果 树 学 报 2018,35(1):1-10
Journal of Fruit Science

DOI:10.13925/j.cnki.gsxb.20170259

桃EXPANSIN基因家族序列特征及其在根结线虫侵染后的诱导表达分析

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摘 要:【目的】探索扩张蛋白(EXPANSIN)基因家族在桃抗南方根结线虫过程中的作用。【方法】首先对桃基因组中的EXPANSIN基因家族进行生物信息学分析,然后利用转录组测序对EXPANSIN基因在南方根结线虫侵染免疫型('红根甘肃桃1号')和高感型('贝蕾')桃种质根系后的不同时期的表达丰度进行分析。【结果】桃EXPANSIN基因家族有27个成员,这些成员分布在8条染色体上,以第2和第5号染色体上最多,均为5个。基因结构分析显示,这些基因包含1~5个外显子,大部分EXPANSIN基因包含DPBB_1和Pollen_allerg_1保守结构域,聚类分析将这27个成员分为2大类,其中有8个与拟南芥中已注释的与线虫侵染过程中巨细胞形成有关的蛋白质聚在一起,均属于EXPA亚类。转录组分析表明,这8个EXPANSIN基因在对南方根结线虫免疫和高感2种种质不同时期的表达趋势存在明显差异,其中*ppa010314m*、*ppa010226m*在'贝蕾'中表达量随侵染上调,而在'红根甘肃桃1号'中上调不明显,这2个基因可能是参与南方根结线虫侵染过程中巨细胞形成的关键基因。【结论】桃EXPANSIN家族成员在结构上高度保守,其中多个成员可能参与调控桃抗南方根结线虫过程。

关键词:桃;EXPANSIN基因家族;南方根结线虫;抗性

中图分类号:S662.1 文献标志码:A 文章编号:1009-9980(2018)01-0001-10

The sequence characters of EXPANSIN genes and the analysis of their induced expression after the infection of root-knot nematodes in peach

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Abstract:【Objective】Expansins are plant cell-wall loosening proteins involved in cell enlargement and a variety of other developmental processes in which cell-wall modification occurs. Members of the expansin family of cell wall proteins disrupt hydrogen bonds within the cell wall polymer matrix and are implicated in cell wall polymer disassembly and cell elongation. The expansin encoding proteins belong to the cell wall zymoprotein, expressing in the plant with a high degree of specificity. Their expression and regulation are controlled not only by the developmental processes of plant, but also by exogenous hormones and environmental factors. Previous studies showed that expansin genes played important roles in plant seed germination, root growth, stem and leaf growth and development, fruit ripening and softening, and organ abscission root-knot nematodes invade host roots and induce formation of giant cell structures that serve them nutrients. The resistances of peach to root-knot nematodes vary with varities. 'Honggengansutao 1' (*Prunus kansuensis*) is immune to *Meloidogyne incognita*. 'Bailey' (*Prunus persica*) is highly susceptible to *M. incognita*. Studies revealed that nematodes changed expression of plant genes encoding cell wall modifying proteins including expansins. Expansins showed unique ability to induce cell wall extension in lower pH. This experiment aimed at exploring the role of expansin gene family during the interac-

收稿日期:2017-07-19 接受日期:2017-09-25

基金项目:中央级科研院所基本科研业务费(Y2017JC37);中国农业科学院科技创新工程项目[CAAS-ASTIP-2017-ZFRI-(01)]

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tion between peach roots and root knot nematodes.【Methods】The locations on the chromosomal information of the expansin gene family member were searched using the GDR, and the amino acid sequences of peach expansin family genes were obtained from the Phytozome. The estimated molecular weight and isoelectric point of the putative protein were obtained from the ExPASY Compute pI/Mw. The amino acid sequences of the *Arabidopsis thaliana* expansin family were obtained from the TAIR database. The structures of expansin proteins were analyzed using the online tools of Gene Structure Display Server, and the maps were built using the software of MapInspect. A multiple alignment analysis of peach expansin proteins was carried out using the Clustal X 2.1 program within the MEGA 5.0 software, and a phylogenetic tree between the peach and *A. thaliana* expansin proteins was constructed using the neighbor joining method and a bootstrap test was set at 1 000 to test the confidence of the tree. Additionally, seedlings of 'Honggengansutao 1' and 'Bailey' were inoculated with *M. incognita* using artificial indoor inoculation. Root tips were observed by staining at 0, 6, 12, 36, 60 and 84 h after inoculation. The expression levels of expansin genes of the seedlings of 'Honggengansutao 1' and 'Bailey' infected by *M. incognita* were detected using RNA-seq technique.【Results】27 expansin candidate genes were found in the peach genome. The lengths of them were typically 241-289 amino acids. The estimated molecular weights and isoelectric points of the putative proteins were 8.98-30.249 ku and 4.40-9.83. The proteins had two conserved domains, named as DPBB_1 superfamily and Pollen_allerg_1 superfamily. A chromosome mapping analysis revealed that expansin genes distributed on 8 chromosomes. Chromosome 2 and 5 each had 5 expansin genes. The results of an intron-exon structure analysis indicated that expansin gene family members were composed of 1-5 exons. Phylogenetic analysis indicated that peach expansin gene family was divided into two groups, ten EXPANSIN associated with giant cell forming proteins during nematode infection in *A. thaliana* belonged to EXPA subclass. We identified 7 081 differential expression genes through comparing the transcriptome of the immune accession 'Honggengansutao 1' and the susceptible accession 'Bailey' at 0, 6, 12, 36, 60 and 84 h after inoculation. 3 380 genes were up-regulated and 3 701 genes were down-regulated, respectively. Transcriptome analysis showed that the expression trends of the 10 expansin genes (*ppa014051m*, *ppa010203m*, *ppa010260m*, *ppa010198m*, *ppa010654m*, *ppa010180m*, *ppa010226m*, *ppa010379m*, *ppa010067m* and *ppa010443m*) were different in two different resistant germplasms. The expression level of *ppa010314m* and *ppa010226m* increased obviously in 'Bailey' as the infection by *M. incognita* and did not increased obviously in 'Honggengansutao 1', indicating that *ppa010314m* and *ppa010226m* might be the key genes for the formation of giant cell during the process of the infection by *M. incognita*.【Conclusion】These results suggested that the EXPANSIN gene family members be highly and structurally conserved. In peach, *ppa010314m* and *ppa010226m* may be involved in the interaction between peach roots and root knot nematodes.

