




冰草*AcSAUR32*基因调控小麦矮秆表型的分子机制研究

The molecular mechanism on regulating dwarf by transferring *A. cristatum AcSAUR32* gene into common wheat

 小组成员：王云、孙吉林、王俊杰、余瑶

 2026.1.10

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冰草

普通小麦

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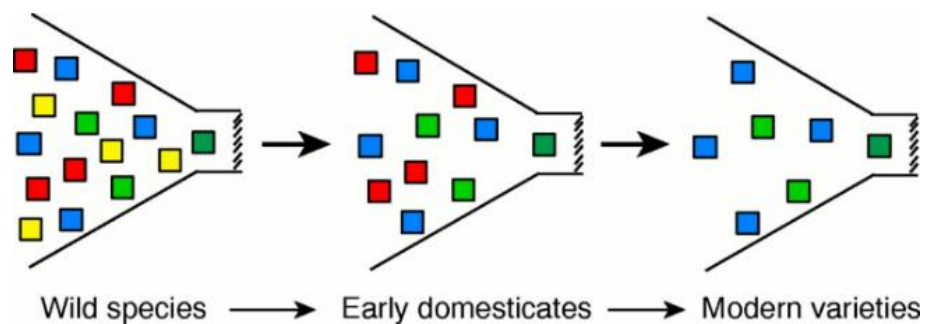
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一、研究背景

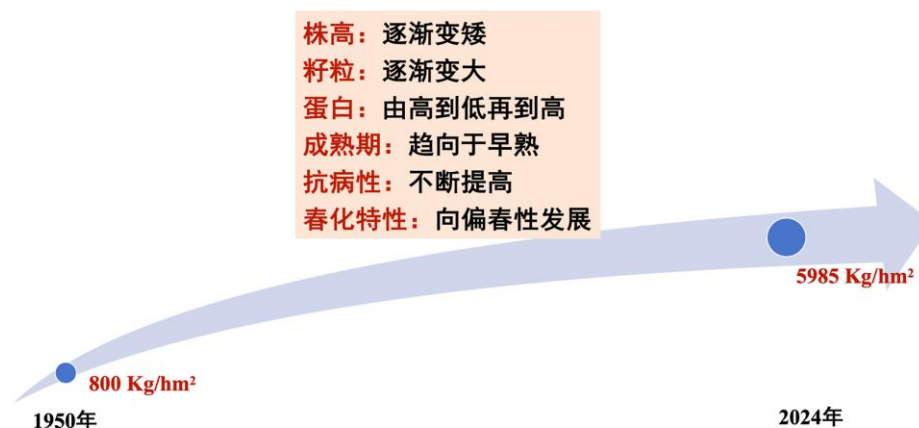
1.1 小麦野生近缘植物对小麦遗传改良有重要意义

普通小麦在长期的驯化过程中，由于**瓶颈效应**，丧失了很多优良基因，限制了其在高产、优质、抗逆等性状改良方面的潜力。随着全球气候的变化和人口的增长，小麦生产面临着产量不足、抗逆性不够的挑战。

小麦属间杂交可以将优良性状相关的基因从野生近缘种转移到栽培小麦中，为小麦的遗传改良提供了新的基因资源，有助于培育出**适应性强、产量高、品质优良**的小麦新品种，从而有效应对气候变化、病虫害威胁以及人口增长带来的粮食需求压力。



遗传瓶颈是指作物在长期的人为选择过程中，在保留后代中遗传多样性逐渐降低的现象



小麦品种的变化趋势

一、研究背景

1.1 小麦野生近缘植物对小麦遗传改良有重要意义



分布于沙漠

冰草属 (*Agropyron L. Gaertn.*)

基因组: 仅含P基因组

高产性状: >300粒/穗, >50穗/株, 穗型近于小麦

理想株型: 株高<60cm, 穗下茎占株高2/3以上, 秆细且弹性强, 旗叶小

品质性状: 籽粒粗蛋白含量18~20%

抗病性状: 经中国农科院植保所鉴定, 1500余份小麦野生近缘中, 只有冰草属物种兼抗白粉、条锈、叶锈、秆锈、黄矮和赤霉等多种病害

抗逆性状: 极强的抗旱和抗寒性, 耐盐碱

小麦改良的最佳外源优异基因供体之一



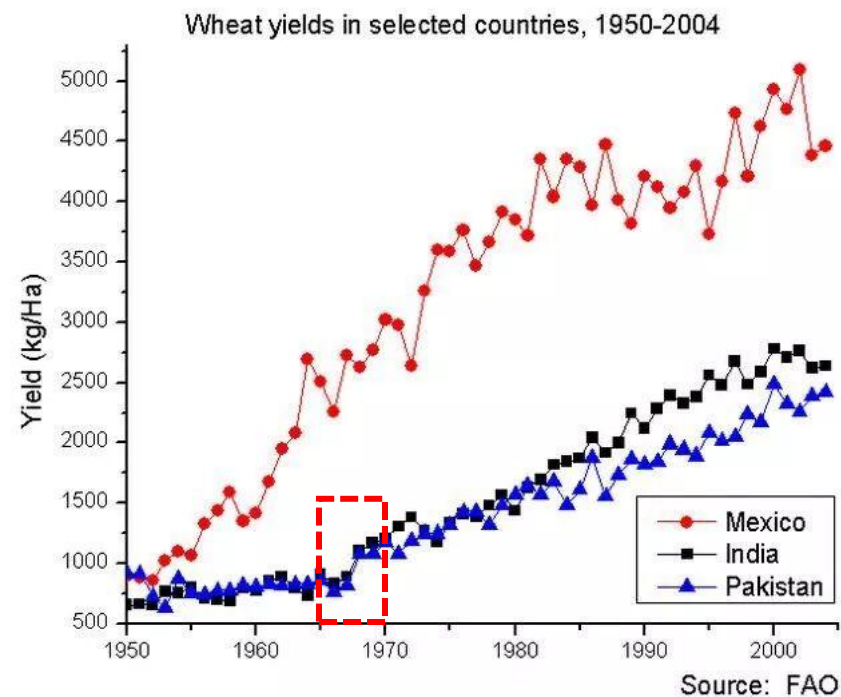
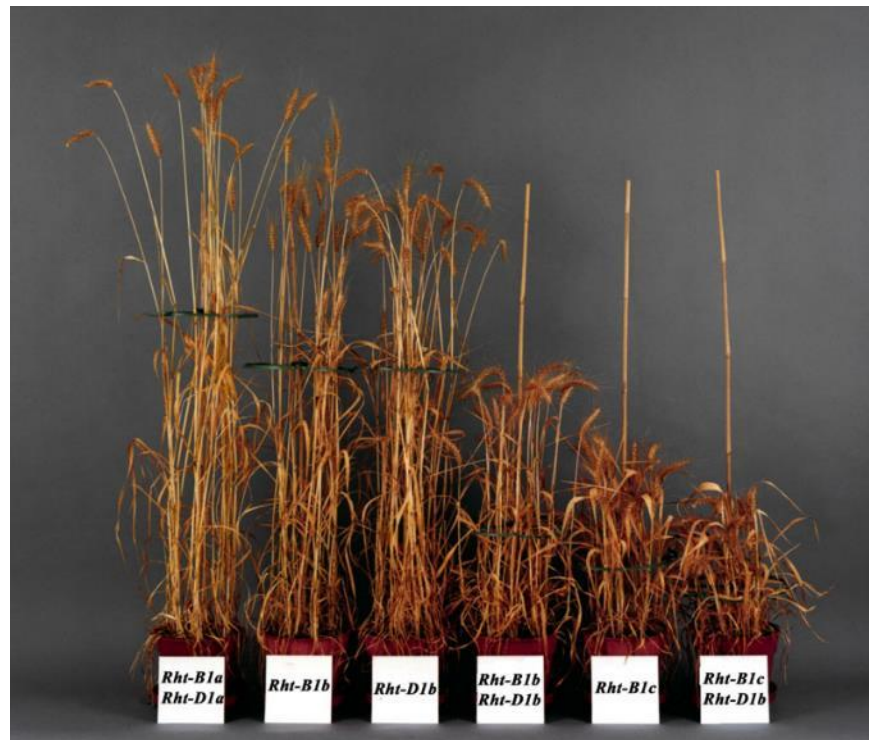
分布于戈壁滩



冰草野生种

一、研究背景

1.2 通过改良作物株型提高种植密度是提高作物产量的有效途径



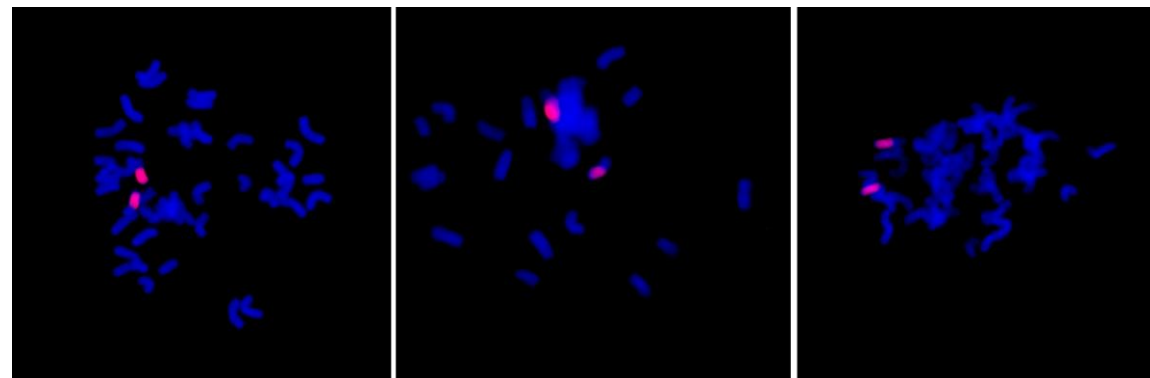
上世纪50年代早期, Dr. Norman E. Borlaug(1914 – 2009)从日本品种**NORIN 10**引入矮秆基因(*Rht1*、*Rht2*)到墨西哥小麦品种, 开创了绿色革命, 1967年印度进口1800吨墨西哥小麦种子, 巴基斯坦随即也引进, 致使小麦产量在五年内翻番。

一、研究背景

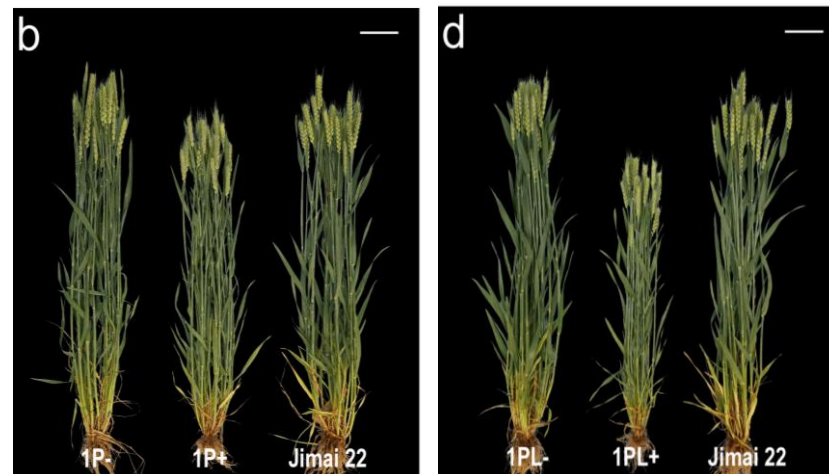
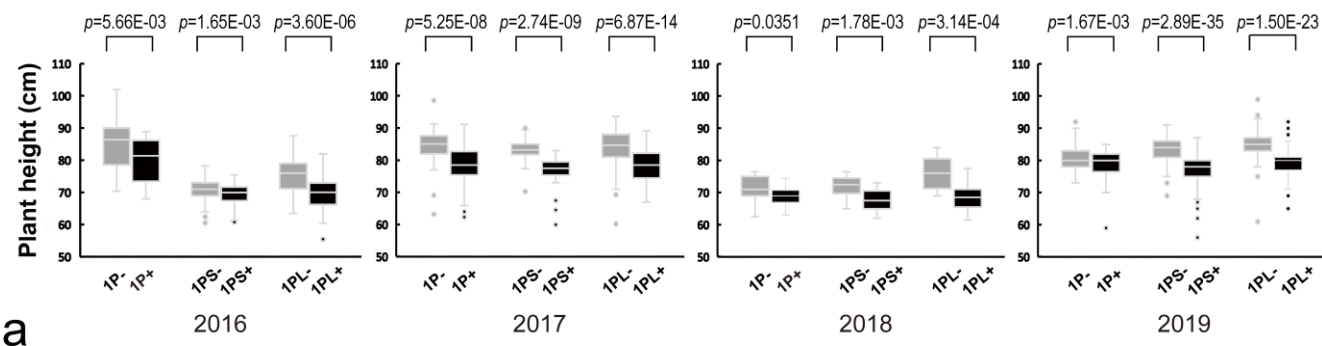
1.3 小麦-冰草1PL易位系株高显著降低

