



# 草地贪夜蛾性信息素生物合成基因的初步探究

Preliminary study on sex pheromone biosynthesis genes of  
*Spodoptera frugiperda*

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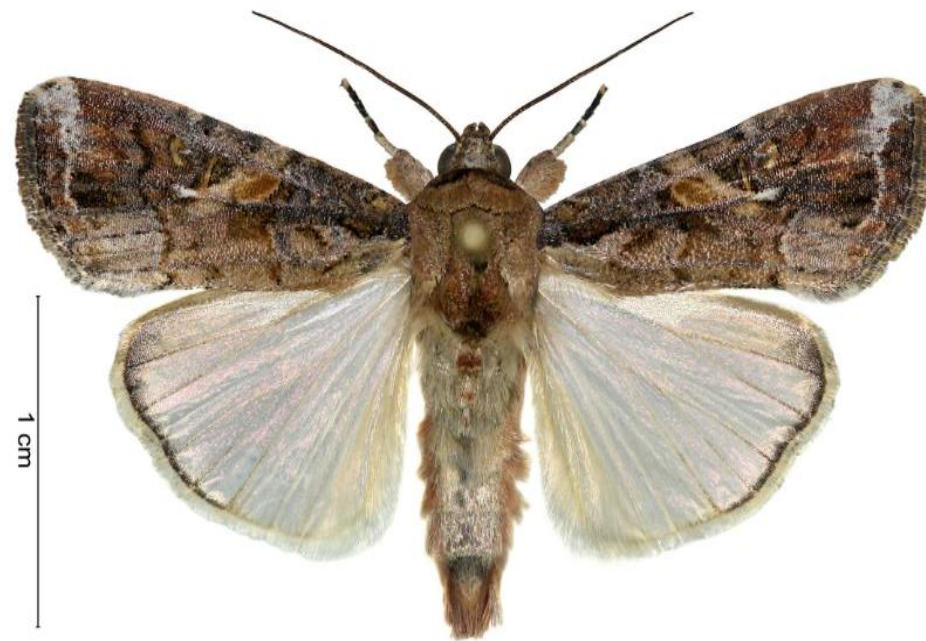
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# 背景介绍

