) model variety and compared them with representatives of the FHY3/FAR1 gene family from *Arabidopsis thaliana*, potato (*Solanum tuberosum*), poplar (*Populus trichocarpa* Torr. & Gray), and tea (*Camellia sinensis*).

Through comparative bioinformatic analyses, a total of 149 FHY3/FAR1 genes were identified in cotton. Among them, 89 homologous genes were confirmed through sequence comparison. Amino acid and coding DNA sequence (CDS) analyses revealed that all identified transcripts possess characteristic domains of the FHY3/FAR1 gene family, including MULE, SWIF, and FAR1/FHY3 DNA-binding domains.

These findings provide a foundation for further studies on the evolution and functional roles of the FHY3/FAR1 gene family in cotton, and contribute to understanding the molecular mechanisms governing cotton growth and development.

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

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

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

KIRISH

Yorug'lik o'simliklarning o'sishi va rivojlanishida eng muhim omillardan biri hisoblanadi. O'simliklar unib chiqishdan boshlab vegetatsiya davrini tugatguncha o'tadigan barcha biomorfologik o'zgarishlar yorug'lik ta'siri ostida bo'ladi [1,2]. O'simliklar genomida uchta asosiy fotorepseptor genlar mavjud. Bular yorug'likning UV-A/ ko'k nur spektrini sezuvchi kriptoxrom va fototropinlar hamda qizil va uzoq qizil nurni sezuvchi fitoxrom genlardir. Bu fotorepseptorlar xususan, fitoxromlar yaxshi o'rganilgan. Fitoxrom fotorepseptorlari kichik genlar oilasini tashkil qilib, *A. thaliana* genomida bir-biridan farqli 5 ta (PHYA-PHYE) genini kodlaydi. Fitoxrom A, B, C, D, E genlari vazifasi jihatidan bir-biriga yaqin hisoblanib, yorug'likning qizil va uzoq qizil nuriga javob beradi. Bulardan farqli ravishda uzoq qizil nurning juda past va juda yuqori kuchlanishlari ta'siri ostida fitoxrom A (PhyA) geni o'simliklarda bir qancha biologik jarayonlarni ya'ni gipokotel uzayishi, urug 'palla bargalarning ochilishi va kengayishi, o'simliklarda gullash, xozilni erta etilishi, anatatsidin eg'ilishini hamda bargalarning yashil tusga kirishini boshqarilishida ishtrok etadi. [3,4,5,6]. Shu bilan bir qatorda Fitoxrom A geni g'ozga o'simligining tola sifat va miqdorining o'zgarishida juda muhim rol o'ynashi aniqlangan [7].

So'ngi yigirma yil ichida PhyA geni faoliyatini o'rganish natijasida uning faollashuvida FAR-RED ELONGATED 1 (FHY1) va uning gomologik FHY1-LIKE (FHL) va FAR-RED ELONGATED 3 (FHY3) va uning gomolog FAR-RED IMPAIRED RESPONSE 1 (FAR1) muhim komponentlar ishtroki aniqlandi [8,9].

BIOLOGIYA

Bu genlar FHY3/FAR1 genlar oilasini tashkil etadi. Ushbu genlar strukturaviy va funksional jihatdan model o'simlik *A.thaliana*da yaxshi o'rganilgan bo'lib, FAR1/FHY3 genlarning oilasining 14 ta FAR1/FHY3 oila a'zolari aniqlangan [10].

FAR1/FHY3 genlar oilasining vakillarini oqsil tuzilishi uchta funksional domenlaridan jumladan, DNK bilan bog'lanish faolligi bo'lgan (C2H2 zinc finger domain) domeni, yadro transpozaza domeni (MLUE domain) domeni va transkripsiya faollashuv faolligi (SWIM zinc finger domain) domenlaridan iborat ekanligi aniqlangan [11].

Ushbu aniqlangan domenlar FHY3/FAR1 genlar oilasining asosini tashkil etadi. Hozirgi kunda o'simlik turlarida FHY3/FAR1 genlar oilasi vakillari ushbu domenlar asosida aniqlanmoqda. FHY3/FAR1 genlar oilasi vakillari bir qancha ekin turlarida sabzovot (kartoshka (*Solanum tuberosum*) [12], pomidor (*Solanum lycopersicum*) [13,14], bodiring (*Cucumis sativus* L.) [15]), donli (sholi (*Oryza sativa*) [16], bug'doy (*Triticum aestivum*) [17]) texnik (choy (*Camellia sinensis*) [18], evkalipt (*Eucalyptus grandis*) [19], kumush qayin (*Betula pendula*) [20], Tibet Prunus [21] terak (*Populus trichocarpa* Torr. & Gray) [22], g'o'za (*G.hirsutum*) [23]) ekinlarda aniqlangan.