我们实验室已经成功创制小麦-冰草1PL易位系，并通过分子标记检测和基因组原位杂交鉴定证实。

经过多年田间农艺性状调查证明：导入冰草1PL能够降低小麦的株高。（注：a,b,d数据来源于原始材料，即1P、1PL、1PS附加系，已经发表）



GISH验证1PL易位系（红色探针为冰草1PL，蓝色为小麦染色体）



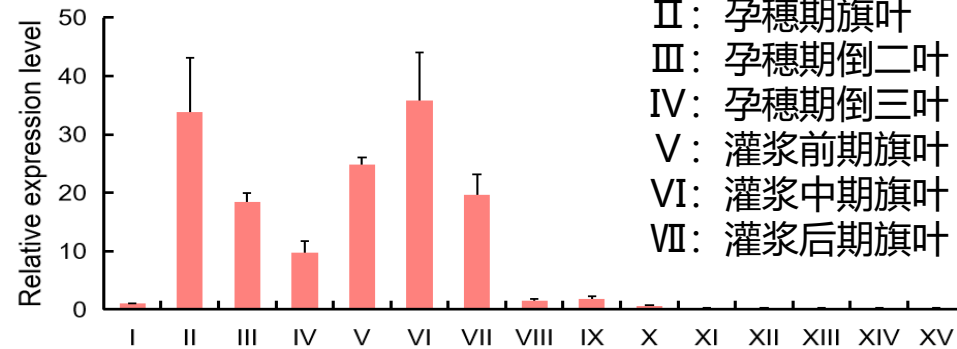
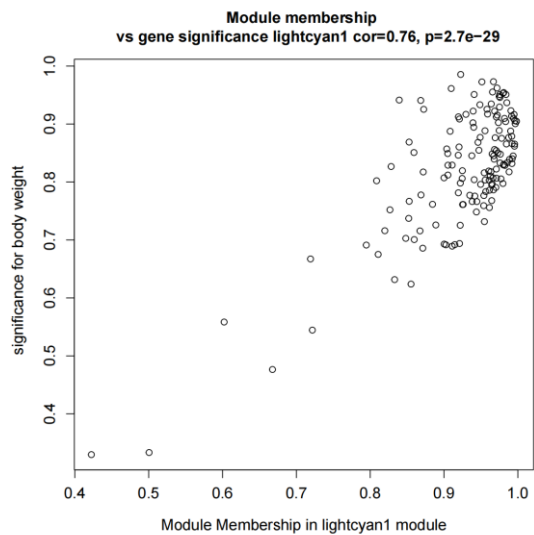
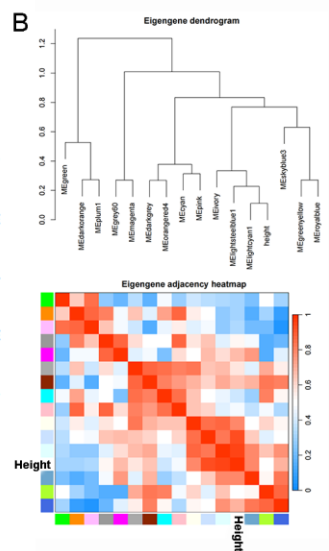
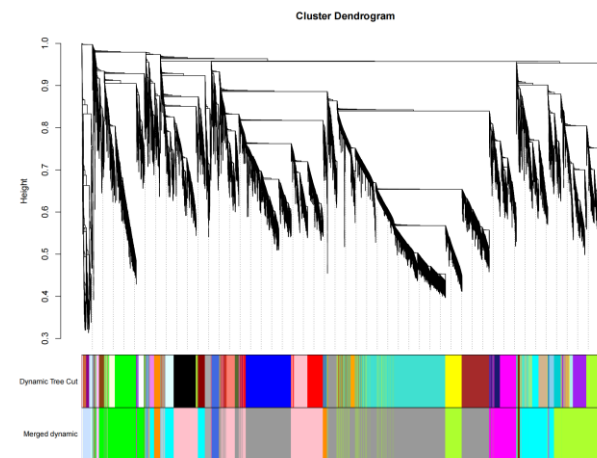
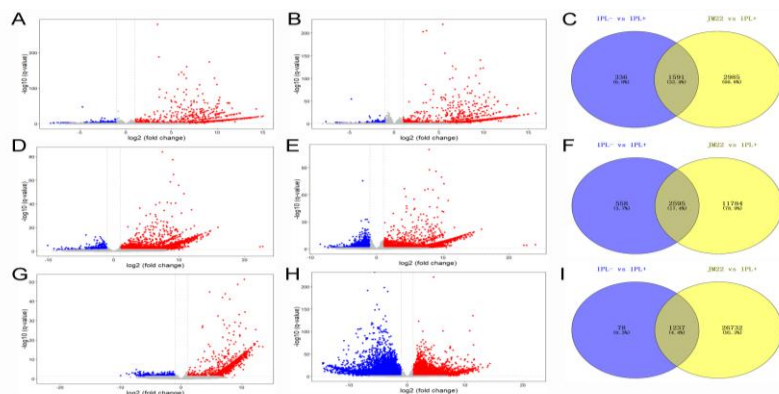
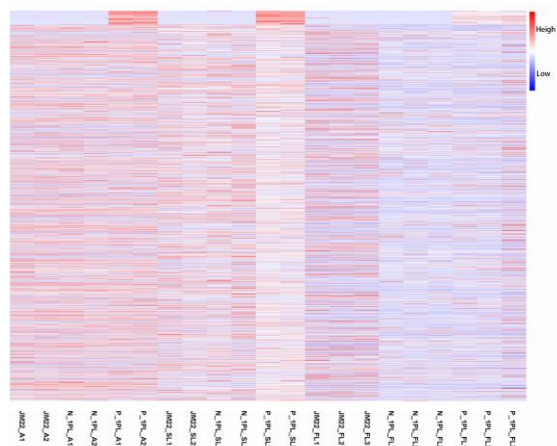
b: 1P附加系阴性植株、阳性植株和济麦22的株型比较对比

d: 1PL附加系阴性植株、1PL阳性植株和济麦22的株型比较对比

一、研究背景

1.4 获得候选基因 *AcSAUR32*

通过转录组分析结合WGCNA分析，获得核心基因 *Acristatum01G026350*。

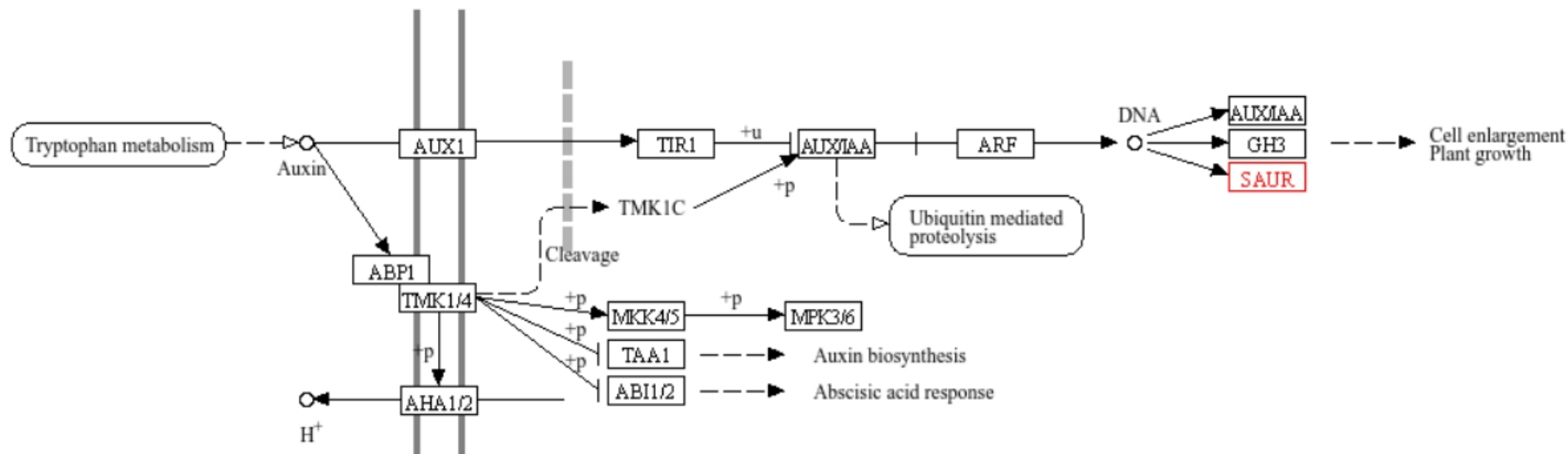


- I : 苗期叶片
- II : 孕穗期旗叶
- III : 孕穗期倒二叶
- IV : 孕穗期倒三叶
- V : 灌浆前期旗叶
- VI : 灌浆中期旗叶
- VII : 灌浆后期旗叶

一、研究背景

1.4 获得候选基因*AcSAUR32*

KEGG分析显示该基因位于生长素信号转导通路，命名为*AcSAUR32* (Small auxin-up RNA, 生长素快速响应基因)



一、研究背景

1.4 获得候选基因*AcSAUR32*

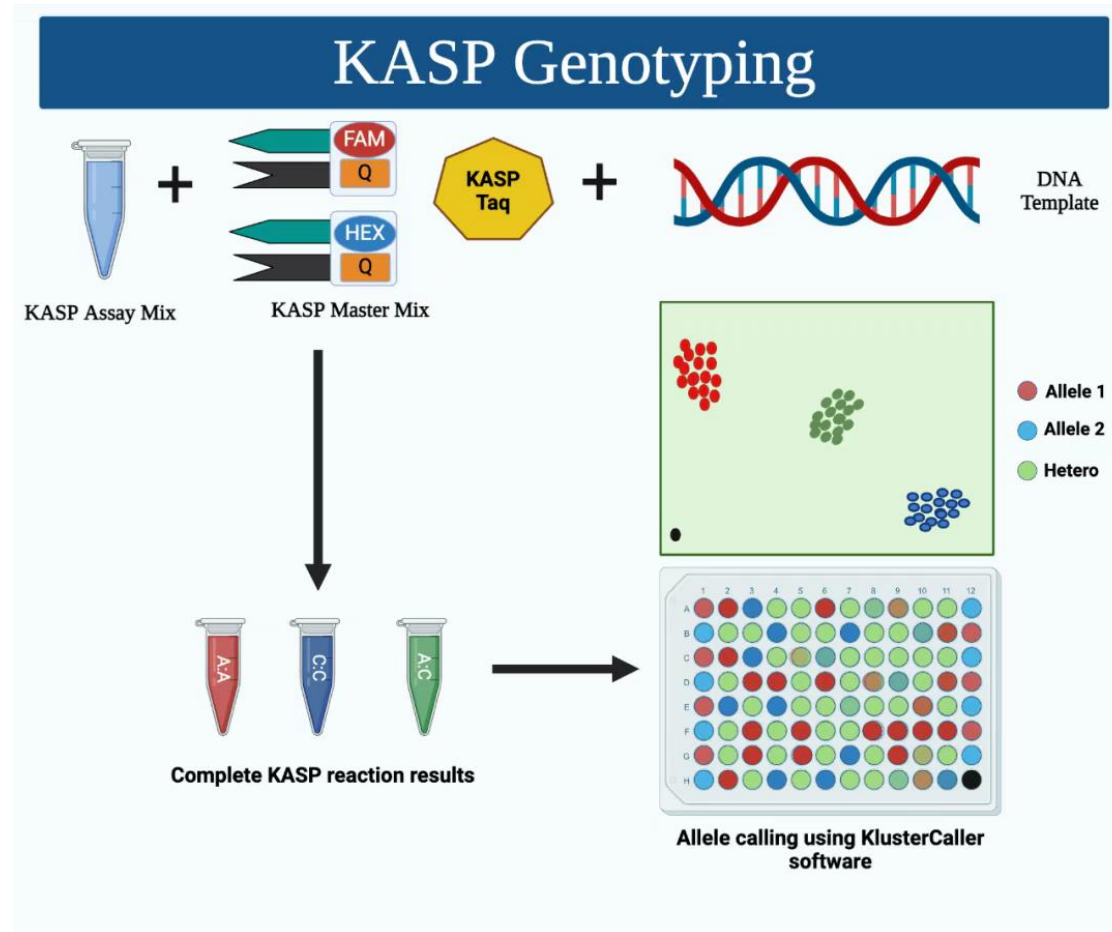
物种	基因名称	主要功能与发现	文献/来源
水稻	OsSAUR45	过表达导致植株 矮化、根系变短 。通过 抑制 生长素合成 (OsYUCCA) 和转运 (OsPIN) 相关基因发挥作用。	Plant Molecular Biology, 2017
水稻	OsSAUR23	正向调控生长素合成与运输。该基因 表达增加 会导致 籽粒变小变轻 ；反之，敲除该基因能获得 籽粒更大更重 的材料。	The Crop Journal, 2025
玉米	ZmSAUR21	在根系优势表达。通过 激活细胞膜上的H⁺-ATP酶活性 ，促进细胞伸长，从而 正向调控玉米幼苗根系总长度 。	扬州大学, 2023
玉米	ZmSAUR15	负向调控 玉米幼胚诱导胚性愈伤组织的能力。敲除该基因能 显著提高 遗传转化中愈伤组织的诱导效率。	The Plant Journal, 2021
棉花	GhSAURX	在 快速伸长的棉纤维 中高表达。在拟南芥中异源表达能 促进主根和下胚轴伸长 ，并上调多个生长素途径基因。	专业期刊, 2024