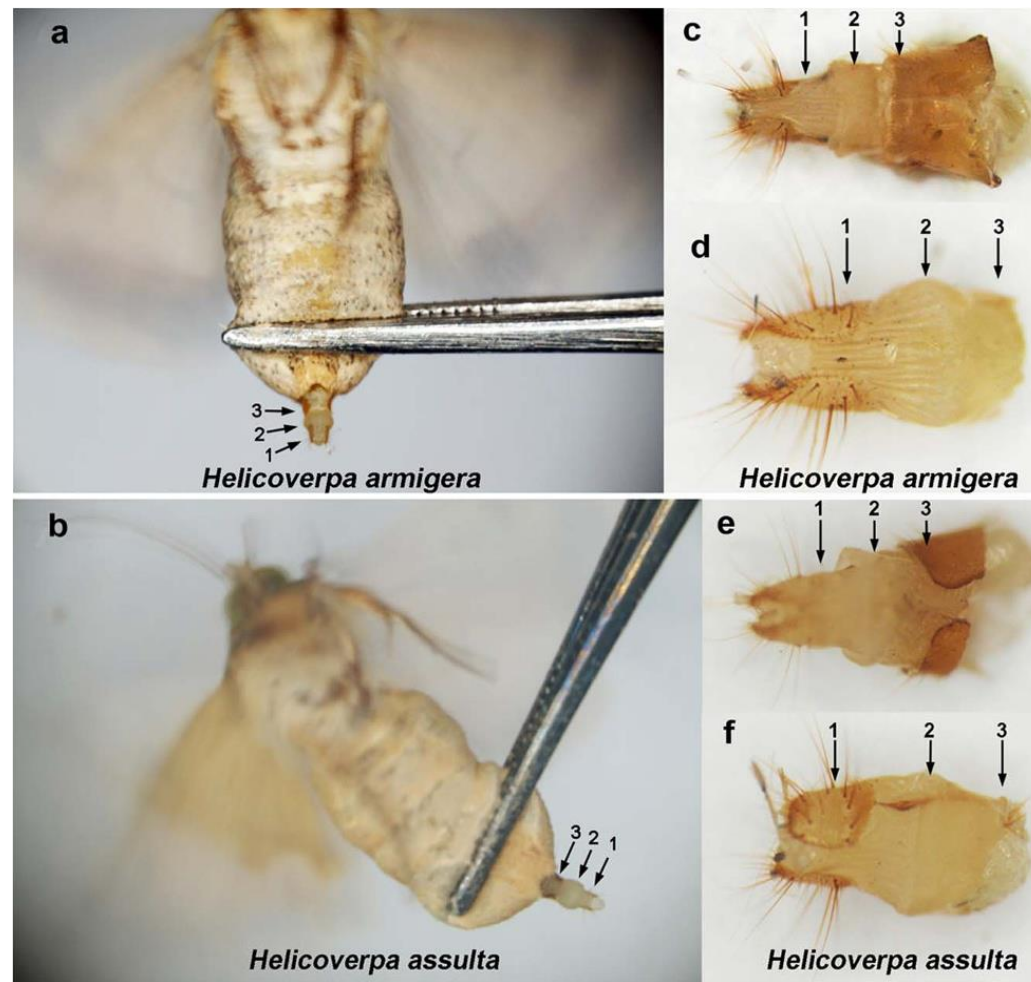
草地贪夜蛾 *Spodoptera frugiperda* 原产于美洲热带地区，是一种杂食性害虫，其寄主植物多达76科350种植物。食量惊人，繁殖量大，同时拥有极强的迁飞能力。于2018年12月11日从缅甸迁入中国。



(Wu 2020)

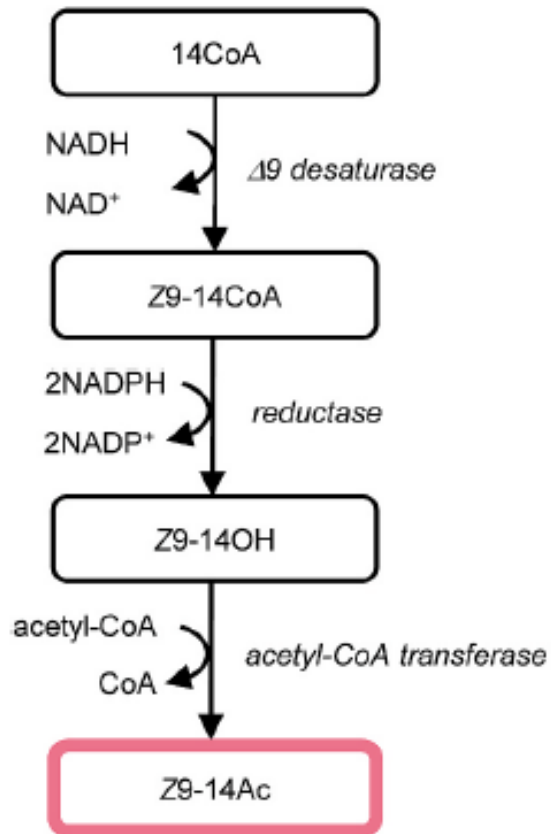
# 背景介绍

性信息素 (sex pheromone) 是由蛾类特殊腺体所释放的微量化学物质，具有物种特异性，已被应用于害虫的监测与防治。



(Li et al. 2015)

# 背景介绍



性信息素的生物合成涉及一系列的酶促反应：脂肪酸的合成（fatty acid synthetase）、去饱和（desaturase）、还原（reducatase）、乙酰化（acetyltransferase）等。

