



中国农业科学院蔬菜花卉研究所

The Institute of Vegetables and Flowers Chinese Academy of Agricultural Sciences

Application of Arabidopsis downy mildew
resistance gene in mapping cabbage resistance
gene

拟南芥抗霜霉病基因在甘蓝抗病
基因定位中的应用

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- Background
- Basic information
- Alignment
- Phylogeny analysis
- Following research

Background

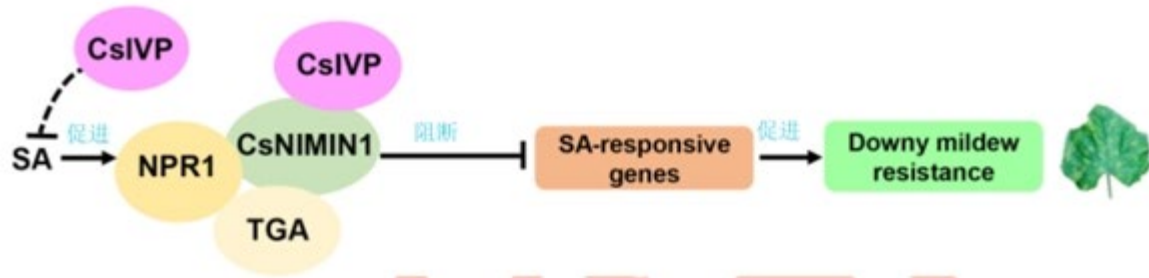
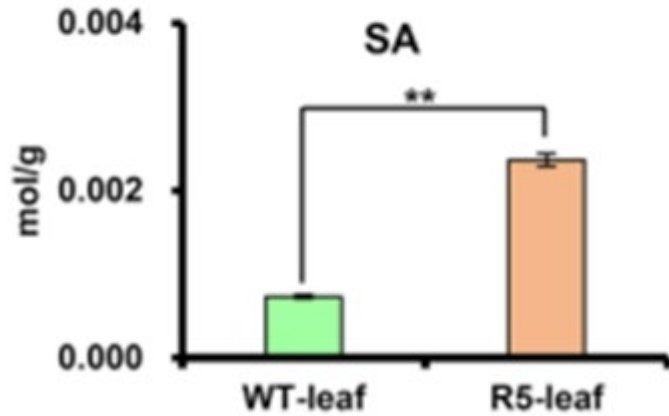
Background



