

O'ZBEKISTON RESPUBLIKASI
OLIIY TA'LIM, FAN VA INNOVATSIYALAR VAZIRLIGI

FARG'ONA DAVLAT UNIVERSITETI

**FarDU.
ILMIY
XABARLAR**

1995-yildan nashr etiladi
Yilda 6 marta chiqadi

5-2025
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ВЕСТНИК.
ФерГУ**

Издаётся с 1995 года
Выходит 6 раз в год

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UO'K: 575.113:577.21:633.51

G'O'ZA (*G.HIRSUTUM* L.) TURI *GhFHY3/FAR1* GENLAR OILASI VAKILLARI CIS-ELEMENT HUDUDLARINI O'RGANISH.**ИЗУЧЕНИЕ ЦИС-ЭЛЕМЕНТНЫХ РЕГИОНОВ ПРЕДСТАВИТЕЛЕЙ СЕМЕЙСТВА ГЕ-НОВ *GhFHY3/FAR1* У ХЛОПЧАТНИКА (*G.HIRSUTUM* L.)****INVESTIGATION OF CIS-ELEMENT REGIONS IN MEMBERS OF THE *GhFHY3/FAR1* GENE FAMILY IN UPLAND COTTON (*G.HIRSUTUM* L.)****Usmanov Dilshod Erkinbaevich¹** ¹O'zbekiston Respublikasi fanlar akademiyasi Genomika va bioinformatika markazi, biologiya bo'yicha PhD**Abdulkarimov Sharofiddin Sayfidinovich²** ²O'zbekiston Respublikasi fanlar akademiyasi Genomika va bioinformatika markazi, kichik ilmiy xodim**Sobirov Botirjon Masharif o'g'li³** ³O'zbekiston Respublikasi fanlar akademiyasi Genomika va bioinformatika markazi, kichik ilmiy xodim**Abdug'afforov Azamat Tojiboy o'g'li⁴** ⁴O'zbekiston Respublikasi fanlar akademiyasi Genomika va bioinformatika markazi, kichik ilmiy xodim**Juraqulov Durbekjon Saydulla o'g'li⁵** ⁵O'zbekiston Respublikasi fanlar akademiyasi Genomika va bioinformatika markazi, stajyor-tadqiqotchi**Xusanbayeva Shahnoza Rustamjon qizi⁶** ⁶O'zbekiston Respublikasi fanlar akademiyasi Genomika va bioinformatika markazi, tayanch doktorant**Sharifjonov Abrorbek Abdurjabbor o'g'li⁷** ⁷O'zbekiston Respublikasi fanlar akademiyasi Genomika va bioinformatika markazi, kichik ilmiy xodim**Buriev Zabardast Tojiboevich⁸** ⁸b.f.d. prof. O'zbekiston Respublikasi fanlar akademiyasi, Genomika va bioinformatika markazi.**Annotatsiya**

O'simliklarning o'sish va rivojlanishi undagi mavjud genlarning murakkab tarmog'ining shakllanishi natijasida amalga oshadi. Bunday murakkab bog'lanish o'simliklarning morfologik jihatdan takomillashuviga olib keladi. Genlarning o'zaro bog'lanishining bir qancha yo'llari bo'lib, shu kabi mexanizmlardan bir bu Cis-Acting Elements (CAE) yoki cis-regulyatsiya modullarini (CRM) hisoblanadi. CRM lar funksiyasini o'rganilishi genlar ekspressiyasini o'rganish uchun yana bir muhim vosita hisoblanadi. O'simliklar genomini zamonaviy texnologiyalar yordamida yuqori sifatli o'qilishi va genomni anotatsiyalash yutuqlarga qaramay, CRM larni identifikatsiyalash, ularning funksiyalarini tushunish va gen ekspressiyasini boshqarilishdagi roli juda kam o'rganilgan. Ushbu maqolada g'o'za (*G.hirsutum* L.) turi *GhFHY3/FAR1* genlar oilasi vakillariga tegishli transkriptlarda CRM larni aniqlash bo'yicha *in-silico* bioinformatik tadqiqotlar o'tkazildi. Bu oila

