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G'O'ZA (*G.HIRSUTUM* L.) TURI *GhFHY3/FAR1* GENLAR OILASI

VAKILLARINI KOLLINEARLIK TAHLILI

*Annotatsiya. FAR-RED ELONGATED HYPOCOTYLS 3 (FHY3) va FAR-RED-IMPAIRED RESPONSE (FAR1) (FHY3/FAR1) genlar oilasi vakillari o'simlik turlarining keng spektrida mavjud bo'lib, o'simliklarni o'sish va rivojlanishi hamda tashqi muhitning noqulay sharoitlariga moslashishda muhim ahamiyat kasb etadi. Bundan tashqari ushbu oila vakillari o'simliklarning abiotik va biotik omillarga chidamliligini ta'minlashda ham markaziy o'rinlarni egallaydi. Ushbu maqolada biz g'o'za GhFHY3/FAR1 genlar oilasi tegishli jami 149 ta gen isoformalarini bir necha o'simlik turlari *A.thaliana*, pomidor (*S.lycopersicum*), kartoshka (*S.tuberosum*), terak (*Populus trichocarpa* Torr. & Gray), kakao (*T.cacao*), choy (*C.sinensis*), tamaki (*N.tabacum*) da mavjud FHY3/FAR1 genlar oilasi vakillari o'rtasida kolerantlik bog'lanishlarni aniqladik. Tahlillar natijasida*

N.tabacumdan boshqa barcha turlarda kolerantlik bog'lanishlar aniqlandi. Eng ko'p kollinearlik bog'lanish Populus trichocarpa Torr. & Gray va C.sinensis o'simlik genamlari o'rtasida borligini ko'rsatdi. Ituzumdoshlar oilasini vakillari S.lycopersicum va S.tuberosum da esa kollinearlik o'rtacha darajadaligi ekanligi namoyon bo'ladi. Ushbu tadqiqot natijalari g'o'za FHY3/FAR1 gen oilasining evolyutsiyasi va funksiyasini o'rganishga hamda bu genlar oilasining g'o'za o'sishi va rivojlanishidagi molekulyar mexanizmi boshqarishni tushunish uchun keyingi tadqiqotlarga asos bo'ladi.

Kalit so'zlar: *G.hirsutum, xromosoma, gen, genom, kollinearlik, FHY3/FAR1*

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АНАЛИЗ КОЛЛИНЕАРНОСТИ ПРЕДСТАВИТЕЛЕЙ ГЕННОЙ СЕМЬИ GhFHY3/FAR1 У ХЛОПЧАТНИКА (*G.HIRSUTUM* L.)

Аннотация. *Представители генной семьи FAR-RED ELONGATED HYPOCOTYLS 3 (FHY3) и FAR-RED-IMPAIRED RESPONSE (FAR1)*

(FHY3/FAR1) обнаружены у широкого спектра видов растений и играют важную роль в их росте, развитии и адаптации к неблагоприятным условиям внешней среды. Кроме того, данные гены занимают центральное место в обеспечении устойчивости растений к абиотическим и биотическим стрессорам. В настоящей работе нами идентифицировано в хлопчатнике 149 изоформ генов, принадлежащих к семейству GhFHY3/FAR1, и проведен сравнительный коллинеарный анализ с представителями данной генной семьи у других растений: *A. thaliana*, томата (*S. lycopersicum*), картофеля (*S. tuberosum*), тополя (*Populus trichocarpa* Torr. & Gray), какао (*T. cacao*), чая (*C. sinensis*) и табака (*N. tabacum*). В результате анализа установлено наличие коллинеарных связей у всех исследованных видов, кроме *N. tabacum*. Наибольшее количество коллинеарных связей наблюдалось между геномами *Populus trichocarpa* Torr. & Gray и *C. sinensis*. У представителей семейства пасленовых (*S. lycopersicum* и *S. tuberosum*) коллинеарность выражена на среднем уровне. Полученные результаты вносят вклад в понимание эволюции и функциональной роли семейства FHY3/FAR1 у хлопчатника, а также служат основой для дальнейших исследований молекулярных механизмов регуляции роста и развития хлопчатника.

