



中国农业科学院

CHINESE ACADEMY OF AGRICULTURAL SCIENCES

Kala4蛋白在水稻多酚合成调控中的功能分析

Functional Analysis of Kala4 Protein in the Regulation of Polyphenol Synthesis in Rice

G13成员：林淑琴 石雯 唐紫瑄 李慧

报告人：唐紫瑄

报告时间：2026.1.11



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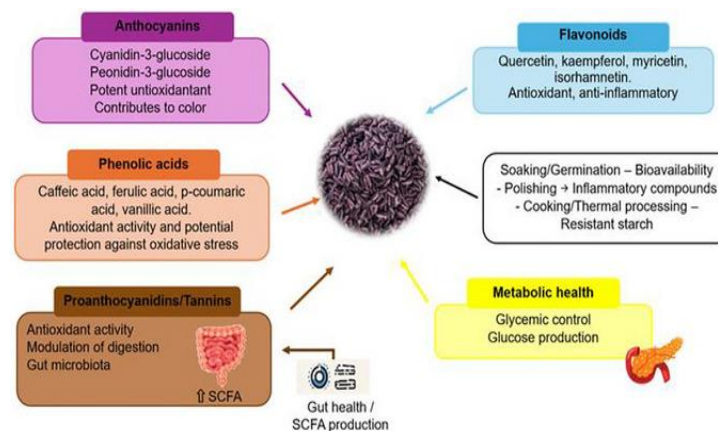
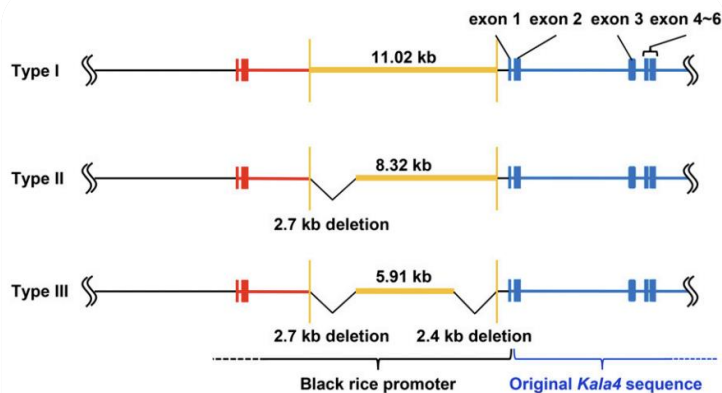
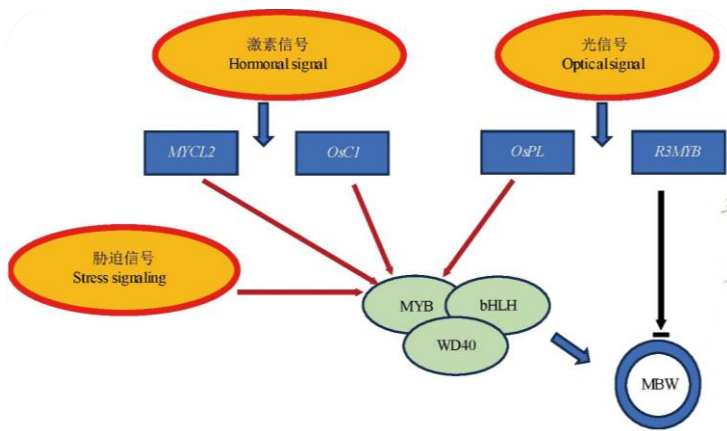
6 下一步计划



