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

Annotatsiya. *O‘simliklarning o‘sishi va rivojlanishida yorug‘likning ahamiyati katta. O‘simliklar yorug‘likning turli spektr to‘lqin uzunliklaridagi nurlari bilan ta’sirlanishi orqali ulardagi mavjud fotoretseptor genlar oqsillari konformatsiyaga uchraydi va o‘simlikning rivojlanishida ishtrok etuvchi boshqa genlar bilan ta’sirlashadi. Fotoretseptor genlar o‘simlikning rivojlanishida kechadigan biokimyoviy jarayonlarning boshqarilishida asosiy rol o‘ynaydi. Ushbu genlar oilasi to‘g‘ridan to‘gri morfobiologik jarayonlarga javob bermasada ular hosil qiladigan oqsillarda mavjud domenlarning ma’lum bir vazifaga javob beruvchi gen oqsillariga bog‘lanish orqali ularning ekspressiyasini*

*boshqarilishida ishtrok etadi. Fotoretseptor genlar oilasi vakil bo‘lgan FHY3/FAR1 genlar oilasi shu kabi genlar oilasi bo‘lib, ularda ushbu oilaga xos bir qancha domenlarning bo‘lishi bilan bir qatorda **N**uclear **L**ocalization **S**ignal (NLS) yoki yadroga ko‘chish signal domeniga ham ega. Ushbu maqolada g‘o‘za (G.hirsutum L.) turi GhFHY3/FAR1 genlar oilasi vakillariga tegishli traskriptlarda NLS domenini aniqlash bo‘yicha in-silico tadqiqotlar o‘tkazdik. Tadqiqotlar natijasida 57% traskriptlar NLS domeniga ega emasligi va qolgan 43% da esa ushbu domenga ega ekanligi tasdiqlandi. Ushbu tadqiqot natijalar g‘o‘za (G.hirsutum L.) turi GhFHY3/FAR1 genla oilasi vakillariga tegishli traskriptlarda ushbu domenini aniqlanishi o‘ziga xos NLS hududlarini ochib berdi va ularning o'simlik rivojlanishini tartibga solishda subhujayra lokalizatsiyasi uchun muhim rol o‘ynashini ko‘rsatdi.*

Kalit so‘zlar: *G.hirsutum, NLS, domen, oqsil, MULE, FAR1, FAR1-DNA binding, Ran-GTP*

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ВЫЯВЛЕНИЕ ДОМЕНА ЯДЕРНОЙ ЛОКАЛИЗАЦИИ (NLS) У ПРЕДСТАВИТЕЛЕЙ СЕМЕЙСТВА ГЕНОВ GHFHY3/FAR1 У ХЛОПЧАТНИКА (*GOSSYPIUM HIRSUTUM* L.) С ИСПОЛЬЗОВАНИЕМ *IN SILICO* АНАЛИЗА

Аннотация. *Свет играет важную роль в росте и развитии растений. Под воздействием света различных спектральных длин волн происходят конформационные изменения в белках фоторецепторных генов, которые далее взаимодействуют с другими генами, участвующими в развитии растений. Хотя семейство фоторецепторных генов напрямую не отвечает за морфобиологические процессы, белки, кодируемые этими генами, через специфические домены связываются с белками других генов и участвуют в регуляции их экспрессии. Одним из таких семейств является FHY3/FAR1, характерной особенностью которого является наличие нескольких доменов, в том числе домена ядерной локализации (Nuclear Localization Signal, NLS). В данной работе были проведены in silico исследования по выявлению NLS-домена в транскриптах представителей семейства GhFHY3/FAR1 у хлопчатника (Gossypium hirsutum L.). По результатам исследования было установлено, что 57% транскриптов не содержат домен NLS, в то время как 43% — обладают этим доменом. Полученные данные позволили идентифицировать уникальные участки NLS у представителей семейства GhFHY3/FAR1 у хлопчатника, что указывает на важную роль этих доменов в субклеточной локализации и регуляции развития растений.*

Ключевые слова: *G. hirsutum, NLS, домен, белок, MULE, FAR1, связывание с ДНК FAR1, Ran-GTP*

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IDENTIFICATION OF THE NUCLEAR LOCALIZATION SIGNAL (NLS) DOMAIN IN GHFHY3/FAR1 GENE FAMILY MEMBERS OF COTTON (*GOSSYPIUM HIRSUTUM* L.) USING *IN SILICO* ANALYSIS