Ключевые слова: *G. hirsutum*, хромосома, ген, геном, коллинеарность, FHY3/FAR1.

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COLLINEARITY ANALYSIS OF GhFHY3/FAR1 GENE FAMILY MEMBERS IN COTTON (*G.HIRSUTUM* L.)

Abstract. *Members of the FAR-RED ELONGATED HYPOCOTYLS 3 (FHY3) and FAR-RED-IMPAIRED RESPONSE (FAR1) (FHY3/FAR1) gene family are present in a wide range of plant species and play crucial roles in plant growth, development, and adaptation to unfavorable environmental conditions. In addition, they occupy a central position in providing resistance to abiotic and biotic stresses. In this study, we identified a total of 149 GhFHY3/FAR1 gene isoforms in cotton and performed a comparative collinearity analysis with representatives of this gene family in other plant species, including A. thaliana, tomato (S. lycopersicum), potato (S. tuberosum), poplar (Populus trichocarpa Torr. & Gray), cacao (T. cacao), tea (C. sinensis), and tobacco (N. tabacum). The analysis revealed collinear relationships in all species except N. tabacum. The highest number of collinear relationships was observed between the genomes of Populus trichocarpa Torr. & Gray and C. sinensis. In Solanaceae representatives (S. lycopersicum and S. tuberosum), collinearity was found to be at a moderate level. These findings contribute to understanding the evolution and functional roles of the FHY3/FAR1 gene family in cotton and provide a foundation for further research on the molecular mechanisms regulating cotton growth and development.*

Keywords: *G.hirsutum*, *chromosome*, *gene*, *genome*, *collinearity*, *FHY3/FAR1*.

Kirish

G'oz (Gossypium ssp.) turkum vakillari yengil sanoatni tabiiy tola bilan ta'minlovchi texnik ekinlar sirasiga kirsada, undan olinadigan mahsulotlardan qishloq xo'jalik, qurilish, aviatsiya sanoatlarining bir qancha tarmoqlarida foydalaniladi. Shu sababdan ham dunyoda 80 ga yaqin paxta yetishtiriladigan mamlakatlarda ushbu ekin strategik ekin hisoblanadi [1]. G'oz turlari ustida olib borilgan ko'plab an'anaviy va molekulyar tadqiqotlar natijasida undagi sifat va miqdorga hamda chidamlilik boshqarilishiga javob beruvchi ko'plab genlar aniqlangan. Lekin g'oz genomini chuqur tahlil etilishi unda yangi genlar funksiyasini kashf qilishga imkon berdi [2]. Shu kabi genlardan biri bu FHY3/FAR1 genlar oilasi hisoblanadi. Ushbu genlar oilasi vakillari o'simliklar turning keng spektrida mavjud bo'lib, o'simliklarni o'sish va rivojlanishi hamda tashqi muhitning noqulay sharoitlariga moslashishda muhim ahamiyat kasb etadi. Bundan tashqari ushbu oila vakillari o'simliklarning abiotik va biotik omillarga chidamliligini ta'minlashda ham markaziy o'rinlarni egallaydi [3].

FHY3/FAR1 genlar oilasi vakillari oilasi funksiyalari manzarali, qishloq xo'jaligi, sanoat o'simlik turlarida aniqlangan [4,5,6,7,8,9,10,11,12,13,14,15,16,17]. Lekin ularning o'simliklarning rivojlanishi va o'sishidagi hamda yorug'lik nuriga bo'lgan reaksiyasi *A.thalinada* atroflicha ochib berilgan [18]. Boshqa ekin turlarida ushbu genlar oilasi vakillarining asosan stress omillarga bo'lgan javob reaksiyalari tadqiq qilingan. Ushbu amalga oshirilgan tadqiqotlar natijasida ushbu oila vakillari o'simliklarning nafaqat o'sish va rivojlanishda balki ularning tashqi sharoitning turli muhitlariga moslashishda hamda stress omillarda asosiy signal vazifasini bajaruvchi genlar tizimi ekanligini ko'rsatdi [4,5,6,7,8,9,10,11,12,13,14,15,16,17]. Masalan, yeryong'oqda (*Arachis hypogaea*) AhJ11-FAR1-5 geni ekspressiyasini kuchayishi natijasida POD, SOD va CAT fermaentlar miqdorini oshishi kuzatilgan [19]. Bu esa o'simlikni