Part
1
背景

背

黑米性状的关键调控基因: **Kala4**



Kala4基因的鉴定

2015年, Oikawa等人鉴定到关键基因Kala4

(Os04g0557500), 它编码bHLH型转录因子, 是玉米花青素调控基因R/B的水稻同源基因。

黑米形成的原因

黑米并非编码区突变所致, 而是Kala4启动子区复杂重排, 使其在种皮异位高表达。Kala4蛋白可激活花青素合成下游基因, 驱动花青素累积。

等位基因的传播

系统进化分析表明, Kala4等位基因最初产生于热带粳稻, 后通过自然杂交与基因渗入传播到籼稻和温带粳稻中。

从“现象发现”到“机制深度解析”的研究缺口

01

保守结构域与DNA结合特异性

Kala4蛋白的保守结构域如何决定其DNA结合特异性尚不明确，这对于理解其在基因调控中的作用机制至关重要。

02

对其他关键基因的调控

除已知靶点，Kala4是否还调控多酚合成通路中的其他关键基因未知，这关系到其在多酚合成调控网络中的全面作用。

03

与Rc基因的异同

与红米基因Rc相比，Kala4在蛋白互作网络与调控逻辑上的异同不清楚，这有助于深入理解不同基因在水稻颜色形成中的作用。

04

启动子结构变异的影响

Kala4启动子结构变异如何影响转录因子结合位点与表观修饰模式未知，这对于揭示基因表达调控机制有重要意义。



Part
析 2

序列分

序列分析



21 条序列已选中 距离树 多序列比对

序列描述	物种命名	最高得分	总得分	覆盖率	期望值	相似度	序列长	序列号
RecName: Full=Anthocyanin regulatory R-S protein [Z...	Zea mays	527	527	81.00%	8.37734e-67	67.35%	612	P13027.1
RecName: Full=Anthocyanin regulatory Lc protein [Z...	Zea mays	527	527	81.00%	7.42692e-67	67.35%	610	P13526.1
RecName: Full=Transcription factor GLABRA3, At1Na...	Arabidopsis thaliana	408	408	81.00%	5.58196e-49	52.26%	637	Q9FN99.1
RecName: Full=Transcription factor EGL1, At1Name...	Arabidopsis thaliana	392	392	82.00%	1.20901e-46	49.02%	596	Q9CAD0.1
RecName: Full=Transcription factor TT8, At1Name_E...	Arabidopsis thaliana	343	343	78.00%	1.93989e-39	44.68%	518	Q9FT81.2
RecName: Full=Basic helix-loop-helix protein A [La...	Pisum sativum	373	373	83.00%	6.70927e-44	44.29%	652	E3SXU4.1
RecName: Full=Truncated basic helix-loop-helix pro...	Pisum sativum	374	374	83.00%	1.72075e-44	44.29%	358	E3SXU5.1
RecName: Full=Transcription factor bHLH42, At1Name...	Actinidia chinensis var. chinensis	375	375	88.00%	4.00323e-44	42.50%	689	A0A2R6QE26.1
RecName: Full=Transcription factor MYC1, Short=AIM...	Arabidopsis thaliana	303	303	80.00%	1.52964e-33	41.77%	526	Q8W2E1.1
RecName: Full=Transcription factor bHLH28, At1Name...	Arabidopsis thaliana	125	125	65.00%	5.42217e-8	34.68%	511	Q9LUK7.1
RecName: Full=Transcription factor MYC3, At1Name...	Arabidopsis thaliana	136	136	71.00%	1.46345e-9	34.56%	592	Q9EIP9.1
RecName: Full=Transcription factor MYC2, Short=LeM...	Solanum lycopersicum	151	151	66.00%	1.26077e-11	33.33%	689	A0A3Q7HRZ6.1
RecName: Full=Transcription factor MYC1, Short=SIM...	Solanum lycopersicum	150	150	66.00%	1.86754e-11	33.06%	630	A0A060KY90.1
RecName: Full=Transcription factor MYC2, Short=AIM...	Arabidopsis thaliana	155	155	72.00%	3.04084e-12	32.85%	623	Q39204.2
RecName: Full=Transcription factor MYC2, Short=OsM...	Oryza sativa Japonica Group	139	139	67.00%	6.36114e-10	32.54%	699	Q336P5.1
RecName: Full=Transcription factor ABA-INDUCIBLE b...	Arabidopsis thaliana	128	128	69.00%	1.75961e-8	30.60%	566	Q9ZPY8.2
RecName: Full=Transcription factor bHLH13, At1Name...	Arabidopsis thaliana	115	115	69.00%	0.00000123304	30.23%	590	Q9LNI5.1
RecName: Full=Transcription factor MYC4, Short=AIM...	Arabidopsis thaliana	145	145	77.00%	9.72987e-11	30.00%	589	Q49687.1
RecName: Full=Transcription factor MTB2, At1Name...	Solanum lycopersicum	115	115	67.00%	0.00000115787	28.35%	579	A0A3Q7HES4.1
RecName: Full=Transcription factor MTB1, At1Name...	Solanum lycopersicum	134	134	69.00%	3.05275e-9	28.13%	613	A0A3Q7ELQ2.1
RecName: Full=Transcription factor bHLH3, At1Name...	Arabidopsis thaliana	93	93	74.00%	0.00115698	24.46%	467	Q23487.1