Key words: *Prunus persica*; Expansin gene family; *Meloidogyne incognita*; Resistance

根结线虫(*Meloidogyne* spp.)是世界上一类分布广泛的植物专性内寄生线虫,种类繁多,寄主范围广[1]。其中南方根结线虫(*Meloidogyne incognita*)是对桃危害最严重的根结线虫种之一[2]。根结线虫诱发病害的典型症状是易感寄主植物根部形成根瘤,具体侵染过程是根结线虫的二龄幼虫通过口针的穿刺作用从植物根尖生长区侵入根系,沿细胞间隙移动,在维管束中建立永久取食位点,形成巨细胞,为线虫发育提供营养,在根系外观上即表现为根瘤。巨细胞形成过程中涉及到的细胞融合和扩增,是基于水解酶、扩张蛋白等细胞壁修饰活性而进行的[3-4]。

扩张蛋白是一类细胞壁酶蛋白,参与细胞膨大以及其他多种细胞壁修饰发生的发育过程[5]。由4类多基因家族编码,分别命名为EXPA、EXPB、EXP-

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like (EXL)A和EXP-like (EXL) B[6]。目前,对EXPANSIN蛋白的研究主要集中在EXPA和EXPB两个亚族,EXPA和EXPB蛋白参与细胞扩张和细胞壁修饰的发育过程[7-8]。而EXLA和EXLB的确切功能尚不清楚[9]。扩张蛋白能够通过打断细胞壁多聚体之间的氢键诱导酸依赖的细胞壁延展和压力松弛,该类蛋白几乎参与了整个植物生长发育过程,除具有增大细胞功能外,对植物种子萌发、根系生长、果实成熟软化、器官脱落以及花粉管生长等方面也起重要作用[10]。扩张蛋白基因的表达受植物激素如生长素、赤霉素、乙烯等的调节[11-14],环境因素如水胁迫[15]、菌根感染[16]、根瘤菌互作[17]等也能诱导扩张蛋白基因的表达。扩张蛋白也参与到了线虫诱导植物根瘤的形成过程中,如在番茄[18-19]、拟南芥[20-21]、大豆[22]、花生[23]上均有报道。线虫的取食可上调*LeEXPA4*和*LeEXPA5*基因表达,但这2个基因表达的位置不一样。*LeEXPA4*在组织分化或多核体细胞膨胀中负责对细胞壁的弱化或拆解,而*LeEXPA5*却是在多核体营养过剩时负责细胞壁的伸展。根结线虫侵染后可导致*AtEXPA1*、*AtEXPA15*基因的上调表达,胞囊线虫侵染后导致*AtEXPA1*、*AtEXPA6*、*AtEXPA8*、*AtEXPA10*和*AtEXPA16*基因的上调表达。南方根结线虫侵染后大豆*EXPA1*、*EXPA5*、*EXPA16*和*EXPA45*基因上调表达。花生根结线虫侵染后花生*EXLB1*基因上调表达。

桃基因组测序的完成和序列释放,为全基因组水平上桃重要功能基因家族的挖掘和功能研究提供了重要的基础数据[24-25]。虽然Hayama等[26]利用基因组数据对桃EXPANSIN蛋白家族基因*PpExp1*、*PpExp1*和*PpExp3*进行了克隆和生物信息分析,但该研究所关注的基因并不全面。笔者以南方根结线虫免疫型和高感型桃不同侵染时期的根部为试材,对桃基因组的EXPANSIN基因家族进行生物信息学和表达分析,明确该基因家族的序列特征及在不同抗性桃各侵染时期的表达特征,为进一步研究该基因家族在桃抗南方根结线虫中的功能奠定基础。

