

www.thedssr.com ISSN Online: 3007-3154 ISSN Print: 3007-3146 Vol. 3 No. 2 (February) (2025)

DIALOGUE SOCIAL SCIENCE REVIEW

Genome-wide identification and characterization of CONSTANS-like gene family in peas (*Pisum sativum*)

Amna BiBi PMAS Arid Agriculture University Rawalpindi. Email: amna181bibi@gmail.com

Sharjeel Ahmad Bahauddin Zakariya University Multan. Email: Sharjeelkhankazmi@gmail.com

Ezzah Rao Bahauddin Zakariya University Multan. Email: Raoezzah231@gmail.com

Shakir shehzad Zhengzhou University, School of Agriculture Science, Henan, China Email: ssqureshi.14@gmail.com

Muhammad Irfan (Corresponding Author) Quaid I Azam University Islamabad. Email: irfanchandia50@gmail.com

Abstract

CONSTANS-like (CO-like, COL) genes play an important role in the circadian clock rhythms, which ensures regular development through complicated biological clocks. COL genes are also involved in plant responses to stress. COL genes are zinc-finger transcription factor. COL genes are also involved in regulating growth and development, and stress responses. COL genes, primarily active in the leaves, play a key role in the photoperiod pathway that regulates flowering. These genes exhibit varying expression levels across different plant varieties, and their amino acid sequences differ, potentially explaining their diverse functions. In this study, 40 PsCOLs genes with complete conserved domain was identified from the genome of Pisum sativum and analysed by bioinformatics. 40 PsCOLs were distributed on 7 chromosomes, encoding 40 PsCOL proteins with different physical and chemical properties. We analyzed their gene structure, phylogenetic relationships, synteny, and expression levels in different tissues. The bioinformatical analysis identified 40 COL transcription factors in the pea genome. The phylogenetic tree constructed with Arabidopsis thaliana and other pulses indicates that PsCOLs of different clusters have different biological functions. The conserved motif prediction showed that the number and distribution of motifs on each PsCOLs is varied. The results provide a foundation for the study of COL transcription factors of Pisum sativum and provide more reference information of the function of COL genes in flowering.

Key words: Pisum sativum, COL (CONSTANS LIKE), circadian clock, flower induction



www.thedssr.com ISSN Online: 3007-3154 ISSN Print: 3007-3146

Vol. 3 No. 2 (February) (2025)

Introduction

The shift from vegetative growth to bolting and flowering is vital for a plant's reproductive success. The transition to flowering in plants is controlled by complex genetic networks influenced by various plant hormones and environmental factors like light, temperature, and day length. In Arabidopsis thaliana, about 180 genes are involved in regulating flowering time through six main pathways: vernalization, autonomous, photoperiod, gibberellin (GA), ambient temperature, and age pathways. These genes work together to ensure flowering happens at the right time. For example, the gene FLOWERING LOCUS C (FLC) acts as a key repressor, integrating signals from both the autonomous and vernalization pathways. Other important genes, such as FLOWERING LOCUS T (FT), SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1 (SOC1), and LEAFY (LFY), act as convergence points, coordinating signals from multiple pathways to initiate flowering.

CONSTANS-like (COL) genes are essential in controlling the flowering of plants through the photoperiod pathway. They work by integrating signals from the circadian clock, light, and specific flowering time genes. As transcription activators specific to the phloem, COL genes promote flowering by boosting the transcription of the FT and TSF genes. However, COL's activity is finely tuned; it is degraded in the dark by the ubiquitin ligase COP1 and in the morning by a pathway activated by the photoreceptor PHYB. This regulation ensures that CONSTANS-like (COL) genes activate the transcription of FT and TSF genes only during long days. This precise timing allows plants to flower at the most appropriate time, aligning their reproductive cycle with favorable environmental conditions.

COL genes are part of an Arabidopsis gene family containing 16 other genes encoding transcription factors. These genes generally have two key conserved domains: a C-terminal CCT domain specific to plants, and an N-terminal zinc finger B-box domain, which is also found in animals. CONSTANS-like (COL) genes are part of the larger B-BOX (BBX) transcription factor family. This family is categorized into five groups based on the presence of one or two B-BOX motifs and the presence or absence of the CCT domain. Previous studies have shown that most COL genes with a CCT domain play a role in controlling flowering time in some plant species. By understanding these mechanisms, we can gain valuable insights into how plants adapt to their environments and improve crop breeding strategies.

The availability of the Arabidopsis genome sequence and its annotation has opened new possibilities for comparing COL transcriptional regulators. Additionally, various tools and databases, like the PlantTFDB database, have been developed to identify, cluster, align, and analyze plant transcription factors.

In Arabidopsis, CO-like genes are grouped into three main categories:

- 1. **Group I**: Includes AtCO and AtCOL1 to AtCOL5, which have two B-boxes.
- 2. Group II: Contains AtCOL6 to AtCOL8 and AtCOL16, each with one B-box.

3. **Group III**: Consists of COL9 to COL15, which have one B-box and an additional diverged zinc finger domain.



www.thedssr.com

ISSN Online: 3007-3154

ISSN Print: 3007-3146

Vol. 3 No. 2 (February) (2025)

Peas (Pisum sativum L.) are an annual diploid (2x=2n=14) species belonging to the Fabaceae family, and they are an economically significant vegetable crop grown worldwide. The main edible parts of peas are their seeds, which are rich in proteins, vitamins, and various medicinal compounds. For successful cultivation, it's crucial to manage the timing of flowering and pod development, as this affects the quality and yield of the pea crop, preventing premature flowering and ensuring optimal production of the desired edible seeds.

