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代谢组和转录组联合分析果树生理机制的研究进展

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摘 要:随着系统生物学研究大数据时代的到来,高通量、高效的多组学联合分析已经成为园艺植物研究领域最热衷的高新技术手段。更多的研究将代谢组学和转录组学联合应用于果树生理遗传机制及其调控的解析,获得了不少研究成果。代谢组和转录组的整合,可以实现组学间的相互验证,既从转录层面预测代谢物的变化,又从代谢层面验证基因转录的结果;可以深入解析代谢谱和转录谱间的相互关系和果树各项生物系统的代谢机制。笔者综述了近年来国内外代谢组和转录组联合分析在果树的果实品质形成与调控、环境响应、免疫互作机制三方面的研究进展。

关键词:果树;生理机制;代谢组学;转录组学;多组学联合分析

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Review of integrated metabolome and transcriptome analysis used for disclosing physiological mechanism in fruit crops

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Abstract: With big data applied into researches on systematic biology, the high-throughput and high-efficient integrated analysis of multi-omics has become the most popularhigh and new technology in the fields of fruit trees. Increasing studies have applied metabolomics and transcriptomics to analyze the physiological-genetic mechanisms and their regulations of fruit trees, bringing out many new discoveries. Integrated analysis of metabolomics and transcriptomics could realize the co-expression analysis of differential metabolites and genes expressed in time series, and explore the causal relationship between genes and metabolites. The key metabolic pathways, genes and metabolites could be found accurately to analyze the correlation between regulation mechanisms and biomolecular functions of fruit trees, combined with various bioinformatics methods like functional annotation and metabolic pathway enrichment. The following is a summary of the successful application of integrated analysis of transcriptomics and metabolomics from three aspects: fruit quality formation and regulation, environmental response, and immune interaction mechanisms. Not only fruit growth, development and maturity, but also fruit flavor, gloss, texture, color, aroma and nutrition are affected by gene transcription and expression, and decomposition and synthesis of metabolite. Flavor quality of fruits is mainly associated with sugars and organic acids in carbohydrate metabolism. High-acid citrus fruit Gao-cheng (*Citrus* sp.) and low-ac-

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id citrus fruit Satsuma mandarin (*Citrus unshiu* Marc.) are selected for study based on metabolomics and transcriptomics, showing that the citric acid degradation of Satsuma mandarin is more active and two transport-related genes named as *CitCHX* and *CitDIC* are up-regulated during the growing period of Satsuma mandarin. The above-mentioned research shows that these genes may be involved in the biological process in that citric acid is exported from the vacuole. Changes in the fruit texture can be divided into some processes involved in softening and lignification. Studies based on metabonomics and transcriptomics indicate that peach fruit softening and fruit lignification may be caused by differentiations in phenylpropane metabolic pathways in fruits; the biosynthesis of phenylalanine to nanngenin chalcone is regulated by mRNA, which encodes chalcone synthase in peach 'Hongli', resulting in active flavonoid synthesis and fruit softening in 'Hongli', while the expression of genes related to coenzyme A ligase like *Pp4CL2* and *Pp4CL2* in peach 'Baili' is higher, which promotes the biosynthesis from phenylalanine to p-coumaric acid in fruits and activates downstream lignin biosynthesis and ethylene precursor synthesis and leads to fruit lignification. In general, anthocyanin biosynthesis at the transcriptional level is controlled by a complex of DNA-binding R2R3 MYB transcription factors, MYC-like basic helix-loop-helix (bHLH) proteins and WD40 proteins. Studies by Wang et al. based on HPLC-MS find that anthocyanin O-malonyl hexanoside plays an important role in the formation of purple phenotype in fig (*Ficus carica* L.); and meanwhile RNA-seq combined with phylogenetic clustering analysis and sequence alignment shows that there may be transposon insertions in the MYB coding sequence in green fig, resulting in the inability to recruit R2R3 MYB transcription factors in MBW, which leads to down-regulation of a series of genes encoding chalcone synthase to UDP glucose-flavonoid 3-O-glycosyltransferase in flavonoid biosynthesis pathway, and various anthocyanins like anthocyanin O-malonylhexoside cannot be synthesized. Fruit during the growth, development and ripening must undergo various environmental changes. Studies based on metabonomics show that cyanidin 3-glucoside and cyanidin 3-(6"-malonyl) glucoside are both significantly lower in the peel of bagged blood orange and bagged purple pummelo, which confirms that light plays an important role in inducing anthocyanin biosynthesis in the peel of blood orange and purple pummelo; while the expressions of *CsRuby1* and *CgRuby1* are strongly inhibited by bagging treatment, and that sequence polymorphism comparison shows that anthocyanin synthesis is regulated by *cis* element on *Ruby1* promoter triggered by light in the peel of blood orange and purple pummelo. Complex defense mechanisms of fruit trees can be activated by microbial infection. To date, initiation of defence mechanisms against necrotrophic, biotrophic and hemi-biotrophic pathogens has been unraveled with global transcriptional analysis, and studies combined with transcriptomics and metabonomics have opened new perspectives in further understanding the biological process of fruit-pathogen interaction recently. A genome-scale metabolic network (GEM) that integrated metabolome and transcriptome datasets obtained from a spontaneous mutant of 'Newhall' navel orange (*Citrus sinensis* Osbeck) with broad-spectrum protections against fungal pathogens indicates that jasmonate biosynthesis and signaling are stimulated by the fatty acid redirection of the mutant, and participate in the tolerance of pathogenic fungi. With the improvement of the resolution of metabolite detection and the completion of whole genome sequencing of more fruit trees, the dynamic changes of genetic transcription and metabolism are expected to be interpreted in greater details, so as to further expand the bioinformatics database and deepen the study on metabonomics and transcriptomics in the metabolic network and regulation mechanism of fruit trees, so as to lay a solid foundation for systematic biology and functional genomics in the future.