1　材料和方法

1.1　材料

选取对南方根结线虫高感的桃种质‘贝蕾’(*Prunus persica*)和免疫种质‘红根甘肃桃1号’(*P. kansuensis*)为供试材料,2者均来自中国农业科学院郑州果树研究所国家桃种质资源圃。果实成熟后,取种子,低温砂藏3~4个月,待发芽出根后备用。

线虫取自感染根结线虫的桃根,经形态学鉴定为南方根结线虫2号生理小种,接种在温室中的番茄上进行繁殖。在适宜接种期,将番茄根系挖出,去离子水洗净,打碎后依次过60、100、200、500目筛子,根结线虫卵留在500目筛上。用36%(φ)蔗糖对虫卵进行浮选浓缩。将浓缩的卵置于铺有一层200目(0.075 mm)网筛和2层滤纸的培养皿中室温孵化,3 d后收集二龄幼虫用于接种。

1.2　桃EXPANSIN家族成员的序列分析、在染色体上的分布分析和进化树的构建

利用蔷薇科基因组数据库(Genome Database for Rosaceae,GDR,http://www. rosaceae. org/)获得桃候选EXPANSIN基因序列。采用MapInspect分析EXPANSIN家族成员在染色体上的分布;利用Gene Structure Display Server(http://gsds1.cbi.pku.edu.cn/)对基因结构进行分析;利用SignalP 3.0 server(http://www.cbs.dtu.dk/services/SignalP-3.0/)对蛋白进行信号肽预测;蛋白质结构域采用SMART(http://smart.embl-heidelberg.de/)进行预测;分子质量及等电点用ExPASY Compute pI/Mw程序(http://web.expasy.org/compute_pi/)计算;采用ClustalX 2.1对桃EXPANSIN蛋白家族序列进行序列比对。

拟南芥EXPANSIN蛋白家族序列从拟南芥基因组数据库(http://www. arabidopsis. org)中获得,桃EXPANSIN蛋白家族序列从phytozome基因组数据库(http://www.phytozome.net/search.php)中检索获得,用ClustalX 2.1进行序列比对,使用MEGA 5.0[27]软件的neighbor-joining法构建系统发育树,其他参数为系统默认值。

1.3　转录组测序

待免疫和高感材料的种子萌发并生长至胚根3 cm左右,参考李海炎等[28]的方法,采用6孔细胞培养板培养,每孔加入5 mL 23%(ω)Pluronic F-127和500条二龄南方根结线虫混匀,接种植株根系,分别在接种后0、6、12、36、60和84 h取‘红根甘肃桃1号’(编号为H0、H1、H2、H3、H4、H5)和‘贝蕾’(编号为B0、B1、B2、B3、B4、B5)根部,每个时期10株,样品混合后置于液氮速冻,-80 ℃保存,用于总RNA提取。

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用CTAB法提取RNA，应用Illumina HiSeq™2000双末端测序技术，按照有参考基因组的转录组测序流程及数据分析方法进行数据分析。测序公司为Macrogen（深圳，中国）公司。

2 结果与分析

2.1 桃EXPANSIN基因家族的全基因组鉴定、在染色体的定位和氨基酸序列分析

利用GDR数据库获得桃候选EXPANSIN基因序列，得到桃EXPANSIN家族27个基因（表1），编码的氨基酸长度为89~289 aa。ProtParam分析显示，EXPANSIN家族的蛋白分子质量为8.900~30.249 ku，等电点4.40~9.83。27个EXPANSIN基因成员分布在桃基因组8条染色体上，每条染色体上的基因数从1个到5个不等。其中第2和第5号染色体上最多，有5个；第1、3和6号染色体上各有4个；第7和第8号染色体有2个；第4号染色体有1个。

SMART分析EXPANSIN家族的蛋白质包含2个结构域（DPBB_1、Pollen_allerg_1）。ClustalX 2.1比对发现几乎所有的EXPANSIN蛋白家族包含完整的结构域，仅*ppa014051m*缺失了结构域Pollen_allerg_1（图1）。