二、基于多序列比对的KASP引物设计

2.1 KASP (Kompetitive Allele Specific PCR, 竞争性等位基因特异性PCR)

原理：一种基于单核苷酸多态性 (SNP) 的高通量基因分型技术。它利用等位基因特异性引物，实现对目标基因位点的精确识别，能够从基因组水平对**SNP**和**InDel**进行精准分型。在PCR扩增过程中，只有与目标DNA匹配的引物或探针才能有效扩增并产生荧光信号。通过检测特定的荧光信号，可以确定样本的基因型。

优势：高通量、低成本、高准确度、特异性高、稳定性高、简单快捷的结果分析、高效率、共显性。

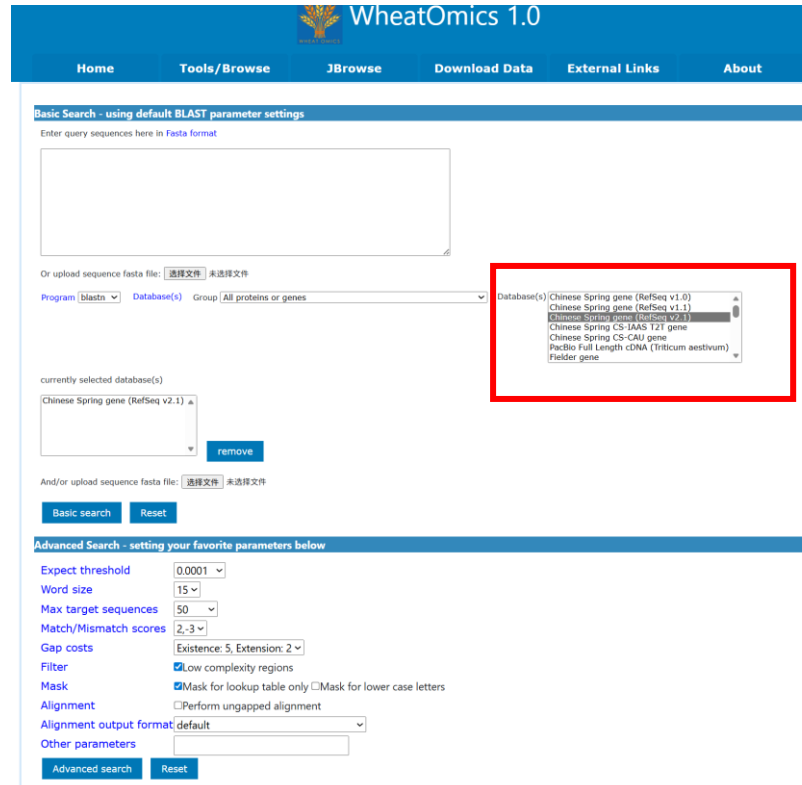
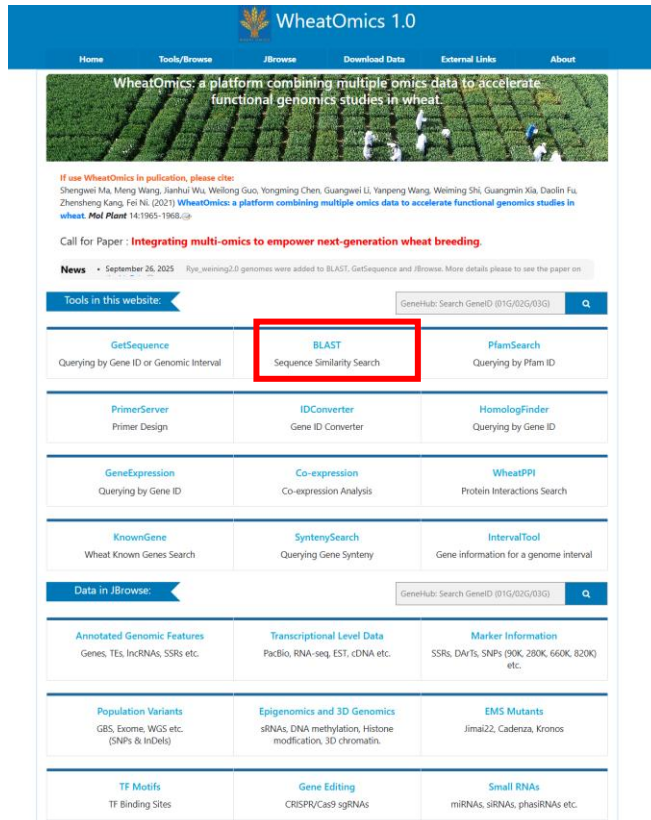


注：由于序列暂时保密，在此以我们实验室对于多序列比对的应用，即KASP引物的设计、验证来代替。

二、基于多序列比对的KASP引物设计

2.2 引物设计

第一步，获得AcSAUR32的小麦同源染色体上的同源基因。在小麦基因组网站WheatOmics 1.0中使用基因的CDS序列进行BLAST，将序列复制粘贴，选择blastn，数据库选中国春2.1，默认参数，获得BLAST结果后下载相似度最高的1A、1B、1D的序列（直接点击）。



二、基于多序列比对的KASP引物设计

2.2 引物设计

第二步，将AcSAUR32和相似度最高的三个1A、1B、1D同源基因整理到同一个FASTA文件中。打开EBI，选择合适的工具进行多序列BLAST，下载结果文件。

第三步，寻找合适的设计位点。

Ac1P01G235900.1	GCCATCTCCA GCTCCGACCC CTGGCCCTTC TCTTCCTAAC CCCAAACCCC
TraesCS1A03G0483200	GCCATCTCCA GCTCCGACCC CTGGCCCTTC TCTTCCTAAC C.CAAACCCC
TraesCS1B03G0589800	GCCATCTCCA GCTCCGACCC CTGGCCCTTC TCTTCCTAAC CCCAAACCCC
TraesCS1D03G0455800.1	GCCATCTCCA GCTCCGACCC CTGGCCCTTC TCTTCCTAAC CCCAAACCCC
Ac1P01G235900.1	TCCT...CCC TCCCGAGCTC GCTCCACCGA TCC.AATCTC TCC.CCTCCT
TraesCS1A03G0483200	GCA..... TCCCGATCTC CC..... TCCC CCCTCCTCCT
TraesCS1B03G0589800	TCCATCCCC TCTCGAGCTC CGCCGTCCGA TCTCCCTCCC CCC.TCTCCT
TraesCS1D03G0455800.1	TCCTCCCGCC TCTCGAGCTC TGCCGTCCGA TCTCCCTCCC CCG.TCTCCT
Ac1P01G235900.1	CCATCTCTC.. AA.....CA AGTCTTGTC GGTCTCTGCGC..CCCGATG
TraesCS1A03G0483200	CCTTCTCTC.. AA.....CA ACTCTTCTCC GGTCTCTGCGC GCCTCCGATG
TraesCS1B03G0589800	CCTTCTCTCGC AACAGCCACA AGACTCGTCC GGTCTCTGCGC..CTCCGATG
TraesCS1D03G0455800.1	CCTTCTCTCGC AACAGCCAGA AGACTCGTCC GGTCTCTGCGC..CTCCGATG
Ac1P01G235900.1	CACCTCAGGC AGC..... ACCAC AGGGCGGAGA TGGTGGCGCC
TraesCS1A03G0483200	CACCTCAGGC AGCAGCAGCA GCAGCAGCAC AGGGCGGAGA TGGTGGCGCC
TraesCS1B03G0589800	CACCTCAGGC AGCAGCAGCA GCACCACAG AGGGCGGATA TGGTGGCGCC
TraesCS1D03G0455800.1	CACCTCAGGC AGCAGCAGCA GCAGCACCAC AGGGCGGAGA TGGTGGCGCC

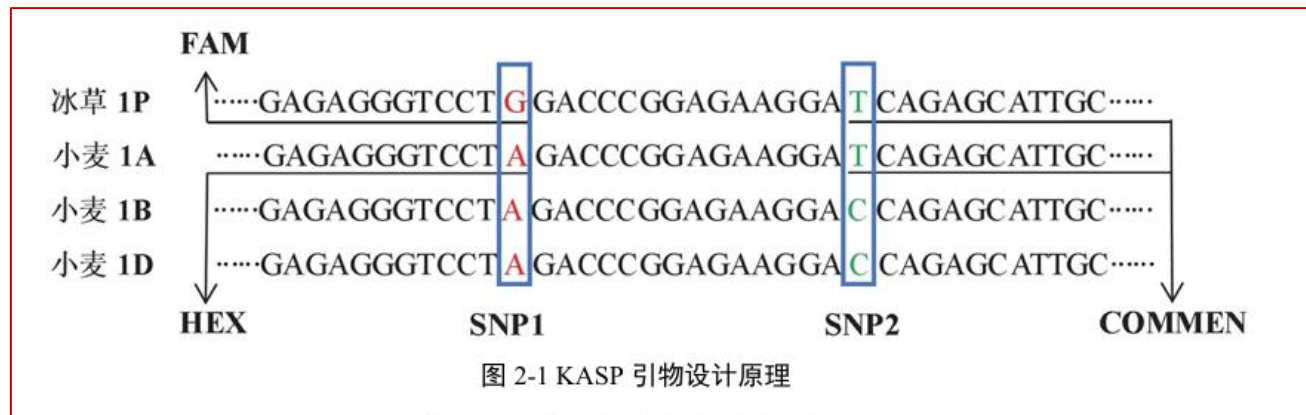


图 2-1 KASP 引物设计原理

如图 2-1，对小麦-冰草 1P/1A 易位系设计引物时，当 5'端前引物为两条的情况下（FAM、HEX），目标 SNP1 为野生近缘种特异即 1P 上位点为 G，但小麦 1A、1B、1D 序列相同即位点为 A，并且目标扩增序列 1A、1P 的 SNP1 位点前，理想状况为没有其它碱基差异。3'端的后引物（COMMEN）是锚定引物，即保证引物只扩增目标序列，目标 SNP2 为冰草 1P、小麦 1A 位点特异即为碱基 T，但小麦 1B、1D 序列相同即位点为 C，类似的，目标扩增序列 1A、1P 的 SNP2 位点后，理想状况为没有其它碱基差异。

二、基于多序列比对的KASP引物设计

2.3 引物验证

引物合成后将三种引物干粉分别稀释至 100 mol/L，工作液 (Primer Mix) 的体积比例按照 12 (FAM) : 12 (HEX) : 30 (通用引物 COMMEN) : 46 (ddH₂O) 混合。384 孔板的 KASP 反应体系如下：每孔总反应体系为 5 μL，1 μL 模板 DNA 稀释液 (50 ng)，0.07 μL Primer Mix，2.5 μL 的 KASP Master Mix (HiGeno 2x Probe Mix B, 北京嘉程生物科技有限公司)，1.43 μL ddH₂O。PCR 反应程序如下：95℃ 预变性 10 min；95℃ 变性 20 s；61℃-55℃ 延伸 40 s，10 个循环；95℃ 变性 20 s，55℃ 复性 40 s，28-34 个循环。

