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**G'O'ZA (*G.HIRSUTUM* L.) TURI *GHFHY3/FAR1* GENLAR OILASI
VAKILLARI COILED-COLI DOMENINI *IN-SILICO* TAHILLAR
YORDAMIDA ANIQLASH**

Annotatsiya. Yorug'lik o'simliklarni o'sishi va rivojlanishida muhim ahamiyat kasb etuvchi omillardan biri hisoblanadi. O'simliklarda kechadigan morfobiologik jarayonlarning barchasi yorug'likning turli spektr uzunligidagi nurlar tasiri ostida yuz beradi. O'simliklarni yorug'lik nuriga javob reaksiyasiga ko'ra asosan uch turdagi fitoxrom (*PhyA-D*), kriptoxrom (*Cry1*, *Cry2*, *CryDash*), fototropin (*Pho1*, *Pho2*) genlar oilasi tasniflanadi. Bu genlardan tashqari ushbu genlar ta'siri ostida ekspressiyalanuvchi *FHY3/FAR1* genlar oilasi ham mavjud. Ushbu genlar oilasi asosan fitoxrom genlar oilasi bilan bog'lanib uning ekspressiyasini boshqarilishida markaziy rol o'ynaydi. *FHY3/FAR1* genlar oilasi

tuzilishiga ko'ra tranpazazalardan kelib chiqqan traskriptom faktor genlari deb qaraladi. Ushbu genlar oilasi tuzilishiga ko'ra juda ko'plab genlarning ekspressiyasini boshqarilishida ishtrok etadi. FHY3/FAR1 genlar oilasi vakillarida genlarni promotor qismiga bog'lovchi coiled-coil domenlari bo'lib, shu domen yordamida genlarga bog'lanib ularni ekspressiyasini boshqarishda ishtirok etadi. Ushbu tadqiqot ishida g'o'za (G.hirsutum L.) turi genomida mavjud FHY3/FAR1 genlar oilasi vakillariga tegishli traskriptlarida mavjud coiled-coil domenlarini tahlil qildik.

Kalit so'zlar: *G.hirsutum, coiled-coil, NLS, domen, oqsil, FHY3/FAR1*

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**ВЫЯВЛЕНИЕ ДОМЕНА COILED-COIL У ПРЕДСТАВИТЕЛЕЙ
СЕМЕЙСТВА ГЕНОВ GHFHY3/FAR1 У ХЛОПЧАТНИКА (GOSSYPIMUM
HIRSUTUM L.) С ИСПОЛЬЗОВАНИЕМ IN SILICO АНАЛИЗА**

Аннотация. Свет является одним из важнейших факторов роста и развития растений. Все морфо биологические процессы в растениях происходят под воздействием света различной длины волны. Растения классифицируются в соответствии с их реакцией на свет на три семейства генов: фитохром (PhyA-D), криптохром (Cry1, Cry2, CryDash) и фототропин (Pho1, Pho2). Помимо этих генов, существует также семейство генов FHY3/FAR1, которое экспрессируется под влиянием этих генов. Это семейство генов в основном взаимодействует с семейством генов фитохрома и играет центральную роль в регуляции его экспрессии. Согласно структуре семейства генов FHY3/FAR1, он считается геном транскрипционного фактора, производным от трансфераз. Согласно структуре этого семейства генов, он участвует в регуляции экспрессии большого количества генов. Гены семейства FHY3/FAR1 содержат домены с coiled-coil которые связывают гены с промоторной областью и участвуют в регуляции экспрессии генов посредством связывания с генами. В данном исследовании мы проанализировали домены с суперспиралью, присутствующие в транскриптах генов семейства FHY3/FAR1 в геноме хлопчатника (*G. hirsutum* L.).