Abstract. *Light plays a crucial role in plant growth and development. Exposure to light of various spectral wavelengths causes conformational changes in photoreceptor gene-encoded proteins, enabling interactions with other genes involved in plant developmental processes. Although photoreceptor gene families are not directly responsible for morphobiological processes, their protein products contain specific domains that interact with other regulatory proteins to modulate gene expression. One such gene family is FHY3/FAR1, which possesses several characteristic domains, including the Nuclear Localization Signal (NLS) domain. In this study, we conducted in silico analyses to identify NLS domains within transcripts of the GhFHY3/FAR1 gene family in cotton (Gossypium hirsutum L.). The results revealed that 57% of the transcripts lacked the NLS domain, while the remaining 43% contained it. These findings highlight the unique NLS regions in GhFHY3/FAR1 transcripts and suggest their important role in subcellular localization and regulation of plant development.*

Keywords: *G. hirsutum, NLS, domain, protein, MULE, FAR1, FAR1-DNA binding, Ran-GTP*

Kirish

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, uning sababi ularning kelib chiqishi deb taxmin qilinadi [1]. FHY3/FAR1 genlar oilasi oila uchun xos bo‘lgan FAR1-DNA binding, SWIM va MULE domenlarga ega. Bundan tashqari ushbu oila vakillarida Coiled-Coil, NLS domenlari ham mavjud [2]. Bu ikki domen oila vakillarining oqsilini boshqa oqsillar bilan bog‘laydi va o‘simlikda kechadigan morfobiologik jarayonlarning boshqarilishidagi ishtrokini taminlaydi. NLS domeni sitoplazmadagi oqsillarni yadroga ko‘chishini taminlovchi domen hisoblanadi. Yadroga oqsillarni ko‘chib o‘tishi muhim jarayon bo‘lib, bunda yadro qobig‘i retseptorlari NLSni aniq taniydigan oqsillar vositasida amalga oshiriladi. NLS uchta qisqa peptid motivlardan iborat bo‘lib, ular importinlar (karyoferinlar) deb nomlanuvchi retseptorlari bilan bog‘lanadi va bog‘langan oqsillarining yadroga ko‘chishiga vositachilik qiladi [3,4,5,6,7]. Oqsillarning yadroga ko‘chishi odatda importin α, importin β1 va maqsadli oqsil bilan uchlamchi kompleks hosil bo‘lishi bilan boshlanadi. Avvalo importin β1 kompleksni NPCga joylashtiradi va Ran-GTP ni importin β1 bilan bog‘lash orqali maqsadli oqsilni yadroga ko‘chiradi [8,9]. Ran-GTP va Ran-YaIM ning yadro va sitoplazma o‘rtasida assimetrik taqsimlanishi maqsadli oqsilni kirishi va chiqishinini nazorat qiladi va bu gradient turli xil Ran bilan bog‘liq tartibga soluvchi omillar tomonidan saqlanadi [10]. O‘simlik oqsillarining deyarli barchasida ushbu domen mavjud bo‘lib, bular yadro oqsillari deb nomalanadi. Kam sonli yani 10% yaqin sitopazmatik oqsillar NLS domeniga ega emasligi aniqlangan. Lekin ushbu oqsillar yadroga ko‘chishida NLS domeniga ega oqsillar bilan kuchli kompleks hosil qiladi [11]. Misol uchun, fotoretseptor genlar oilasining eng ko‘p o‘rganilgan vakillaridan fitoxrom genlarining yadroga ko‘chishi uchun uning ostida rivojlanuvchi FHY3/FAR1 genlar oilasining vakillari