The genome sequence of peas (Pisum sativum L.) has been a significant focus of research due to its importance as a vegetable crop. The Pea Genome International Consortium launched a program to develop a high-quality reference draft sequence for peas. The reference genome sequence of the pea cultivar 'Caméor' was produced, with a genome assembly length of approximately 3.92 Gb, composed of 24,623 scaffolds. This comprehensive genome sequence provides valuable insights into the genetic basis of various traits and facilitates the improvement of pea crops through genome-informed breeding strategies.

In this study we analyzed their gene structure, phylogenetic relationships, synteny, and expression levels in different tissues. The results provide insights into the genetic networks regulating flowering in peas.

Materials and Methods

Discovering and Cataloging COL Genes in Peas

The genome, genes and corresponding protein sequences of the peas were downloaded from the Pulse Crop Database (<u>https://www.pulsedb.org/</u>).

Analyzing the Evolutionary Relationships of COL Genes

Protein sequences from various species were collected for a phylogenetic study in the Planta journal. The sequences were aligned using the Clustal X2 program with the Gonnet protein weight matrix. A maximum likelihood phylogenetic tree was then built using the MEGA program (v6.06) with the Jones-Taylor-Thornton (JTT) model. The analysis used 1000 bootstrap replicates and the full CDS sequence for a partial 70% length. Uniform rates and homogeneous lineages were used, with gaps/missing data treated using partial deletion with a site coverage cutoff of 70%. Branch frequencies higher than 50% were shown in the results. The figure was beautified with information from the group using iTOL software (https://itol.embl.de/).

Breakdown of Gene Structure and Key Motifs

The gene structure was analyzed using the Gene Structure Display Server tool (http://gsds.cbi. pku.edu.cn/, v2.0). MEME software (http://meme.nbcr.net/meme/, v4.12.0) was used to search for motifs among the proteins. The motif search window ranged from 10 to 100 base pairs (bp). Only motifs that appeared in at least 3 different protein sequences were kept. These motifs were illustrated in two separate figures, matching the phylogenetic trees. The top 10 motifs with the lowest E-values were highlighted and shown in a specific pattern.



www.thedssr.com

ISSN Online: 3007-3154

ISSN Print: 3007-3146

Vol. 3 No. 2 (February) (2025)

Gene expression analysis

Gene expression analysis was carried out using TBtool in the form of heatmap.

Results and Discussion

Genome-wide identification of COL genes in peas

The bioinformatics analysis discovered 40 CONSTANS-like (COL) transcription factors in the pea genome. All the pea COL genes were found to be well conserved. They were designated as `PsCOL' followed by a serial number and sorted based on the E-value of their CCT domain. (S1 Table).

			Туре	Organis	Sourc	
#	Name	Unique name		m	е	Location
					Pisum	
					sativu	
					m	
					Cameo	
				р.	r	chr1LG6:
_		0 1 = = =		Pisum	0	6179629
1	Psat1g004200.1	via	А	sativum	e v1a	6182102
					Pisum	
					sativu	
					m Cameo	
					cameo r	chr2LG1:
		Psat2g054040.1_Ps_Cameor_	mRN	Pisum	r genom	96225535
2	Psat2g054040.1		A	sativum	e v1a	9622 <u>33</u> 33 96227308
_	2 000-800404012				Pisum	<u> </u>
					sativu	
					m	
					Cameo	chr2LG1:
					r	422791882
		0	mRN	Pisum	genom	
3	Psat2g184400.1	v1a	А	sativum	e v1a	422793178
					Pisum	
					sativu	
					m	1
					Cameo	chr3LG5:
				D:	r	192414403
		Psat3g094880.1_Ps_Cameor_		Pisum sativum	genom	
4		v1a	A	sativuili	e via	192418130
		Destor 146040 1 De Comean y	DN	Digum		chr3LG5:
_		Psat3g146040.1_Ps_Cameor_v	A	sativum	sativu	283230002
5	Psat3g146040.1	la	A	sativum	m	••



www.thedssr.com

ISSN Online: 3007-3154

ISSN Print: 3007-3146

Vol. 3 No. 2 (February) (2025)

			I		Come o o	00000000
					Cameo	283232920
					r	
					genom	
					e v1a	
					Pisum	
					sativu	
					m	
					Cameo	
				_	r	chr4LG4:
	Psat4g049800.1	Psat4g049800.1_Ps_Cameor_				83108351
6		v1a	А	sativum	e v1a	83114427
					Pisum	
					sativu	
					m	
					Cameo	
					r	chr5LG3:
		Psat5g013840.1_Ps_Cameor_v	mRN	Pisum	genom	23305529
7		1a	A	sativum	e v1a	23306747
Ĺ					Pisum	
					sativu	
					m	
					Cameo	
						chr5LG3:
		Psat5g047080.1_Ps_Cameor_	mRN	Pisum		85890798
8	Psat5g047080.1		A	sativum	e via	85900143
_					Pisum	-0)10
					sativu	
					m	
					Cameo	
						chr5LG3:
		Psat5g071920.1_Ps_Cameor_v	mRN	Pisum		131131454
9	Psat5g071920.1			sativum		131131454 131135493
9	1 50(350/1920.1	1α	11	Sativuili	Pisum	131130493
					sativu	
					m Comoo	ahn=I Car
					cameo	chr5LG3:
10		Deateropy 440 1 De Cameer w	mDN	Pisum	aonom	139279057
10		Psat5g077440.1_Ps_Cameor_v			genom	
\square	Psat5g077440.1	1a	А	sativum	e v1a	139282202
			DV	. .		chr5LG3:
		Psat5g105240.1_Ps_Cameor_v		Pisum	sativu	187478164
11	Psat5g105240.1	1a	A	sativum	m	••