qurg'oqchilik stressiga chidamliligini oshishiga olib kelgan. Lekin ushbu oilaning boshqa bir vakillari FHY3 va FAR1 genlarining ekspressiyasini to'xtatilishi, o'simliklarni tuz, osmotik, qurg'oqchilikka chidamlilik darajasini pasaytirgan [3]. Bunga sabab, FHY3 va FAR1 genlari auksin va strigolakton signalizatsiyasini boshqarilishida ishtrok etadi va o'simliklarda shoxlanish va stressga chidamlilikni oshiradi. Sholida (*O.sativa*) FHY3/FAR1 genlar oilasi issiqlik ta'sirida TSD1 genini ekspressiyasini kuchaytiradi va buning natijasida o'simlikda boshqoq morfogenezi jarayonida uning issiq stressiga bo'lgan chidamliligi kuchaydi [20]. Natijada boshqoqlarda doning puch bo'lib qolish yoki changlanishning abnormal bo'lish kamayadi. Tadqiq etilayotgan gen oilasi vakillari qator o'simlik turlarida aniqlangan va funksiyalari ochib berilgan. Ushbu genlar oilasi g'o'za ekinida ham tadqiq qilinganiga qaramay uning o'simlikdagi funksiyalari to'liq ochib berilmagan [14]. FHY3/FAR1 genlar oilasi vakillarini funksiyasini g'o'za (*G.hirsutum* L.) turida o'rganish maqsadida GhFHY3/FAR1 genlarini boshqa ekin turlari FHY3/FAR1 genlari bilan kollinearlik bog'liqligini o'rganishni maqsad qildik. Buning natijasida GhGHY3/FAR1 genlar oilasi vakillari g'o'za ekinida qanday funksiyani boshqarishda ishtrokini oldindan taxmin qilishimiz mumkin bo'ladi.

Gossypium ssp turida FHY3/FAR1 genlarining funksiyasini o'rganish ularning erta gullash, abiotik va biotik stress omillarga chidamli genotiplarni olishga imkon beradi.

Material va metodlar

G'o'za (*G.hirsutum* L.) GhFHY3/FAR1 genlar oilasi vakillarini boshqa ekin turlari bilan kollinearlikni aniqlash uchun cottongen.org ma'lumotlar bazasidan Oxford Nanopore PromethION; PacBio Sequel (HiFi v. 0.7) usuli yordamida sekvenslangan *Gossypium hirsutum* (AD1) 'TM-1'T2T genome JZU_v1.0 tizmasi va Arabidopsis Information Resource (TAIR) (<https://www.arabidopsis.org/>) bazasidan *A.thaliana* hamda EnsemblPlants (<http://plants.ensembl.org/info/data/ftp/index.html>) bazasidan esa *S.lycopersicum*, *S.tuberosum*, *Populus trichocarpa* Torr. & Gray, *T.cacao*, *C.sinensis*, *N.tabacum* aminokislotalar ketma-ketliklari yuklab

olindi va bioinformatik solishtirish tahlillarida foydalanildi. O'simlik genomlari va genlar o'rtasidagi kollinearlikni bioinformatik tahlil qilishda TBtools-II (v2.119) dasturidan foydalanildi.