Key words: Fruit trees; Physiological mechanism; Metabonomics; Transcriptomics; Multi-omics

随着现代分子生物学和生物信息的迅猛发展，生物学研究进入了系统生物学的大数据时代。近年来，组学技术成为探索生命奥秘的重要手段，继基因组学、转录组学和蛋白质组学之后，代谢组学也迅速发展起来，成为系统生物学的一个重要组成部分[1]。在园艺科研领域，为了系统地研究各种生物学现象，仅使用单一组学方法往往比较局限，而借助多组学解析园艺植物的遗传特性、代谢途径和新表型则能更为透彻[2]。随着技术的改进和生物信息数据库的更新，转录组学和代谢组学得以快速升级，双组学联合分析在果树研究领域发挥着越来越重要的作用[3-4]。

转录组学（Transcriptomics）是一门在整体水平上研究细胞中基因转录情况及转录调控规律的学科，其研究对象是植物细胞在特定功能状态下转录出的所有RNA的总和，包括多聚腺苷酸信使RNA（mRNA）、前体mRNA（pre-mRNA）和非编码RNA（noncoding RNA）。转录组同时受到内源因子和外源因子调控，是联系基因组遗传信息与功能蛋白质组的桥梁[5]。该组学的应用改变了以前选取单个或少数基因逐个突破的研究模式[6]，将生物学研究由分散转向整合。目前，转录组学研究技术已经历多次更新换代，与Sanger测序和微阵列等方法相比，第二代的转录组测序（RNA-seq）[7]和第三代的单分子测序（SNS）[8]在测序无偏倚、高通量及高分辨率方面更具优势，可量化基因表达[9]、发掘新转录本[10]、鉴定选择性剪接基因和检测等位基因[11]，已在柑橘[12]、苹果[13]、猕猴桃[14]、荔枝[15]和火龙果[16]等果树研究中获得高质量转录组数据，为果实品质形成、环境响应、免疫互作等方面的研究奠定了基础。

代谢组学（Metabonomics/Metabolomics）是效仿基因组学、转录组学、蛋白质组学的研究思想而诞生的学科，该组学旨在反映某一生物体的组织或细胞内全部代谢物或某类代谢物的合成、分解和转化规律[17]。代谢组检测涉及到的是分子质量50~1 500 Da的小分子代谢物[1,18]，这些代谢物是基因转录以及蛋白修饰的最终产物，在细胞信号传递和能量传递等方面发挥了重要的调控作用[19]，最能反映细胞在功能水平上的活动[20]。在果树研究中，代谢组分离鉴定技术以气相色谱质谱联用（GC-MS）[21]、液相色谱质谱联用（LC-MS）[22]和核磁共振技术（NMR）[23]为主，常用于评估果实品质[24]、确定果实代谢指纹图谱[25]、分析果树代谢网络[22]等研究。得益于代谢组学高通量的特点，果树代谢组学突破了传统代谢物化学成分分析的局限，将最初单纯的代谢分析或单一代谢途径分析转向多个代谢通路关联解析[20,26]。