www.thedssr.com

ISSN Online: 3007-3154

ISSN Print: 3007-3146

					Comos	10-401400
					cameo n	187481433
					Г — — — — — — —	
					genom	
					e via	
					Pisum	
					sativu	
					m	
						chr5LG3:
1.0			DN	D:		404947942
12		Psat5g199360.1_Ps_Cameor_v		Pisum	genom	
	Psat5g199360.1	18	A	sativum		404956872
					Pisum	
					sativu	
					m	1 -1 C
						chr5LG3:
				. .		407506973
13		so s = = =		Pisum	genom	
	Psat5g200320.1	via	A	sativum	e v1a	407511905
					Pisum	
					sativu	
					m ~	1 - ~
						chr5LG3:
			DM	D '		522397014
14		Psat5g265480.1_Ps_Cameor_			genom	
	Psat5g265480.1	via	A	sativum	e v1a	522401790
					Pisum	
					sativu	
					m	1
					Cameo	chr5LG3:
			DV	. .	r	526039434
15		30 / = = =		Pisum	genom	
	Psat5g267200.1	via	A	sativum		526041217
					Pisum	
					sativu	
					m	
					Cameo	chr5LG3:
				D .	r	547667071
16		30 – – –		Pisum	genom	
	Psat5g282000.1	v1a	A	sativum	e v1a	547668574
						chr6LG2:
	-	0 111 = = =		Pisum	sativu	2980326
17		v1a	A	sativum	m	2984035



DIALOGUE SOCIAL SCIENCE REVIEW

www.thedssr.com

ISSN Online: 3007-3154

ISSN Print: 3007-3146

					Comos	
					Cameo	
					r	
					genom	
					e v1a	
					Pisum	
					sativu	
					m	
					Cameo	
. 0			DN	р.	r	chr6LG2:
18		Psat6g107360.1_Ps_Cameor_v		Pisum		179347411
	Psat6g107360.1	18	A	sativum		179352245
					Pisum	
					sativu	
					m	
					Cameo	chr6LG2:
					r	233659887
19		Psat6g124840.1_Ps_Cameor_v		Pisum	genom	
	Psat6g124840.1	1a	A	sativum		233675414
					Pisum	
					sativu	
					m	
					Cameo	chr6LG2:
					r	252713969
20		Psat6g131680.1_Ps_Cameor_v		Pisum	genom	
	Psat6g131680.1	1a	A	sativum		252717993
					Pisum	
					sativu	
					m	
						chr6LG2:
				_		441355586
21		Psat6g223840.1_Ps_Cameor_			genom	
	Psat6g223840.1	v1a	А	sativum		441358728
					Pisum	
					sativu	
					m	
						chr6LG2:
						459822830
22		0 0 = = =	mRN	Pisum	genom	
	Psat6g228360.1	v1a	A	sativum		459824927
						chr7LG7:
23		Psat7g011960.1_Ps_Cameor_v	mRN	Pisum	sativu	18571500
	Psat7g011960.1	1a	А	sativum	m	18574594



DIALOGUE SOCIAL SCIENCE REVIEW

www.thedssr.com

ISSN Online: 3007-3154

ISSN Print: 3007-3146

			1		0	
					Cameo	
					r	
					genom	
					e v1a	
					Pisum	
					sativu	
					m	
					Cameo	
					r	chr7LG7:
24		Psat7g031600.1_Ps_Cameor_v	mRN	Pisum	genom	51210245
	Psat7g031600.1	1a	A	sativum	e v1a	51212076
					Pisum	
					sativu	
					m	
					Cameo	
					r	chr7LG7:
25		Psat7g037680.1_Ps_Cameor_	mRN	Pisum	genom	63533061
	Psat7g037680.1		A	sativum		63536130
	1000/803/00011			Sutivuili	Pisum	0000100
					sativu	
					m	
						chr7LG7:
						166775673
26		Psat7g101680.1_Ps_Cameor_v	mDN	Pisum		
	$\mathbf{D}_{\text{cot}} = \pi_1 \circ 160 \circ 1$			sativum	genom	
	Psat7g101680.1	1a	A	sativuili	e v1a	166780076
					Pisum	
					sativu	
					m	
						chr7LG7:
			D 1 -	. .		445763618
27		Psat7g221720.1_Ps_Cameor_v		Pisum	genom	
	Psat7g221720.1	1a	A	sativum		445769891
					Pisum	
					sativu	
					m	
					Cameo	chr7LG7:
					r	488732676
28		Psat7g260760.1_Ps_Cameor_	mRN	Pisum	genom	
	Psat7g260760.1	v1a	A	sativum	e v1a	488734148
					Pisum	chr7LG7:
29		Psat7g260880.1_Ps_Cameor_	mRN	Pisum		488750731
	Psat7g260880.1	,0 = = =	A	sativum	m	
			1		1	