(Holkenbrink et al. 2020)

# 基因筛选

## SCIENTIFIC REPORTS

OPEN *Two fatty acyl reductases involved in moth pheromone biosynthesis*

Binu Antony<sup>1</sup>, Bao-Jian Ding<sup>2</sup>, Ken'Ichi Moto<sup>3</sup>, Saleh A. Aldosari<sup>1</sup> & Abdulrahman S. Aldawood<sup>1</sup>

脂肪酰基还原酶（FAR）参与生物脂肪酸和合成，同时也是参与昆虫性信息素合成的关键基因；以此篇文献为基础，基于BLAST筛选草地贪夜蛾中可能的FAR基因；

# 序列分析

## Function<sup>i</sup>

Catalyzes the reduction of fatty acyl-CoA to fatty alcohols.

UniRule annotation

## Catalytic activity<sup>i</sup>

• a long-chain fatty acyl-CoA + 2 H<sup>+</sup> + 2 NADPH = a long-chain primary fatty alcohol + CoA + 2 NADP<sup>+</sup> UniRule annotation

EC:1.2.1.84 UniRule annotation

Source: Rhea. « Hide

## Family & Domains<sup>i</sup>

### Domains and Repeats

Feature key	Position(s)	Description	Actions	Graphical view	Length
Domain <sup>i</sup>	37 – 304	NAD_binding_4 UniPro annotation	Add BLAST		268
Domain <sup>i</sup>	366 – 457	Sterile UniPro annotation	Add BLAST		92

## Sequence similarities<sup>i</sup>

Belongs to the fatty acyl-CoA reductase family. UniRule annotation ARBA annotation

# 基因筛选

- 以文献中验证过一条斜纹夜蛾FAR基因 (GenBank 登录号 KR781119) 为query序列, 对草地贪夜蛾CDS序列进行本地BLAST (序列数据来源于 Insect Base) ;

NUCLEOTIDE SEQUENCE

**Spodoptera littoralis FAR-like protein VII (pgFARI) mRNA, complete cds**

Spodoptera littoralis

1,431 bp mRNA sequence

KR781119.1

FASTA

Download

BLAST

Windows PowerShell

```
PS E:\blast\blast-2.11.0+db> makeblastdb -in Spodoptera_frugiperda.cds.fa -dbtype nucl -out Sfrudb
```

```
Building a new DB, current time: 04/28/2022 20:42:18
```

```
New DB name: E:\blast\blast-2.11.0+db\Sfrudb
```

```
New DB title: Spodoptera_frugiperda.cds.fa
```

```
Sequence type: Nucleotide
```

```
Keep MBits: T
```

```
Maximum file size: 1000000000B
```

```
Adding sequences from FASTA; added 22202 sequences in 0.672193 seconds.
```

```
PS E:\blast\blast-2.11.0+db> tblastx -query target.seq.txt -db Sfrudb -out Sfru_FAR.txt -outfmt 7
```