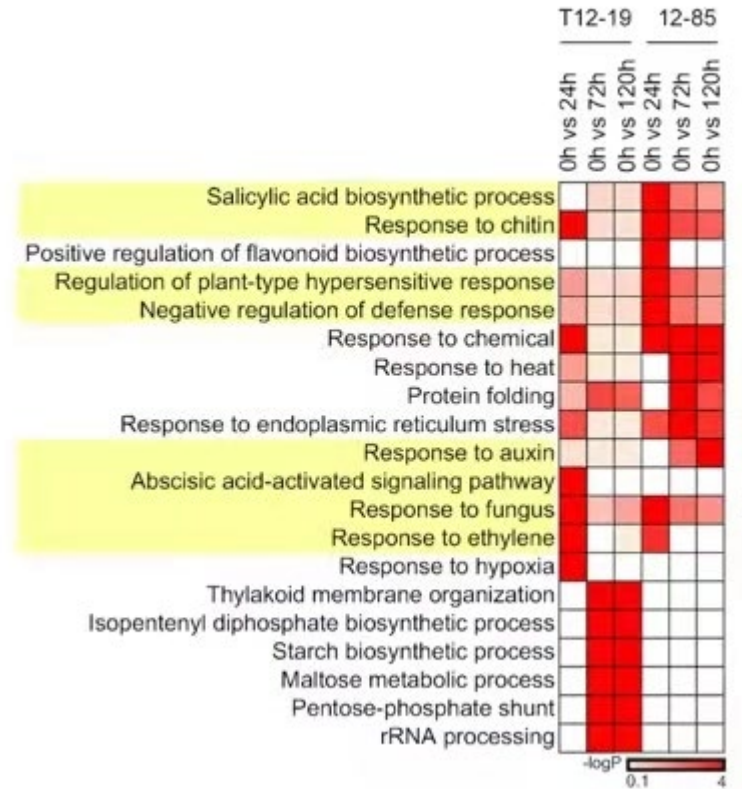
严重危害叶菜类蔬菜的生产

李明远等.当代蔬菜. 2004

Background



Yan et al. Plos biology 2020



Zhang et al. Horticulture research 2021

Basic information

序列登录号: Q9FLV0

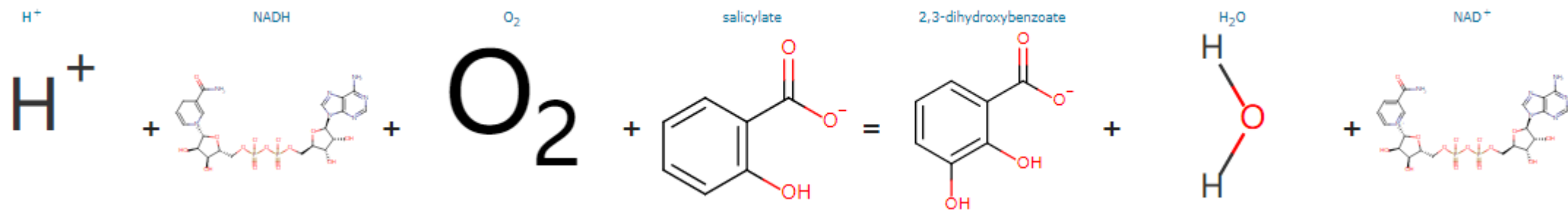
蛋白名: Protein downy mildew resistance 6