DIALOGUE SOCIAL SCIENCE REVIEW

www.thedssr.com

ISSN Online: 3007-3154

ISSN Print: 3007-3146

					Comoo	488754266
					cameo r	400/54200
					aonom	
					genom	
					e v1a	
					Pisum	
					sativu	
					m	
					Cameo	CC 1 1
				D '	r	scaffold037
		Psatos3732g0240.1_Ps_Came			\sim	32: 88975
	0.1	or_v1a	A	sativum	e v1a	90064
					Pisum	
					sativu	
					m	
					Cameo	
					r	scaffold018
	-	Psatos1849g0080.1_Ps_Came			genom	
	0.1	or_v1a	A	sativum	e v1a	105287
					Pisum	
					sativu	
					m	
						chr3LG5:
						414219815
32		Psat3g193520.1_Ps_Cameor_v			genom	
	Psat3g193520.1	1a	А	sativum	e v1a	414222685
					Pisum	
					sativu	
					m	
					Cameo	
					r	chr5LG3:
33		Psat5g032240.1_Ps_Cameor_			\sim	61613251
	Psat5g032240.1	v1a	А	sativum		61615757
					Pisum	
					sativu	
					m	
					Cameo	
					r	chr6LG2:
34		Psat6g025680.1_Ps_Cameor_	mRN	Pisum		20093622
	Psat6g025680.1	v1a	А	sativum	e v1a	20095774
					Pisum	chr3LG5:
35		Psat3g024360.1_Ps_Cameor_	mRN		sativu	52122308
	Psat3g024360.1	v1a	А	sativum	m	52125247



www.thedssr.com

ISSN Online: 3007-3154

ISSN Print: 3007-3146

Vol. 3 No. 2 (February) (2025)

				1	Comoo	1
					Cameo	
					r	
					genom	
					e v1a	
					Pisum	
					sativu	
					m	
					Cameo	chr7LG7:
						416598234
36		Psat7g210000.1_Ps_Cameor_	mRN	Pisum	genom	
	Psat7g210000.1		A	sativum	0	416601139
	1 546/8-1000011				Pisum	110001107
					sativu	
					m	
						chr5LG3:
~ -		Dasterson a Da Compon	DN	Diaum		555813839
37				Pisum	genom	
	Psat5g289520.1	VIa	A	sativum		555815702
					Pisum	
					sativu	
					m	
					Cameo	chr2LG1:
					r	386656323
38		Psat2g155840.1_Ps_Cameor_v	mRN	Pisum	genom	••
·	Psat2g155840.1	1a	А	sativum	e v1a	386658929
					Pisum	
					sativu	
					m	
						chr2LG1:
						105544927
30	Psat22060680 1	Psat2g060680.1_Ps_Cameor_	mRN	Pisum	genom	
57	-	v1a	A	sativum	-	 105549131
┝─┤		1 44	<u> </u>	Such vann	Pisum	100047101
					sativu	
					m Corrector	
					Cameo	1 (10)
				.		chr6LG2:
			has D N	IL/1 CI 1 PO	Janom	0748000
40	Psat6g005440.1	Psat6g005440.1_Ps_Cameor_	iiikn A	Pisum sativum	•	3748932 3751167

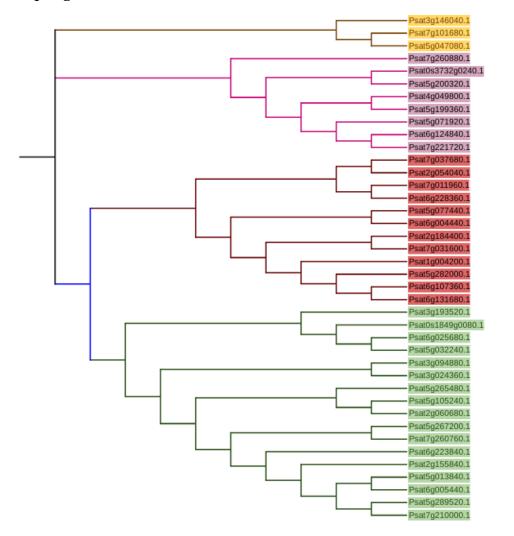
Table S1 Phylogenetic Tree



DIALOGUE SOCIAL SCIENCE REVIEW

www.thedssr.com ISSN Online: 3007-3154 ISSN Print: 3007-3146 Vol. 3 No. 2 (February) (2025)

To provide insight into the evolution of COL genes in different sequences of the pea plant, we performed a comparative analysis using the genes from a total of 40 gene sequences of pea genome.



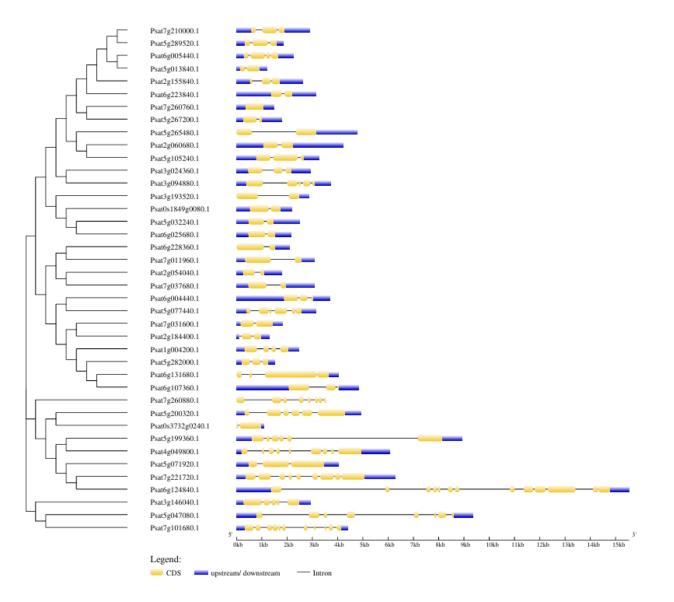
Gene structure

To compare the pea COL genes, their exon-intron structures were predicted, and the results are shown in Fig



www.thedssr.com ISSN Online: 3007-3154 ISSN Print: 3007-3146 Vol. 3 No. 2 (February) (2025)