Ключевые слова: *G. hirsutum*, суперспираль, NLS, домен, белок, FHY3/FAR1

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IDENTIFICATION OF THE COILED-COIL DOMAIN IN GHFHY3/FAR1 GENE FAMILY MEMBERS OF COTTON (*GOSSYPIUM HIRSUTUM* L.) USING *IN SILICO* ANALYSIS

Annotation. *Light is one of the most important factors in the growth and development of plants. All morpho biological processes in plants occur under the influence of light of different wavelengths. Plants are classified according to their response to light into three gene families: phytochrome (PhyA-D), cryptochrome (Cry1, Cry2, CryDash), and phototropin (Pho1, Pho2). In addition to these genes, there is also the FHY3/FAR1 gene family, which is expressed under the influence of these genes. This gene family mainly interacts with the phytochrome gene family and plays a central role in controlling its expression. According to the structure of the FHY3/FAR1 gene family, it is considered to be a transcriptome factor gene derived from transferases. According to the structure of this gene family, it participates in controlling the expression of a large number of genes. Members of the FHY3/FAR1 gene family contain coiled-coil domains that bind genes to the promoter region and are involved in regulating gene expression by binding to genes. In this study, we analyzed the coiled-coil domains present in the transcripts of members of the FHY3/FAR1 gene family in the genome of cotton (*G. hirsutum* L.).*

Keywords: *G. hirsutum, coiled-coil, NLS, domain, protein, FHY3/FAR1*

Kirish

Coiled-coil domen eukariot va prokariot organizimlar genomida uchraydi, umumiy ravishda genomning 3% tashkil etadi. Ushbu domen α -spiral shaklda

tuzilgan bo'lib, spirallar soni 2 ta dan 7 tagacha bo'lishi mumkin [1]. Coiled-coil domenlar turli xil funksiyalarga bog'liq bo'lgan oqsillardagi oligomerik spiral strukturaviy birliklardir.

Ushbu domenlar katalitik faollikka ega ekanligi bilan boshqa domenlardan farqlanadi. Ularning bajaradigan vazifalari ularning tuzilishidan kelib chiqadi. Coiled-coil domenlar genda mavjud domenlarni ajratib turadigan yoki bog'laydigan molekulalar bo'shliqlar hisoblanadi [2,3].

Coiled-coil domenlar bir-biridan uzoq masofada yotgan katta supermolekulyar tuzilmalari oqsillarining turli tomonlaridan bog'lanishni ta'minlaydi [4]. Coiled-coil domenlar parallel yoki antiparallel joylashuvga ega bo'lib, ular bir xil bo'linmaning zanjir ichidagi o'zaro ta'siri yoki alohida polipeptid zanjirlari orasidagi zanjirlararo aloqalar orqali hosil bo'lishi mumkin [5]. Bu domenlar organizmlarda mavjud oqsillarining 5-10% da mavjud ekanligi aniqlangan [6]. Coiled-coil domenlarni funksiyasini o'rganish natijasida ushbu domenga ega oqsillar talaygina biologik funksiyalarda genlar ekspressiyani boshqarishda, o'simliklarda biotik va abiotik omillarga javob reaksiyasini shakllanishida, o'sish va rivojlanishni boshqarilishida ishtirok etishi aniqlangan. Ularning asosiy xususiyati oqsillarning biri biriga o'zaro ta'sirini ta'minlaydi va oqsillar yoki domenlarni bir-biriga bog'laydi [7].

Coiled-coil domeni tuzilishi jihatidan ikki sinfga bo'lish mumkin: Olti yoki yettita heptaddan iborat qisqa takroriy o'ralishidan hosil bo'lgan domenlar, *Leucine zippers* deb ham ataladi. Qisqa takroriy domenlar ko'p hollarda transkripsiya omillarida gomo va geterodimer motivlari sifatida aniqlangan [8,9]. Birinchi sinf domenlaridan farqli o'laroq, bir necha yuzlab aminokislotalarning spiral hosil qilishidan hosil bo'ladigan uzun o'ralgan domenlardir. Ikkinchi sinf domenlari funksional oqsil komplekslarini Golji, sentrosomalar, sentromerlar yoki yadro qobig'i kabi yirik hujayrali tuzilmalarga biriktirishda ishtirok etadi [10].

Ushbu tadqiqot ishida biz g'oz (*G.hirsutum*) turi genomida mavjud FHY3/FAR1 genlar oilasi vakillariga tegishli transkriptlarida mavjud coiled-coil domenlarini tahlil qildik. Coiled-coil domeni *A.thaliana* AtFHY3/FAR1 genlar

oilasi vakillarida o'rganilgan bo'lib, faqatgina FRS3 va FRS8 genlarida ushbu domen yo'qligi aniqlangan [11]. FHY3/FAR1 genlar oilasi vakillari boshqa ekin turlarida ham aniqlanganligiga qaramasdan ularda ham ushbu domenlar qay darajada ekanligi tahlil qilinmagan [12,13,14,15,16,17,18,19,20,21,22].