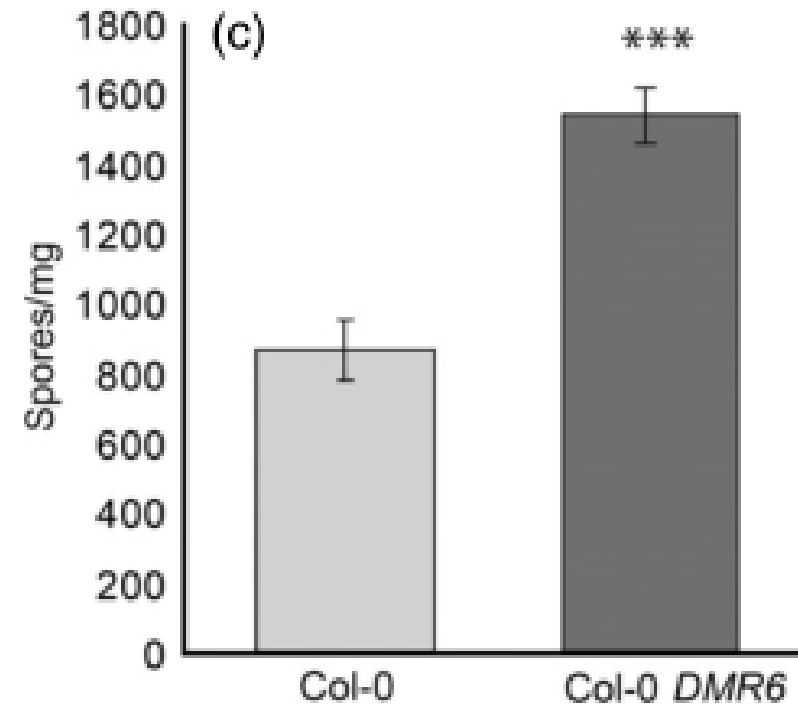
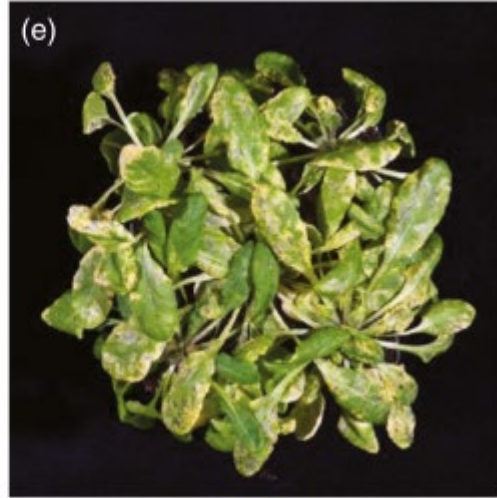
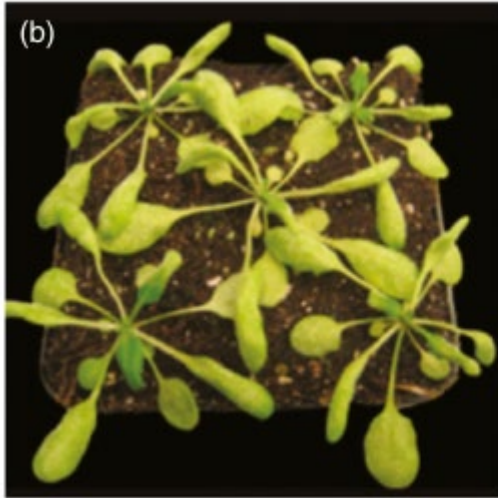
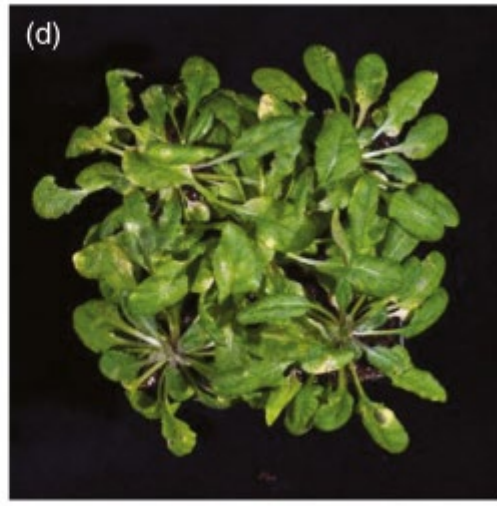
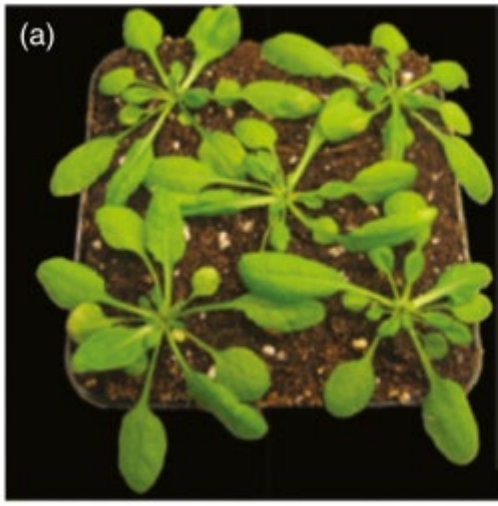
物种: 拟南芥 *Arabidopsis thaliana*