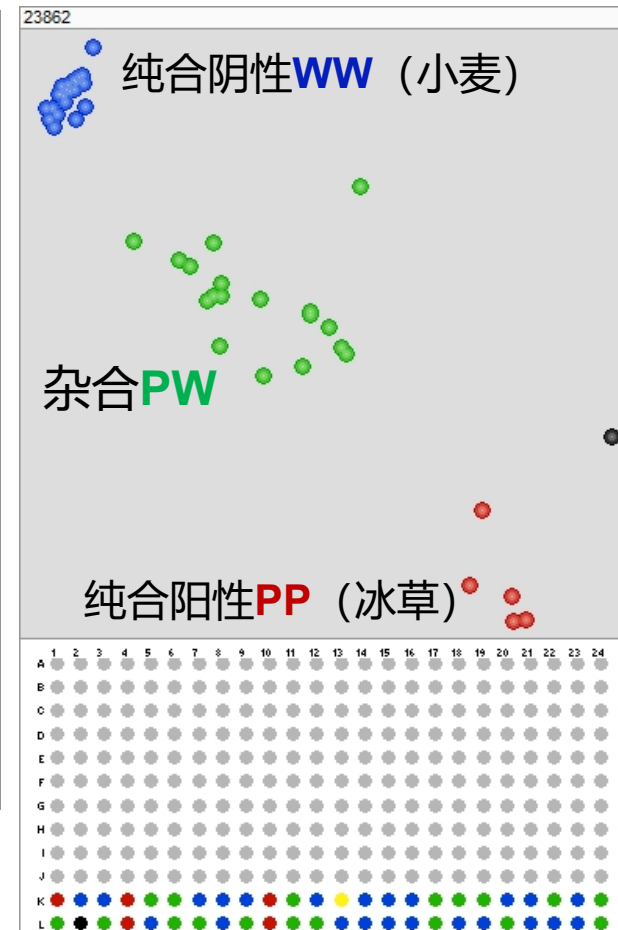
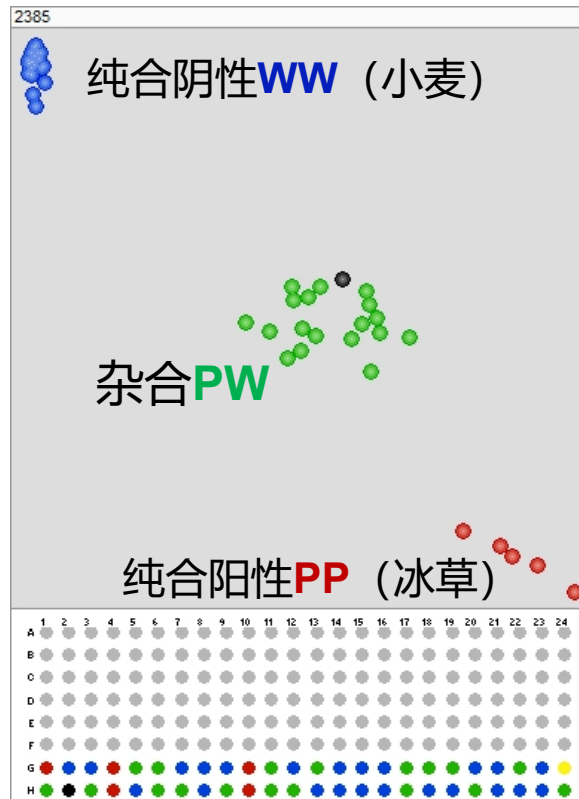
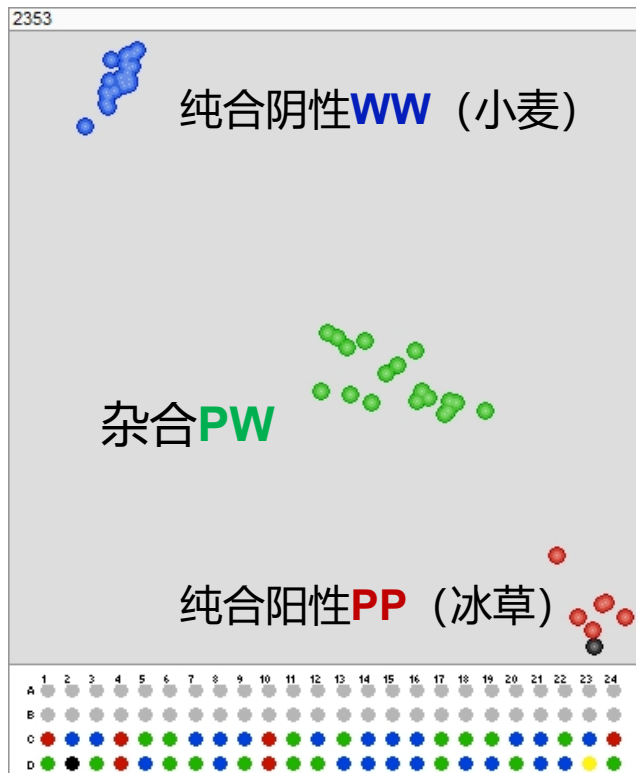
PCR 程序完成后在 BMG LABTECH FLUO star Omega SNP 仪器上读取扩增的荧光值，数据分析使用 Cluster caller 软件。



适用于小麦 (异源六倍体)，其他作物可以通过查找文献，探索合适的体系、程序和参数

二、基于多序列比对的KASP引物设计

2.3 引物验证



验证时，使用一定量的群体，建议使用同一DNA模板，可以相互佐证，筛选准确、分型好的引物

二、基于多序列比对的KASP引物设计

上述多序列比对方法仅适用于少量基因，若进行**大批量**的引物设计，建议使用**本地BLAST**，以1PL纯合易位系为例，先在**ensembl**中下载小麦参考基因组数据FASTA，再用Tbtools将1A1B1D的数据提取出来，另存为文档，后续BLAST建库即可进行大批量的多序列比对，可以在结果文件中大批量的设计引物。

Search

Search Bread wheat... Go

e.g. TraesCS3D02G273600 or 3D:2685940-2634711 or Carboxy*

For information about the assembly and annotation please view the [IWGSC announcement](#).

The previous wheat assembly ([TIGACv1](#)) and every other plant from release 37 is available in the [Ensembl Plants archive](#) site.

About *Triticum aestivum*

Triticum aestivum (bread wheat) is a major global cereal grain essential to human nutrition. Wheat was one of the first cereals to be domesticated, originating in the [fertile crescent](#) around 7000 years ago. Bread wheat is hexaploid, with a genome size estimated at ~17 Gb, composed of three closely-related and independently maintained genomes that are the result of a series of naturally occurring hybridisation events. The ancestral progenitor genomes are considered to be *Triticum urartu* (the A-genome donor) and an unknown grass thought to be related to *Aegilops speltoides* (the B-genome donor). This first hybridisation event produced tetraploid [emmer wheat](#) (AABB, *T. dicoccoides*) which hybridized again with *Aegilops tauschii* (the D-genome donor) to produce modern bread wheat.

Guidelines for gene nomenclature in wheat can be found in the 2013 edition of the Wheat Gene Catalogue available in [GrainGenes](#). The Wheat Gene Catalogue is the internationally agreed rules of nomenclature for wheat genes.

Taxonomy ID [4565](#)

Data source [International Wheat Genome Sequencing Consortium](#)

[More information and statistics](#)

Genome assembly: [IWGSC](#)

[More information and statistics](#)

[Download DNA sequence \(FASTA\)](#)

[Convert your data to IWGSC coordinates](#)

[Display your data in Ensembl Plants](#)

Other cultivars

This species has data on 18 additional cultivars. [View list of cultivars](#)

View karyotype

Example region

Gene annotation

What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

[More about this genebuild](#)

[Download genes, cDNAs, ncRNA, proteins - FASTA - GFF3](#)

[Update your old Ensembl IDs](#)

Carboxy* CAB
ADH F-box
PSII

Example gene

Example transcript

```
1P1Gresults.fasta
D: > a-blast-2.16.0+ > results > 1P1Gresults.fasta
465710
465711
465712
465713 Query_1785 1 ATGGCCGCGGACGGCAGAGGTGGGTGGGCTGGCGGTGGACTTCTCGGAGGGGAGCCGC 60
465714 TraesCS1A02G106600.1 1 .....T..... 60
465715 TraesCS1B02G124100.2 1 .....T..... 60
465716 TraesCS1D02G108300.1 1 .....T.....G..... 60
465717 TraesCS1B02G124100.1 1 .....T..... 60
465718
465719 Query_1785 61 GCGGCGCTGCAGTGGGCGGCGGACAACCTGCTCCGCTCCGGCGACAACCTGCTCCTCCTG 120
465720 TraesCS1A02G106600.1 61 .....T..... 120
465721 TraesCS1B02G124100.2 61 .....G..... 120
465722 TraesCS1D02G108300.1 61 .....G..... 120
465723 TraesCS1B02G124100.1 61 .....G..... 120
465724
465725 Query_1785 121 CACGTCCTCAAGGACCCCGACTACGAGCAGGGGAGACCCCTCTGGGAGGCTCCGGC 180
465726 TraesCS1A02G106600.1 121 .....C..... 180
465727 TraesCS1B02G124100.2 121 .....C..... 180
465728 TraesCS1D02G108300.1 121 .....C..... 180
465729 TraesCS1B02G124100.1 121 .....C..... 180
465730
465731 Query_1785 181 TCGCCTTAAATCCCCTCTCGGAGTTCTCTCACCTTCAACCGCAAAGAAATACGGGGTG 240
465732 TraesCS1A02G106600.1 181 .....G.....T.....T..... 240
465733 TraesCS1B02G124100.2 181 ..C....G.....T.....T..... 240
465734 TraesCS1D02G108300.1 181 .....G.....TT.....G..T..T... 240
465735 TraesCS1B02G124100.1 181 ..C....G.....T.....T..... 240
465736
```

三、进化分析

3.1 氨基酸序列的获得

拟南芥：在TAIR-Home中直接搜索SAUR，然后下载所有结果的氨基酸序列，与AcSAUR32保存在一起。

小麦：在WheatOmics 1.0中进行BLAST，选择blastn，数据库选中国春2.1，默认参数。去除低置信结果后，下载全部CDS序列，使用在线软件翻译为氨基酸序列，也与AcSAUR32保存在一个txt文件中。

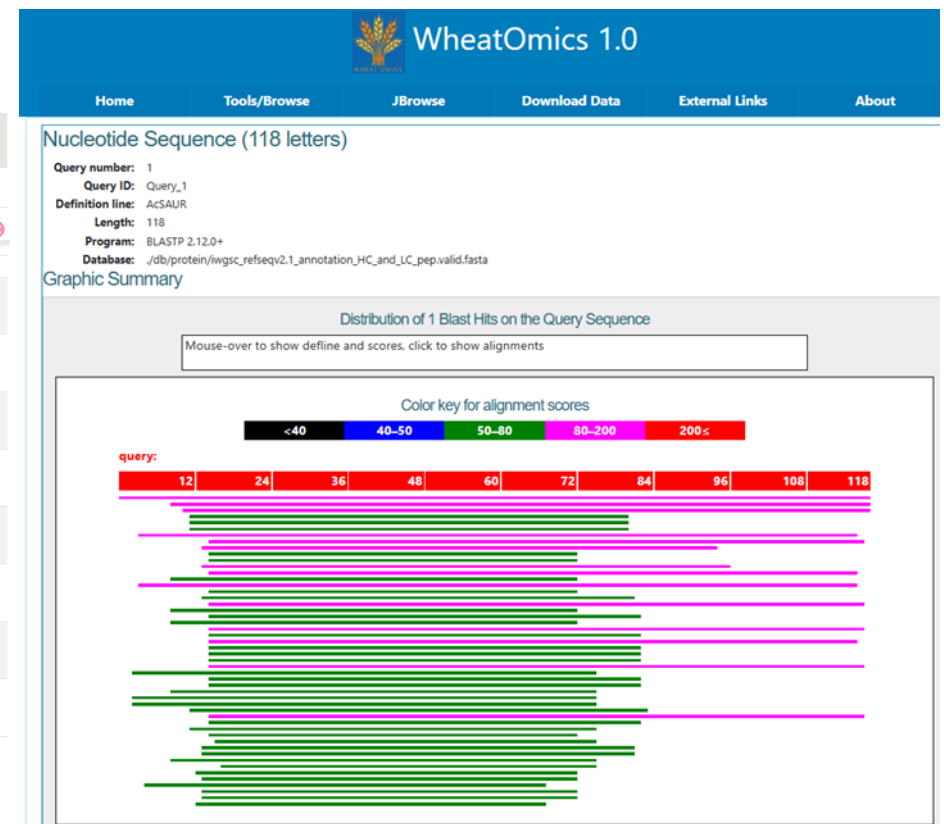
TAIR Search Results

New Search Download All Download Checked
Get GO Annotations Get PO Annotations Get Sequences Get Gene Descriptions Get Locus History Get Microarray Elements

Your query for genes where gene name, description, phenotype, locus name, uniprot id or GenBank accession contains the term SAUR resulted in 90 matches

Select All Clear Selected Displaying 1 - 25 of 90 results Results per page (top): 25 1 2 3 4