Material va metodlar

G'o'za (*G.hirsutum* L.) GhFHY3/FAR1 genlar oilasi vakillarini aminokislotalar ketma-ketliklarida mavjud coiled-coil domeni COILED-COILS PREDICTION- NPS – IBCP (https://npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_lupas.html) va Waggawagga Coiled-coil and single alpha-helix prediction (<https://waggawagga.motorprotein.de/>) online dasturi yordamida *in-silico* tahlili amalga oshirildi.

Natija va muhokama

G'o'za (*G.hirsutum* L.) turi genomida 149 ta FHY3/FAR1 genlar oila a'zolariga tegishli traskriptlar aniqlangan bo'lib, ushbu 149 ta FHY3/FAR1 gen tomonidan kodlangan oqsillarning aminokislotalar ketma-ketliklari COILED-COILS PREDICTION - NPS – IBCP va Waggawagga Coiled-coil and single alpha-helix prediction online dasturi yordamida *in-silico* tahlili amalga oshirildi. Ushbu tahlillar natijasiga ko'ra g'o'za (*G.hirsutum* L.) turi genomida mavjud FHY3/FAR1 genlar oilasiga tegishli 149 ta traskriptlarning 30,2% da bitta, 18,2% da ikkita, 1,3% da uchta coiled-coil domeniga ega ekanligini ko'rsatdi. Qolgan 50,3% da esa ushbu domenga ega emasligi tasdiqlandi.

Ushbu domen eukariot va prokariot organizmlar genomining umumiy holda 3% tashkil etsada organizmdagi oqsillarning 5-10% da mavjud [1,6]. Ushbu domen oqsillar o'rtasida o'zaro bog'lanishni ta'minlash bilan bir qatorda ularning boshqarilishida ishtrok etadi. Shu sababli ushbu domenga ega gen yoki genlar oilasi organizmda kechadigan qator morfobiologik jarayonlarning boshqarilishida ishtrok etadi. Shu kabi genlar oilasidan biri bu FHY3/FAR1 genlar oilasidir. FHY3/FAR1 genlar oilasi vakillari bir qancha ekin turlarida o'rganilganligiga qaramay ularda mavjud coiled-coil domeni haqida ma'lumotlar keltirilmagan [12,13,14,15,16,17,18, 19,20,21,22]. Ushbu domen *A.thaliana* AtFHY3/FAR1

genlar oilasi vakillarida o'rganilgan bo'lib, oilaning 14 vakilidan ikkitasida ya'ni FRS3 va FRS8 larda coiled-coil domeni yo'qligi keltirilgan [11]. Biz o'rgangan FHY3/FAR1 oilasiga tegishli transkriptlarda ham 1, 2 va 3 ta coiled-coil domenlar aniqlandi. Lekin ushbu domenga ega bo'lmagan transkriptlar katta miqdorni tashkil

etdi. Coiled-coil domenlarga ega oqsillar o'simliklarda abiotik va biotik stress omillarda javob reaksiyasi sifatida ishlashi adabiyotlarda keltirilgan. Demak, biz olib borgan tadqiqot natijasida aniqlangan coiled-coil domeniga ega transkriptlarni amaliy jihatdan chuquroq o'ragnishni talab etadi.

Xulosa

G'o'za (*G.hirsutum L.*) genomida aniqlangan FHY3/FAR1 genlar oilasiga tegishli 149 ta transkript oqsillarini *in-silico* tahlil qilish natijasida ularda mavjud coiled-coil domenlari aniqlandi. FHY3/FAR1 genlar oilasi transkriptlarida ushbu domenlar 1 tadan 3 tagacha ekanligi ma'lum bo'ldi. Coiled-coil domenlarini aniqlanishi ushbu domen ega oqsillarning o'simlik rivojlanishining qaysi jarayonlarida faol ishtrok etishi yoki qaysi oqsillarni ekspressiyalanishini boshqarishini ko'rsatadi. Ushbu domenlarni o'rganilishi u ta'sir etadigan oqsillarning negativ yoki pozitiv boshqarilishi haqidagi ma'lumotlarni beradi. Bu esa amaliy jihatdan ushbu domenga ega genlarni biotexnologik usullar yordamida ekspressiyasini kuchaytirish yoki susaytirishga olib keladi.