果实生长发育或响应外界胁迫时，内源因子或外源因子会诱导细胞信号转导，进一步调节相关基因的表达[27-28]，经过转录后修饰[29-30]、蛋白质翻译[31-32]、翻译后修饰[33-34]后，转录结果最终在代谢水平上呈现，这是一个涉及多代谢通路的复杂的调控过程，单从转录、翻译或代谢一方面研究都不能较完整地阐释其中的机制。多组学关联分析成为突破单一组学研究瓶颈的一种有效方法，不同组学分别由不同层面反映果树基因转录到代谢的情况，实现数据互补，更完整地理解果树的各种生理现象背后的调控过程。其中，代谢组学和转录组学关联分析，可实现时序表达的差异基因与差异代谢物的共表达分析，探究基因和代谢物间的因果关系，同时结合功能注释和代谢通路富集等生物功能分析，锁定重点代谢通路、关键基因和关键代谢物，系统解析果树调控机制和生物分子功能间的关联性[2,35]。近年来，代谢组学和转录组学关联分析已被广泛应用于大豆[36]、水稻[37-39]、马铃薯[40]、烟草[41]等植物的研究，而果树这方面的研究也在不断增加。以下将从果树的果实品质形成与调控、环境响应、免疫互作机制三个方面对转录组学和代谢组学联合分析的成功应用作一综述。

1　基于双组学的果实品质形成和调控研究

基因转录与代谢物的分解和合成不仅影响果实生长、发育和成熟，也参与果实风味、光泽、质地、颜色、香气和营养等品质的形成与调控[42-44]。

果实风味品质主要涉及碳水化合物代谢中的糖和有机酸。基于高效液相色谱（HPLC）和实时定量荧光PCR（qRT-PCR）的研究已经确定，苹果发育前期主要积累淀粉和有机酸，成熟期积累果糖、葡萄糖和蔗糖[45]，*INV*、*SS*和*SPS*等基因调控了蔗糖和淀粉间的转化[46]。代谢组学和转录组学研究进一步解析苹果糖代谢，发现6-磷酸海藻糖可能是调节苹果蔗糖和淀粉代谢等糖代谢途径的信号物质，*TPS*、*TPP*和*TREH*参与调控了果实发育后期的海藻糖代谢[47]。双组学分析葡萄坐果期三个阶段的转录和代谢变化，发现半乳糖醇可作为信号糖调节坐果期葡

萄的MYB转录因子，抑制下游的次生代谢，编码蔗糖转运蛋白SUC2和双向糖转运蛋白SWEET1、SWEET4、SWEET5和SWEET14的基因表达下调，限制蔗糖和葡萄糖的运输，这抑制了库中营养物质的积累，最终糖信号协同植物激素信号促进葡萄坐果[48]。代谢组学和转录组学关联分析不仅能发掘关键代谢物和关键基因，还能通过功能注释和代谢通路富集将代谢物和基因与代谢通路联系，实现由点到面探究果实的糖酸代谢，在椪柑果实糖酸代谢的调控研究中，Lin等[49]研究发现，成熟末期椪柑果实的蔗糖代谢由蔗糖合成转变为蔗糖分解，糖酵解和三羧酸循环加快，碳水化合物流向能量代谢，因此延迟采收会降低碰柑的果实品质。Lin等[50]运用代谢组学和转录组学分析高酸柑橘‘高橙’和低酸柑橘‘温州蜜柑’，发现温州蜜柑的柠檬酸降解更活跃，温州蜜柑果实发育期间两个运输相关基因*CitCHX*和*CitDIC*表达上调，可能参与了柠檬酸向液泡外运输的生物过程，而被输出的柠檬酸是通过*CitAco3-CitGS2-CitGDU1*催化的谷氨酰胺途径来降解的，该研究进一步揭示了柑橘的柠檬酸降解过程。Lu等[51]通过代谢谱确定‘大红甜橙’和‘冰糖橙’两种甜橙的有机酸代谢以及柠檬酸积累的关键阶段，对关键阶段中的两种甜橙果实作转录组分析，筛选出5个调节柠檬酸积累的候选基因，差异表达基因分析表明，成熟期间‘大红甜橙’的三羧酸循环出现显著变化，推测柠檬酸的积累能力较高和分解代谢受阻是‘大红甜橙’柠檬酸含量高的成因，该研究较深入地解析了甜橙柠檬酸积累的分子过程。