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vakillari transkriptlarini *in-silico* bioinformatik tahlil qilish natijasida yorug'likni va gibrellin, auksin, sitokinin kabi gormonlar sistemasini boshqaruvchi genlar ekspressiyasini boshqarishda ishtirok etishini ko'rsatdi. Ushbu gormonlar tizimi o'simliklarni o'sishi va rivojlanishini boshqarish bilan bir qatorda ularda abiotik va biotik omillarga qarshi turish mexanizmlarini ham tartibga soladi. Mazkur tadqiqot natijalari g'oz (G. hirsutum L.) turi GhFHY3/FAR1 genlar oilasi vakillariga tegishli transkriptlarda ushbu CRM larni aniqlanishi oila vakillarining abiotik va biotik omillarga qarshi turish mexanizmlarini boshqarilishida ishtirok etishini ochib berdi.

Аннотация

Рост и развитие растений происходят в результате формирования сложной сети генов, присутствующих в их геноме. Такие сложные взаимодействия приводят к морфологическому совершенствованию растений. Существует несколько способов взаимодействия генов, и одним из таких механизмов являются Cis-Acting Elements (CAE) или цис-регуляторные модули (CRM). Изучение функций CRM является важным инструментом для исследования экспрессии генов. Несмотря на достижения в области высококачественного секвенирования и аннотации растительных геномов с использованием современных технологий, идентификация CRM, понимание их функций и роли в регуляции генной экспрессии остаются недостаточно изученными. В данной статье были проведены *in silico* биоинформационные исследования по выявлению CRM в транскриптах представителей семейства генов GhFHY3/FAR1 у хлопчатника (*Gossypium hirsutum* L.). Результаты *in silico* анализа транскриптов показали, что представители этого семейства участвуют в регуляции экспрессии генов, контролирующих световую сигнализацию и гормональные системы, включая гиббереллины, ауксины и цитокинины. Эти гормональные системы регулируют не только рост и развитие растений, но и механизмы устойчивости к абиотическим и биотическим факторам. Полученные результаты указывают, что выявленные CRM в транскриптах представителей семейства GhFHY3/FAR1 хлопчатника (*G. hirsutum* L.) играют роль в регуляции механизмов устойчивости растений к неблагоприятным условиям.

Abstract

The growth and development of plants occur as a result of the formation of a complex network of genes present in their genome. Such intricate interactions contribute to the morphological advancement of plants. There are several pathways for gene interaction, and one of these mechanisms is represented by Cis-Acting Elements (CAE) or cis-regulatory modules (CRM). Studying CRM functions is an important tool for investigating gene expression. Despite the achievements in high-quality genome sequencing and annotation of plant genomes using modern technologies, the identification of CRM, the understanding of their functions, and their role in gene expression regulation remain insufficiently explored. In this study, *in silico* bioinformatic analyses were conducted to identify CRM in transcripts of members of the GhFHY3/FAR1 gene family in upland cotton (*Gossypium hirsutum* L.). The *in silico* analysis of the transcripts revealed that members of this family are involved in the regulation of gene expression controlling light signaling and hormonal systems, including gibberellins, auxins, and cytokinins. These hormonal systems regulate not only plant growth and development but also mechanisms of resistance to abiotic and biotic factors. The results of this research indicate that the identified CRM in transcripts of GhFHY3/FAR1 gene family members of cotton (*G. hirsutum* L.) play a role in regulating plant resistance mechanisms against adverse environmental conditions.

Kalit so'zlar: *G. hirsutum* L., CRM, FHY3/FAR1, oqsil.

Ключевые слова: *Gossypium hirsutum* L., CRM, FHY3/FAR1, белок.

Key words: *Gossypium hirsutum* L., CRM, FHY3/FAR1, protein.