Ushbu genlar oilasi g'o'za ekinida aniqlanishiga qaramay, biz ushbu genni g'o'za genomidan qayta tahlil qilishga qaror qildik. Ushbu genlar oilasini qayta tahlil qilishimizga sababi ushbu genlar tahlil qilganda g'o'za genomini hozirgi darajada sifatli emasligi va solishtirilishda faqat MULE, SWIF, FAR domenlariga taqqoslab o'rganilganligini asos qilib keltirish mumkin. Ushbu ishda biz nafaqat MULE, SWIF, FAR domenlariga balki kartoshka, terak, choy ekinlarining FHY3/FAR1 genlar oilasi vakillariga ham solishtirib o'rgandik.

MATERIAL VA TADQIQOT USLUBLARI

G'o'za (*G.hirsutum* L.) Gh FHY3/FAR1 genlar oilasi vakillarini aniqlash uchun Pfam ma'lumotlar bazasidan FAR1/FHY3 DNA binding (PF03101), SWIM (PF04434) va MULE transpozaza (PF10551) domenlari (<http://pfam.xfam.org>) [24], kartoshka, choy, terak kabi o'simliklarning o'rganilgan FHY3/FAR1 genlari oilasi vakillari aminokislotalar ketma-ketligi (<https://plantfdb.gao-lab.org/>) va *A.thaliana* AtFHY3/FAR1 genlarining aminokislotalar ketma-ketliklari Arabidopsis Information Resource (TAIR) (<https://www.arabidopsis.org/>) yuklab olindi. Yuklab olingan domenlar va ekin turlarining FHY3/FAR1 aminokislotalar ketma-ketliklarini solishtirish maqsadida Oxford Nanopore PromethION; PacBio Sequel (HiFi v. 0.7) usuli yordamida sekvenslangan *Gossypium hirsutum* (AD1) 'TM-1' T2T genome JZU_v1.0 tizmasining aminokislotalar ketma-ketliklaridan foydalanildi (<https://www.cottongen.org/node/13354882/>).

G'o'za genomidan FHY3/FAR1 genlarini solishtirish va ajratishda HMMER 3.0 dasturi (<http://www.ebi.ac.uk/Tools/hmmer/search/hmmscan/>) foydalanildi. HMMER 3.0 ning E qiymati 0,01 ga to'g'irlandi. Solishtirish natijasida olingan GhFHY3/FAR1 aminokislota ketma-ketliklari NCBI CDD (Conserved Domains) ma'lumotlar bazasi (<https://www.ncbi.nlm.nih.gov/cdd>) va Interpro (<https://www.ebi.ac.uk/interpro/>) on-line bazalari yordamida qayta tekshiruvdan o'tkazildi va FHY3/FAR1 genlar oilasiga tegishli bo'lmagan hamda o'zida konservativ domenlarga ega bo'lmagan aminokislotalar ketma-ketliklari olib tashlandi.

NATIJALAR VA MUHOKAMA

G'o'za (*G.hirsutum*) o'simligi genomini choy, kartoshka, arabidosis, terak va FAR1/FHY3 DNA binding (PF03101), SWIM (PF04434) va MULE transpozaza (PF10551) domenlari solishtirma bioinformatik tahlil qilish natijasida GhFHY3/FAR1 genlar oilasiga tegishli 149 ta genlar mavjudligi ma'lum bo'ldi. Ushbu solishtirish *G.hirsutum* turiga massub TM1 genomi ya'ni (AD1) ustida o'tkazilganligi bois aniqlangan 149 ta genning 77 tasi At genomdan, 72 tasi esa Dt genomdan kelganligi aniqlandi. Aniqlangan genlarni aminokislotalar va oqsil kodlovchi nukleotidlar ketma-ketliklarini (CDS) bir-biriga o'zaro solishtirish natijasida bir-birga o'xshash ketma-ketliklar birlashtirildi. Natijada g'o'za genomida ushbu oila vakillari 89 tani tashkil etdi.

O'simlik turlarida aniqlangan FHY3/FAR1 oilasi vakillarining g'o'za genomi bilan bioinformatik solishtirish natijalariga ko'ra choy CsFHY3/FAR1 geni oilasi vakillariga solishtirilmasi eng yuqori natija berdi. Choy o'simligida jami 25 ta CsFHY3/FAR1 gen oilasi vakillari aniqlangan bo'lib, ushbu genlarni g'o'za genomiga solishtirishda 25 ta yangi g'o'za FHY3/FAR1 genlari aniqlandi. Boshqa ekin turlari (*A.thaliana*, terak, kartoshka) FHY3/FAR1 genlar oilasi vakillarini solishtirish natijalari bir-biriga taqqoslaganda olingan solishtirish natijalari bir-birga o'xshash ekanligini ko'rsatdi.