Jadval-1

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

№	Traskript ID	Coiled-Coil Domain	Coiled-Coil Domain position	№	Traskript ID	Coiled-Coil Domain	Coiled-Coil Domain position
1	GhChrA10G0742.1	1	453-487	75	GhChrA08G1173.1	-	-
2	GhChrD10G0830.1	1	446-480	76	GhChrD08G1130.1	-	-
3	GhChrD02G1404.1	1	191-240	77	GhChrD02G1666.1	-	-
4	GhChrA05G1169.1	1	160-203	78	GhChrD05G1161.1	-	-
5	GhChrD05G1160.1	1	41-79	79	GhChrD13G1566.1	-	-
6	GhChrD07G1931.1	1	175-220	80	GhChrA10G0952.1	-	-
7	GhChrA09G1160.1	1	252-293	81	GhChrD10G1089.1	-	-
8	GhChrD09G1069.1	1	252-293	82	GhChrA02G0602.1	-	-
9	GhChrA11G0812.1	1	347-388	83	GhChrA02G0603.1	-	-
10	GhChrD11G0814.1	1	506-547	84	GhChrD02G0621.1	-	-
11	GhChrA05G2646.1	1	129-149	85	GhChrA09G2866.1	-	-
12	GhChrD05G2597.1	1	129-149	86	GhChrD09G2678.1	-	-
13	GhChrD09G0509.1	1	507-548	87	GhChrA09G1360.1	-	-
14	GhChrD04G1966.1	1	403-441	88	GhChrD09G1249.1	-	-
15	GhChrD01G2274.1	1	75-95	89	GhChrA11G0813.1	-	-
16	GhChrD10G1394.1	1	108-151	90	GhChrA09G2749.1	-	-
17	GhChrA02G0115.1	1	187-232	91	GhChrD09G2571.1	-	-
18	GhChrA03G1680.1	1	25-77	92	GhChrA06G1499.1	-	-
19	GhChrA05G4627.1	1	214-263	93	GhChrD06G1411.1	-	-
20	GhChrA10G2453.1	1	214-263	94	GhChrA09G0411.1	-	-
21	GhChrD01G1715.1	1	171-220	95	GhChrD09G0385.1	-	-
22	GhChrA10G2155.1	1	467-503	96	GhChrA05G2881.1	-	-
23	GhChrA01G1653.1	1	326-360	97	GhChrA10G2249.1	-	-
24	GhChrD01G1635.1	1	428-465	98	GhChrA01G2174.1	-	-
25	GhChrA03G1247.1	1	261-308; 680-720	99	GhChrA06G0967.1	-	-
26	GhChrD02G1297.1	1	233-277	100	GhChrA10G1746.1	-	-
27	GhChrD06G1208.1	1	616-639	101	GhChrD01G2104.1	-	-
28	GhChrD07G2281.1	1	352-400	102	GhChrA11G3724.1	-	-
29	GhChrA05G4637.1	1	140-160	103	GhChrD01G2273.1	-	-
30	GhChrA08G3083.1	1	483-519	104	GhChrD04G1174.1	-	-
31	GhChrA09G1359.1	1	351-396	105	GhChrA11G1671.1	-	-
32	GhChrA10G2154.1	1	186-223	106	GhChrD05G3176.1	-	-
33	GhChrA11G1770.1	1	675-715	107	GhChrD07G2331.1	-	-
34	GhChrA12G1454.1	1	57-106	108	GhChrA08G2390.1	-	-
35	GhChrD05G3261.1	1	134-168	109	GhChrA09G0337.1	-	-
36	GhChrD07G2588.1	1	64-113	110	GhChrD11G0875.1	-	-
37	GhChrD08G1075.1	1	555-603	111	GhChrA03G0863.1	-	-
38	GhChrD11G2816.1	1	121-157	112	GhChrD03G1167.1	-	-
39	GhChrD12G0852.1	1	18-52	113	GhChrA07G2371.1	-	-
40	GhChrD09G1114.1	1	380-424	114	GhChrA11G3512.1	-	-
41	GhChrA05G3603.1	1	283-318	115	GhChrD11G3399.1	-	-
42	GhChrA05G3605.1	1	291-340	116	GhChrA01G1459.1	-	-
43	GhChrA05G3606.1	1	316-365	117	GhChrA01G2175.1	-	-

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