kerak bo‘ladi. Shu sababli FHY3/FAR1 va fitoxrom genlar ortasida kuchli bog‘lanish hosil bo‘ladi. Ushbu bo‘g‘lanishning buzilishi yani FHY3/FAR1 genlar oilasi vakillarining ekspressiyasini to‘xtatilishi fitoxrom genlar ekspressiyasini ham tushishiga olib keladi [2]. Oqsillarda mavjud domenlarni o‘rganish ular bilvosita va bevosita ta’sir ko‘rsatadigan gen oqsillari haqida bilimlarimizni oshishiga olib keladi. FHY3/FAR1 genlar oilasining vakillarida NLS domenlari aniqlangan bo‘lib, bu oqsillar faqatgina *A.thalina* model o‘simligiga tegishli hisoblanadi [2]. Oxirgi 5 yillikni qaraydigan bo‘lsak o‘simlik turlarida FHY3/FAR1 genlar oilasi chuqur molekulyar tadqiqotlar ko‘plab amlaga oshirilmoqda [12,13,14,15,16,17,18,19,20, 21,22,23,24]. Ushbu gen oilasi ustida olib borilayotgan bioinformatik tadqiqotlarda ulardagi mavjud NLS domenlari qay darajada tuzilganligi keltirilmagan. Shundan kelib chiqib ushbu tadqiqotda g‘o‘za (*G.hirsutum L.*) turida mavjud FHY3/FAR1 genlar oilasi vakillariga tegishli transkriptlarida NLS domenini aniqlashga qaror qildik.

Material va metodlar

G‘o‘za (*G.hirsutum L.*) GhFHY3/FAR1 genlar oilasi vakillarini aminokislotalar ketma-ketliklarida mavjud NLS domeni NucPred - Predicting Nuclear Localization of Proteins (https://nucpred.bioinfo.se/nucpred/) va NLStradamus (http://www.moseslab.csb.utoronto.ca/NLStradamus/) online dasturi yordamida *in-silico* tahlili amalga oshirildi. Aminokislotalar ketma-ketligin tahlil qilishda NLS chegarasini aniqlash NucPred - Predicting Nuclear Localization of Proteins da keltirilgan qonuniyat asosida amalga oshirildi [25].

Natija 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 aminokislotlar ketma-ketliklari domeni NucPred - Predicting Nuclear Localization of Proteins va NLStradamus online dasturlari yordamida *in-silico* tahlili amalga oshirildi. Ushbu tahlilar Brameier M [25] tomonidan ishlab chiqilgan aminokislotalar ketma-ketligida mavjud NLS domelarni ishonchliligi aniqlovchi maxsus algoritm asosida hisoblandi. Ushbu

algoritmga ko‘ra NucPred ballining chegarasi qancha past bo‘lsa uning ishonchliligi hamda yadroda saqlanib qolishi vaqti oz bo‘lishi bilan tavsiflangan. Aminokislotalar ketma-ketligida mavjud NLS domenlar boshqa dastur yoki algoritmlarda ham hisoblashda NLS balining chegarasi O‘rtacha 0.6 deb qabul qilingan. Lekin ushbu chegaradan kam ball olgan NLS domenlar hisobga olinmaydi. Ba’zi NLS domenlarning balli kam bo‘lsada ular birikib yadroga olib kiradigan oqsillarning ahamyati katta hisoblanadi [26]. Shu bois ham biz FHY3/FAR1 genlar oilasi vakillariga tegishli transkriptalar kodlaydigan aminokislotalar ketma-ketligida mavjud NLS domenlarini 0.00 dan 1.00 gacha ball chegarasida tahlil qildik. Olingan natijalari asosida tahlil qilingan 149 ta traskriptlarning 57% NLS domeniga ega emasligi va qolgan 43% da esa ushbu domenga ega ekanligi tasdiqlandi. Ba’zi traskriptlarda 2 hatto 3 ta NLS domenlari aniqlandi. NLS domeniga ega aminokislotalar ketma-ketligini ball chegarasi va ishonchliligi 1-jadvalda keltirilgan.

NLS domenlariga ega oqsillar yadro oqsillari deb ham nomlanib, o‘simlik oqsillarining deyarli barchasida ushbu domen mavjud ekanligi tasdiqlangan. Kam sonli yani 10% yaqin sitopazmatik oqsillar NLS domeniga ega emasligi aniqlangan. Lekin ushbu oqsillar yadroga ko‘chishida NLS domeniga ega oqsillar bilan kuchli kompleks hosil qiladi [11]. Ushbu domenlarning transkripsiya omillarida ko‘plab uchrashi ulardagi aminokislotalar ketma-ketligi arginin (R) va lizin (K) kabi aminokislotalar bilan boyitilgani bilan tavsiflanadi [27,28,29]. NLS domenini FHY3/FAR1 genlar oilasi vakillarida uchrashiga asosiy sabablardan biri ushbu oila vakillarining traskripsiya omillaridan kelib chiqqanligi deb qarash mumkin [1]. Ba’zi o‘simlik transkripsiya omillarida NLS domeniga ega bo‘lmasligi mumkin va ular yadroga ushbu signallarga ega bo‘lgan oqsillar bilan dimerizatsiya yordamida ko‘chishi taminlanadi deb qaraladi [30]. Ushbu domenga ega bo‘lgan aminokislotalar ketma-ketligi ma’lum bir oqsillar bilan bo‘glanib ularning yadrodagi ekspressiyasini ta’minlaydi. Misol uchun, FHY3/FAR1 genlar oilasi vakillari asosan fitoxrom oilasi vakillari bilan bog‘lanib ularning ekspressiyasini boshqarilishida ishtirok etadi [31].