表1 桃基因组中EXPANSIN蛋白家族的特征

Table 1 Characteristics of EXPANSIN family in peach genome

桃基因组第1版登录号 *Prunus persica* v1.0 number	桃基因组第2版登录号 *Prunus persica* v2.0 number	定位染色体 Chromosome number	预测的蛋白 Predicted protein		
			氨基酸长度 Amino acid length/aa	分子质量 Molecular weight/ku	等电点 Isoelectric point
ppa010242m	*Prupe.1G360700*	1	257	27.775	9.14
ppa019174m	*Prupe.1G516600*	1	253	28.134	9.10
ppa010379m	*Prupe.1G276700*	1	252	26.742	9.33
ppa019560m	*Prupe.1G516700*	1	262	29.346	9.18
ppa019150m	*Prupe.2G136500*	2	289	30.249	4.86
ppa009786m	*Prupe.2G274400*	2	277	29.547	6.58
ppa016148m	*Prupe.2G121800*	2	260	28.743	8.59
ppa010198m	*Prupe.2G237000*	2	259	27.832	9.41
ppa010382m	*Prupe.2G263600*	2	252	26.743	6.92
ppa010067m	*Prupe.3G014800*	3	265	28.669	8.60
ppa010654m	*Prupe.3G265800*	3	241	26.118	9.32
ppa010041m	*Prupe.3G155600*	3	266	28.584	8.83
ppa024239m	*Prupe.3G256600*	3	259	28.512	8.89
ppa015148m	*Prupe.4G183400*	4	265	29.105	9.83
ppa014051m	*Prupe.5G043800*	5	89	8.900	4.40
ppa010376m	*Prupe.5G057900*	5	252	27.983	7.46
ppa017982m	*Prupe.5G047300*	5	255	27.698	4.69
ppa010443m	*Prupe.5G195200*	5	249	26.217	9.08
ppa016612m	*Prupe.5G087100*	5	263	28.991	9.39
ppa010314m	*Prupe.6G042000*	6	254	27.267	8.43
ppa010180m	*Prupe.6G075100*	6	260	28.020	9.58
ppa010226m	*Prupe.6G256500*	6	258	27.956	8.59
ppa010260m	*Prupe.6G292300*	6	257	27.509	8.92
ppa021118m	*Prupe.7G124900*	7	266	29.498	8.84
ppa009524m	*Prupe.7G125000*	7	288	31.555	8.57
ppa010171m	*Prupe.8G174500*	8	261	28.216	8.84
ppa010203m	*Prupe.8G182000*	8	259	28.572	8.28

2.2 桃EXPANSIN蛋白家族相似性和进化树分析

利用进化树分析软件MEGA5.0对已知桃的27个和拟南芥的34个EXPANSIN蛋白序列进行进化分析，结果（图2）显示，桃和拟南芥的EXPANSIN蛋白主要分为group 1（EXPA）和group 2（EXPB、expansin-like）2大类，group 1中含有9个AtEXPASIN和6个PpEXPASIN，group 2中含有25个AtEXPASIN和21个PpEXPASIN。其中拟南芥中与线虫侵染过程中巨细胞形成有关的蛋白分别有AtEXP1、AtEXP4、AtEXP6、AtEXP8、AtEXP10、AtEXP15、AtEXP16和AtEXP20。该类蛋白与ppa014051m、ppa010203m、ppa010260m、ppa010198m、ppa010654m、ppa010-180m、ppa010226m、ppa010379m、ppa010067m和ppa-010443m聚为一类。

通过EXPANSIN家族基因CDS区域的碱基序列与基因组序列比对得到各个基因外显子和内含子在

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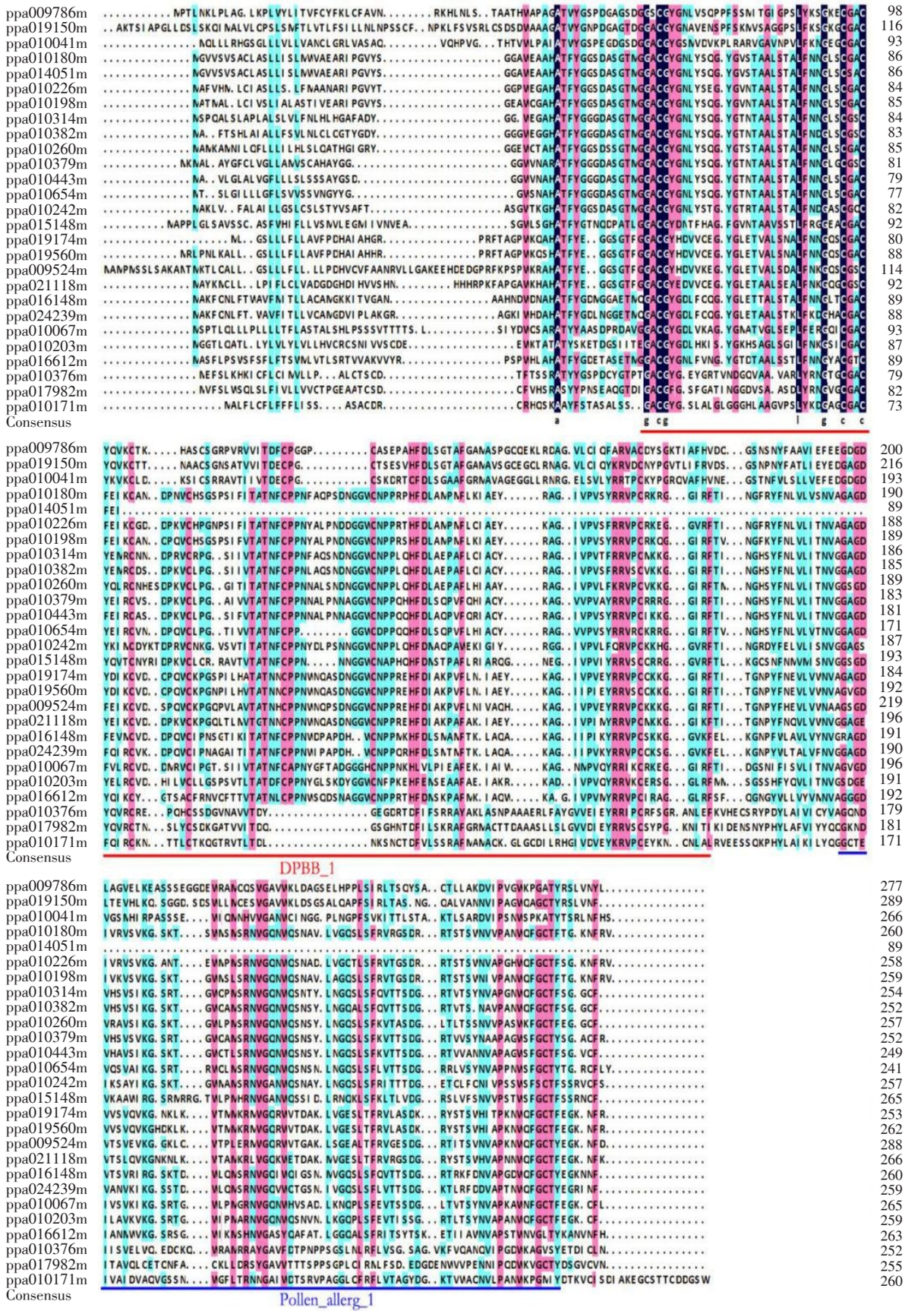