Natija va muhokama

Kollinearlik tahlili genomlarning differentsiatsiyasi va evolyutsiyasi jarayonini aniqlashda muhim vosita hisoblanib, o'simlik turlari genlari o'rtasida aniqlangan kollinearlik bog'lanishlar natijasida ularni bajaradigan funksiyalarini oldindan taxmin qilish mumkinligini ko'rsatadi [21]. G'o'za (*G.hirsutum* L.) turi GhFHY3/FAR1 genlar oilasi vakillarini kovariatsiyasini o'rganish uchun biz *G.hirsutum*, *A. thaliana*, *S.lycopersicum*, *S.tuberosum*, *Populus trichocarpa* Torr. & Gray, *T.cacao*, *C.sinensis*, *N.tabacum* FHY3/FAR1 genlar oilasini vakillari o'rtasida kollinear bog'lanishni aniqladik (1-rasm). Olingan ma'lumotlarni tahlil natijalariga ko'ra *G.hirsutum* va *A.thaliana* o'rtasida 21 ta kombinatsiya aniqlanib GhFHY/FAR1 oilasi vakillarining 17 ta transkripti *A.thaliana* AtFHY3/FAR1 genlar oilasining 21 ta transkriptlari bilan kollinearlik bog'lanishida ekanligi ma'lum bo'ldi (1-jadval). 17 ta transkript bo'lishiga sabab GhFHY3/FAR1 genlar oilasining 1 ta transkripti AtFHY/FAR1 genlar oilasining 2 ta transkripti bilan kollinearlik bog'lanishlar hosil qildi. Qolgan ekin turlar o'rtasida olib borilgan kollinearlik tahlil natijalari 1-jadvalda keltirilgan.