KIRISH

1960-yillarda bakteriyalarda birinchi cis-regulyatsiya modullari (CRM) aniqlangandan beri o'simliklarda ko'plab CRM lar aniqlandi va ularning o'simlik genetikasidagi ahamiyati keng o'rganildi. Cis-ta'sir qiluvchi elementlar o'simlik rivojlanishi, stressga javob berish va atrof-muhit o'zgarishlariga moslashish jarayonida gen ekspressiyasini tartibga solishda hal qiluvchi rol o'ynaydi [1].

CRM gen ekspressiyasini boshqarishda transkripsiya omillari (transcription factors (TFs)) bilan bog'lana oladigan qisqa, kodlanmagan DNK ketma-ketliklaridan iborat [2]. Ushbu ketma-ketliklar TF-bog'lash joylari (TFBS) yoki motivlar deb ham ataladi. CRM larni keng qamrovli identifikatsiyalash maqsadli genlar ekspressiyasini o'rganish hamda TF lar va ularning maqsadli genlari ekspressiyasiga o'zaro ta'sir ko'rsatadigan genlarni tartibga soluvchi tarmoqlarni (TST) identifikatsiyalash uchun juda muhimdir. TST lar o'simliklarning o'sishi va stress reaksiyalarini boshqaradigan signalizatsiya yo'llarining molekulyar regulyatorlarini aniqlash uchun keng qo'llaniladi [3,4,5,6]. Ularning identifikatsiyasi o'simliklarning o'sishi va rivojlanishida hamda tashqi muhit sharoitiga moslashishda ishtirok etadigan genlarning transkripsiyaviy boshqaruvini o'rganish uchun muhim vositalardan biri hisoblanadi. Shundan kelib chiqib ularning uch toifaga bo'lib o'rganiladi, ya'ni promoterlar, enhanserlar va saylenserlar. Har bir turdagi CMR alohida tuzilish va funksiyaga ega ekanligi bilan bir-biridan farq qilishi adabiyotlarda o'rganilgan [7].

O'simliklar genomini tadqiq qilish mobaynida bir necha CRM lar aniqlangan bo'lib, ular o'simliklarning biotik va abiotik omillarga javob reaksiyalarida, to'qimalarga xos genlarning espres-

siyasida va morfologik xususiyatlarni rivojlantirishi kabi jarayonlarni amalga oshishida asosiy roli ega ekanligi ko'rsatilgan [8,9,10]. Masalan, kartoshka (*Solanum tuberosum*) StFAR3 va StPOD7 genlarning ekspressiyasi L1-Box elementi tomonidan boshqariladi, bu uzun zanjirli yog' kislotalari biosintezi orqali kutin va suberin rivojlanishini va StHAP3 va StCASP1 genlarda mavjud bo'lgan MBSII elementi esa hujayra differentsiatsiyasini boshqarilishida ishtrok etadi [11]. CRM lar- ning funksiyasini o'rganish o'simliklarda mavjud morfologik rivojlanish, stress omillariga javob reaksiyalari hamda hujayra differentsiatsiyasi va to'qimlarga xos genlar ekspressiyasini boshqarilishini o'rganish imkonini beradi.

FHY3FAR1 genlar oilasi ham katta genlar oilasi sirasiga kirib, o'simlikning rivojlanishining har bir bosqichida ishtirok etadi. O'rganilgan adabiyotlardan bizga ma'lumki, FHY3/FAR1 genlar oilasi tuzilishiga ko'ra transpozazalardan kelib chiqqan trankripsiya omillari xususiyatiga ega genlar oilasi hisoblanadi. Ushbu oila vakillari ko'p domenga ega bo'lib, bunga sabab ularning kelib chiqishi deb taxmin qilinadi [12]. Oxirgi yillarda ushbu genlar oilasi vakillarini o'simlikdagi funksiyasini o'rganishga bag'ishlangan molekulyar tadqiqotlar ko'plab amalga oshirilmoqda [13,14,15,16,17,18,19,20,21,22,23,24,25]. Bu gen oilasi ustida olib borilayotgan bioinformatik tadqiqotlarda ulardagi mavjud CRM larning bajaradigan funksiyalari keltirilgan [13,14,15,16,17,18,19,20,21,22,23,24,25]. Ammo, g'o'za (*G.hirsutum* L.) turi FHY3/FAR1 genlar oilasi ushbu o'simlik turida o'rganilganligiga qaramay, ushbu gen promoter qismlarida mavjud CRM haqida ma'lumotlar keltirilmagan. Shundan kelib chiqib, biz tadqiqotimizda g'o'za (*G.hirsutum* L.) turida mavjud FHY3/FAR1 genlar oilasi vakillariga tegishli transkriptlarida CRM larni aniqlashga qaror qildik.