序列分析

BLAST



<input type="checkbox"/> sp A0A3Q7HRZ6 MYC2_SOLLC	S S T S A S T L S A A A T V D A S K S M P F F N Q E T L Q Q R L Q A L I D G A R E T W T Y A I F W Q S S V V D F S S P S V L G W G D	132
<input type="checkbox"/> sp Q8W2F1 BH012_ARATH	M A D G V E A - - - - - A A G R S K R Q N S L L R K Q L A L - - A V R S V Q W S Y A I F W S S S L - - - T O P G V L E W G E	56
<input type="checkbox"/> sp E3SXU5 IBHLHM_PEA	M T - - - - - A P T P E N G C N K L Q N M L Q A - - A V Q S V Q W T Y S L F W Q I C P - - - Q Q L I L V W G D	45
<input type="checkbox"/> sp A0A2R6QE26 BHL42_ACTCC	- - - - - M A A P P S T R L Q G M L Q T - - A V Q S V Q W T Y S L F W Q L C P - - - Q Q G I L V W G D	41
<input type="checkbox"/> sp Q9FN69 GL3_ARATH	M A T G Q N - - - - - R T T V P E N L K K H L A V - - S V R N I Q W S Y G I F W S V S A - - - S Q S G V L E W G D	47
<input type="checkbox"/> sp Q9CAD0 EGL1_ARATH	M A T G E N - - - - - R - T V P D N L K K Q L A V - - S V R N I Q W S Y G I F W S V S A - - - S Q P G V L E W G D	46
<input type="checkbox"/> sp P13027 ARRS_MAIZE	M A V S A S R V Q - - - - Q A E E L L Q R P A E R Q L M R S Q L A A - - A A R S I N W S Y A L F W S I S D - - - T O P G V L T W T D	57
<input type="checkbox"/> tr A0A0P0WDK6 A0A0P0WDK6_ORYSJ	M A - S A P - - P - - - V Q E E A L Q - - P G T N H F R S R L A A - - A V R S I S W S Y T I F W S T S T - - - S L P G V L T W N D	52
A0A3Q7HRZ6:Chain		
<input type="checkbox"/> sp A0A3Q7HRZ6 MYC2_SOLLC	G Y Y K G E E D K A K R K L S V S S P A Y I A E Q E H R K K V L R E L N S - L I S G A P P G - - - - - - - - - - - - - - - T	178
<input type="checkbox"/> sp Q8W2F1 BH012_ARATH	G C Y N G D M K K R K K S Y E S H - - - Y K Y G L - Q K S K E L R K L Y L S M L E G D S G T T V S T T H D N L N D D D D N C H S T S	118
<input type="checkbox"/> sp E3SXU5 IBHLHM_PEA	G Y Y N G A I K T R K T V Q P M E V S A E E A S L - Q R S Q Q L R E L Y E S L S A G E T N P - - - - - - - - - - - P T R R P C	96
<input type="checkbox"/> sp A0A2R6QE26 BHL42_ACTCC	G Y Y N G A I K T R K T V L P I E V S A E E A S L - Q R S Q Q L R E L Y D S L S A G E S N Q - - - - - - - - - - - Q T R R P C	92
<input type="checkbox"/> sp Q9FN69 GL3_ARATH	G Y Y N G D I K T R K T I Q A S E I K A D Q L G L - R R S E Q L S E L Y E S L S V A E S S S S G V A A G S - - - - - Q V T R R A S A	107
<input type="checkbox"/> sp Q9CAD0 EGL1_ARATH	G Y Y N G D I K T R K T I Q A A E V K I D Q L G L - E R S E Q L R E L Y E S L S L A E S S A S G - - - S S - - - - - Q V T R R A S A	103
<input type="checkbox"/> sp P13027 ARRS_MAIZE	G F Y N G E V K T R K I S N S V E L T S D Q L V M - Q R S D Q L R E L Y E A L L S G E G D R - - - - - - - - - - - R A A P A R P A	110
<input type="checkbox"/> tr A0A0P0WDK6 A0A0P0WDK6_ORYSJ	G F Y N G E V K T R K I S N L E D L T A D Q L V L - R R S E Q L S E L Y S L L S G E C D H - - - - - - - - - - - R A - - R K P V	103
A0A3Q7HRZ6:Chain		
<input type="checkbox"/> sp A0A3Q7HRZ6 MYC2_SOLLC	D D A V D E E V T D T E W F F L I S M T Q S F V N G S G L P G Q A L Y S S S P I W V A G T E K L A A S H C E R V R Q A Q G F G L Q T	244
<input type="checkbox"/> sp Q8W2F1 BH012_ARATH	M M L S P D D L S D E E W Y Y L V S M S Y V F S P S Q C L P G R A S A T G E T I W L C N A Q Y A E N K L F S R S L L A R S A S I Q T	184
<input type="checkbox"/> sp E3SXU5 IBHLHM_PEA	A S L S P E D L T E S E W F Y L M C V S F S F P P G V G L P G K A Y A R R O H V W L T G A N E V D S K T F S R A I L A K S A N I Q T	162
<input type="checkbox"/> sp A0A2R6QE26 BHL42_ACTCC	A A L S P E D L T E S E W F Y L M C V S F S F P P G V G L P G K A Y A K R O H V W L T G A N E V D S K V F S R A I L A K S A R V Q T	158
<input type="checkbox"/> sp Q9FN69 GL3_ARATH	A A L S P E D L A D T E W Y Y L V C M S F V F N I G E G M P G R T F A N G E P I W L C N A H T A D S K V F S R S L L A K S A A V K T	173
<input type="checkbox"/> sp Q9CAD0 EGL1_ARATH	A A L S P E D L T D T E W Y Y L V C M S F V F N I G E G I P G G A L S N G E P I W L C N A E T A D S K V F T R S L L A K S A S L Q T	169
<input type="checkbox"/> sp P13027 ARRS_MAIZE	G S L S P E D L G D T E W Y Y V V S M T Y A F R P G Q G L P G R S F A S D E H V W L C N A H L A G S K A F P R A L L A K S A S I Q S	176
<input type="checkbox"/> tr A0A0P0WDK6 A0A0P0WDK6_ORYSJ	A A L S P E D I A D T E W Y Y V V C M T Y A F R P G Q G L P G R S Y A S N R S V W L C N A Q S A D S K T L T S T C A L S E E R V Y - S	168
A0A3Q7HRZ6:Chain		
<input type="checkbox"/> sp A0A3Q7HRZ6 MYC2_SOLLC	I V C I P S A N G V V E L G S T E L I V Q S S D L M N K V R V L F N F S N D L G S G S W A V Q P E S D P S A L - - - - - - - - - -	299
<input type="checkbox"/> sp Q8W2F1 BH012_ARATH	V V C F P Y L G G V I E L G V T E L I S E D H N L L R N I K S C L M E I S A H Q D N D - - - - - - - - - - - D E - -	229
<input type="checkbox"/> sp E3SXU5 IBHLHM_PEA	V V C I P V L D G V V E I G T T D K V Q E D L N F I K H V R S F F I D H H S L - P P K - P A L S E H S T S N P T - - - - - - - Y S T	219
<input type="checkbox"/> sp A0A2R6QE26 BHL42_ACTCC	V V C I P L L D G V V E L G N T E R V Q E D I G F I H Q V K S F F I D H H P P P P K - P A L S E H S T S N L A - - - - - - - T S S	216
<input type="checkbox"/> sp Q9FN69 GL3_ARATH	V V C F P F L G G V V E I G T T E H I T E D M N V I Q C V K T S F L E A P D P Y A T I L P A R S D Y H I D N V L D P Q Q I L G D E I	239
<input type="checkbox"/> sp Q9CAD0 EGL1_ARATH	V V C F P F L G G V L E I G T T E H I K E D M N V I Q S V K T L F L E A P P - Y T T I - S T R S D Y Q - - E I F - - - - - D P L S D D K	228
<input type="checkbox"/> sp P13027 ARRS_MAIZE	I L C I P V M G G V L E L G T T D T V P E A P D L V S R A T A A F W E P Q C P T Y S E E P S S S P S S G R A N E - - - T G E A A A D D -	239
<input type="checkbox"/> tr A0A0P0WDK6 A0A0P0WDK6_ORYSJ	D N C L H P L H E -	180

在CNCB中进行BLAST，结果包含21条同源蛋白序列的核心参数，涵盖玉米（Zea mays）、拟南芥（Arabidopsis thaliana）、番茄（Solanum lycopersicum）、豌豆（Pisum sativum）、猕猴桃（Actinidia chinensis）。

序列分析



百分比一致性矩阵 (Percent Identity Matrix)

Percent Identity Matrix

<input type="checkbox"/> sp A0A3Q7HRZ6 MYC2_SOLLC	100.00%	22.59%	28.21%	26.76%	24.62%	26.41%	25.94%	27.01%
<input type="checkbox"/> sp Q8W2F1 BH012_ARATH	22.59%	100.00%	36.32%	30.02%	39.15%	39.62%	33.61%	41.04%
<input type="checkbox"/> sp E3SXU5 BHLHM_PEA	28.21%	36.32%	100.00%	66.67%	36.36%	37.67%	34.00%	41.42%
<input type="checkbox"/> sp A0A2R6QE26 BHL42_ACTCC	26.76%	30.02%	66.67%	100.00%	35.03%	35.83%	28.17%	40.61%
<input type="checkbox"/> sp Q9FN69 GL3_ARATH	24.62%	39.15%	36.36%	35.03%	100.00%	78.52%	34.24%	50.00%
<input type="checkbox"/> sp Q9CAD0 EGL1_ARATH	26.41%	39.62%	37.67%	35.83%	78.52%	100.00%	36.22%	46.51%
<input type="checkbox"/> sp P13027 ARRS_MAIZE	25.94%	33.61%	34.00%	28.17%	34.24%	36.22%	100.00%	61.11%
<input type="checkbox"/> tr A0A0P0WDK6 A0A0P0WDK6_ORYSJ	27.01%	41.04%	41.42%	40.61%	50.00%	46.51%	61.11%	100.00%