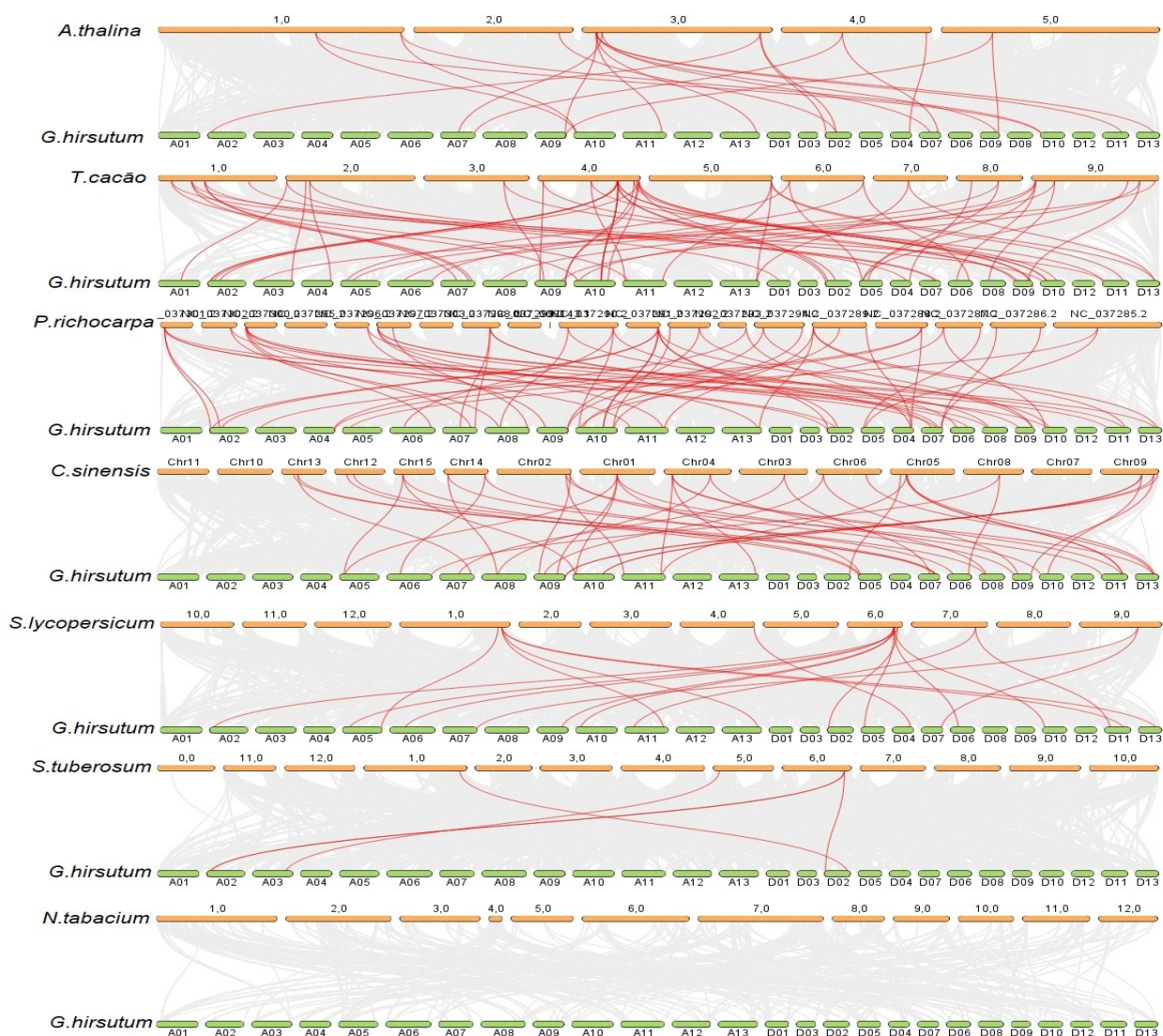
Jadval-1

FHY3/FAR1 genlar oilasi vakillarining *G.hirsutum* va 6 ta ekin turlari genomi o'rtasidagi kollinearlik bog'lanishlar soni

Kollinearlik kombinatsiyalar	Kollinearlik transkriptlar soni asosiy genomda	Kollinearlik transkriptlar soni solishtirilayotgan genomda
<i>G.hirsutum</i> vs <i>A.thaliana</i>	<i>G.hirsutum</i>	<i>A.thaliana</i>
21	17	21
<i>G.hirsutum</i> vs <i>T.cacão</i>	<i>G.hirsutum</i>	<i>T.cacão</i>
61	56	61
<i>G.hirsutum</i> vs <i>P.richocarpa</i>	<i>G.hirsutum</i>	<i>P.richocarpa</i>
60	40	60
<i>G.hirsutum</i> vs <i>C.sinensis</i>	<i>G.hirsutum</i>	<i>C.sinensis</i>

45	36	45
<i>G.hirsutum</i> vs <i>S.lycopersicum</i>	<i>G.hirsutum</i>	<i>S.lycopersicum</i>
19	19	19
<i>G.hirsutum</i> vs <i>S.tuberosum</i>	<i>G.hirsutum</i>	<i>S.tuberosum</i>
4	4	4

Ushbu tahlilda *G.hirsutum* x *T.cacao* va *G.hirsutum* x *C.richocarpa* genomlari o'rtasida FHY3/FAR1 genlar oilasi vakillarini solishtirilishi tahlilida kollinearlik bog'lanishlar sonining ko'pligi bilan boshqa kombinatsiyalardan farq qildi. Kam kollinearlik bog'lanishlar *G.hirsutum* x *S.tuberosum* kombinatsiyasi o'rtasida borligi ma'lum bo'ldi. Ushbu solishtirishda *G.hirsutum* x *N.tabacum* kombinatsiyasi ham amalga oshirildi. Lekin ushbu kombinatsiyada ikki genom o'rtasida FHY3/FAR1 genlar oilasi vakillari bo'yicha kollinearlik bog'lanish aniqlanmadi. Kollinearlik bog'lanish tahlillari g'o'za genomi *A.thalina* genomidan ko'ra *T.cacão*, *P.richocarpa*, *C.sinensis* ekin turlari genomlariga yaqinroq ekanini ko'rsatdi. Bu esa ushbu ekin turlari evolutsion rivojlanishda bir-birga yaqin bo'lgan bo'lishi mumkin degan taxminni keltirib chiqaradi.



**1-rasm. FHY3/FAR1 genlr oilasi vakillarining *G.hirsutum* va 6 ta ekin turlari
genomi oʻrtasidagi kollinearlik tahlili**