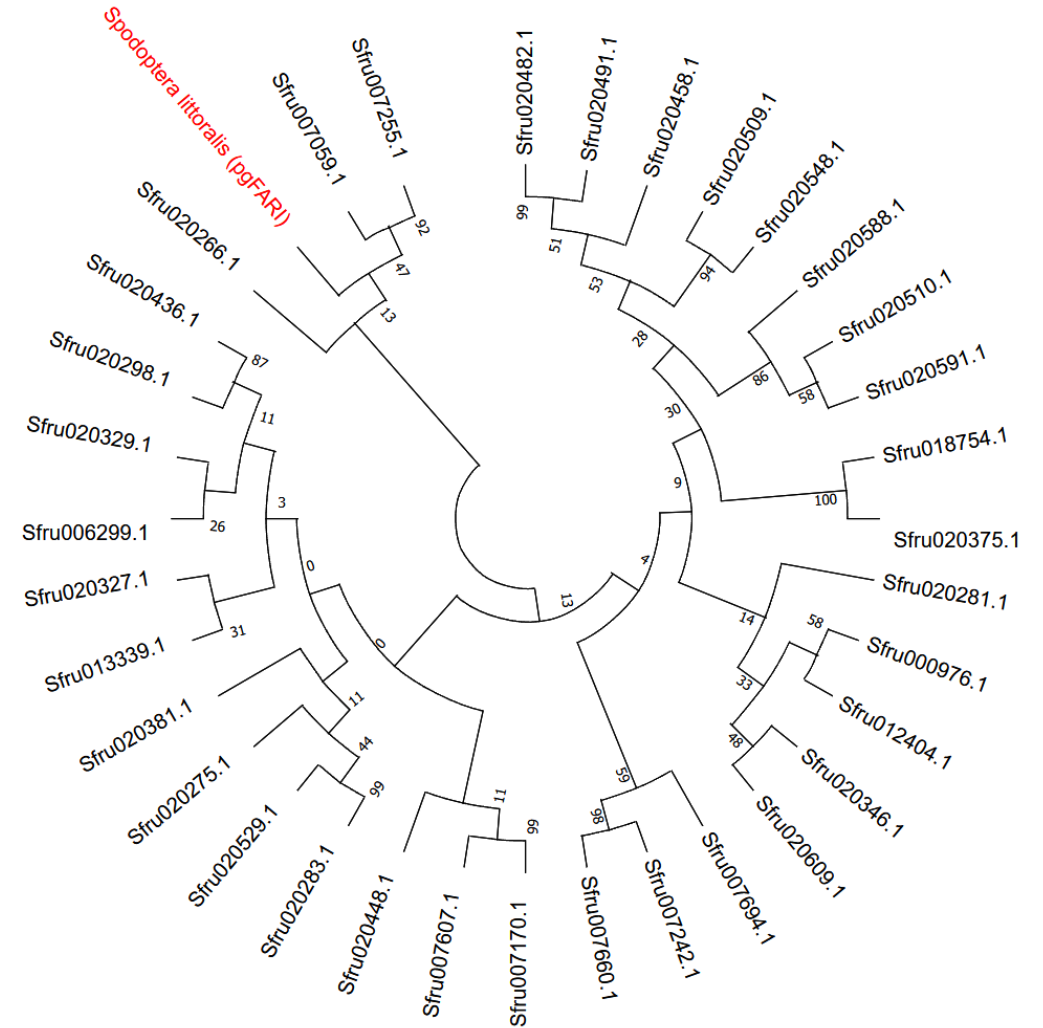
# 基因筛选

- 采用tBlastx程序, e值为0.00001, 共检索到34条相似序列;

```
文件(F) 编辑(E) 格式(O) 查看(V) 帮助(H)
# TBLASTX 2.11.0+
# Query: KR781119.1 Spodoptera littoralis FAR-like protein VII (pgFARI) mRNA, complete cds
# Database: Sfrudb
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens, q. start, q. end, s. start, s. end, evalue,
bit score
# 262 hits found
KR781119.1      Sfru007660.1      87.302   315    40     0      5     949    1     945    0.0
654
KR781119.1      Sfru007660.1      71.154   312    90     0     940    5     936    1     0.0
474
KR781119.1      Sfru007660.1      88.112   143    17     0     953   1381   943   1371   0.0
311
```

# 序列分析

- 把所检索出来的34条序列与参考序列翻译成蛋白序列后，采用MUSCLE进行了多序列比对，并使用MEGA7进行了系统发育树的构建（邻接法），以寻找与参考序列同源关系最近的序列；