Xulosa. G‘o‘za (*G.hirsutum L.*) genomida aniqlangan FHY3/FAR1 genlar oilasiga tegishli 149 ta taranskript oqsillarini *in-silico* tahlil qilish natijasida ularda mavjud NLS domenlari aniqlandi. FHY3/FAR1 genlar oilasi tarnskriptlarining 57% NLS domeniga ega emasligi va qolgan 43% da esa ushbu domenga ega ekanligi tasdiqlandi. Bundan tashqari ushbu transkriptlarda NLS domeni 1 tadan 3 tagacha ekanligi ma’lum bo‘ldi. Oxirgi 5 yillikni qaraydigan bo‘lsak o‘simlik turlarida FHY3/FAR1 genlar oilasi chuqur molekulyar tadqiqotlar ko‘plab amalga oshirilmoqda [12,13,14,15,16,17,18, 19,20,21,22,23,24]. Ushbu gen oilasi ustida olib borilayotgan bioinformatik tadqiqotlarda ulardagi mavjud NLS domenlari qay darajada tuzilganligi keltirilmagan. Shundan kelib chiqib ushbu tadqiqotda g‘o‘za (*G.hirsutum L.*) turida mavjud FHY3/FAR1 genlar oilasi vakillariga tegishli transkriptlarida NLS domenini aniqlanishi ushbu oila vakillarini qay darajada hujayrada kechadigan biofizikaviy jarayonlarda ishtrok etishini ko‘rsatadi. Bu esa amaliy jihatdan ushbu domenlarni chuqurroq bioinfarmatik tahlil qilish bitoxnologiyaning yangi yo‘nalishlariga asos soladi.

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Jadval-1

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

#	Sequence-ID	NucPred-score threshold	Specificity fraction of proteins predicted to be nuclear that actually are nuclear	Sensitivity fraction of true nuclear proteins that are predicted (coverage)	Position	NLS sequence
1	GhChrA01G1459.1	0.14	0.45	0.88		No
2	GhChrA01G1653.1	0.83	0.84	0.32		no
3	GhChrA01G2174.1	0.05	0.50	100		no
4	GhChrA01G2175.1	0.12	0.45	0.88	91-94	KKAK
5	GhChrA02G0115.1	0.18	0.45	0.88	105-143/205-208	LSRSRRDGSAIGRALVCNKEGFRMPDKREKIMRHRAETR/KKRS
6	GhChrA02G0116.1	0.55	0.70	0.62	133-160	KSIRVRVRKRESKREGCMARMNVKREKP
7	GhChrA02G0602.1	0.57	0.70	0.62		no
8	GhChrA02G0603.1	0.29	0.52	0.83		no
9	GhChrA02G1020.1	0.52	0.70	0.62		no
10	GhChrA03G0469.1	0.60	0.71	0.53		no
11	GhChrA03G0862.1	0.28	0.52	0.83		no
12	GhChrA03G0863.1	0.97	0.88	0.21		no
13	GhChrA03G0946.1	0.24	0.52	0.83	104-123	KLLPDRELRRKPKGRPYWSG
14	GhChrA03G1145.1	0.24	0.52	0.83	96-123	VSIRGKFGPVRKPRPSTREGCKAMIHIK
15	GhChrA03G1185.1	0.92	0.88	0.21		no
16	GhChrA03G1247.1	0.74	0.81	0.44		no