蛋白家族: iron/ascorbate-dependent oxidoreductase family

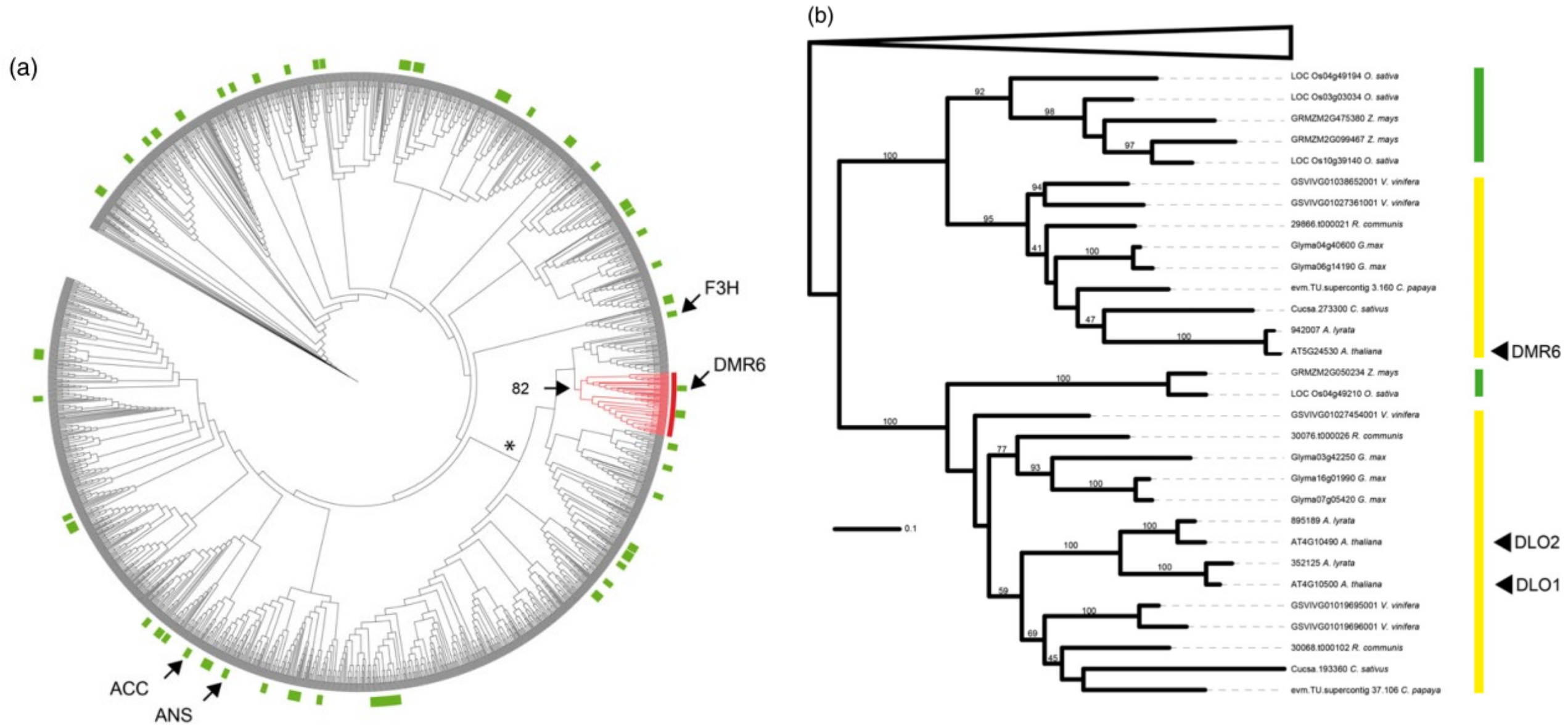
Domain: 188-288

function: Fe2OG dioxygenase





Tieme Zeilmaier et al. *the plant journal*. 2015






Tieme Zeilmaker et al. the plant journal. 2015

BLAST search 

New job

Clear form




 Configure this page Custom tracks Export data Share this page Bookmark this page[Ensembl Plants is produced in collaboration with Gramene](#)

Sequence data:

```
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MAAKLI STGFRHTL PENYVRPI SDRPRLSEVS QLED FPLIDL SSTD RSFLIQQIHQACA
RFGFFQVINHG VNKQI IDEMVS VAREFF SMSMEEKMKLYSDDPTKTR LSTSFNVKKEEV
NNWRDYLR LHCYPI HKYVNEWPSNPPS FKEIVSKYSREVREVGFKIEELISESLGLEKDY
MKKVLGEQGQHM AVNYYPPCEPELTYGLPAHTDPNALTILLQD TTVCGLQILIDGQWFA
VNPHPDAFVINIGDQLQAL SNGVYKSVWHRAVINTENPRLSVASFLCPADCAVMSPAKPL
WEAEDDET KPVYKDFTYAEYYKKFWSRNL DQEHCL ENFLNN
```

[Add more sequences](#) (1 sequence added, 29 more sequences allowed) Protein DNA

Search against:

 Brassica_oleracea [Add/remove species](#) Protein databaseProteins 

TO1000数据库:

http://plants.ensembl.org/Brassica_oleracea/Info/Index

Subject name	Subject description	Gene hit	Genomic Location	Orientation	Length	Score	E-val	%ID
Bo2g159320.1	pep chromosome:BOL:C2:49875930:49881835:-1 gene:Bo2g159320 transcript:Bo2g159320.1 gene_biotype:protein_coding transcript_biotype:protein_coding	Bo2g159320	C2:49875933-49881835 [Sequence]	Reverse	341 [Sequence]	1589	0.0	88.3 [Alignment]
Bo7g096760.1	pep chromosome:BOL:C7:37450642:37451706:-1 gene:Bo7g096760 transcript:Bo7g096760.1 gene_biotype:protein_coding transcript_biotype:protein_coding	Bo7g096760	C7:37450645-37451688 [Sequence]	Reverse	193 [Sequence]	901	8.8e-117	89.1 [Alignment]
Bo7g096770.1	pep chromosome:BOL:C7:37457223:37458034:-1 gene:Bo7g096770 transcript:Bo7g096770.1 gene_biotype:protein_coding transcript_biotype:protein_coding	Bo7g096770	C7:37457226-37458034 [Sequence]	Reverse	149 [Sequence]	690	1.6e-87	87.2 [Alignment]
Bo3g044790.1	pep chromosome:BOL:C3:18629218:18630075:1 gene:Bo3g044790 transcript:Bo3g044790.1 gene_biotype:protein_coding transcript_biotype:protein_coding	Bo3g044790	C3:18629218-18629652 [Sequence]	Forward	145 [Sequence]	462	6.3e-56	62.8 [Alignment]