DIALOGUE SOCIAL SCIENCE REVIEW



Motif Analysis

To explore the conserved domains and motifs, MEME software was employed to analyze the sequence alignment of the COL proteins in radish. The motifs were listed using serial numbers for Motif 1 to Motif 15 according to the ascending E-value of the alignment.



www.thedssr.com ISSN Online: 3007-3154 ISSN Print: 3007-3146 Vol. 3 No. 2 (February) (2025)

DIALOGUE SOCIAL SCIENCE REVIEW

Name	<i>p</i> -value	Motif Locations
Psat2g155840.1	7.24e-45	
Psat2g060680.1	0.00e+0	
Psat6g005440.1	4.55e-48	
Psat5g105240.1	0.00e+0	
Psat6g228360.1	4.78e-99	
Psat3g094880.1	2.11e-76	
Psat6g223840.1	1.09e-48	
Psat7g011960.1	3.69e-112	
Psat1g004200.1	1.13e-68	
Psat2g054040.1	7.65e-29	
Psat6g131680.1	0.00e+0	
Psat7g031600.1	2.28e-46	
Psat5g265480.1	2.88e-98	
Psat5g282000.1	1.16e-38	
Psat7g037680.1	7.93e-51	
Psat5g199360.1	0.00e+0	
Psat4g049800.1	0.00e+0	
Psat2g184400.1	4.26e-23	

Expression Analysis

We investigated the expression of each COL gene using published RNA-seq data for different pea tissues during vegetative and reproductive development.



www.thedssr.com ISSN Online: 3007-3154 ISSN Print: 3007-3146

Vol. 3 No. 2 (February) (2025)