目标水稻序列与玉米同源序列一致性达61.11%，呈现显著的禾本科物种近缘特征

猕猴桃序列与豌豆序列一致性为66.67%，拟南芥两条同源序列一致性高达78.52%，体现了双子叶植物 bHLH家族的种间保守性；

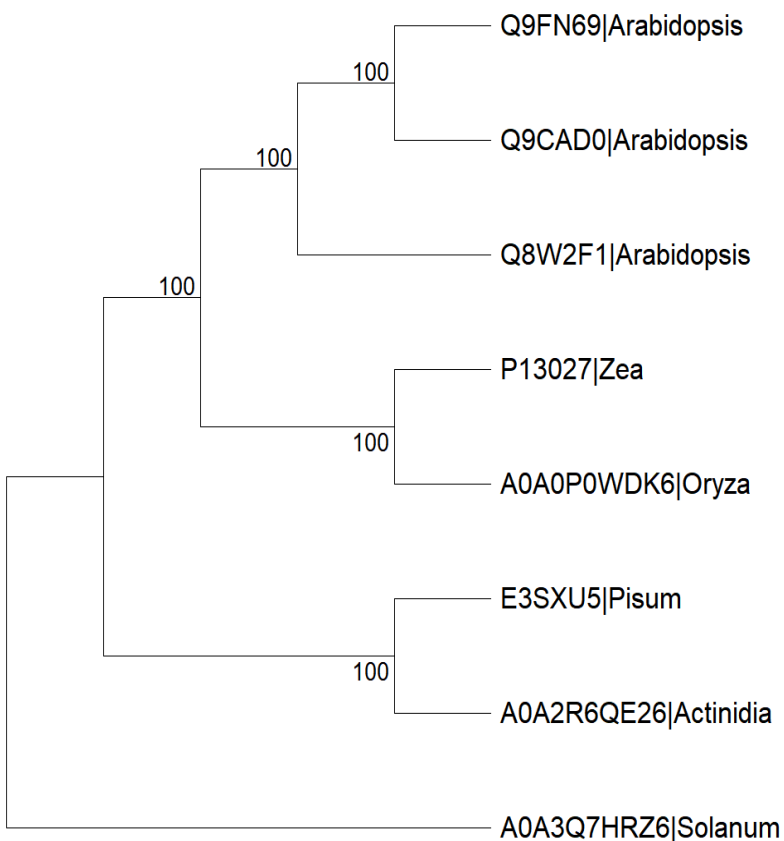
番茄同源序列与其他物种序列一致性均低于28%，属于分化程度较高的独立分支。

序列分析

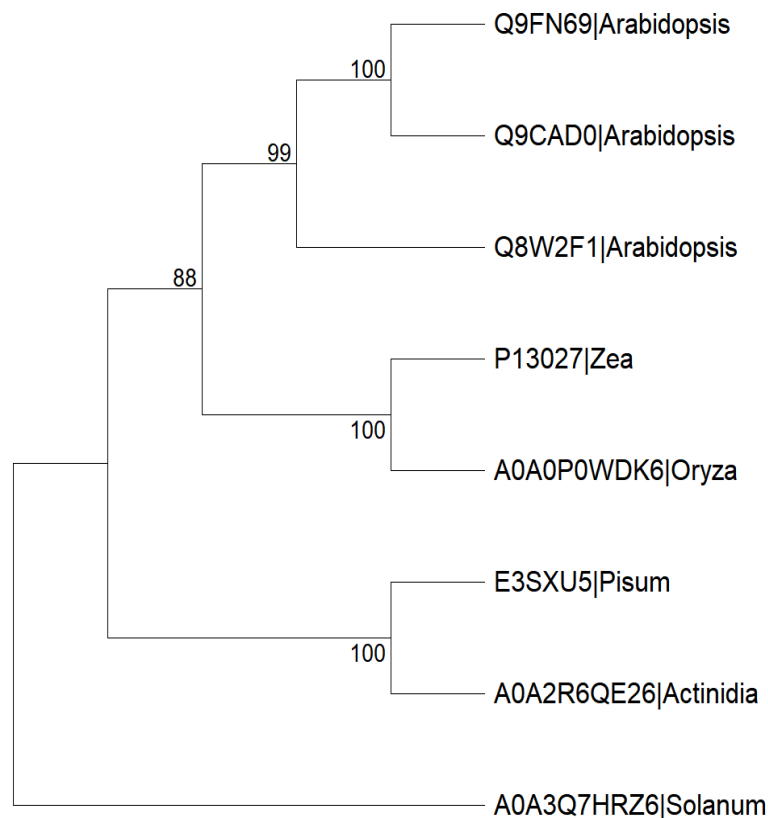
系统发育树构建



最大似然法 (ML)



邻接法 (NJ)



邻接法仅基于序列遗传距离构建进化树，最大似然法结合进化模型，更贴合基因在植物系统发育中的真实演化路径

bHLH基因在植物祖先分化为单子叶、双子叶支系之前，就已发生旁系同源基因复制事件，产生了多个基因亚型；

番茄基因单独成支是因该bHLH基因亚型在茄科物种演化中发生了适配其特有功能的序列分化



Part **3**

蛋白理化数据分析

蛋白理化数据分析



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Number of amino acids: 180

Theoretical pI: 5.80

Molecular weight: 20260.64

Extinction coefficients:

Extinction coefficients are in units of $M^{-1} cm^{-1}$, at 280 nm measured in water.

Ext. coefficient 46660

Abs 0.1% (=1 g/l) 2.303, assuming all pairs of Cys residues form cystines

Ext. coefficient 46410

Abs 0.1% (=1 g/l) 2.291, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is M (Met).

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).

>20 hours (yeast, in vivo).

>10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 60.47

This classifies the protein as unstable.