图1　桃 EXPANSIN 蛋白家族序列比对

Fig. 1 Multiple alignments of peach EXPANSIN proteins

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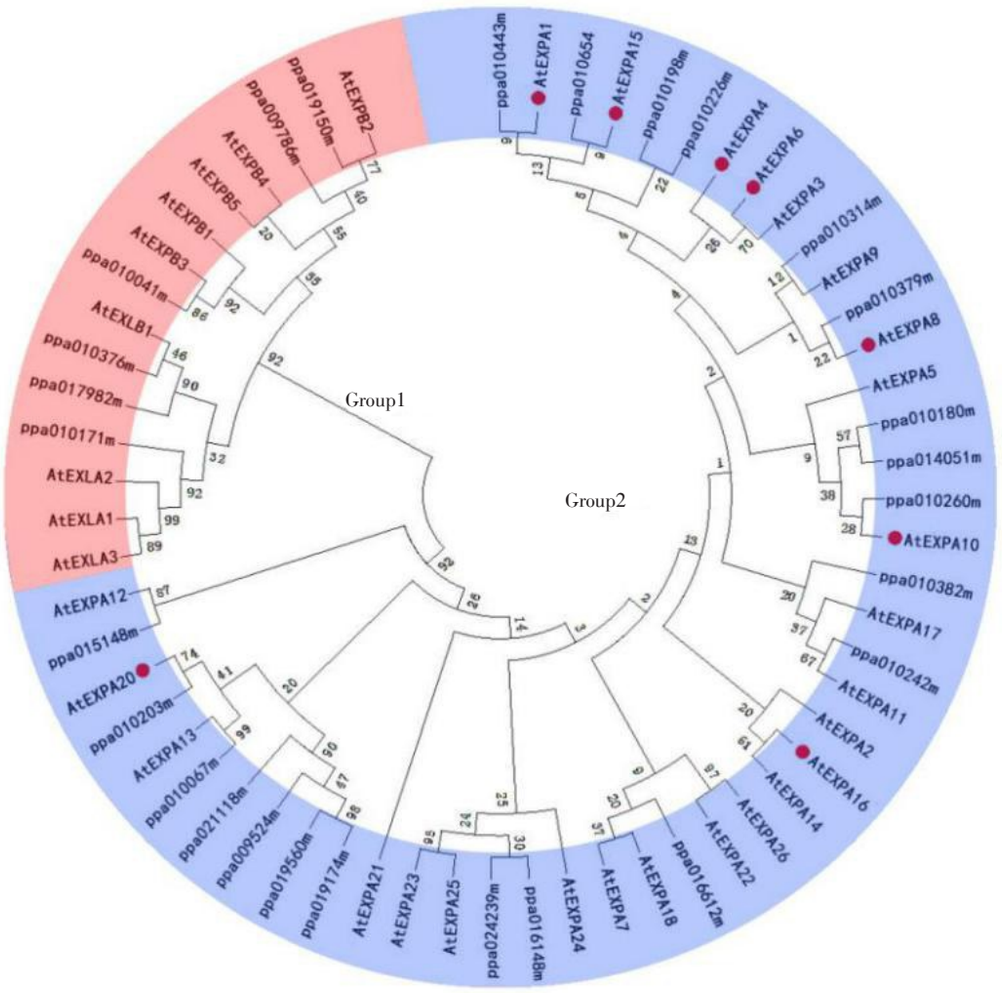

进化树由 MEGA 5.0 的邻接法绘制，参数设置为 1 000 次重复。其中红色圆圈标注的为拟南芥中与线虫侵染过程中巨细胞形成有关的蛋白质。

The unrooted tree was generated using MEGA 5.0 program by neighbor-joining method. Bootstrap values from 1 000 replicates are indicated at each-branch. The marked red circles are *Arabidopsis* proteins associated with giant cell formation during the nematode infection.