MATERIAL VA METODLAR

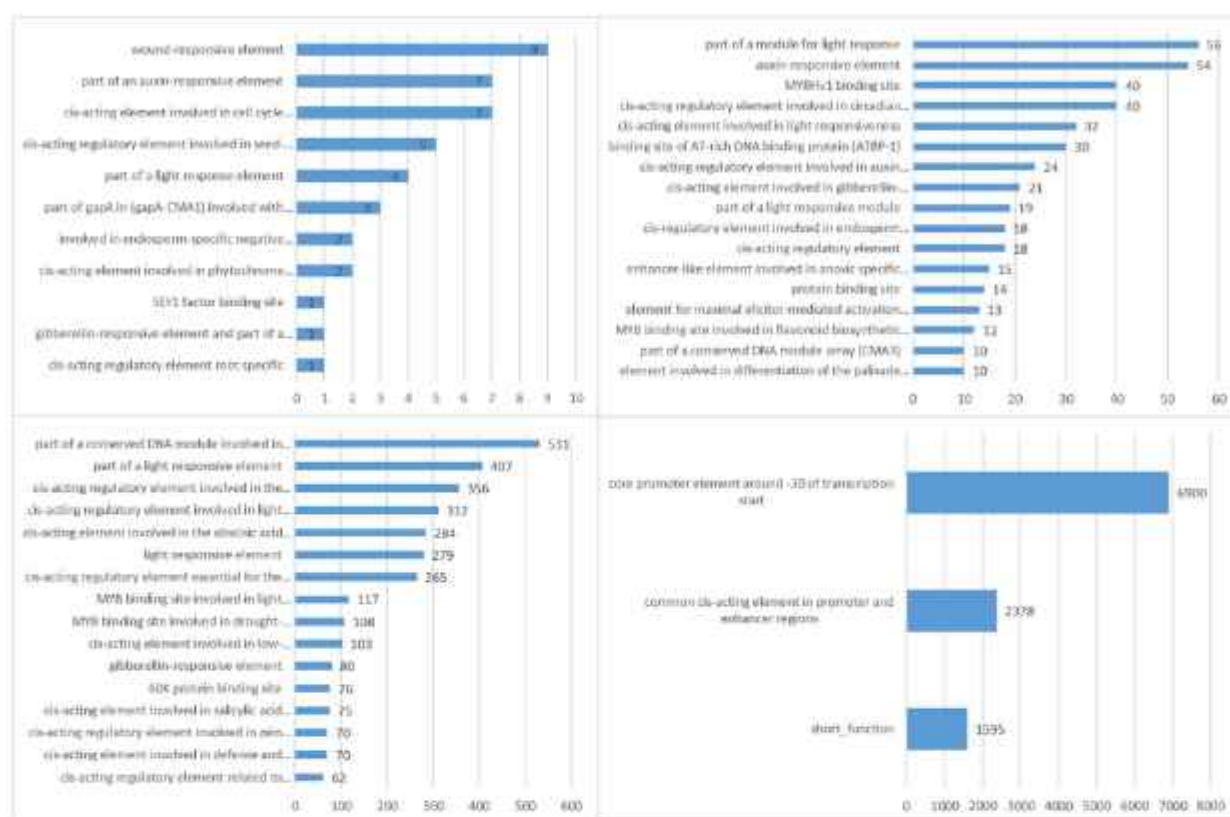
G'o'za (*G.hirsutum* L.) GhFHY3/FAR1 genlar oilasi vakillarini oqsil kodlovchi nukleotidlar ketma-ketligining (CDS) yuqori qismidan 2000 bp (2kb) nukleotidlar ketma-ketligi TBtool dasturi yordamida ajratib olindi. So'ngra ajratib olingan nukleotidlar ketma-ketligi cis-elementlarni tekshirish uchun on-line Plant CARE veb-saytida (<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>) tekshiruvdan o'tkazildi [26]. Cis-elementlasri xaritasini tuzish TBtools dasturi yordamida amalga oshirildi [27].