Aliphatic index: 75.39

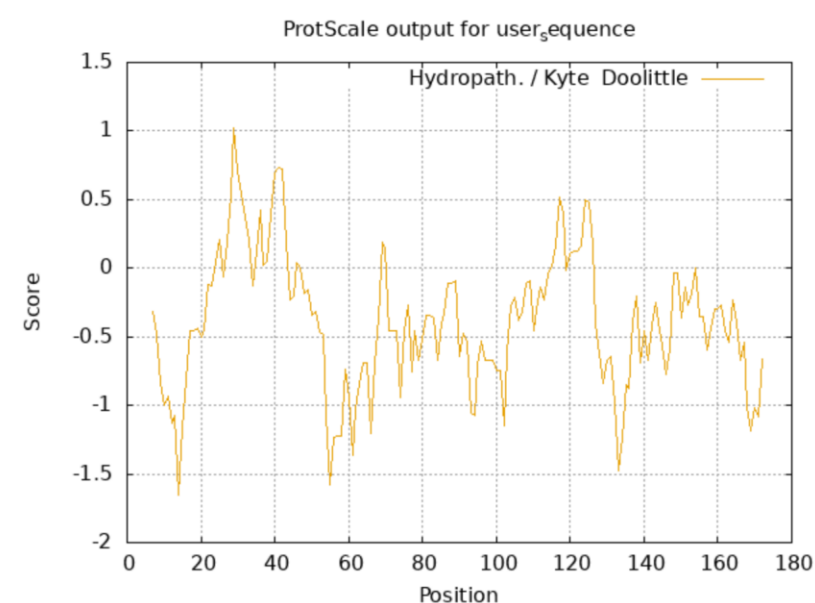
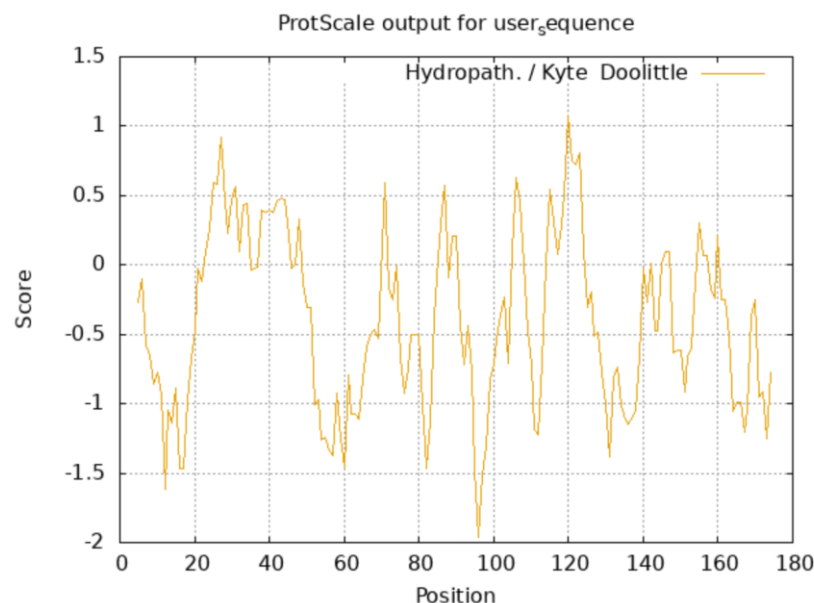
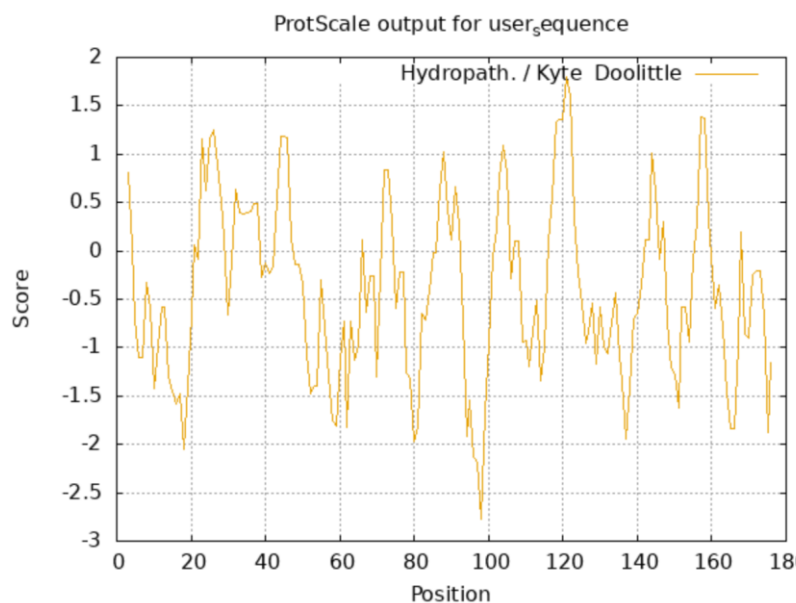
Grand average of hydropathicity (GRAVY): -0.401

● 该蛋白质属于中等长度，略偏酸性，属于小分子量蛋白，该蛋白N端氨基酸为甲硫氨酸

● 为“不稳定蛋白”，推测蛋白在体外易降解。

● 蛋白整体偏亲水，更易溶于水相环境。

整体偏亲水，无连续、高强度的疏水区域，有稳定的强亲水区。





Part **4**

蛋白结构分析

Transcription factor GLABRA 3

Download files

AF-Q9FN69-F1-v6 • [Google Deepmind dataset](#) •  

Tell us what you think of the new look [Share your feedback](#)

Summary and Model Confidence

Domains

Annotations

Similar Proteins

Protein

Transcription factor GLABRA 3

Gene

GL3

Source organism

Arabidopsis thaliana (Mouse-ear cress) [go to search](#)

UniProt

Q9FN69 [go to UniProt](#)

Biological function

Transcription activator, when associated with MYB75/PAP1, MYB90/PAP2 or TT2. Involved in epidermal cell fate specification. Negatively regulates stomata formation, but, in association with TTG1 and MYB0/GL1, promotes trichome formation, branching and endoreplication. Also regulates trichome cell wall maturation. Together with MYB66/WER, promotes the formation of non-hair cells in root epidermis cells in the N position. Whereas together with CPC, promotes the formation of hair cells in root epidermis cells in the H position by inhibiting non-hair cell formation. Also seems to play a role in the activation of anthocyanin biosynthesis, probably together with MYB75/PAP1. Activates the transcription of GL2. [Show less](#) [go to UniProt](#)

Experimental structures

1 structure in PDB for Q9FN69 [go to PDBe-KB](#)