激活 Windows

激活 Windows


```

oleracea      MAAKLLSTGFRHSTLFPENYVRPLSDRPRLSQVSQLDFPLIDISSDRSRLVQKIHQACA 60
Raphanus     MAAKLISTGFRHTTLFPENYVRPLSDRPRLSQVSQLDFPLIDISSDRSRLVQKIHQACA 60
DMR6_ARATH   MAAKLISTGFRHTTLFPENYVRPISDRPRLSEVSQLDFPLIDLSSDRSFLIQQIHQACA 60
rapa         MAAKLISTGFRHTTLFPENYVRPLSNRPCLSDVSPLEDFPIIDLSSDRSRLVQKIHQACS 60
napus        MAAKLISTGFRHTTLFPENYVRPLSNRPCLFDVSPLEDFPIIDLSSDRSRLVQKIHQACS 60
*****:*****:*****:***:*** * :** *****:***:***:*** * :*:*****:

oleracea      RFGFFQVINHGVS KATIDEMVSV AHEFFGMPMDEKMKLYSDDPTKTPRLSTSPNVKEEEV 120
Raphanus     RFGFFQVINHGVR KATIDEMVSV AHEFFGMSMDEKMKLYSDDPTKTPRLSTSPNVKEEEV 120
DMR6_ARATH   RFGFFQVINHG VNKQIIDEMVSV AHEFFSMSMEBKMKLYSDDPTKTTRLSTSPNVKEEEV 120
rapa         RFGFFQVINHRV SKETIDGMVSV ANEFFSMSMEBKMKLYSDDPTKTTRLSTSPNVKEEEV 120
napus        RFGFFQVINHRV SKETIDGMVSV ANEFFSMSMEBKMKLYSDDPTKTTRLSTSPNVKEEEV 120
***** * * ** *****:***:*** * :*****:***** *****:***

oleracea      NNWRDYLRRLHCYPIDKYVHEWPSNPPSFKEVVSKYSREIRELGKIBELISESLGLEKDY 180
Raphanus     NNWRDYLRRLHCYPIDKYVHEWPSNPPSFKEVVSKYCREVRELGFTIBELISESLGLEKDY 180
DMR6_ARATH   NNWRDYLRRLHCYPIDKYVNEWPSNPPSFKEIVSKYSREVREVGFKIBELISESLGLEKDY 180
rapa         NNWRDYLRRLHCYPIDKYVHEWPSKPPSFKEVVSRVSTEVRELGFTIBELISESLGLEKDH 180
napus        NNWRDYLRRLHCYPIDKYVHEWPSKPPSFKEVVSRVSTEVRELGFTIBELISESLGLEKDH 180
***** ***** ***:***:*****:***:*** * :**:*: :*****:*****:

oleracea      MKKVLGEGGQHMAVNYYPPCPEPELTYGLPAHTDPNALTILLQDATVCGLQILIDGHWFA 240
Raphanus     MKNVLGEGGQHMAVNYYPPCPEPELTYGLPAHTDPNALTILLQDATVCGLQILIDGHWFA 240
DMR6_ARATH   MKKVLGEGGQHMAVNYYPPCPEPELTYGLPAHTDPNALTILLQDITVCGLQILIDGQWFA 240
rapa         MRKVLGEGGQHMAVNYYPPCPEPELTYGLPAHTDPNALTILLQDATVCGLQILIDGQWFA 240
napus        MRKVLGEGGQHMAVNYYPPCPEPELTYGLPAHTDPNALTILLQDATVCGLQILIDGQWFA 240
* :*****:*****:*****:*****:*****:*****:*****:*****:

oleracea      VNPRPDAFVINIGDQLQALSNGVYKSVWHRAVTNTEKPRLSVASFLCPDCAVISPAKPL 300
Raphanus     INPRPDAFVINIGDQLQALSNGVYKSVWHRAVTNTEKPRLSVASFLCPDCAVISPAKPL 300
DMR6_ARATH   VNPHPDAFVINIGDQLQALSNGVYKSVWHRAVTNTEKPRLSVASFLCPDCAVISPAKPL 300
rapa         VNPHPDAFVINIGDQFQALSNGVYKSVWHRAVTNTEKPRLSVASFLCPDCAVISPAKPL 300
napus        VNPHPDAFVINIGDQFQALSNGVYKSVWHRAVTNTEKPRLSVASFLCPDCAVISPAKPL 300
*:*****:*****:*****:*****:*****:*****:*****:*****:

oleracea      WEAKEEBAKPIYRDYTYABYYKKFWSRNLQEHCLNENFLND 341
Raphanus     WEAKEEBAKPIYRDYTYABYYKKFWSRNLQEHCLNENFLND 341
DMR6_ARATH   WEAEDEBKPVYKDFTYABYYKKFWSRNLQEHCLNENFLNN 341
rapa         WEAEDEBAKPIYRDYTYABYYKKFWSRNLQEHCLNENFLNH 341
napus        WEAEDEBAKPIYRDYTYABYYKKFWSRNLQEHCLNENFLNH 341
*****: :*:**:*:*:*****:*****:*****:*****:*****:

```

Domain: 188-288
function: Fe2OG dioxygenase

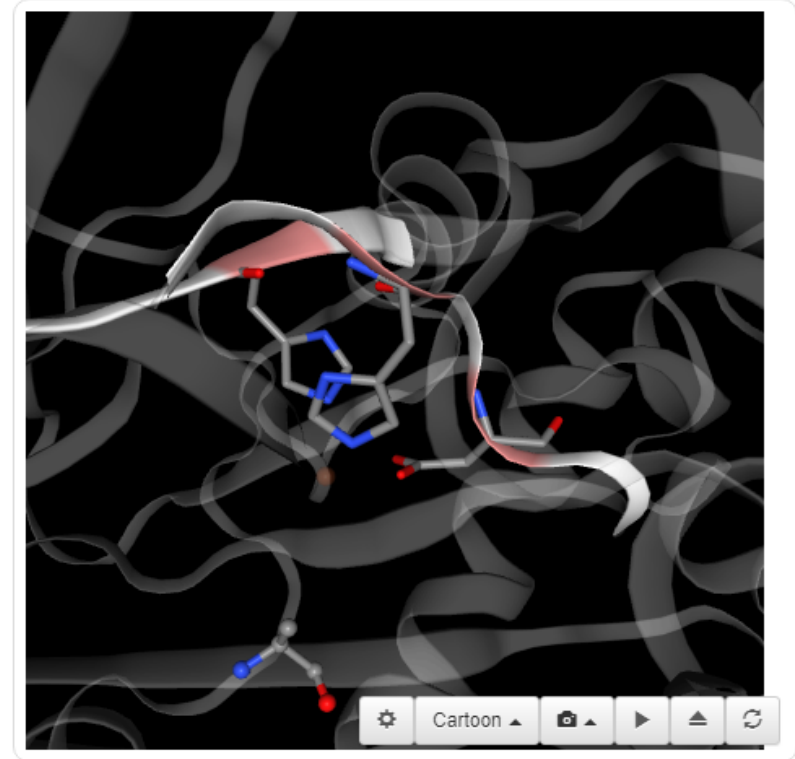
position	function
212	metal binding
214	metal binding
269	metal binding
279	2-oxoglutarate