Yuksak oʻsimliklarda oʻsishi va rivojlanishini boshqarilishi fotoretseptor genlar tizimi tomonidan amlga oshiriladi. Yorugʻlik nuridagi qizil va uzoq qizil spektri oʻsimliklarning oʻsishi va rivojlanishiga taʼsir qiluvchi ikkita asosiy ekologik omil hisoblanadi [22]. Ushbu nurlarga javob beruvchi FHY3/FAR1 genlar oilasi phyA vositachiligida uzoq qizil yorugʻlik signali yoʻlining muhim tarkibiy qismi sifatida dastlab *A.thalinada* aniqlangan va tavsiflangan. *A.thalianada* gen tuzilishi, molekulyar morfologiyasi va biologik funksiyalarining yuqori gomologiyasiga ega jami 14 ta FHY3/FAR1 yoki FRS genlari aniqlangan [23]. Ushbu genlar oilasi vakillarini tadqiq etish oxirgi 5 yillikda keskin oshdi va qator oʻsimliklarda aniqlandi. Ushbu tadqiqotlar natijasida aniqlangan FHY3/FAR1 genlar oilasining vakillari oʻsimlik turlariga qarab bir-biridan farqli vazifalarni

bajarishda ishtirok etishi aniqlandi [4,5,6,7,8,9,10,11,12,13,14,15,16,17]. Bunga sabab ular o'rtasidagi evolutsion kollinearlik bog'lanish deb taxmin qilish mumkin. Shu sababdan ham biz g'o'za (*G.hirsutum* L.) genomida mavjud GhFHY3/FAR1 genlar oilasi vakillarini turli ekin genomlarida mavjud FHY3/FAR1 genlar oilasi bilan solishtirish tahlillarini amalga oshirdik. Buning natijasida GhFHY3/FAR1 genlar oilasi vakillari model o'simlik *A.thaliana*ga qarganda daraxtsimon o'simliklar FHY3/FAR1 genlar oilasiga yaqin ekanligini ko'rsatdi. Bu esa g'o'za GhFHY3/FAR1 genlar oilasini vakillarini shunga o'xshash biologik vazifalarni boshqarilishida ishtirok etishi mumkinligini ko'rsatadi.

Xulosa

Ushbu tadqiqotda g'o'za (*G.hirsutum* L.) genomida mavjud GhFAR1/FHY3 gen oilasi vakillarini *A. thaliana*, *S.lycopersicum*, *S.tuberosum*, *Populus trichocarpa* Torr. & Gray, *T.cacao*, *C.sinensis*, *N.tabacum* FHY3/FAR1 genlar oilasi vakillari o'rtasida kollinearlik bog'lanishlar bioformatik jihatdan tahlil qilindi. Tahlillar natijasida *G.hirsutum* x *T.cacao* va *G.hirsutum* x *C.richocarpa* genomlari o'rtasida FHY3/FAR1 genlar oilasi vakillarida kollinearlik bog'lanishlar sonining ko'pligi bilan boshqa kombinatsiyalardan farq qildi. Bu natija asosida g'o'za (*G.hirsutum* L.) GhFHY3/FAR1 genlar oilasini vakillarini o'simliklarning o'sish va rivojlanishida yoki abiotik va biotik omillarga chidamlilikni boshqarilishida ishtirok etishini oldindan taxmin qilish mumkinligini ko'rsatadi. Qolaversa, g'o'za ekinini o'ta murakkab tetraploid genomini dekodlash orqali g'o'zaning o'sishi, rivojlanishi va stressga chidamliligidagi GhFHY3/FAR1 mexanizmlari haqida chuqurroq tushunchaga ega bo'lamiz, bu esa kelgusida iqlim o'zgarishiga chidamli va yuqori hosildorlikka ega yangi g'o'za navlarini rivojlantirish uchun nazariy asos bo'ladi.

FOYDALANILGAN ADABIYOTLAR

1. Vitale, G.S.; Scavo, A.; Zingale, S.; Tuttolomondo, T.; Santonoceto, C.; Pandino, G.; Lombardo, S.; Anastasi, U.; Guarnaccia, P. Agronomic Strategies for

Sustainable Cotton Production: A Systematic Literature Review. *Agriculture* 2024, 14, 1597. <https://doi.org/10.3390/agriculture14091597>

2. Abbas, M., Abid, M. A., Meng, Z., Abbas, M., Wang, P., Lu, C., et al. (2022). Integrating advancements in root phenotyping and genome-wide association studies to open the root genetics gateway. *Physiologia Plantarum* 174, e13787. doi: 10.1111/ppl.13787

3. Tang et al. (2013). Tang W, Ji Q, Huang Y, Jiang Z, Bao M, Wang H, Lin R. FAR-RED ELONGATED HYPOCOTYL3 and FAR-RED IMPAIRED RESPONSE1 transcription factors integrate light and abscisic acid signaling in Arabidopsis. *Plant Physiology*. 2013;163(2):857–866. doi: 10.1104/pp.113.224386.