No.	Locus	Description
1	AT1G29430	Other Names: SAUR62;SMALL AUXIN UPREGULATED RNA 62 SAUR762 expression is induced during pollination and expressed in pollen tubes. SAUR62 likely functions in translation of proteins required for pollen tube development/function.
2	AT1G79130	Other Names: SAUR40;SMALL AUXIN UPREGULATED 40 SAUR-like auxin-responsive protein family.(source: Araport11)
3	AT1G56150	Other Names: SAUR71;SMALL AUXIN UPREGULATED 71 SAUR-like auxin-responsive protein family.(source: Araport11)
4	AT1G29490	Other Names: SAUR68;SMALL AUXIN UPREGULATED 68 SAUR-like auxin-responsive protein family.(source: Araport11)
5	AT3G12830	Other Names: SAUR72;SMALL AUXIN UPREGULATED 72 SAUR-like auxin-responsive protein family.(source: Araport11)
6	AT1G17345	Other Names: SAUR77;SMALL AUXIN UPREGULATED RNA 77 SAUR-like auxin-responsive protein family.(source: Araport11)
7	AT4G34800	Other Names: SAUR4;SMALL AUXIN UPREGULATED RNA 4 SAUR-like auxin-responsive protein family.(source: Araport11)
8	AT4G34770	Other Names: SAUR1;SMALL AUXIN UPREGULATED RNA 1 SAUR-like auxin-responsive protein family.(source: Araport11)

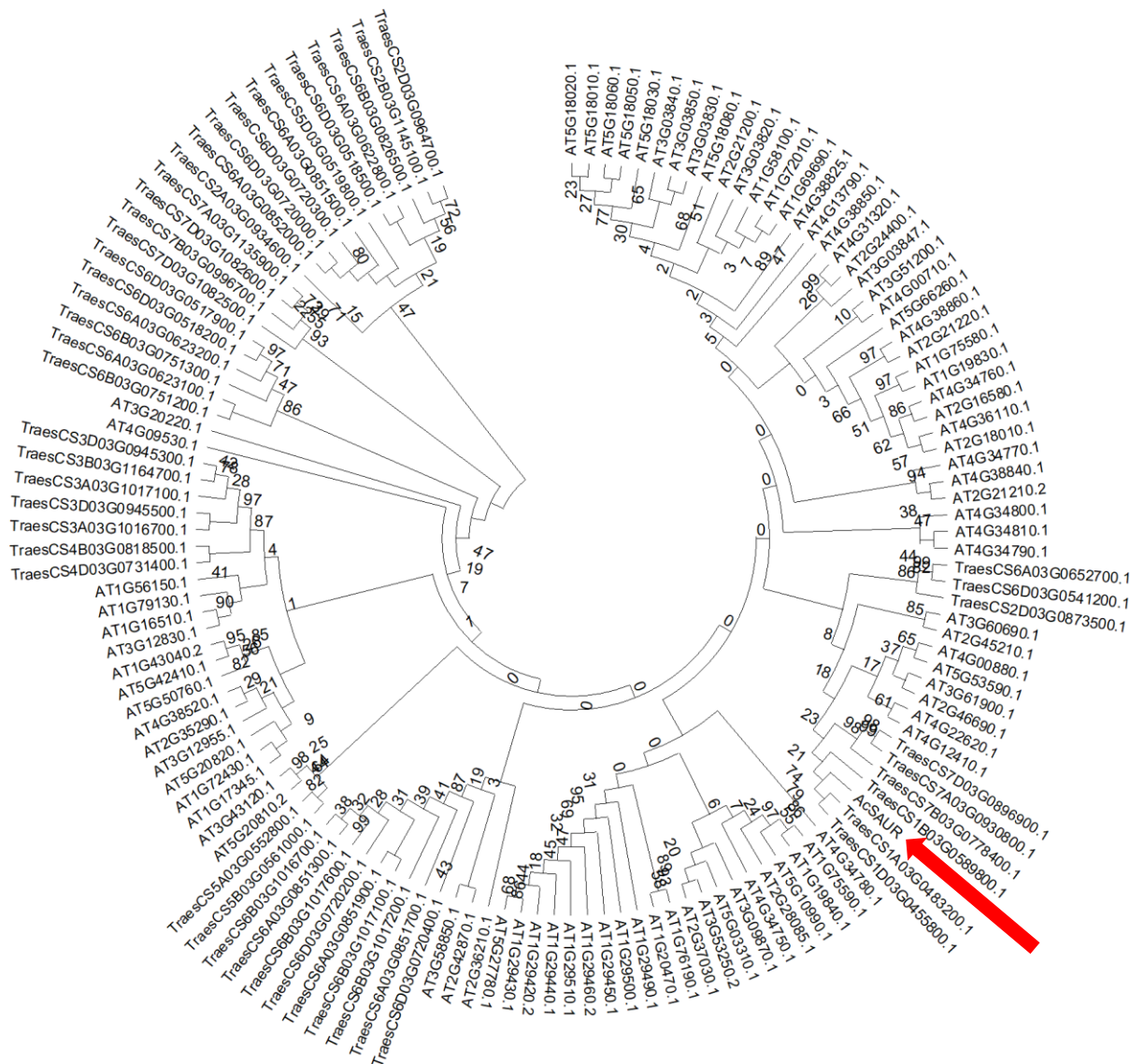


三、进化分析

3.2 进化树构建

打开MEGA12，选蛋白质，用MUSCLE（较大规模的远缘序列），默认参数进行对齐。去除拟南芥中的两个假基因（存在非法字符，会报错），基于远缘序列、氨基酸长度较短、序列数较多，考虑到模型和计算时间，最后选择邻接法（Neighbor-joining）、自举法，为获得较准确的结果，Bootstrap replicates设置为1000，选择JTT模型，其他参数默认。因为序列较多，调整为环形图、改变进化树尺寸和字体大小。

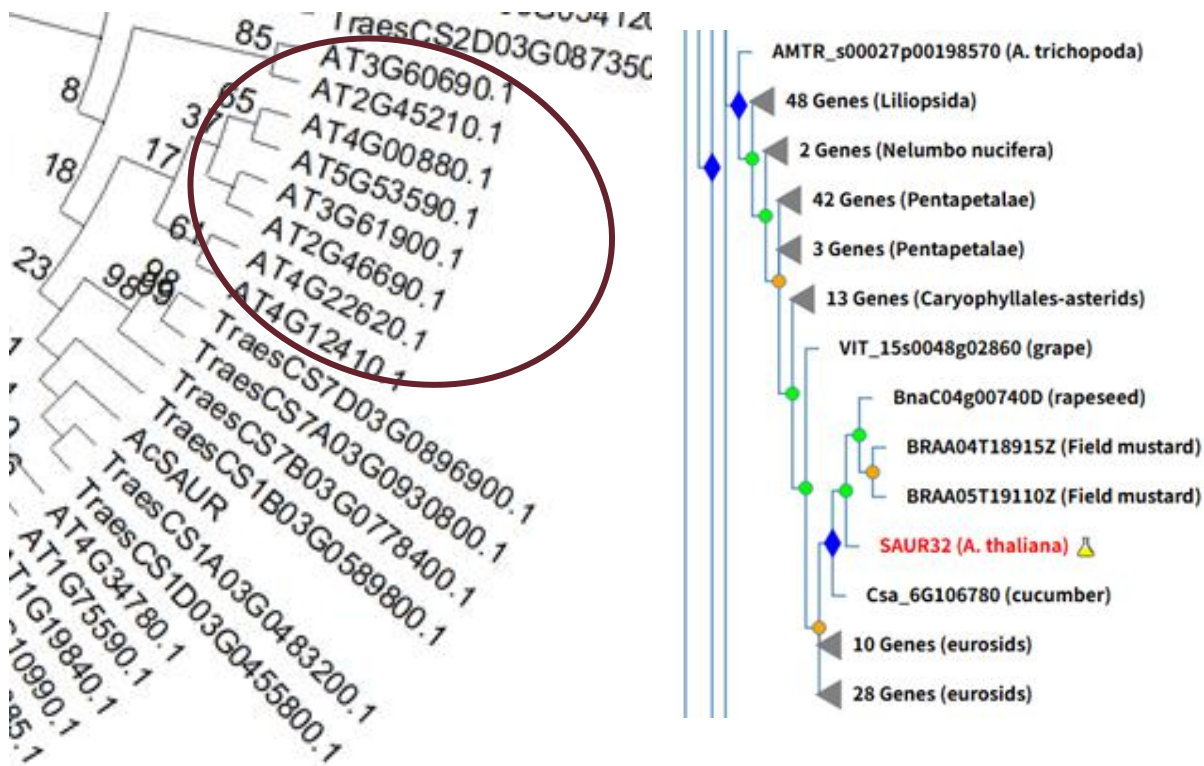
红色箭头所指即为AcSAUR32所在类群，可以发现该基因与同源群1A、1D上的同源基因聚在一起，符合预期。



三、进化分析

3.3 进化分析

由于小麦网站里面没有找到基因名称，因此从距离最近的拟南芥基因ID入手，发现与拟南芥的SAUR59、36、32等同属一个类群。在此我们选择同源基因SAUR32，通过DeepSeek找到一个关于SAUR家族分类的文献（划分为10个分支和3个亚家族）。



数据来源说明

尽管主要权威数据库收录了SAUR32，但它们并未提供分类信息。具体如下：

- TAIR数据库 (拟南芥信息库) 确认了 AT2G46690 就是 SAUR32 基因，并显示其蛋白质含有 SAUR_fam 结构域，但没有涉及家族内部的分类 1。
- 专业学术论文中有一项于2021年发表的关于SAUR32功能的研究，论文详细探讨了它在干旱胁迫和ABA信号通路中的作用，但同样未提及该基因在SAUR家族中的具体类别 3 5 7。

后续查询建议

要找到这个问题的答案，你可以尝试以下方法：

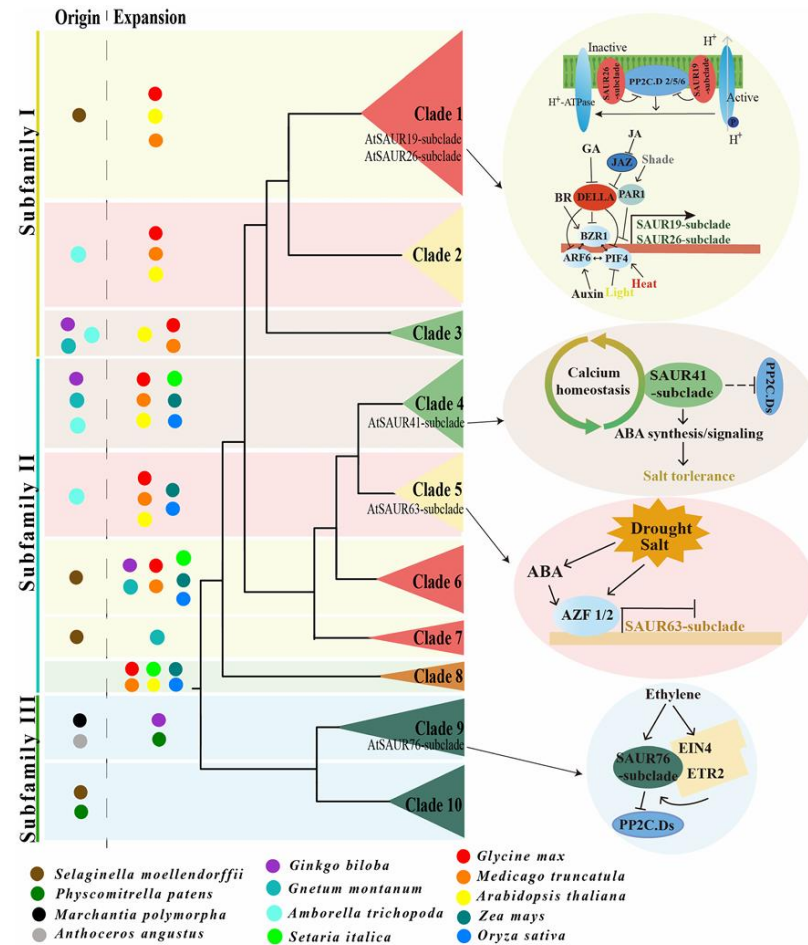
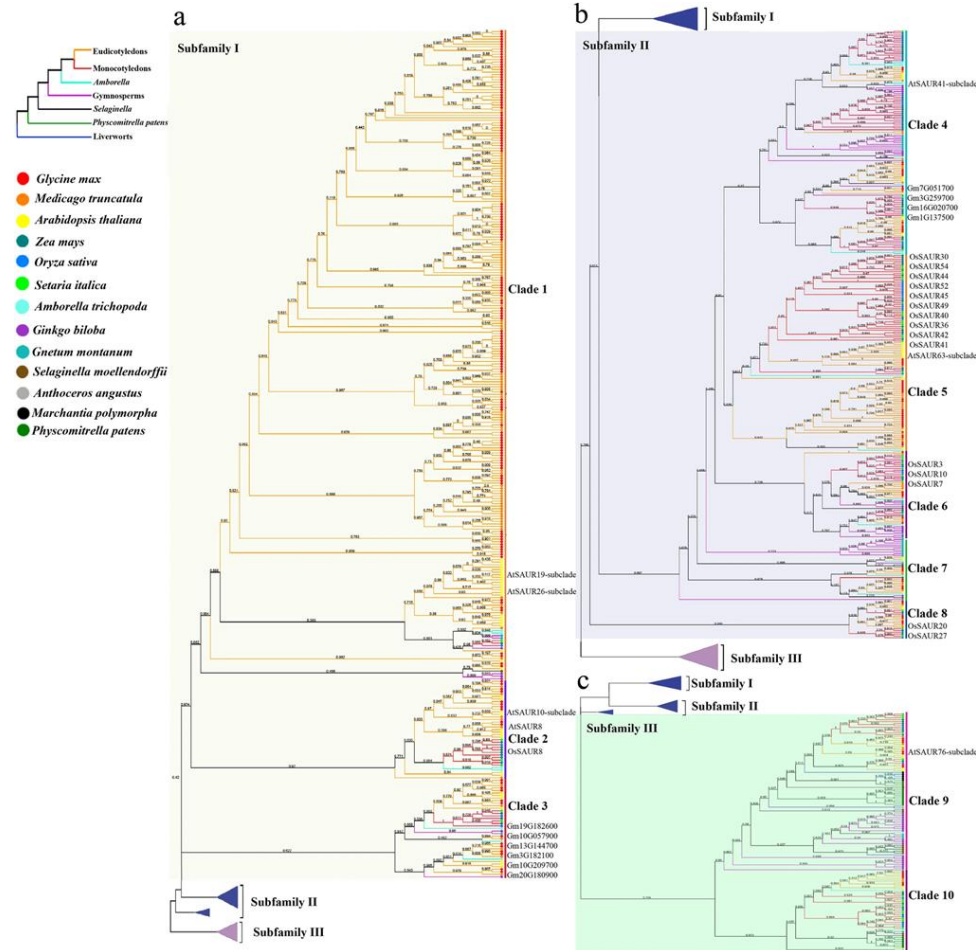
1. 查阅全面的SAUR家族分类文献
根据另一项系统研究 SAUR蛋白家族可被划分为 10个分支 (clade) 和3个亚家族 (subfamily) 8。
你可以查找这类对拟南芥全部SAUR成员进行系统进化分析的研究，其中通常包含详细的分类树状图或附表，列出每个基因（包括SAUR32）的归属。
2. 使用更专业的生物信息学工具
你可以尝试在 Phytozome、Ensembl Plants 等植物基因组平台上，直接调取拟南芥所有SAUR蛋白的序列，并利用 MEGA 等软件自行构建系统进化树进行分析。