图 2 桃 EXPANSIN 的进化关系

Fig. 2 Phylogenetic relationship of peach EXPANSIN proteins

DNA序列上的分布(图3)。各个基因含有的外显子数从1到5不等，来自group 2的基因即EXPB和expansin-like类通常含有4~5个外显子、3~4个内含子；group 1的基因即EXPA类含有1~3个外显子和0~2个内含子。

2.3 桃 EXPANSIN 基因在南方根结线虫侵染‘红根甘肃桃1号’‘贝蕾’根系不同时期的表达

采用Illumina HiSeq™2000技术对南方根结线虫接种后不同时期‘红根甘肃桃1号’和‘贝蕾’的根系组织进行转录组测序，共获得509 786 660个测序reads，平均每个样本4 248 222个reads，每个read长101 bp。将免疫的‘红根甘肃桃1号’和感病的‘贝蕾’相同时期的转录组比较，发现在转录水平上响应根结线虫侵染过程中的差异表达基因有7 081个。

从中将EXPANSIN家族基因表达量数据提取出，剔除表达量值小于1.0的基因，绘制热图(图4)。根据基因层次聚类可将这些基因分为4类：Ⅰ类基因在‘贝蕾’中表达量随侵染先上调后下调，而在‘红根甘肃桃1号’中上调不明显；Ⅱ类基因在0时期表达量最高，而后随侵染在‘贝蕾’中呈波动性表达，在‘红根甘肃桃1号’中下调表达；Ⅲ类基因在‘贝蕾’中基本不表达，在‘红根甘肃桃1号’中表达量随侵染先上调后下调；Ⅳ类基因在‘贝蕾’中均上调表达，整体表达量较低，其中Ⅳ-1在‘红根甘肃桃1号’中表达量上调

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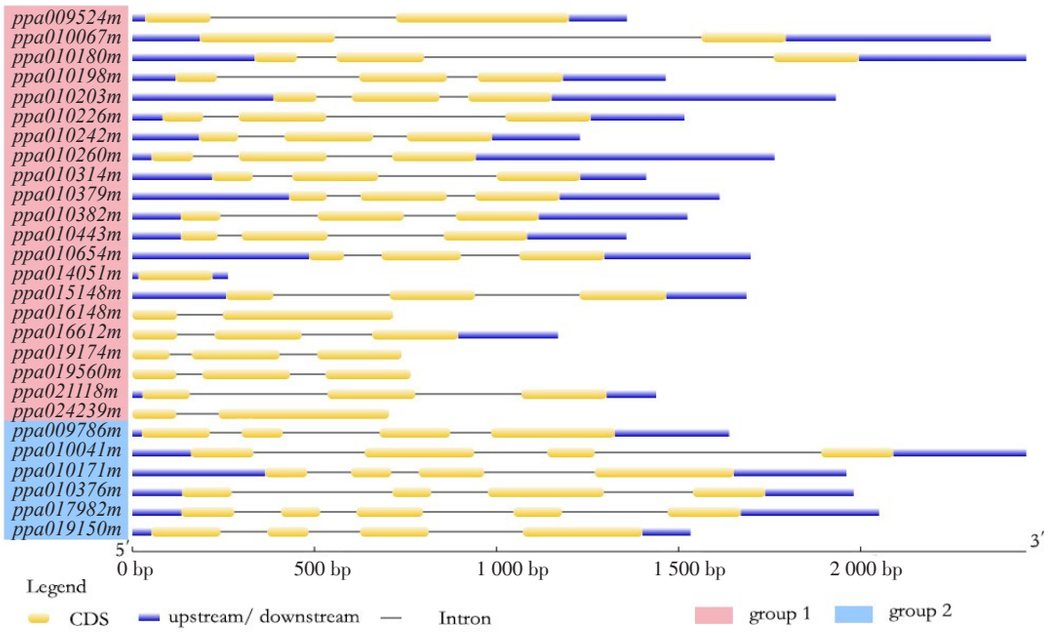

黄色代表外显子,细线代表内含子,蓝色代表编码区上下游的非翻译区。

The exons are represented by yellow boxes, the introns are represented by lines, and upstream/downstream regions are represented by blue boxes.