4. Wang, F.; Wang, X.; Zhang, Y.; Yan, J.; Ahammed, G.J.; Bu, X.; Sun, X.; Liu, Y.; Xu, T.; Qi, H.; et al. SlFHY3 and SlHY5 act compliantly to enhance cold tolerance through the integration of myo-inositol and light signaling in tomato. *New Phytol.* 2022, 233, 2127–2143.

5. 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.

6. 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>

7. 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.

8. 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.

9. 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.
10. 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.
11. Zeps, M.; Kondratovičs, T.; Grigžde, E.; Jansons, Ā.; Zeltniš, P.; Samsone, I.; Matisons, R. Plantlet Anatomy of Silver Birch (*Betula pendula* Roth.) and Hybrid Aspen (*Populus tremuloides* Michx. × *Populus tremula* L.) Shows Intraspecific Reactions to Illumination In Vitro. *Plants* 2022, 11, 1097. <https://doi.org/10.3390/plants11081097>.
12. 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.
13. 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>
14. 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.
15. Yao, H. Zheng, Y. Sun, Y. Liu, Y. Genome-Wide Identification and Expression Analysis of the FAR1-RELATED SEQUENCE (FRS) Gene Family in Grape (*Vitis vinifera* L.). *Int. J. Mol. Sci.* 2025, 26, 4675. <https://doi.org/10.3390/ijms26104675>
16. Huaijun Tang, De Jing 2, Cheng Liu, Xiaoqing Xie, Lei Zhang, Xunji Chen, Changyu Li. Genome-Wide Identification and Expression Analyses of the FAR1/FHY3 Gene Family Provide Insight into Inflorescence Development in Maize. *Curr Issues Mol Biol.* 2024 Jan 2;46(1):430–449. doi: 10.3390/cimb460107

17. Lescot, M.; Dehais, P.; Thijs, G.; Januaryal, K.; Moreau, Y.; Van de Peer, Y.; Rouze, P.; Rombauts, S. PlantCARE, a database of plant cis-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences. *Nucleic Acids Res.* 2002, 30, 325–327.
18. Ma, L.; Li, G. FAR1-RELATED SEQUENCE (FRS) and FRS-RELATED FACTOR (FRF) family proteins in Arabidopsis growth and development. *Front. Plant Sci.* 2018, 9, 692.
19. Yan et al. Yan CL, Sun C, Zhang Q, Wang H, Yuan J, Shan C, Zhao S, X Cloning and function analysis of FAR1-5 transcription factor in peanut. *Peanut Science.* 2020; 49:16–20. doi: 10.14001/j.issn.1002-4093.2020.02.003.
20. Cai et al. (2023).Cai Z, Wang G, Li J, Kong L, Tang W, Chen X, Qu X, Lin C, Peng Y, Liu Y, Deng Z, Ye Y, Wu W, Duan Y. Thermo-sensitive spikelet defects 1 acclimatizes rice spikelet initiation and development to high temperature. *Plant Physiology.* 2023;191(3):1684–1701. doi: 10.1093/plphys/kiac576.
21. Huang, L., Zhang, L., Zhang, P. et al. Molecular characteristics and expression pattern of the FAR1 gene during spike sprouting in quinoa. *Sci Rep* 14, 28485 (2024). <https://doi.org/10.1038/s41598-024-79474-0>.
22. Huang, X., Ouyang, X., Yang, P., Lau, O. S., Li, G., Li, J., et al. Arabidopsis FHY3 and HY5 positively mediate induction of COP1 transcription in response to photomorphogenic UV-B light. *Plant Cell* 24, 2012. 4590–4606. doi: 10.1105/tpc.112.103994.
23. 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