Qizil va uzoq qizil yorug'lik o'simliklarning o'sishi va rivojlanishini, ayniqsa fotomorfogenezni boshqarilishiga ta'sir etuvchi muhim omil hisoblanadi. PhyA qizil va uzoq qizil nurni qabul qiluvchi va ularga javob beradigan asosiy fotoretseptor gen hisoblanadi. Transposazadan kelib chiqqan FHY3/FAR1 oqsillari FHY1 va FHL hujayradagi ekspressiyasini bevosita faollashtirib, PhyA genini yadroga kirishini modulyatsiya qiladi. Oldingi tadqiqot shuni ko'rsatdiki, FAR1/FHY3 asosan maqsadli genlarning yorug'lik tasirida induksiyalangan transkripsiyasini faollashtiradi [25]. FHY3/FAR1 genlar oilasi *A.thaliana*da yaxshi o'rganilgan bo'lib, uning genomida ushbu oilaning 14 vakili ya'ni AtFHY3, AtFAR1 va 12 ta AtFRS aniqlangan va ular tuzilishi, morfologiyasi va funksiyalari jihatidan yuqori gomologiyaga ega [26]. *A.thaliana* AtFHY3/FAR1 genlar oilasi vakillari ustida olib borilgan tadqiqotlarda FRS genlarning o'simliklarning o'sishi va rivojlanishidagi muhim rolini ochib berildi [25]. Shundan so'ng sabzavot (kartoshka [12], pomidor [13,14], bodirring [15]), donli (sholi [16], bug'doy [17]) texnik (choy [18], evkalipt [19], kumush qayin (*Betula pendula*) [20], Tibet Prunus [21] terak [22], g'oz [23]) kabi bir nechta ekin turlarda FRS bo'yicha tadqiqotlar boshlangan.

FHY3/FAR1 genlar oilasi vakillarini g'ozda genomidan aniqlash bo'yicha 2018 yilda tadqiqotlar o'tkazilgan bo'lib [23], solishtirma tahlillar FAR1/FHY3 DNA binding (PF03101), SWIM (PF04434) va MULE transposaza (PF10551) domenlari asosida amalga oshirilgan. Biz ushbu tadqiqotda solishtirishda ushbu domenlar bilan birgalikda *A.thaliana*, terak, kartoshka, choy o'simliklarda aniqlangan FHY3/FAR1 genlar oilasini vakillaridan ham foydalandik. Bundan tashqari biz solishtirishda yuqori texnologiya asosida nukleotidlar ketma-ketligi aniqlangan g'ozda genomidan foydalandik. Bu esa FHY3/FAR1 genlar oilasini yangi vakillarini aniqlashda katta ahamiyatga ega. G'ozda genomini choy o'simlik turida aniqlangan CsFHY3/FAR1 genlar oilasi vakillari bilan solishtirish natijasida 25 ta yangi FHY3/FAR1 oilasi vakillari aniqlandi.

G'ozda genomida aniqlangan FHY3/FAR1 genlar oilasining vakillarini strukturaviy va funksional jihatdan o'rganilish, ushbu genlar ishtrokida g'ozaning biotik va abiotik omillarga chidamli, serhosil va tola sifat yaxshilangan navalarini olishga muhim manba bo'lib xizmat qiladi.

XULOSA

Ushbu tadqiqotda g'ozda (*G.hirsutum*) genomida mavjud 89 ta FAR1/FHY3 gen oilasi vakillarini FAR1/FHY3 DNA binding (PF03101), SWIM (PF04434) va MULE transposaza (PF10551) domenlari, *A.thaliana*, kartoshka, choy, terak kabi o'simliklarda o'rganilgan FHY3/FAR1 genlar oilasi vakillarining aminokislotalari ketma-ketligiga solishtirib aniqladik hamda har tomonlama va tizimli tahlil qilindi. Bundan tashqari, g'ozda ekinini o'ta murakkab tetraploid genomini dekodlash orqali g'ozaning o'sishi, rivojlanishi va stressga chidamliligidagi Gh FHY3/FAR1 mexanizmlari haqida chuqurroq tushunchaga ega bo'lamiz, bu esa kelgusida iqlim o'zgarishiga chidamli va yuqori hosildorlikka ega yangi g'ozda navlarini rivojlantirish uchun nazariy asos bo'ladi.

ADABIYOTLAR RO'YXATI

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