图3　EXPANSIN家族基因结构

Fig. 3 Structure of peach EXPANSIN proteins

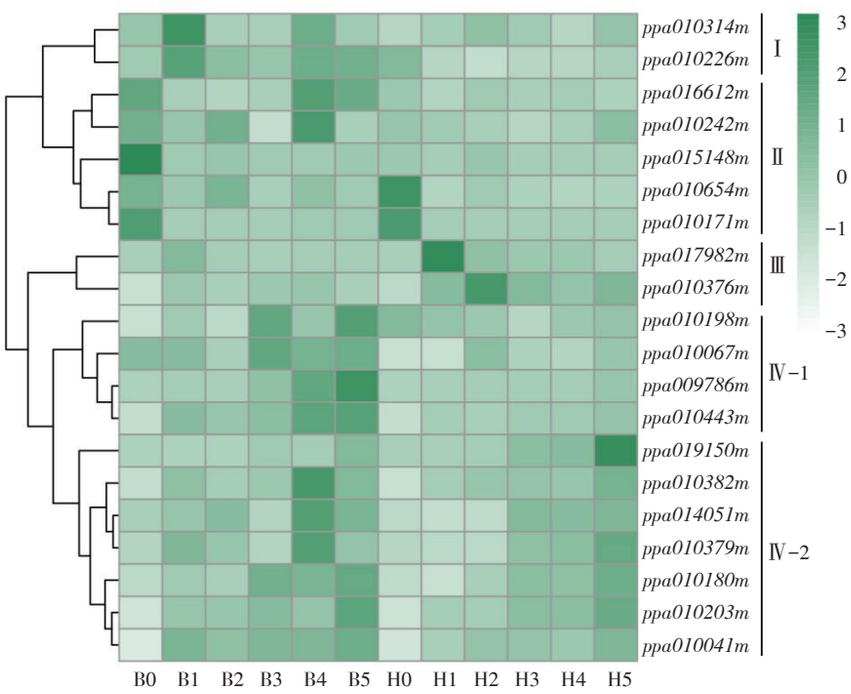

图4　EXPANSIN家族基因在'红根甘肃桃1号'和'贝蕾'南方根结线虫各侵染时期的表达

Fig. 4 Expression of EXPANSIN genes in 'Honggengansutao 1' and 'Bailey' sampled at different *Meloidogyne incognita* infection stages

不明显,Ⅳ-2在'红根甘肃桃1号'中上调表达。

由于桃巨细胞形成主要在南方根结线虫侵染后36 h[29],因此,笔者关注在'贝蕾'侵染后期上调表达、在'红根甘肃桃1号'中不表达或上调不明显的基因。同时,从27个桃和34个拟南芥EXPANSIN蛋白序列的进化树(图3)可以看出,10个桃EXPANSIN

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基因编码的蛋白质与拟南芥中已注释的与线虫侵染过程中巨细胞形成有关的蛋白AtEXPA1、AtEXPA4、AtEXPA6、AtEXPA8、AtEXPA10、AtEXPA15、AtEXPA16和AtEXPA20聚在一起，均属于EXPA类，表明这些蛋白的功能可能具有相似性。由图4可知，*ppa010314m*、*ppa010226m*、*ppa010198m*、*ppa010067m*、*ppa009786m*和*ppa010443m*在‘贝蕾’侵染后期上调表达，在‘红根甘肃桃1号’中上调表达不明显；*ppa019150m*、*ppa010382m*、*ppa014051m*、*ppa010379m*和*ppa010180m*、*ppa010203m*和*ppa010041m*在‘贝蕾’和‘红根甘肃桃1号’中均呈上调表达。由以上分析可知，*ppa010314m*、*ppa010226m*、*ppa010198m*、*ppa010067m*和*ppa010443m*既与拟南芥中已注释的与线虫侵染过程中巨细胞形成相关蛋白聚为一类，同时表达规律为在‘贝蕾’侵染后期上调表达，在‘红根甘肃桃1号’中上调表达不明显，推测*ppa010314m*、*ppa010226m*、*ppa010198m*、*ppa010067m*和*ppa010443m*可能与南方根结线虫侵染过程中桃根部巨细胞的形成有关，参与桃抗南方根结线虫过程。

2.4 南方根结线虫侵染桃过程中激素对EXPANSIN基因表达的调控

笔者将Aux/IAA基因家族提取，进而提取这些基因的表达量数据，剔除表达量值小于1.0的基因，剩余15个基因绘制热图（图5）。基因层次聚类分为2类，Ⅰ类基因在‘贝蕾’中表达随侵染先上调后下调，在‘红根甘肃桃1号’中上调表达不明显；Ⅱ类基因在抗、感材料中表达规律不明显。其中，Aux/IAA基因家族Ⅰ类基因与EXPANSIN基因家族Ⅰ类基因表达趋势相似，且EXPANSIN基因家族Ⅰ类基因表达滞后于Aux/IAA基因家族Ⅰ类基因，推测*ppa010314m*和*ppa010226m*可能是参与南方根结线虫侵染过程中巨细胞形成的关键基因。