# 序列分析

将进化关系最近的Sfru007059.1与检索序列进行双序列比对；相似度

67.9%

```
                *           20           *           40           *           60           *           80
Spodoptera : YVSVEDFYAGKTIFITGGTGFLGKVFLEKLLYSCKDVEIVYILIREKKGKTPQQRVEDLNFNKPISRLKQKDSQCMKKVTAIIGD : 85
Sfru007059 : YQSVADFYSGKSVFMTGGTGFLGKVYMEKLLYSCKPKLDKLYLLIREKKGVSAADKRIADLFENPLFERLKSSNPDFMKKVVLVEGD : 85
                YQSVADFYAGK36F6TGGTGFLGKV56EKLLYSCKD6DK6Y6LIREKKGK3ADKR6ADLFEKP6FERLKQK1PDCMKKVTA6IGD

                *           100          *           120          *           140          *           160          *
Spodoptera : LSEPGGLGISKDDEELLLOKVSUVFVHVAANVQFYKEFKEIINTNVGGTKYVLQLCQRIKDIKAFVHISTAYCHTDQKVLEERIYEF : 170
Sfru007059 : LGLFNLGISPSECTLIDKVSUVYHAGATVREYEPPLPVSININFDGTRKMLELSQRMKNIEAFIYVSTAFACANAKVLVETAYES : 170
                LGEPGLGISKDDE2LL6DKVSUV5HAAANVQFYEEFKEIININFDGT4K6L2LCQR6K1IEAF6H6STA5AHA1AKVLEERAYFP

                180          *           200          *           220          *           240          *
Spodoptera : PAELSEVLKFLQCFQHDKKQIKEIFKKQPNSTYFAKALAEITYIAENCGRVPTIIIRPSIISASLKEFLFGWVDSWNGATGLITAS : 255
Sfru007059 : PAKVEDVYKFIIEHGHDKHAVKKFISGSHFGTYAFKALSEAYIAKNHGKVPVAVIIRPSAVTATKDGFEVKGWLDNWFGEASVILYYI : 255
                PAE6EDVLKF622HGHDKHA6KEFFGKHFG3YAFKALAEAYIAENCG4VPA6IIRPSA63A3KDEF6KGW6DNWFGEA3G66TAI

                260          *           280          *           300          *           320          *           340
Spodoptera : YNGANRVLLGEGSNFLDLIPVDFVANLAIVAA--AKCTSSLKVYNCCSSGCNPI-----TLKQ--LVSHMNNVGFQKNSIIF : 329
Sfru007059 : NEGVIKRVLHGHNHTIDFIPVDYVSNLCIISALRAKESNEVQVYNSTSTSDNPVNWDITFNTMKEEKTLGKKNKFFY---LSMTY : 337
                NEGAIKRVLHGEGNH6DFIPVD5VANLAI6AALRAKC3NE6KVYNCCS3GCNPN6NWDITFNT6K2EKL6SGKKNKFG5DKN6S6I5

                *           360          *           380          *           400          *           420
Spodoptera : TNNKASLSTLTFFIQTTPSFTADMFLRVTKGSPRYMKIQSKLTIARNAINFFTCHSWVMKADNSRRIYASLSLHDRHTFPDPTD : 414
Sfru007059 : VDSKIALQLGTTFFIQITPAVLADLWLKIKGKIPKYLKVVAQALTIARNAYDYFTTNNFILRSDRTREIHSSLSPEDEEFPCDPTQ : 422
                TINKAALQLGTTFFIQITPAFLAD65L46KGKIP4Y6K6QAKALIARNAL15FTCHN5664ADN3REIHASLSLEDREEFPCDPTD

                *           440
Spodoptera : IDWKKYINIYIEGINQFL : 432
Sfru007059 : IRWPEYLKDNMNGIYKYL : 440
                IDWKEY6KDN6EGINK5L
```

# 蛋白预测

- 用Phyre对该基因的蛋白结构进行预测，结果显示属于氧化还原酶类；进一步推测该基因可能参与草地贪夜蛾的性信息素合成。



# 功能验证

- 基因克隆
- 表达定量
- 基因干扰
- 行为试验

# 参考文献

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