														1									L	
		30.16	7.10	25.41	27.08	47.97	62.26	50.95	108.01	69.19	81.72	22.89	7.50	20.49	19.06	13.73	107.43	105.50	185.30	152.60	205.88	101.42	152.49	D
		14.38	7.90	11.05	15.46	74.91	51.23	50.65	66.93	49.95	51.07	25.90	33.25	15.97	4.55	3.48	52.75	68.51	91.03	97.94	110.86	161.43		Psat7g210000
		62.99	13.53	20.83	42.98	27.58	34.72	31.33	43.44	32.74	71.05	18.82	5.52	22.15	25.59	20.99	13.92	38.66	71.52	48.02	84.06	72.35	64.06	Psat6g025680 Psat2g155840
		47.86	11.43	35.89	42.99	22.44	3.58	3.35	37.48	49.54	40.17	8.86	5.00	13.11	10.02	7.03	64.83	69.38	49.64	92.04	198.67	101.17	109.07	Psat0s1849g0080
		7.45	0.05	8.25	5.45	10.28	1.12	1.53	21.59	14.01	16.21	0.19	0.47	1.47	2.27	1.77	87.62	79.03	39.09	58.14	108.27	119.65	158.52	Psat7g011960
		13.31	0.26	1.42	9.89	16.73	0.65	0.82	18.33	10.16	30.45	1.10	0.24	0.94	3.33	1.18	29.40	70.87	31.95	44.91	132.00	82.32	73.06	Psat5g289520
		184.48	143.86	157.90	135.63	1.23	0.55	1.06	12.84	6.28	2.11	93.80	102.87	65.12	33.85	30.98	8.34	8.78	9.26	9.07	11.18	8.00	6.35	Psat6g005440
		48.63	39.56	61.31	43.29	17.47	27.75	26.77	53.03	32.40	14.77	85.49	71.41	89.91	101.21	102.51	14.76	13.70	59.68	55.09	14.44	14.59	17.27	Psat6g004440
		5.81	10.86	13.43	6.78	0.70	1.37	1.85	7.27	5.14	2.83	13.03	7.69	5.62	2.96	2.25	27.34	12.32	3.42	7.30	17.41	3.34	2.53	Psat5g105240
	[16.08	9.18	14.62	11.83	6.83	14.33	12.39	11.92	7.30	9.31	8.32	5.32	11.97	7.22	6.52	7.12	6.61	14.85	12.70	16.44	8.75	8.57	Psat5g047080
	Ľ	5.89	3.00	6.72	3.67	0.37	3.95	3.06	8.21	1.69	1.46	7.02	4.72	17.99	4.96	4.10	11.49	7.09	10.76	11.68	28.10	13.17	9.45	Psat5g071920
		4.67	4.97	6.77	4.34	6.96	9.73	9.30	4.74	13.24	10.17	8.59	8.67	6.34	2.44	1.73	16.66	10.67	3.52	5.75	7.92	4.29	4.30	Psat3g094880
l		9.09	7.61	11.03	8.20	8.73	13.73	12.00	6.85	7.51	9.36	7.49	2.19	7.99	6.68	5.67	5.96	5.48	7.33	4.76	4.96	3.92	5.62	Psat7g260880
		3.68	5.32	3.35	3.25	11.60	2.17	2.81	10.89	9.20	4.07	12.42	7.24	0.80	0.73	0.88	4.33	4.58	10.37	5.26	1.74	0.36	0.64	Psat5g077440
		3.19	3.85	4.38	3.10	4.58	6.64	5.70	4.06	4.99	5.61	21.79	9.72	3.25	2.54	1.98	5.57	4.24	4.16	2.73	4.31	2.25	3.44	Psat5g199360
		5.07	5.28	10.74	5.90	0.79	6.36	5.43	2.43	1.33	2.18	6.68	4.80	3.76	1.87	0.77	13.40	5.40	2.23	2.77	7.55	1.39	1.08	Psat4g049800
	ľL	1.87	1.58	0.90	3.49	1.24	10.55	9.37	3.87	1.16	2.89	9.30	3.12	1.90	0.97	0.27	1.01	1.72	5.42	8.33	3.44	6.23	7.62	Psat7g260760
		0.02	0.03	0.02	0.00	1.46	12.39	11.21	6.41	0.50	4.61	0.09	0.18	0.22	1.21	0.56	0.90	0.64	22.92	3.46	3.54	1.37	1.48	Psat6g107360
L		0.00	0.15	0.32	0.00	0.13	0.08	0.13	0.48	1.79	0.40	0.22	0.34	0.03	0.00	0.00	13.71	5.00	0.93	1.24	3.29	1.29	2.31	Psat2g054040
		1.11	1.93	1.73	1.59	0.11	0.19	0.31	2.64	0.68	1.51	0.32	0.32	0.46	0.21	0.17	7.42	9.13	1.31	1.66	3.21	1.73	2.02	Psat6g223840
	Ίг	4.19	5.91	2.63	3.75	6.48	0.06	0.03	2.17	3.05	1.85	0.57	0.32	0.36	0.19	0.11	0.53	0.98	1.29	3.31	0.69	0.73	0.81	Psat5g282000
		2.66	2.55	2.39	1.95	2.00	4.81	5.41	0.74	2.71	1.46	2.89	1.89	2.60	2.23	1.96	0.95	0.83	1.27	0.77	1.19	0.85	1.20	Psat7g101680
		1.56	1.96	1.44	1.24	1.43	2.25	1.76	1.70	1.90	2.50	1.24	0.68	0.57	0.68	0.54	1.42	1.03	2.02	1.46	1.76	1.17	1.56	Psat5g265480
		1.49	2.02	2.21	1.41	3.30	2.54	3.04	2.15	2.88	3.80	1.66	1.63	0.60	0.74	0.54	5.69	2.94	2.40	1.76	2.72	0.89	1.18	Psat2g060680
		1.90	4.33	1.11	1.28	0.21	2.91	1.69	0.85	0.19	0.26	6.97	6.21	0.07	0.00	0.00	0.00	0.05	1.86	0.68	0.25	0.12	0.21	Psat2g184400
		0.95	0.57	0.70	0.40	0.47	0.53	0.58	0.21	1.07	0.33	0.31	0.38	0.53	0.49	0.28	0.15	0.16	0.24	0.17	0.25	0.02	0.17	Psat3g146040
		0.02	0.00	0.05	0.02	0.03	0.00	0.07	0.06	0.09	0.04	0.00	0.15	0.02	0.02	0.04	0.00	0.04	0.08	0.09	0.35	0.02	0.14	Psat0s3732g0240
		2.48	4.53	3.16	2.40	0.36	0.07	0.00	0.01	0.98	0.10	0.54	0.21	0.90	0.37	0.41	0.23	0.15	0.00	0.06	0.00	0.00	0.00	Psat5g013840
		3.00	4.91	2.33	2.63	0.80	3.20	2.31	0.19	0.06	0.40	0.54	0.09	0.18	0.00	0.00	0.00	0.04	0.36	0.11	0.00	0.00	0.08	Psat7g031600
l		0.14	0.03	0.11	0.09	0.11	0.03	0.00	11.26	1.13	2.14	1.26	0.72	0.10	0.00	0.10	2.85	2.29	2.32	2.79	2.27	0.46	0.44	Psat1g004200
		0.03	0.05	0.03	0.06	0.00	0.00	0.00	0.15	0.06	7.93	0.02	0.10	0.09	0.00	0.00	1.45	1.14	0.01	1.13	5.39	0.78	0.86	Psat6g131680
	r	6.06	1.31	3.10	2.87	5.78	9.57	6.89	16.51	7.08	8.52	4.86	2.42	2.37	3.31	2.49	5.46	9.47	25.17	26.39	34.18	22.14	29.63	Psat5g200320
		1.00	0.34	0.45	0.42	3.41	0.16	0.15	9.25	8.78	8.72	0.11	0.13	1.04	0.89	0.23	14.31	29.72	13.24	22.99	44.68	26.37	30.79	Psat3g193520
		0.87	0.49	1.38	0.69	9.58	6.92	6.93	7.81	8.96	6.74	0.52	1.42	0.39	0.24	0.27	13.57	17.46	10.24	12.66	8.97	16.66	18.63	Psat6g228360
		1.44	1.73	2.20	2.14	26.77	13.30	15.93	19.75	24.22	21.46	4.38	4.16	0.32	0.19	0.36	16.45	20.22	19.38	14.33	20.03	12.86	14.56	Psat7g037680
[17.09	3.24	3.54	9.25	21.16	23.82	23.19	29.93	19.09	25.28	43.07	33.60	20.39	3.96	3.41	10.91	22.21	39.36	39.51	45.67	51.49	46.28	Psat5g267200
L		28.14	9.71	39.75	15.79	15.35	18.70	16.16	43.43	34.15	30.54	5.91	3.67	16.96	13.39	8.96	49.55	31.16	38.82	41.81	83.35	39.24	50.79	Psat7g221720
l		11.63	12.24	14.81	15.13	34.70	22.60	28.43	33.01	26.79	25.51	13.07	23.63	8.73	4.39	5.93	36.11	41.94	28.46	34.62	50.24	35.85	33.20	Psat5g032240
	ſ	14.82	11.54	26.16	12.28	10.65	18.70	16.22	22.62	18.26	22.24	11.97	7.03	17.26	12.41	8.40	33.13	20.47	18.15	20.91	45.23	19.94	20.21	Psat6g124840
		11.58 Z	9.57 Z	16.09 Z	12.74 Z	4.15 Z	9.95 a	9.39 Ħ	19.41 Z	6.29 Z	13.50 Z	6.49	4.47	3.57 Z	2.30 Z	1.72 Z	33.75 Z	24.72 Z	27.26 Z	34.13 Z	55.92 Z	40.72 Z	49.08 Z	Psat3g024360
		Root_B_LN	Root_F_LN	otSys_A_HN	otSys_A_LN	Pods_C_LN	eeds_12dap	.12dap_mut	Stem_BC_LN	Node_B_LN	lower_B_LN	seeds_5dai	ds_5dai_mut	odule_G_LN	Jodule_A_LN	lodule_B_LN	Shoot_A_HN	Shoot_A_LN	Iuncle_C_LN	ndril_BC_LN	Leaf_B_LN	erLeaf_C_LN	erLeaf_C_LN	
		Ro	Ra	ootS	potS	Por	beed	5_12	Sten	cNoi	Flow	Sei	sb.	Nodu	Nodt	NodL	Sho	Sha	dunc	indri	Le	erLe	erLe	