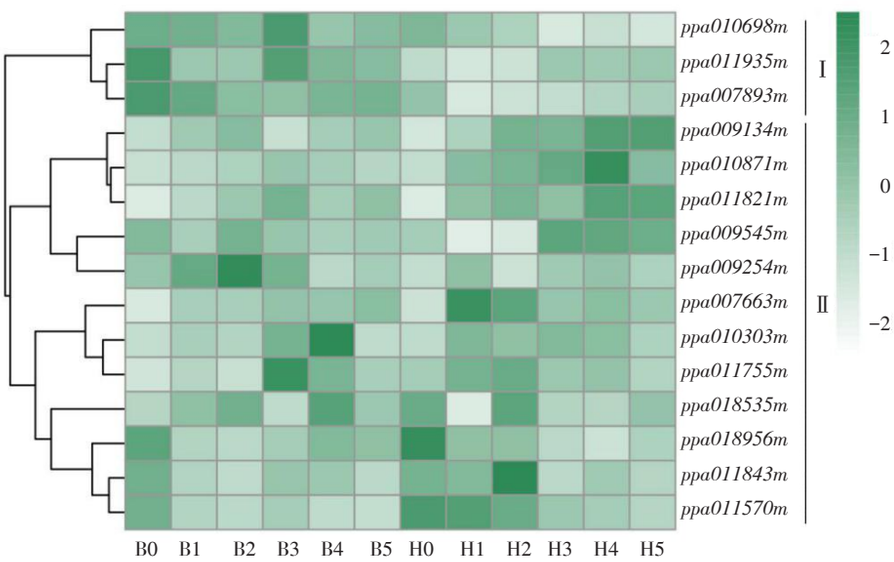

图5 Aux/IAA基因家族在‘红根甘肃桃1号’和‘贝蕾’南方根结线虫各侵染时期的表达

Fig. 5 Expression of Aux/IAA genes in ‘Honggengansutao 1’ and ‘Bailey’ sampled at different *Meloidogyne incognita* infection stages

3 讨 论

笔者通过桃全基因组分析，获得了27个桃的EXPANSIN家族基因。所有的EXPANSIN蛋白除*ppa014051m*缺失了结构域Pollen_allerg_1外，均包含2个结构域。进化分析表明，桃EXPANSIN蛋白主要分为group 1（EXPA）和group 2（EXPB和expansin-like）2大类，这些数据证实了该基因家族在进化过程中的保守性。Sampedro等[10]也报道了EXPANSIN蛋白通常含250~275个氨基酸，由2个结构域（结构域1和结构域2）以及1个信号肽构成，主要分为EXPA和EXPB两类。这一结果进一步证明了EXPANSIN基因家族在进化过程中的保守性。

目前，对线虫侵染植物根部的基因表达调控知

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之甚少,有2个被人们广泛接受的植物基因特异激活方式[30]:一是植物基因通过其启动子中的调节元件与线虫分泌物的直接相互作用而激活,如在辣椒中,EXPANSIN基因*upa6*的启动子由细菌Ⅲ型效应AvrBs3激活,同样胞囊线虫也可能具有一种蛋白质负责直接激活扩张蛋白启动子;二是侵染后的根部基因的表达由植物激素间接激活,如生长素参与了巨细胞的形成[31]。EXPANSIN基因的表达受激素调控,不同的EXPANSIN类型调控模式也不一样,很多EXPA类型基因受到生长素[32-33]、赤霉素[34]、细胞分裂素[35]和乙烯[36]等的调控,在水稻EXPANSIN启动子区域就有相应的反应元件[37]。在与激素关系的研究中,生长素与EXPANSIN基因的关系研究最清楚,生长素诱导质子泵理论得到普遍认同,生长素作为酶的变构效应剂与ATP结合并使之活化,促进H^+分泌到细胞壁中,导致细胞壁基质pH下降,EXPANSIN基因及降解细胞壁的酶被活化,使半纤维素与微纤丝之间的氢键被切断,细胞壁松弛变软,导致细胞壁机械性能的变化[38]。在番茄中,生长素不仅可以正调控内切木葡聚糖酶,还可以正调控LeExp2mRNA的表达[39]。Karczmarek等[40]认为生长素在根结线虫成功侵染过程中是必需的,Aux/IAA基因家族成员被生长素快速诱导,并参与生长素诱导的转录调控。本研究中通过构建桃、拟南芥EXPANSIN蛋白序列进化树,发现10个桃EXPANSIN基因编码的蛋白质与拟南芥中已注释的与线虫侵染过程中巨细胞形成相关的蛋白聚在一起,均属于EXPA类,表明这些蛋白的功能可能具有相似性。比较分析EXPANSIN基因家族在南方根结线虫侵染'红根甘肃桃1号'(免疫)和'贝蕾'(高感)根系不同时期的表达量发现,*ppa010314m*、*ppa010226m*、*ppa010198m*、*ppa-010067m*和*ppa010443m*既与拟南芥中已注释的与线虫侵染过程中巨细胞形成相关蛋白聚为一类,同时表达规律为在'贝蕾'侵染后期上调表达,在'红根甘肃桃1号'中上调表达不明显,推测*ppa010314m*、*ppa010226m*、*ppa010198m*、*ppa010067m*和*ppa01-0443m*可能与南方根结线虫侵染过程中桃根部巨细胞的形成有关,参与桃抗南方根结线虫过程。将Aux/IAA基因家族和EXPANSIN基因家族在南方根结线虫侵染'红根甘肃桃1号''贝蕾'根系不同时期的表达做对比分析,发现Aux/IAA基因家族Ⅰ类基因与EXPANSIN基因家族Ⅰ类基因表达趋势相似,且EXPANSIN基因家族Ⅰ类基因表达滞后于Aux/IAA基因家族Ⅰ类基因,推测*ppa010314m*、*ppa010226m*可能是参与南方根结线虫侵染过程中巨细胞形成的关键基因。但这些基因在参与桃抗南方根结线虫过程中如何参与巨细胞形成有待进一步的证明。前人对EXPANSIN的研究大多是影响器官发育、果实成熟软化等方面,围绕抗性的研究非常少。因此,本研究获得的EXPANSIN基因将有助于研究桃在响应病原菌侵染时的表达模式。

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