17	GhChrA03G1680.1	0.70	0.81	0.44	268-288	RKMPRRPKKNRRMAKDEPKKL
18	GhChrA03G2410.1	0.37	0.57	0.77	68-84	NRRKPIDESAECIRRRR
19	GhChrA04G1493.1	0.36	0.57	0.77		no
20	GhChrA05G0713.1	0.93	0.88	0.21		no
21	GhChrA05G1169.1	0.59	0.70	0.62	706-724	LDPPKRRKKKYIHKGPFKR
22	GhChrA05G1306.1	0.29	0.52	0.83	82-112	RKTKERYRGKISCSSAGFKKKSEANRPRPET
23	GhChrA05G2646.1	0.33	0.57	0.77	100-134	KWRKYGKKKIKNNPNPRHYYRCSMEGCKVKKRVER
24	GhChrA05G2881.1	0.09	0.50	100		no
25	GhChrA05G3603.1	0.48	0.63	0.69		no
26	GhChrA05G3605.1	0.50	0.70	0.62		no
27	GhChrA05G3606.1	0.48	0.63	0.69		no
28	GhChrA05G4627.1	0.29	0.52	0.83	655-671	AGKKIASVKKNVAKVRP
29	GhChrA05G4637.1	0.07	0.50	100	23-83	KLRLKNPKSTIKMGVNRVTSESPPHFKRFYVYFETLKRGWKERYKPILGLDGCFLKGPFKG
30	GhChrA06G0836.1	0.12	0.45	0.88	8-18	RKVKTRLVSMR
31	GhChrA06G0967.1	0.27	0.52	0.83		no
32	GhChrA06G1242.1	0.33	0.57	0.77	80-104/147-166	RTKKKERYRAKLSCSSAGFKKKSEA/KRFYKSHKKMILAARKARPP
33	GhChrA06G1499.1	0.53	0.70	0.62	123-139/148-152	RKYGKKKVKNNPNPRNY/KVKKR
34	GhChrA06G1652.1	0.21	0.52	0.83		no
35	GhChrA06G2180.1	0.70	0.81	0.44		no
36	GhChrA07G1988.1	0.59	0.70	0.62	100-119	GFRKLRPRRSENRKPRAITR
37	GhChrA07G1989.1	0.53	0.70	0.62		no
38	GhChrA07G2371.1	0.82	0.84	0.32	696-697	KK
39	GhChrA07G2540.1	0.46	0.63	0.69		no
40	GhChrA08G1173.1	0.68	0.71	0.53	114-124/203-212	AKRKKKATAAR/KRRRTASWKR
41	GhChrA08G2390.1	0.81	0.84	0.32		no

42	GhChrA08G2725.1	0.06	0.50	100	52-55/173-209	KSKD/HIHANFKKMILEARGKPILTMMEIVRTKIMLLIVKKK
43	GhChrA08G2982.1	0.31	0.57	0.77	545-573	IRPPKTRRPPGRPKKKVLCVENLKRPKRV
44	GhChrA08G3083.1	0.18	0.45	0.88	496-500	RKKNS
45	GhChrA09G0337.1	0.10	0.45	0.88	223-239	FKKAGFRTKELKDLLWK
46	GhChrA09G0411.1	0.60	0.71	0.53		no
47	GhChrA09G0480.1	0.70	0.81	0.44		no
48	GhChrA09G0553.1	0.66	0.71	0.53		no
49	GhChrA09G1160.1	0.55	0.70	0.62		no
50	GhChrA09G1359.1	0.41	0.63	0.69		no
51	GhChrA09G1360.1	0.51	0.70	0.62		no
52	GhChrA09G2749.1	0.55	0.70	0.62		no
53	GhChrA09G2866.1	0.71	0.81	0.44	712-722	KRPPGRPKKKQ
54	GhChrA10G0742.1	0.30	0.57	0.77		no
55	GhChrA10G0952.1	0.90	0.88	0.21	68-70/75-77	RRK/KRK
56	GhChrA10G1477.1	0.68	0.71	0.53	441-452	RPPGRPTKVRRK
57	GhChrA10G1713.1	0.38	0.57	0.77	123-125	HRK
58	GhChrA10G1714.1	0.34	0.57	0.77		no
59	GhChrA10G1715.1	0.52	0.70	0.62		no
60	GhChrA10G1746.1	0.29	0.52	0.83		no
61	GhChrA10G1915.1	0.30	0.57	0.77		no
62	GhChrA10G2154.1	0.28	0.52	0.83	182-187	RTKKLK
63	GhChrA10G2155.1	0.79	0.81	0.44		no
64	GhChrA10G2249.1	0.74	0.81	0.44	511-523	RRPPGRPTKVKRK
65	GhChrA10G2406.1	0.26	0.52	0.83		no
66	GhChrA10G2453.1	0.22	0.52	0.83	116-125	FRIERKDGKK
67	GhChrA11G0812.1	0.30	0.57	0.77		no