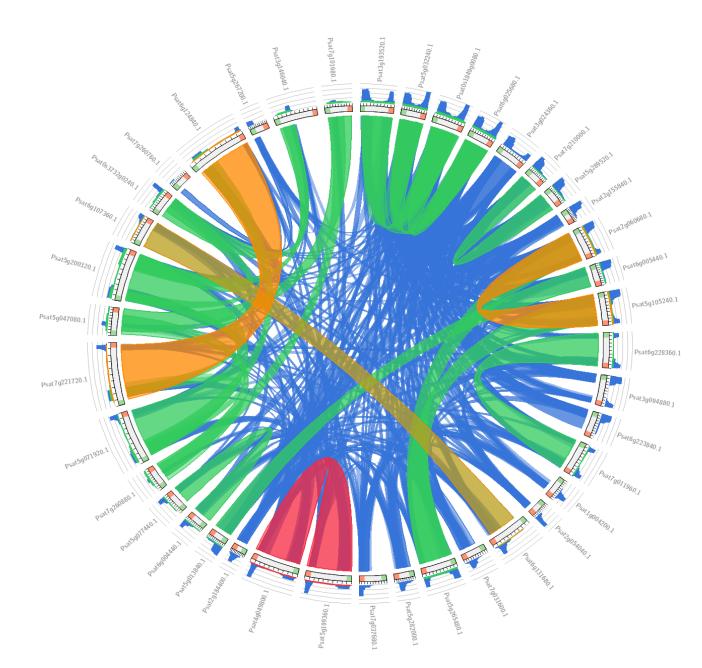
210.00
180.00
150.00
120.00
90.00
-60.00
- 30.00
0.00



www.thedssr.com ISSN Online: 3007-3154 ISSN Print: 3007-3146 Vol. 3 No. 2 (February) (2025)

Syntany Analysis

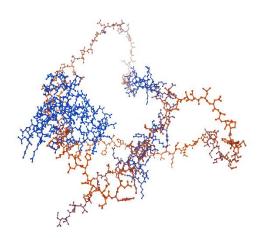
Syntany analysis was performed using Circos Software

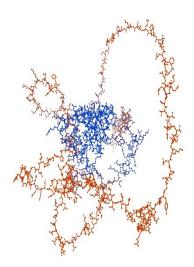




www.thedssr.com ISSN Online: 3007-3154 ISSN Print: 3007-3146 Vol. 3 No. 2 (February) (2025)

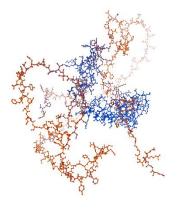
3D Protein Structure 3D protein structure was made using Swiss Model Tool

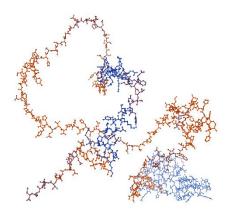




www.thedssr.com ISSN Online: 3007-3154 ISSN Print: 3007-3146 Vol. 3 No. 2 (February) (2025)



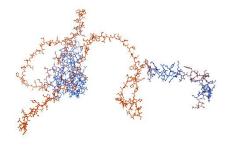






www.thedssr.com ISSN Online: 3007-3154 ISSN Print: 3007-3146 Vol. 3 No. 2 (February) (2025)