Average pLDDT

63.34 (Low)

pLDDT distribution

■ 26.2% Very high
■ 20.7% High
■ 9.3% Low
■ 43.8% Very low

蛋白结构分析

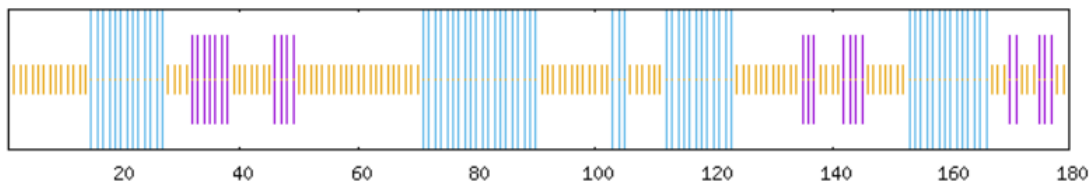
二级结构

10 20 30 40 50 60 70
MASAPPVQEEALQPGTNHFRLAAAVRSISWSYTIWFSTSTSLPGVLTWNDGFYNGEVKTRKISNLEDL
ccccccccccccchhhhhhhhhhhcc
TADQLVLRREQLSELYSLLSGECDHRARKPVAALSPEDIADTEWYVVCMTYAFRPGQLPGRSYASN
chhhhhhhhhhhhhhhhhhhhhccccccccccccchhhccccchhhhhhhhhhhcccccccccccccccc
RSVWLCNAQSADSKTLSTCALSEERVYSDNCLHPLHEWRA
ccccccccccccchhhhhhhhhhhhhcccccccccccc

Sequence length : 180

SOPMA :

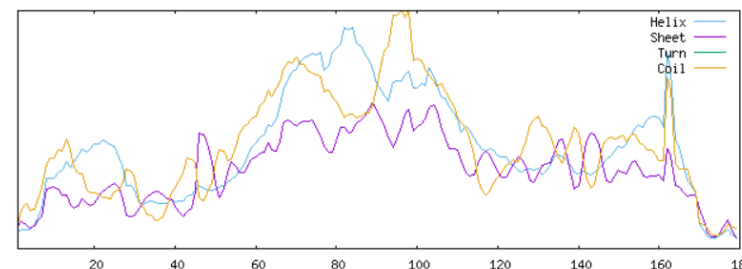
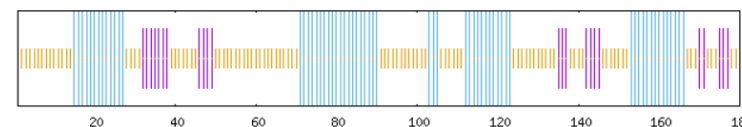
Alpha helix (Hh) :	62 is	34.44%
3 ₁₀ helix (Gg) :	0 is	0.00%
Pi helix (Ii) :	0 is	0.00%
Beta bridge (Bb) :	0 is	0.00%
Extended strand (Ee) :	24 is	13.33%
Beta turn (Tt) :	0 is	0.00%
Bend region (Ss) :	0 is	0.00%
Random coil (Cc) :	94 is	52.22%
Ambiguous states (?) :	0 is	0.00%
Other states :	0 is	0.00%



该蛋白二级结构以“高柔性无规卷曲 + 中等占比 α -螺旋”为核心， β -折叠占比适中，结构特征匹配转录因子的功能需求。



Alpha helix (Hh) :	62 is	34.44%
3 ₁₀ helix (Gg) :	0 is	0.00%
Pi helix (Ii) :	0 is	0.00%
Beta bridge (Bb) :	0 is	0.00%
Extended strand (Ee) :	24 is	13.33%
Beta turn (Tt) :	0 is	0.00%
Bend region (Ss) :	0 is	0.00%
Random coil (Cc) :	94 is	52.22%
Ambiguous states (?) :	0 is	0.00%
Other states :	0 is	0.00%



Parameters :
Window width : 17
Similarity threshold : 8
Number of states : 3

Prediction result file (text): [\[SOPMA\]](#)

Intermediate result files (text): [\[PSI-BLAST on UniProtKB 50% identity\]](#) [\[KALIGN MSA in CLUSTAL W format\]](#)

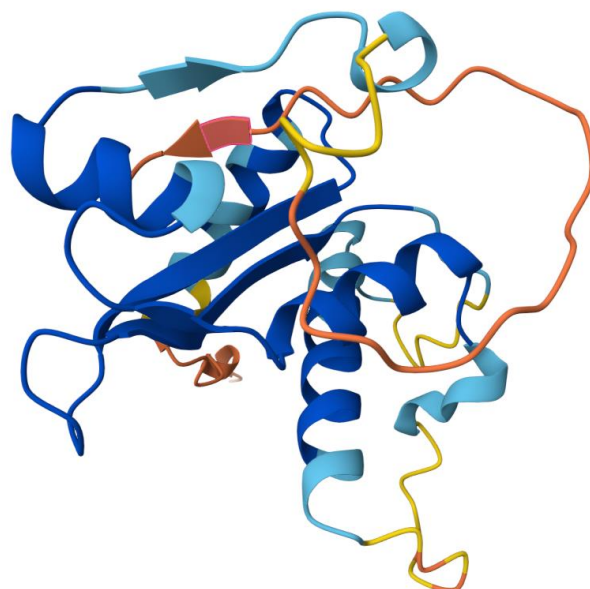
Last modification time : Fri Jan 2 14:11:20 2026. Current time : Fri Jan 2 14:11:20 2026. User : public@114.246.37.230.

蛋白结构分析

kala4蛋白结构预测



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None available in the PDB

72.5 (High)

40% Very high	Very high (pLDDT > 90)
23.3% High	High (90 > pLDDT > 70)
13.9% Low	Low (70 > pLDDT > 50)
22.8% Very low	Very low (pLDDT < 50)

Os04g0557500 protein, Sequence length 180

[Copy sequence](#)

```
1 MASAPPVQEEALQPGTNHFRSRLAAAVRSISWSYTI11FWST21STSLPGVLTW31NDGFYNGEVK41TRKISNLEDL51TADQLVLR61RRSEQ71LSELYYSLLSGECDHRARK81PVAALS91PEDIADTEWY101VVVCMTYAFR111PGQLPGR121SYASNR131SVWLCNAQ141SADSK151  
161 TLSTCALSEERVYSDNCLHPLHEWRA171
```

模型整体置信度较高

Very high/High 置信度, 对应 KALA4 的bHLH 核心结构域 (α -螺旋 + HLH 区, 是功能关键区)