68	GhChrA11G0813.1	0.46	0.63	0.69		no
69	GhChrA11G1671.1	0.40	0.63	0.69		no
70	GhChrA11G1770.1	0.93	0.88	0.21		no
71	GhChrA11G2041.1	0.09	0.50	100		no
72	GhChrA11G3026.1	0.45	0.63	0.69	139-168	KTIPGRPKKNRRKAKNELKKVKPGQHSRAG
73	GhChrA11G3512.1	0.51	0.70	0.62		no
74	GhChrA11G3724.1	0.82	0.84	0.32	621-639	RPKKNRRMAKDEPKKLKPG
75	GhChrA12G1454.1	0.24	0.52	0.83		no
76	GhChrA13G2087.1	0.27	0.52	0.83	541-574/547-573	KLDITVRPPKIRRPPGRPKKKVLRVENLKRPKRV/ RPPKIRRPPGRPKKKVLRVENLKRPKR
77	GhChrA13G2387.1	0.43	0.63	0.69		no
78	GhChrD01G1635.1	0.88	0.84	0.32		no
79	GhChrD01G1715.1	0.27	0.52	0.83		no
80	GhChrD01G2104.1	0.19	0.45	0.88		No
81	GhChrD01G2273.1	0.06	0.50	100		no
82	GhChrD01G2274.1	0.49	0.63	0.69		no
83	GhChrD02G0121.1	0.42	0.63	0.69	129-140	PDKREKIMRRRA
84	GhChrD02G0621.1	0.67	0.71	0.53		no
85	GhChrD02G1254.1	0.47	0.63	0.69		no
86	GhChrD02G1268.1	0.22	0.52	0.83	97-126	SIRGKFGPVRKPRPSTREGCKAMIHIKFNK
87	GhChrD02G1297.1	0.73	0.81	0.44		no
88	GhChrD02G1404.1	0.92	0.88	0.21		no
89	GhChrD02G1666.1	0.00	0.50	100	117-133	NRRVGFKTPLSMIFKNS
90	GhChrD02G2399.1	0.37	0.57	0.77	68-74/81-85	NRRKPID/IRRRR
91	GhChrD03G0495.1	0.14	0.45	0.88	116-141	ERKWPPVSVAPFKLLPDRELRRKPKG
92	GhChrD03G0496.1	0.65	0.71	0.53		no

93	GhChrD03G1166.1	0.71	0.81	0.44		no
94	GhChrD03G1167.1	0.97	0.88	0.21		no
95	GhChrD04G1174.1	0.08	0.50	100	42-66	AMKVRINAKILRRYGRRISKNFYKF
96	GhChrD04G1966.1	0.38	0.57	0.77		no
97	GhChrD05G0715.1	0.83	0.84	0.32		no
98	GhChrD05G1160.1	0.02	0.50	100	110-195/310-343	ARLSTTKLFLIKKMSETHTCGAGNSSSRHPKVSSKLVKFLVKEKLRD SPNAKPREIINEILQDYGFKARYAHVWRGVESAKEKPQV /QPVTFVADRRVGFKKPISMIFKNSHHGYCLHRLI
99	GhChrD05G1161.1	0.55	0.70	0.62	142-159	DPPKRRKKKYIHKGPFKR
100	GhChrD05G1286.1	0.28	0.52	0.83	82-112	RKTKERYRGKLSCSSAGFKKKSEANRPRPET
101	GhChrD05G2597.1	0.34	0.57	0.77	100-134	RWRKYGKKKIKNNPNPRHYYRCSREGCKVKKRVER
102	GhChrD05G3176.1	0.29	0.52	0.83		no
103	GhChrD05G3261.1	0.32	0.57	0.77	241-243	KKK
104	GhChrD06G1208.1	0.26	0.52	0.83	83-112/150-170	FRTKKKERYRAKLSCSSAGFKKKSEANNPR/ IKRFYKSHKKMILAARKARPP
105	GhChrD06G1411.1	0.51	0.70	0.62	99-129	WRKYGKKKVKNNPNPRNYYQCSSEGCKVKKR
106	GhChrD06G2121.1	0.71	0.81	0.44		no
107	GhChrD07G1088.1	0.33	0.57	0.77		no
108	GhChrD07G1730.1	0.56	0.70	0.62	572-580	ELRRKPKGR
109	GhChrD07G1770.1	0.61	0.71	0.53	119-130	KKYKRKKQRERA
110	GhChrD07G1931.1	0.62	0.71	0.53	100-118	GFRKLRPRRSENRKPRAIT
111	GhChrD07G1932.1	0.51	0.70	0.62		no
112	GhChrD07G2281.1	0.82	0.84	0.32		no
113	GhChrD07G2331.1	0.56	0.70	0.62		no
114	GhChrD07G2425.1	0.33	0.57	0.77	102-111	GQEKKPRPSA
115	GhChrD07G2588.1	0.60	0.71	0.53	714-738	PRLLQPPARPKKRRARAENAGRAKR