NATIJA VA MUHOKAMA

G'o'za (*G.hirsutum* L.) turi genomida 149 ta FHY3/FAR1 gen oilasiga tegishli transkriptlar aniqlangan bo'lib, 149 ta FHY3/FAR1 genining oqsil kodlovchi nukleotidlar ketma-ketligining (CDS) yuqori qismidan 2000 bp (2kb) nukleotidlar ketma-ketligi ajratib olindi. So'ngra ajratib olingan nukleotidlar ketma-ketligi cis-elementlarni tekshirish uchun on-line PlantCARE tekshiruvdan o'tkazildi [26]. Natijada FHY3/FAR1 genlar oilasiga tegishli transkriptlarda jami 117 ta cis-elementlar aniqlandi. Ushbu 117 ta cis-elementlar 5 turdagi, ya'ni yorug'likka, stress omillarga, o'sish va rivojlanishga, gormonlar sinteziga javob beruvchi genlarning ekspressiyalanishida muhim rol o'ynashini ko'rsatdi (1-diagramma).

Diagramma-2

GhFHY3/FAR1 genlar oilasi transkriptlarining cis-elementlarining statistikasi va tasnifi.



Aniqlangan 117 turdagi cis-elementlar 47 ta turdagi biologik jarayonlar ishtirok etish ushbu oila vakillarining o'simliklar o'sish va rivojlanishida katta ahamiyat kasb etishini ko'rsatadi. Mazkur aniqlangan cis-elementlarning katta qismi stress omillarda hamda o'sish va rivojlanishda katta ahamiyatga ega ekanligini ko'rsatdi (diagramma-2).

XULOSA

G'o'za (*G.hirsutum* L.) genomida aniqlangan FHY3/FAR1 genlar oilasiga tegishli 149 ta transkript promoter qismlarini *in-silico* tahlil qilish natijasida ularda mavjud 117 turdagi CRMlar aniqlandi. Bundan tashqari ushbu CRM lar 5 turdagi ya'ni yorug'likka, stress omillarga, o'sish va rivojlanishga, garmonlar sinteziga javob beruvchi genlarning ekspressiyalanishida muhim ro'l o'ynashini ko'rsatdi. FHY3/FAR1 genlar oilasi vakillari ustida olib borilgan chuqur molekulyar tadqiqotlar natijasida ushbu oila vakillari o'simliklarning rivojlanishida kechadigan ko'plab biologik jarayonlarda ishtiroki borligi aniqlangan [13,14,15,16,17,18,19,20, 21,22,23,24,25]. FHY3/FAR1 gen oilasi ustida olib borilayotgan amaliy tadqiqotlar natijasida ushbu oila vakillari asosan stress va yorug'lik reaksiyalarida faol ekanligi keltrilgan [13,14,15,16,17,18,19,20,21,22,23,24,25]. Shundan kelib chiqib ushbu tadqiqotda g'o'za (*G.hirsutum* L.) turida mavjud FHY3/FAR1 genlar oilasi vakillariga tegishli transkriptlarida CRM hududlarini aniqlanishi ushbu oila vakillarining qay darajada hujayrada kechadigan biofizikaviy jarayonlarda ishtirok etishini ko'rsatadi. Bu esa amaliy jihatdan ushbu CRMlarni chuqurroq bioinformatik tahlil qilish biotexnologiyaning yangi yo'nalishlariga asos soladi.

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