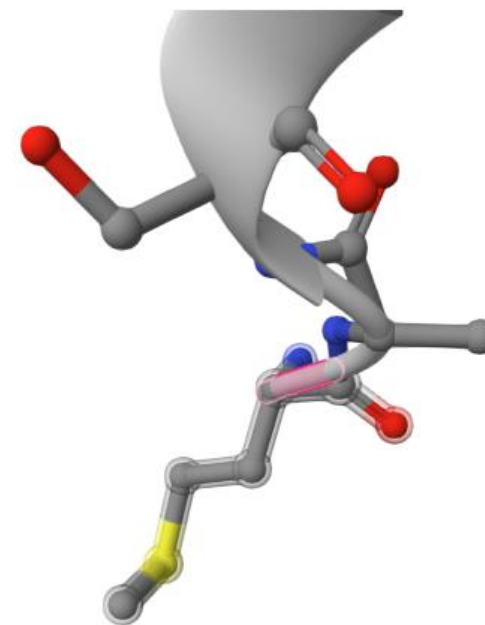
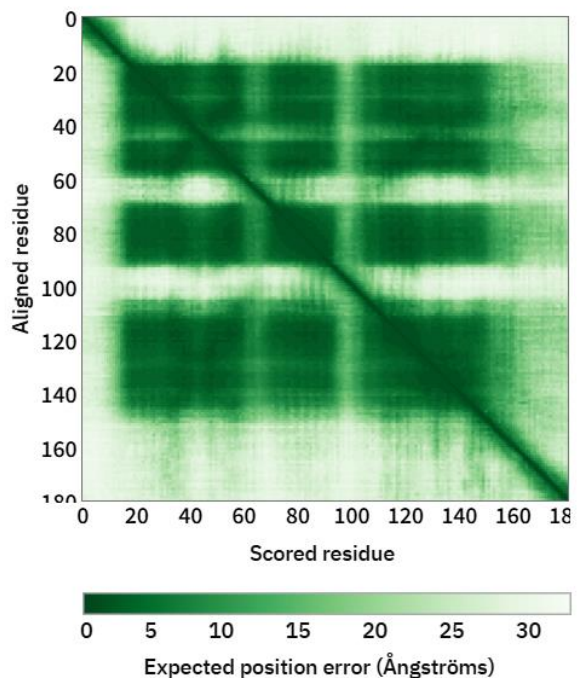
Low/Very low 置信度, 对应之前 SOPMA 预测的“无规卷曲”, 是柔性调控区

蛋白结构分析

kala4蛋白结构域3D结构



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PAE 热图中大部分区域呈深绿色，说明蛋白核心区域的残基相对位置很稳定，进一步印证了核心结构域的可靠性。

图中绿色区域是蛋白的核心折叠区，是 KALA4 作为 bHLH 转录因子的核心功能域。

蛋白结构分析

三级结构,以7fdo.1.A为模板



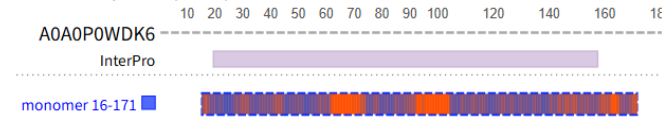
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A0A0P0WDK6 (A0A0P0WDK6_ORYSJ) *Oryza sativa subsp japonica (Rice)*

Os04g0557500 protein ☆ UniProtKB InterPro STRING Interactive Modelling

180 aa; Sequence (Fasta)



It is possible new templates exist for this target since these models were created.

Rebuild Models

Available Structures

1 SWISS-MODEL model

Template	Oligo-state	QMEAN DisCo	Range	Ligands	Trg-Tpl Seq id (%)
7fdo.1.A	monomer	0.63			48.72

Download Model report Compare Structure Assessment

Alignments

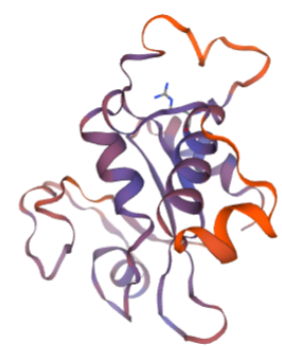
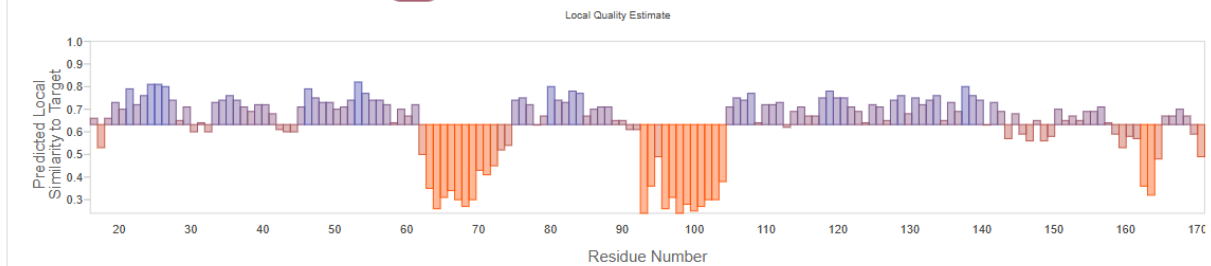
Model based on 7fdo.1.A Transcription factor EGL1

MODEL	TNHFRSRLAAAVRSISW	SYTIFWSTSTSLPGVLTW	NDGFYNGEVK	60
7fdo.1.A	PDNLKQQLAVSVRNIQ	WVSYGIFWVSVASQPGVLE	WGDGYNGDIK	47
MODEL	TRKISNLEDLTDQLVLR	RSEQLSELYSLLSGECD	-----HRA	99
7fdo.1.A	TRKTIQAABVKIDQLGL	RSEQLRELYFSLSLAESSAS	GSSQVTR	92
MODEL	RKPVAAALSPEDIADTE	WYVVCMTYAFRPGQGLPGR	SYASNRSVW	144
7fdo.1.A	RASAAALSPEDLTDTE	WYVVCMTYAFRPGQGLPGR	SALNNGEPIW	137
MODEL	LCNAQSADSKTLSTCAL	SE-----ERVYSDNC		171
7fdo.1.A	LCNAETADSKVFTRSLL	AKSASLQTVVCFPFL		169

SWISS-MODEL based on 7fdo.1.A, SMTL Version 2025-08-20; Trg-Tpl Seq Id 48.72%. *Crystal structure of transcription factor CPC in complex with EGL3*