116	GhChrD08G1075.1	0.24	0.52	0.83	622-641	KLLPDRELRHKPKGRPCSTR
117	GhChrD08G1130.1	0.67	0.71	0.53	114-125/203-214/231-237	AKRKKKATAARP/KRRRTASWKRAA/KTPPRKK
118	GhChrD08G1405.1	0.19	0.45	0.88		No
119	GhChrD09G0385.1	0.52	0.70	0.62	319-330	DKRDLNIKRPRK
120	GhChrD09G0509.1	0.26	0.52	0.83		no
121	GhChrD09G0554.1	0.17	0.45	0.88		No
122	GhChrD09G0681.1	0.07	0.50	100	20-29/178-197	RARRWALKEI/HRVSARHLYANWRNKNPRRD
123	GhChrD09G1069.1	0.46	0.63	0.69		no
124	GhChrD09G1114.1	0.76	0.81	0.44		no
125	GhChrD09G1244.1	0.07	0.50	100		no
126	GhChrD09G1249.1	0.44	0.63	0.69		no
127	GhChrD09G2571.1	0.63	0.71	0.53		no
128	GhChrD09G2678.1	0.70	0.81	0.44	711-722	KRPPGRPKKKQP
129	GhChrD10G0830.1	0.31	0.57	0.77		no
130	GhChrD10G1089.1	0.91	0.88	0.21	69-70	RK
131	GhChrD10G1394.1	0.23	0.52	0.83	167-183	RGLRRNPRGRPQSSRIR
132	GhChrD10G1416.1	0.57	0.70	0.62		no
133	GhChrD10G1417.1	0.34	0.57	0.77		no
134	GhChrD10G1418.1	0.42	0.63	0.69	119-128	AKHAHRKDRV
135	GhChrD10G1532.1	0.62	0.71	0.53		no
136	GhChrD10G1575.1	0.36	0.57	0.77	210-225	KLLPDRELRRKPKGRP
137	GhChrD10G2065.1	0.69	0.71	0.53		no
138	GhChrD10G2448.1	0.42	0.63	0.69		no
139	GhChrD11G0757.1	0.09	0.50	100		no
140	GhChrD11G0814.1	0.31	0.57	0.77		no

141	GhChrD11G0875.1	0.34	0.57	0.77		no
142	GhChrD11G1767.1	0.93	0.88	0.21		no
143	GhChrD11G2816.1	0.20	0.52	0.83	308-311	RKKA
144	GhChrD11G3399.1	0.56	0.70	0.62		no
145	GhChrD12G0852.1	0.60	0.71	0.53	235-254	PGRPKQIRRKEINEVRKSGP
146	GhChrD13G1101.1	0.05	0.50	100	135-183	VGIGKKKSSPDGPSCYPSCVAGLYISVIGKRAKLGHWLQPAIGLEKGNI
147	GhChrD13G1566.1	0.00	0.50	100	92-124	QPVTFVADRRIGFKRPISMIFKNSHHGYCLHRL
148	GhChrD13G1980.1	0.30	0.57	0.77	541-574/547-574	KLDITIRPPKIRRPPGRPKKKVLRVENLKRPKRV/ RPPKIRRPPGRPKKKVLRVENLKRPKR
149	GhChrD13G2270.1	0.41	0.63	0.69		no