DIALOGUE SOCIAL SCIENCE REVIEW



References

- AmasinoRM,MichaelsSD(2010)The timing of flowering. Plant Physiol 154: 516520. https://doi.org/ 10.1104/pp.110.161653 PMID: 20921176
- Nie S, XuL,WangY,HuangD,MulekeEM,SunX,etal.(2015) Identification of boltingrelated micro RNAsandtheir targets reveals complex miRNA-mediated floweringtime regulatory networks in radish (Raphanus sativus L.). Sci Rep 5: 14034.https://doi.org/10.1038/srep14034 PMID: 26369897
- Srikanth A, Schmid M(2011) Regulation of flowering time: all roads lead to Rome. Cell Mol Life Sci 68: 20132037. https://doi.org/10.1007/s00018-011-0673-y PMID: 21611891
- Fornara F, de MontaiguA, CouplandG(2010)SnapShot:Control of flowering in Arabidopsis. Cell 141: 550, 550 e551552. https://doi.org/10.1016/j.cell.2010.04.024 PMID: 20434991
- Michaels SD, Amasino RM (1999) FLOWERINGLOCUS Cencodesa novel MADS domain proteinthat acts as arepressor of flowering. Plant Cell 11: 949956. PMID: 10330478
- LeeJ, LeeI(2010) Regulation and function of SOC1, a flowering pathwayintegrator. J Exp Bot 61: 22472254. https://doi.org/10.1093/jxb/erq098 PMID: 20413527
- Berns MC, Nordström K, Cremer F, Tóth R, Hartke M, Simon S, Klasen JR, Bürstel I, Coupland G (2014) Evening expression of Arabidopsis GIGANTEA is controlled by combinatorial interactions among evolutionarily conserved regulatory motifs. Plant Cell 26:3999–4018. https://doi.org/10. 1105/tpc.114.129437
- Blazquez MA, Soowal LN, Lee I, Weigel D (1997) LEAFY expression and flower initiation in Arabidop sis. Development 124:3835–3844. https://doi.org/10.1242/ dev.124.19.3835
 Borner R, Kampmann G, Chandler J, Gleissner R, Wisman E, Apel K, Melzer S (2000) A MADS domain gene involved in the transition to



DIALOGUE SOCIAL SCIENCE REVIEW

www.thedssr.com

ISSN Online: 3007-3154

ISSN Print: 3007-3146

Vol. 3 No. 2 (February) (2025)

flowering in Arabidopsis. Plant J 24:591–599. https://doi. org/10.1046/j.1365-313x.2000.00906.x

- Brandoli C, Petri C, Egea-Cortines M, Weiss J (2020) Gigantea: Uncovering new functions in flower development. Genes 11:1142<u>https://doi.org/10.3390/genes11101142</u>
- Choi H-y, Hong J-h, Kang J-y, Kim SY (2000) ABFs, a family of ABA-responsive element binding fac tors. J Biol Chem 275:1723–1730. https://doi.org/10.1074/jbc.275.3.1723
- Fowler S, Lee K, Onouchi H, Samach A, Richardson K, Morris B, Coupland G, Putterill J (1999) GIGANTEA: A circadian clock-controlled gene that regulates photoperiodic flowering in Arabidop sis and encodes a protein with several possible membrane-spanning domains. EMBO J 18:4679 4688. https://doi.org/10.1093/emboj/18.17.4679 Gray JA, Shalit-Kaneh A, Chu DN, Hsu PY, Harmer SL (2017) The REVEILLE clock genes inhibit growth of juvenile and adult plants by control of cell size. Plant Physiol 173:2308–2322. https://doi.org/10.1104/pp.17.00109
- Hall A, Bastow RM, Davis SJ, Hanano S, McWatters HG, Hibberd V et al (2003) The TIME FOR COF FEE gene maintains the amplitude and timing of Arabidopsis circadian clocks. Plant Cell 15:2719 2729. <u>https://doi.org/10.1105/tpc.013730</u>
- Han Y, Zhang X, Wang Y, Ming F (2013) The suppression of WRKY44 by GIGANTEAmiR172 pathway is involved in drought response of Arabidopsis thaliana. PLoS ONE 8:e73541. https://doi.org/ 10.1371/journal.pone.0124854
- Harmer SL, Hogenesch JB, Straume M, Chang HS, Han B, Zhu T, Wang X, Kreps JA, Kay SA (2000) Orchestrated transcription of key pathways in Arabidopsis by the circadian clock. Science 290:2110–2113. https://doi.org/10.1126/science.290.5499. 2110
- Helfer A, Nusinow DA, Chow BY, Gehrke AR, Bulyk ML, Kay SA (2011) LUX ARRHYTHMO encodes a nighttime repressor of circadian gene expression in the Arabidopsis core clock. Curr Biol 21:126 133. <u>https://doi.org/10 .1016 /j.cub</u> .2010.12.021
- Hernandez-Garcia CM, Finer JJ (2014) Identification and validation of promoters and cis-acting regula tory elements. Plant Sci 217–218:109–119. https://doi.org/ 10.1016/j.plantsci.2013.12.007
- Jackson SD (2008) Plant responses to photoperiod. New Phytol 181:517–531. https:// doi.org/10.1111/j. 1469-8137.2008.02681.x
- Jose J, Bánfalvi Z (2019) The role of GIGANTEA in flowering and abiotic stress adaptation in plants. Columella 6:7–18 Kawamura H, Ito S, Yama