Q9CAD0

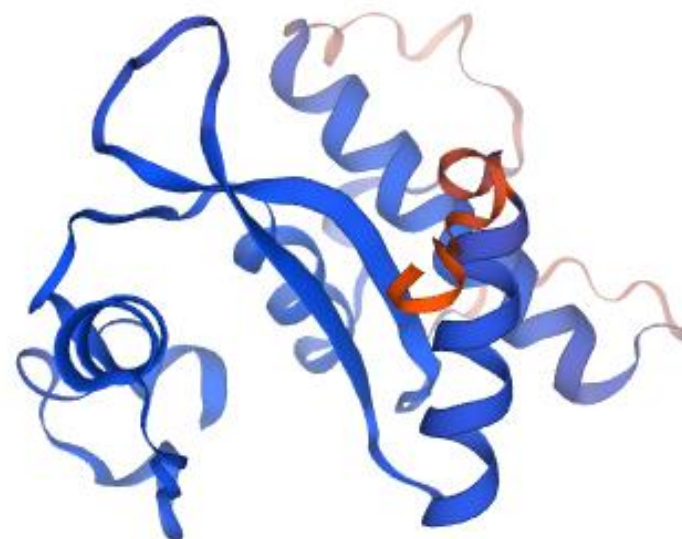
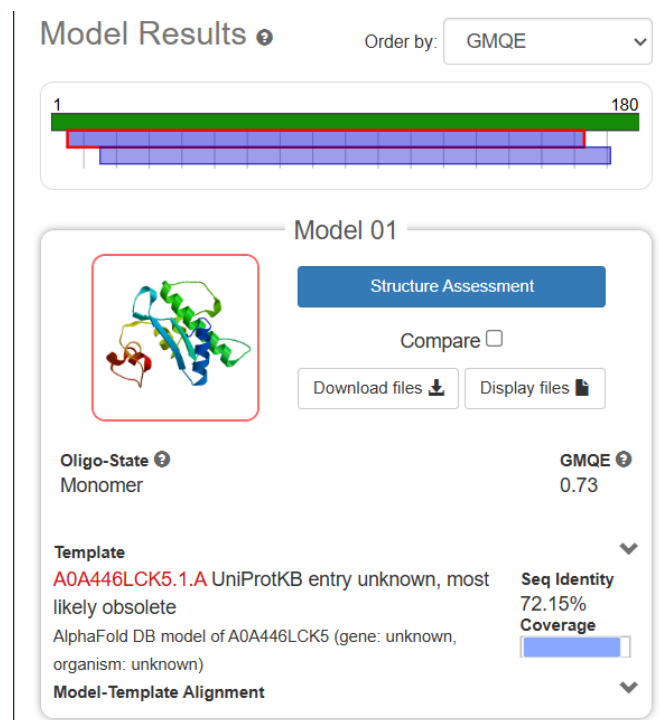
Average Model Confidence (QMEANDisCo): 0.63 ± 0.07; Local Confidence



Cartoon Camera Play Home

蛋白结构分析

三级结构,以A0A446LCK5.1.A为模板



以A0A446LCK5.1.A为模板 (来自 AlphaFold DB 的预测模型), 目标蛋白与模板的序列一致性高达 72.15% (远高于之前模型的 48.72%) —— 序列相似度越高, 模型的结构参考性越强。

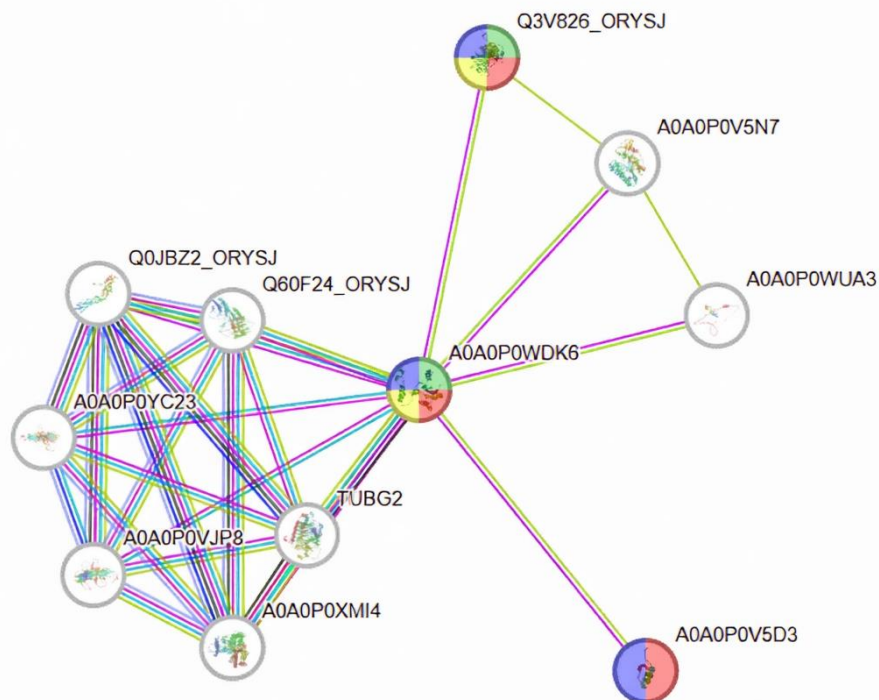


Part
系 5

互作关

互作关系

互作网络



number of nodes: 11
number of edges: 27
average node degree: 4.91
avg. local clustering coefficient: 0.913

expected number of edges: 12
PPI enrichment p-value: 0.0002
your network has significantly more interactions than expected (what does that mean?)

GO:0009957	Epidermal cell fate specification	2 of 9	2.95	1.86	0.00042	●
GO:0090558	Plant epidermis development	3 of 170	1.85	1.45	0.0011	●
GO:0009624	Response to nematode	2 of 28	2.45	1.42	0.0024	●
GO:0010026	Trichome differentiation	2 of 56	2.15	1.12	0.0079	●
GO:0030154	Cell differentiation	3 of 565	1.32	0.71	0.0255	●

KALA4 作为 bHLH 转录因子，通过与 10 个功能关联蛋白互作，核心参与植物表皮发育、毛状体分化（bHLH 家族经典功能），同时协同调控“微管组织、细胞周期”等过程，支撑表皮细胞的形态建成。



Part **6**

下一步计划



1. 蛋白保守结构与亚细胞定位预测

2. 启动子顺式元件分析

小组成员及分工



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G13A-林淑琴:互作关系、蛋白二、三级结构

G13B-石雯:进化树构建、蛋白理化数据分析

G13C-唐紫瑄: PPT汇报

G13D-李慧: PPT制作



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