如果你需要，我可以帮你查找进行SAUR家族全基因组鉴定与进化分析的相关文献，以确定其具体类别。

三、进化分析

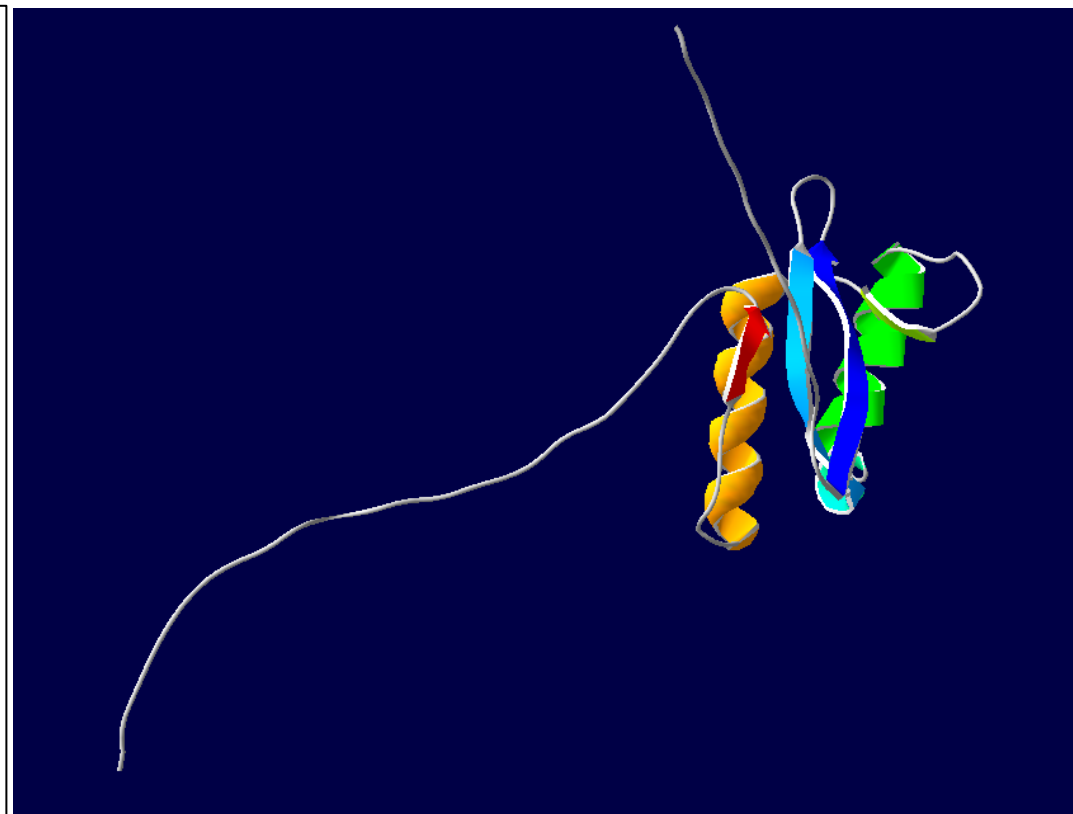
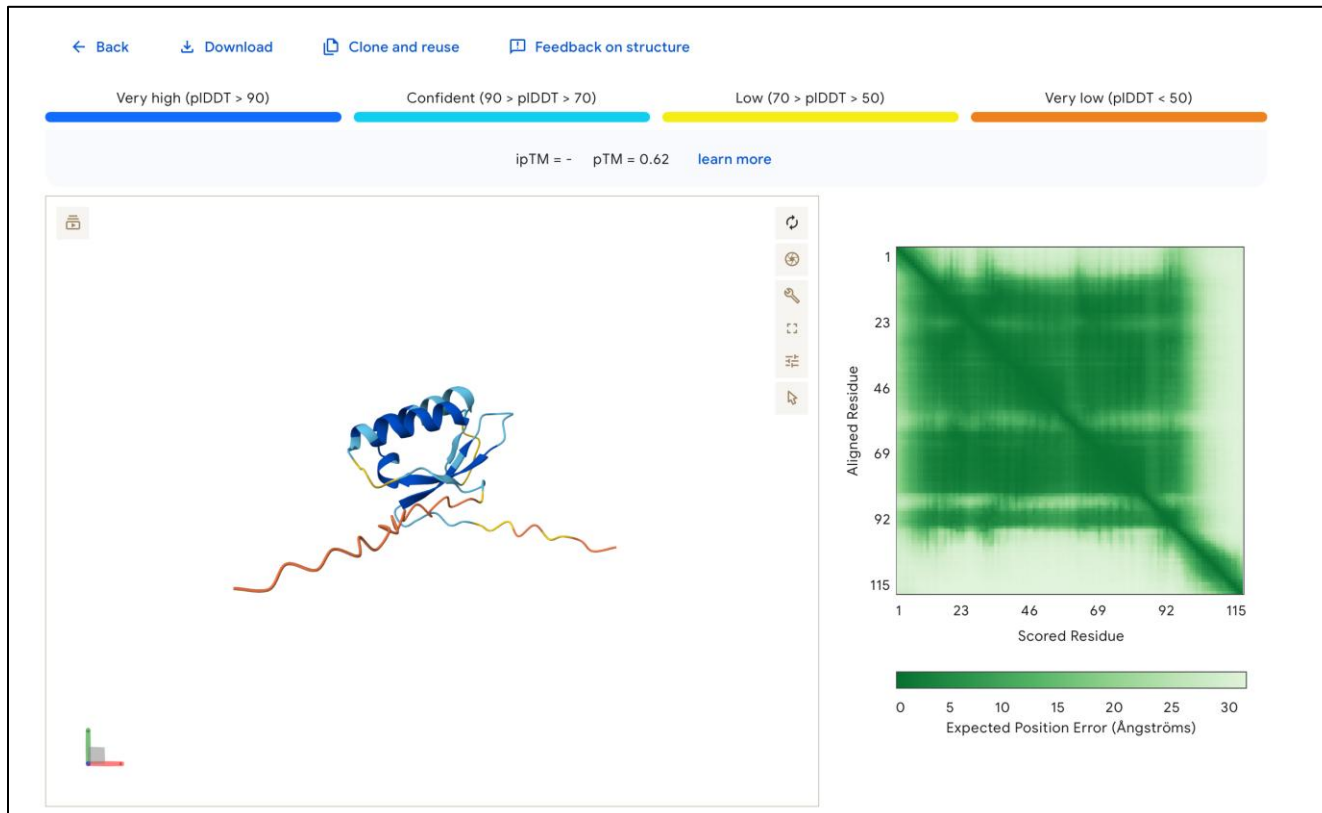
3.3 进化分析

通过分析文献中分类，确定AcSAUR32属于Clade 4。



四、结构与功能分析

AlphaFold3预测AcSAUR32蛋白结构

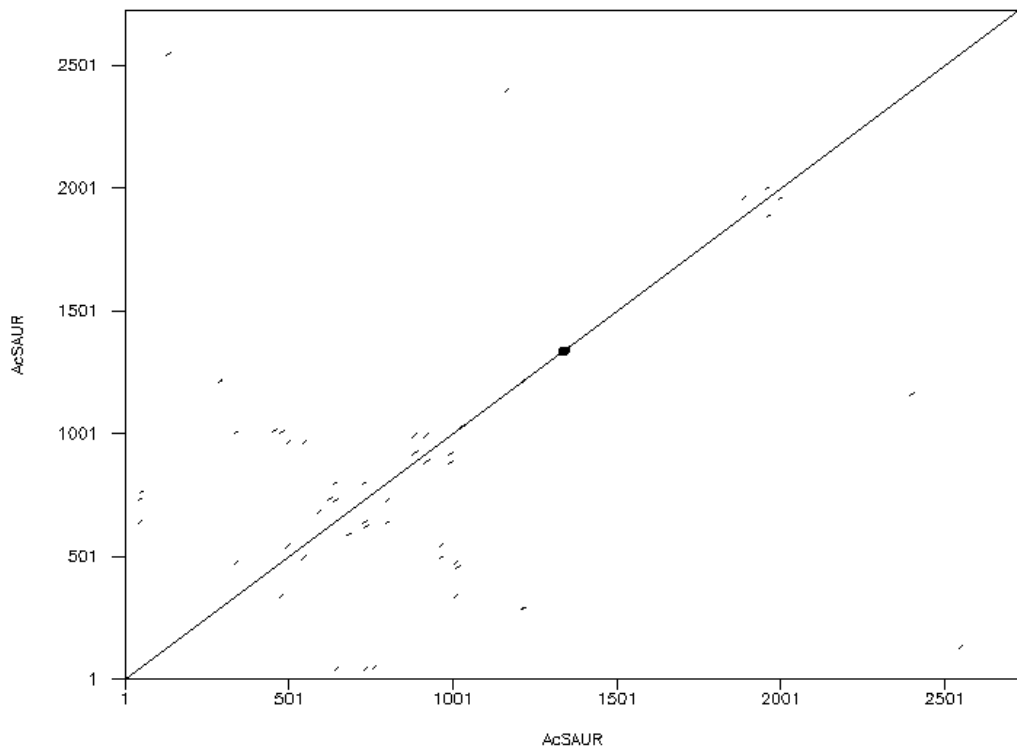


四、结构与功能分析

使用EBI Dottup，输入目前扩增出来的最长核苷酸序列，发现序列中不存在大片段的重单元。

使用ProtParam，输入氨基酸序列，计算蛋白质的各种物理和化学参数。

Dottup: fasta::emboss-dottup-l20251229-070001-0350-30901...
Mon 29 Dec 2025 07:00:06



Number of amino acids: 117
Theoretical pI: 6.94
Molecular weight: 13250.13

Amino acid composition: [CSV format](#)

Ala (A)	11	9.4%
Arg (R)	12	10.3%
Asn (N)	0	0.0%
Asp (D)	7	6.0%
Cys (C)	4	3.4%
Gln (Q)	4	3.4%
Glu (E)	8	6.8%
Gly (G)	11	9.4%
His (H)	15	12.8%
Ile (I)	3	2.6%
Leu (L)	12	10.3%
Lys (K)	2	1.7%
Met (M)	2	1.7%
Phe (F)	6	5.1%
Pro (P)	5	4.3%
Ser (S)	1	0.9%
Thr (T)	2	1.7%
Trp (W)	0	0.0%
Tyr (Y)	1	0.9%
Val (V)	11	9.4%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	0	0.0%

Extinction coefficients:

This protein does not contain any Trp residues. Experience shows that this could result in more than 10% error in the computed extinction coefficient. Extinction coefficients are in units of $M^{-1} cm^{-1}$, at 280 nm measured in water.
Ext. coefficient 1740
Abs 0.1% (=1 g/l) 0.131, assuming all pairs of Cys residues form cystines

Ext. coefficient 1490
Abs 0.1% (=1 g/l) 0.112, 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 16.69
This classifies the protein as stable.