从NCBI上blast的结果显示结构域在五个物种中相对保守，因此，其功能相差可能并不大。所以DMR6在甘蓝中的同源蛋白可能也参与水杨酸的氧化还原反应

Sequence Alignments ^

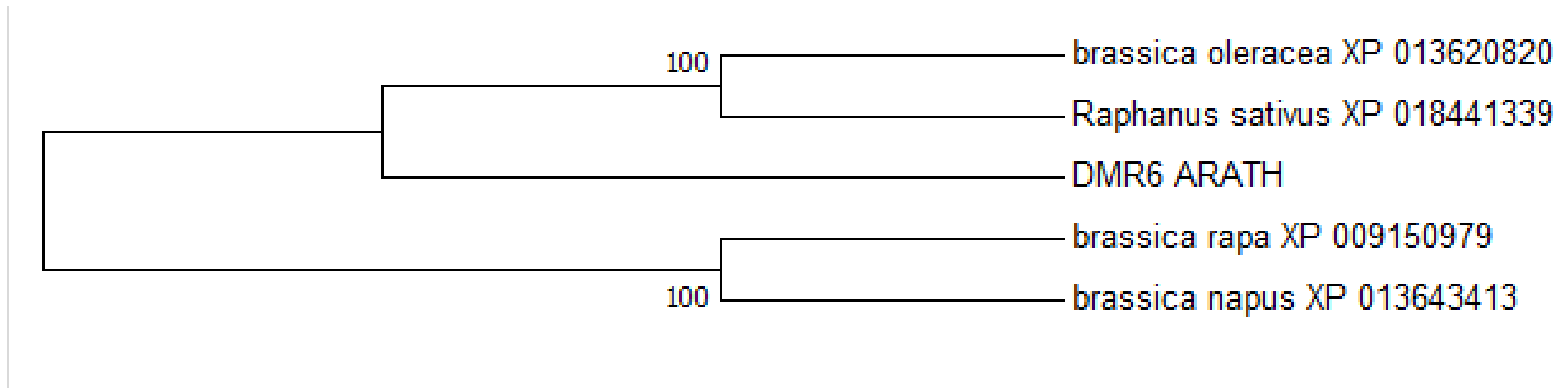
Model based on 6lsv.1.A Probable 2-oxoglutarate-dependent dioxygenase At5g05600

MODEL	RHTTLPENYVRPISDRPRL-SEVSQLEDFFLIDLST-----DRSFLIQQIHQACARFGFFQVINHGUNKQIID	78
6lsv.1.A	NLSSLPDRYIKPASLRPTTTEADAPTATNIPIIDLEGLFSEEGLSDDVIMARISEACRGWGFFQVNVHGVPKPELMD	91
MODEL	EMVSVAREFFSMSMEEKMKLYSDDPTKTTTRLSTSFNVKKEEVNNWRDYRLHLCYP-IHKYVNEWPSNPPSFKEIV	152
6lsv.1.A	AARENWREFFHMPVNAKETYSNSP-RTYEGYGSRLGVEKGASLDWSDYYFLHLLPHHLKDFNKWPSFPPTIREVI	165
MODEL	SKYSREVREVGFKIEELISESLGLEKDYMKKVLGE--QGQHMVNNYPPCPEBELTYGLPAHIDPNALTILLQDT	225
6lsv.1.A	DEYGEELVKLSGRIMRVLSTNLGLKEDKFQEAFFGENIGACLRVNNYYPKCPPELALGLSHIDPQGM TILLPDD	240
MODEL	TVCGIQILIDGQWFAVNPHPDFAVINIGDQLQALSNGVYKSVWHRAVNTNENPRLSVASFLLCPADCAVMSPAKPL	300
6lsv.1.A	QVFGIQVRKDDTWTITVKKPHAFIVNIGDQIQILSNSTYKSVHRVIVNSDKERVSLAFFYNPKSDIPIQLQEL	315
MODEL	WEAEDDET KPVYKDFTYAEYYKFWSRNLDQEHCLN	337
6lsv.1.A	VS---THNPPLYPPMTFDQYRLFIRTQGGPQKSHVES	349



在Uniprot数据库中找到其3D结构，发现其金属离子结合位点也只有212、214、269三个位置的氨基酸，因此，可以确定，如果这三个位置发生突变，会对蛋白质的功能造成很大影响，甚至使蛋白质失去它原有的功能

Phylogeny analysis



下一步思路：

设计引物，在抗病和感病甘蓝中扩增*DMR6*的同源基因，看该基因在抗感株系中是否发生变异

如果有变异，则构建载体，将这个基因导入抗病株系中，进行接种实验观察导入该基因是否会使抗病株系获得感病表型



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请老师和各位同学批评指正

谢谢！