Aliphatic index: 86.67

Grand average of hydropathicity (GRAVY): -0.312

Total number of negatively charged residues (Asp + Glu): 15
Total number of positively charged residues (Arg + Lys): 14

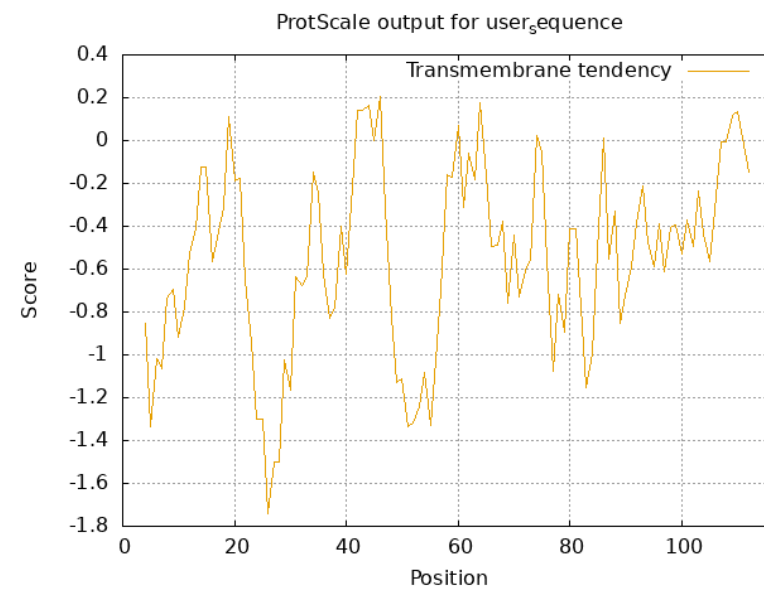
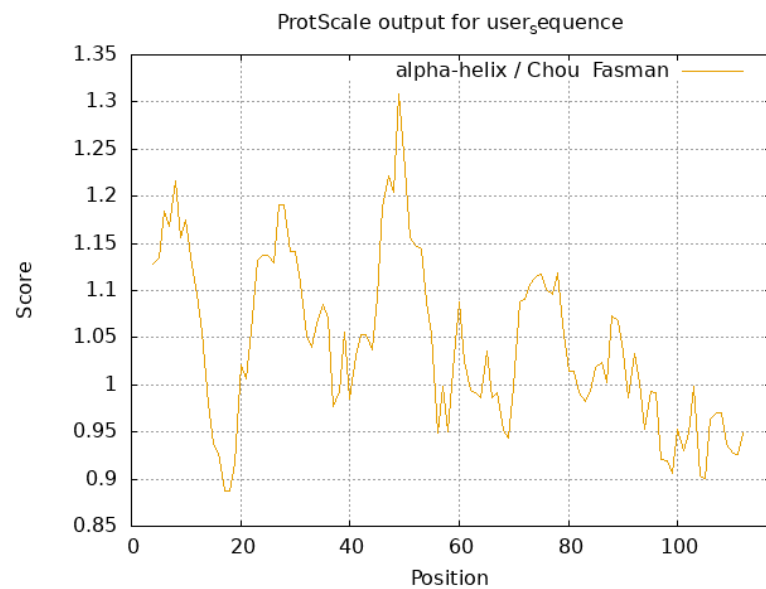
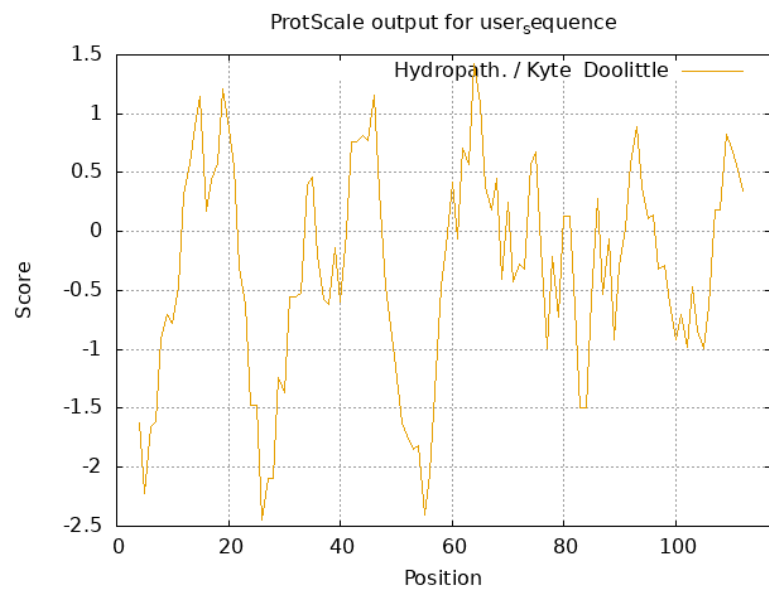
Atomic composition:

Carbon	C	583
Hydrogen	H	905
Nitrogen	N	189
Oxygen	O	156
Sulfur	S	6

Formula: $C_{583}H_{905}N_{189}O_{156}S_6$
Total number of atoms: 1839

四、结构与功能分析

使用ProtScale，输入氨基酸序列，分别对疏水性、 α -螺旋、跨膜倾向性进行分析。



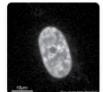
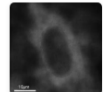
四、结构与功能分析

4.2 亚细胞定位预测

Welcome to *openGPS*

openGPS Home Predict Results Submit About Contact us →

Prediction Results

NO.	Protein ID	Localization	Nucleus Image	Protein Image
1	AcSAUR	Nucleoplasm		

openGPS (预测在细胞质)

AcSAUR
 Predicted localizations: Cell membrane
 Predicted membrane association: Peripheral
 Predicted signals:

Localization	Cytoplasm	Nucleus	Extracellular	Cell membrane	Mitochondrion	Plastid	Endoplasmic reticulum	Lysosome/Vacuole	Golgi apparatus	Peroxisome
Probability	0.2590	0.4166	0.0570	0.5585	0.1950	0.2121	0.2292	0.4071	0.0743	0.0219

Membrane association	Peripheral	Transmembrane	Lipid anchor	Soluble
Probability	0.5990	0.0910	0.5480	0.4350

DeepLoc-2.1 (预测在细胞核、细胞膜、液泡)

14 Nearest Neighbors

id	site	distance	identity	comments
At1g24735.1	cyto	246.742	13.8462%	[Arath]
GTH_SILCU	cyto	248.789	12.5%	[Uniprot] SWISS-PROT45:Cytoplasmic.
ADH2_LYCES	cyto	274	10.2632%	[Uniprot] SWISS-PROT45:Cytoplasmic.
ADH3_SOLTU	cyto	290.277	10%	[Uniprot] SWISS-PROT45:Cytoplasmic.
ADH1_SOLTU	cyto	291.576	10%	[Uniprot] SWISS-PROT45:Cytoplasmic.
ADH1_TRIRP	cyto	291.904	10%	[Uniprot] SWISS-PROT45:Cytoplasmic.
ADH1_PETHY	cyto	294.166	9.42408%	[Uniprot] SWISS-PROT45:Cytoplasmic.
ADH2_SOLTU	cyto	298.535	10%	[Uniprot] SWISS-PROT45:Cytoplasmic.
SODM_MAIZE	mito	303.421	12.3404%	[Uniprot] SWISS-PROT45:Mitochondrial matrix.
At4g02520.1	plas	307.115	12.7358%	[Arath]
CB48_MAIZE	chlo	309.089	12.8788%	[Uniprot] SWISS-PROT45:Chloroplast thylakoid membrane.
ADH1_PEA	cyto	313.297	9.73684%	[Uniprot] SWISS-PROT45:Cytoplasmic.
SOD2_MESCR	cyto	315.838	12.1795%	[Uniprot] SWISS-PROT45:Cytoplasmic.
FER1_ORYSA	chlo	317.542	14.3885%	[Uniprot] SWISS-PROT45:Chloroplast.

WoLFPSORT (预测在细胞质、线粒体、叶绿体)

Analysis Report:

SVM	LOCALIZATION	RELIABILITY
Amino Acid Comp.	Nuclear	0.236
N-peptide Comp.	Mitochondrial	0.489
Partitioned seq. Comp.	Mitochondrial	0.348
Physico-chemical Comp.	Mitochondrial	0.356
Neighboring seq. Comp.	Cytoplasmic	0.389

CELLO Prediction:

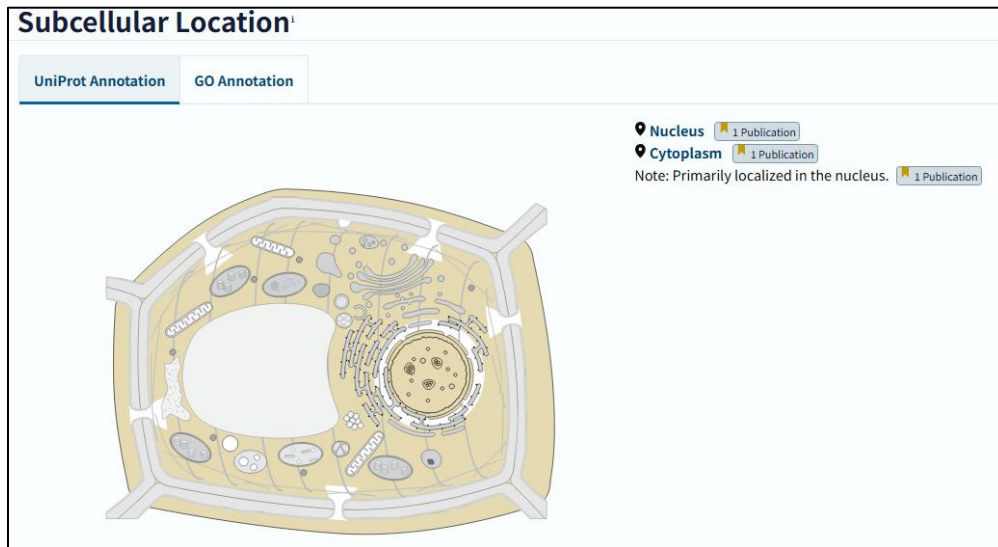
Mitochondrial	1.547 *
Cytoplasmic	1.246 *
Nuclear	0.860
Chloroplast	0.462
Extracellular	0.460
PlasmaMembrane	0.179
Peroxisomal	0.116
ER	0.040
Cytoskeletal	0.033
Lysosomal	0.020
Golgi	0.018
Vacuole	0.018

CELLO (预测在线粒体、细胞质)

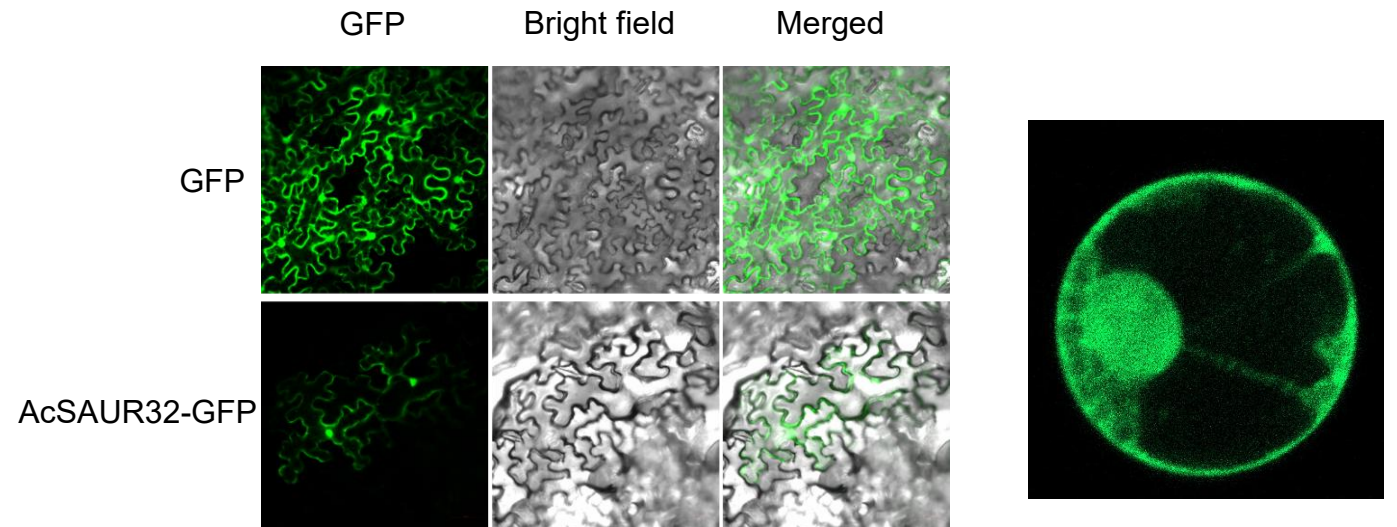
四、结构与功能分析

参考UniProt中SAU32_ARATH, 结果都指向细胞核和细胞质。

通过实验发现, *AcSAUR32*亚细胞定位 (烟草和原生质体) 在细胞核和细胞质上。可见同源基因之间亚细胞定位和预测的结果可以提供参考。



UniProt (*SAU32_ARATH*定位在核、质)

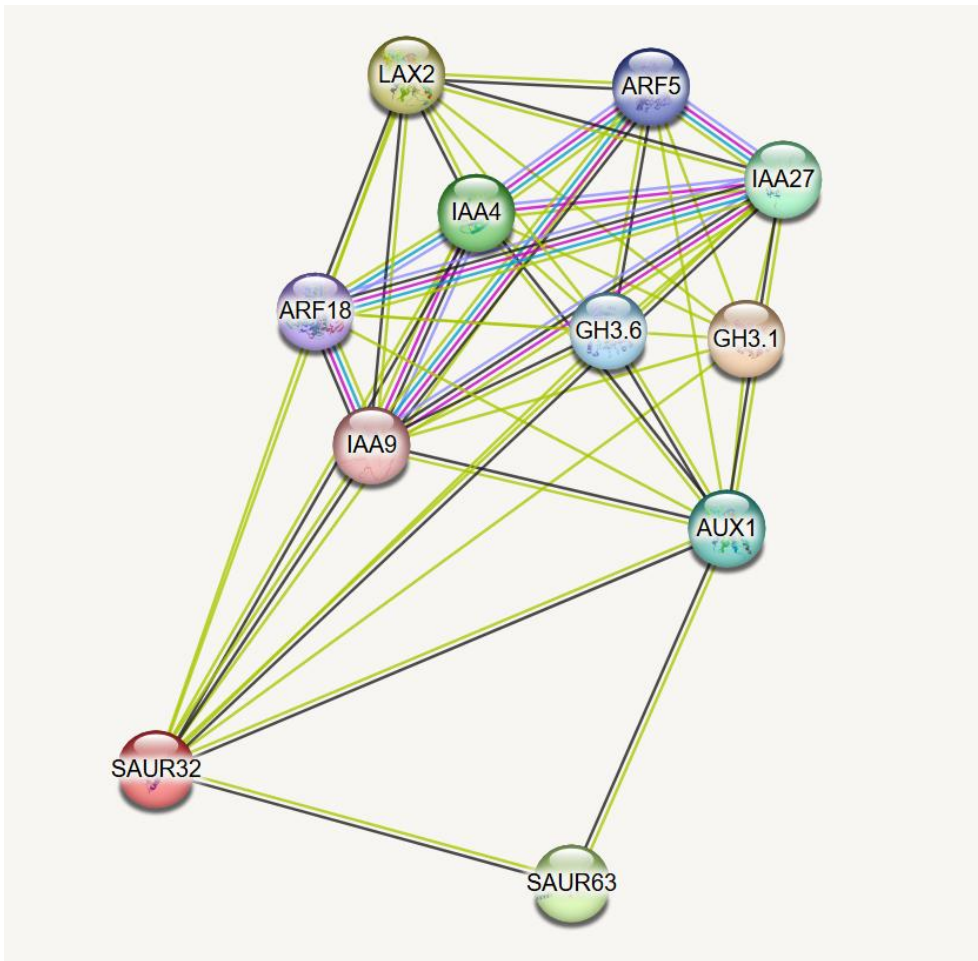


烟草
(图片还未处理)

小麦原生质体
(噪点太多, 需重做)

四、结构与功能分析

4.3 拟南芥中同源蛋白SAU32互作



Nodes:

Network nodes represent proteins
splice isoforms or post-translational modifications are collapsed, i.e. each node represents all the proteins produced by a single, protein-coding gene locus.

Node Color

- colored nodes: query proteins and first shell of interactors
- white nodes: second shell of interactors

Node Content

- empty nodes: proteins of unknown 3D structure
- filled nodes: a 3D structure is known or predicted

Edges:

Edges represent protein-protein associations
associations are meant to be specific and meaningful, i.e. proteins jointly contribute to a shared function; this does not necessarily mean they are physically binding to each other.

Known Interactions

- from curated databases
- experimentally determined

Predicted Interactions

- gene neighborhood
- gene fusions
- gene co-occurrence

Others

- textmining
- co-expression
- protein homology

Your Input:

- SAUR32 Auxin-responsive protein SAUR32; May play a role in the apical hook development. Belongs to the ARG7 family. (121 aa)

Predicted Functional Partners:

	Neighborhood	Gene Fusion	Cooccurrence	Coexpression	Experiments	Databases	Textmining	[Homology]	Score
GH3.1 Probable indole-3-acetic acid-amido synthetase GH3.1; Catalyzes the synthesis of indole-3-acetic acid (IAA)-amino acid conjug...									0.719
LAX2 Auxin transporter-like protein 2; Carrier protein involved in proton-driven auxin influx. Mediates the formation of auxin gradient f...									0.718
SAUR63 Auxin-responsive protein SAUR63; May promote auxin-stimulated organ elongation, such as hypocotyls, stamen filaments and ...									0.697
IAA4 Auxin-responsive protein IAA4; Aux/IAA proteins are short-lived transcriptional factors that function as repressors of early auxi...									0.678
IAA27 Auxin-responsive protein IAA27; Aux/IAA proteins are short-lived transcriptional factors that function as repressors of early au...									0.637
AUX1 Auxin transporter protein 1; Carrier protein involved in proton-driven auxin influx. Mediates the formation of auxin gradient from...									0.600
GH3.6 Indole-3-acetic acid-amido synthetase GH3.6; Catalyzes the synthesis of indole-3-acetic acid (IAA)-amino acid conjugates, prov...									0.599
ARF5 Auxin response factor 5; Auxin response factors (ARFs) are transcriptional factors that bind specifically to the DNA sequence 5...									0.598
ARF18 Auxin response factor 18; Auxin response factors (ARFs) are transcriptional factors that bind specifically to the DNA sequence ...									0.598
IAA9 Auxin-responsive protein IAA9; Aux/IAA proteins are short-lived transcriptional factors that function as repressors of early auxi...									0.597

参考STRING中SAU32_ARATH的蛋白互作

四、结构与功能分析

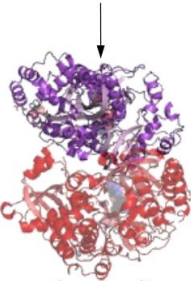
参考STRING中SAU32_ARATH的蛋白互作

GH3.1

Information
Probable indole-3-acetic acid-amido synthetase GH3.1; Catalyzes the synthesis of indole-3-acetic acid (IAA)-amino acid conjugates, providing a mechanism for the plant to cope with the presence of excess auxin; Belongs to the IAA-amido conjugating enzyme family.
Identifier: O82333, GH3.1
Organism: Arabidopsis thaliana

UniProt e! KEGG Pfam

- show protein sequence
- homologs among STRING organisms



1 588

Pfam GH3

1 of 4
PDB structure (4b2g)
identity: 80.4%

PDB

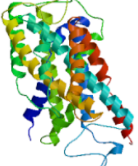
植物应对过量生长素的存在机制

LAX2

Information
Auxin transporter-like protein 2; Carrier protein involved in proton-driven auxin influx. Mediates the formation of auxin gradient from developing leaves (site of auxin biosynthesis) to tips by contributing to the loading of auxin in vascular tissues and facilitating acropetal (base to tip) auxin transport within inner tissues of the root apex, and basipetal (tip to base) auxin transport within outer tissues of the root apex (By similarity); Belongs to the amino acid/polyamine transporter 2 family. Amino acid/auxin permease (AAP) (TC 2.A.18.1) subfamily.
Identifier: Q9S836, LAX2
Organism: Arabidopsis thaliana

UniProt e! KEGG Pfam

- show protein sequence
- homologs among STRING organisms



39 398

Pfam Aa_trans

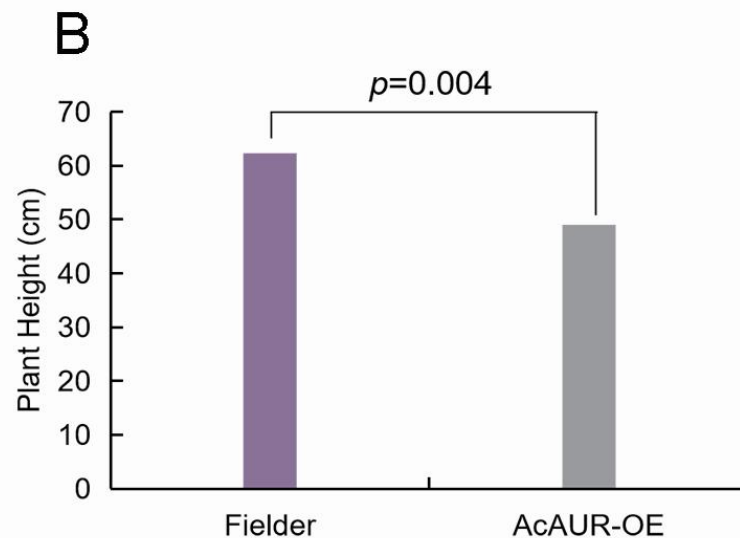
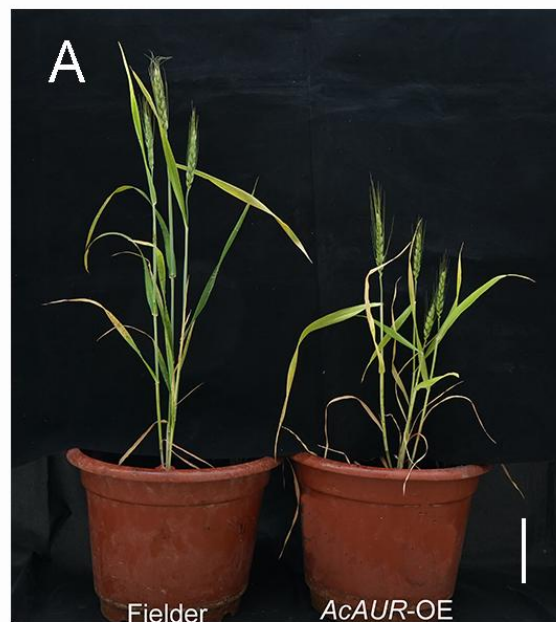
1 of 2
homology model (Q9S836 / 7kgvA)
identity: 15.3%

生长素的装载和运输

四、结构与功能分析

4.4 *AcSAUR32*转基因功能验证

构建冰草中的*AcSAUR32*基因的过表达载体质粒，将质粒转入受体小麦Fielder中。对T₁代植株进行农艺性状考察后发现*AcSAUR32*转基因植株的株高较受体材料Fielder降低，初步证实冰草1PL染色体中的特异基因*AcSAUR32*参与小麦的生长发育过程，能够降低小麦株高。（目前在T₃代）



T₁代

五、后续研究计划

正在进行：亚细胞定位（原生质体）
转基因材料的筛选（聚焦表型）
酵母双杂筛库（筛互作蛋白）
基因敲除（预计年后获得T₀代种子）

后续计划：Western blot实验
启动子活性分析LUC实验
筛出互作蛋白后开展验证实验
进一步分析氨基酸序列差异（可能会往蛋白质结构上进行一些研究）
阐明分子机制，构建模型



国家作物种质库（新库）


G06小组全体成员



G06A王云、G06B孙吉林、G06C王俊杰、G06D余瑶（从左到右）



Thank you for listening

 2026.1.10