果实角质层在果实发育期间形成，影响果实外观品质和贮藏品质[52-54]。前人通过研究苹果、木莓、醋栗、黑穗醋栗和葡萄已经确定角质层的主要组分是角质和蜡质，二者的合成受不同代谢机制调控[55-57]，但果实角质层形成的分子机制和调控因素尚不明确。双组学研究果实膨大期到贮藏期间6个阶段的‘纽荷儿’脐橙果皮角质层形成过程，发现角质组分中酚类化合物和甘油、脂肪族单体、十六酸和十八酸三类代谢物具有各自的代谢规律，蜡质中的ABA与蜡质形成相关基因*CRE1*、*CRE3*和*CRE4-1*以及蜡质的单糖有很强的相关性，说明ABA可能参与脐橙的蜡质形成；3个酮酰辅酶A合成酶成员KCS1、KCS11和KCS17在角质层形成关键时期表达上调，涉及蜡质合成的醛脱羰化酶CER1、脂肪酰辅酶A还原酶FAR1和CER26相关基因随之上调，角质、蜡质和木质素生物合成基因在果实发育后期被诱导[58]。在梨果实表皮蜡质形成的分子机制研究中，GC-MS分析表明梨的蜡质主要包括烷烃、伯醇、脂肪酸、醛类、萜类等化合物，差异表达基因的KEGG通路分析表明，亚油酸代谢、脂肪酸降解、醚脂代谢途径与蜡质生物合成密切相关，差异代谢物-基因的共表达网络鉴定出参与果实蜡质生物合成、运输和调控的*KCS2*等15个结构基因和*PbrMYB30_1*等12个编码转录因子的基因，这些基因进一步完善了梨果皮蜡质的生物合成通路[59]。

果实质地的变化包括果实软化和木质化[60]。果实软化涉及细胞壁变化和植物激素调节，其中，细胞壁降解受聚半乳糖醛酸酶和果胶酯酶作用[61-62]，而植物激素调节以乙烯生物合成最为关键[63]。果实木质化与果实木质素积累有关[64]，苯丙氨酸解氨酶、肉桂醇脱氢酶等共同参与木质素合成[65]。代谢组学和转录组学研究发现，桃的软化和木质化可能是果实中苯丙烷代谢途径的分支差异造成的两种结果，‘红丽’桃中编码查尔酮合成酶的mRNA正调控苯丙氨酸到南瓜皂苷查尔酮的生物合成，导致类黄酮合成活跃以及果实软化；‘白丽’桃中辅酶A连接酶相关基因*Pp4CL2*和*Pp4CL2*的高表达促进果实由苯丙氨酸到对香豆酸的生物合成，激活下游的木质素生物合成和乙烯前体合成，引起果实木质化[66]。

果实色泽是重要的外观品质，红色或紫色的花色苷、绿色的叶绿素、橙色的类胡萝卜素和红色的番茄红素都影响果实色泽。拟南芥和葡萄的研究已证实黄酮类化合物可通过维管束中特定的转运蛋白进行长距离运输[67-68]，Gutierrez等[69]通过代谢组学和转录组学方法发现黑莓的叶到果实间也存在黄酮类化合物的转运现象。HPLC-MS和RNA-seq分析表明，黑莓转色期前果实积累较多的儿茶素，但儿茶素生物合成基因表达未见增加，说明儿茶素来源于果实外部，而叶中积累的黄酮醇是果实的6倍，叶片编码的UDP-糖基转移酶、ABC转运蛋白和谷胱甘肽-S-转移酶的基因大量表达，表明叶片合成的儿茶素可能被运输到果实，最终，儿茶素作为原花青素前体在多个*RuMYB*正调控下参与原花青素的生物合成[69]。花青素生物合成的转录调控一般由DNA结合的R2R3-MYB转录因子、MYC碱性螺旋-环-螺旋（bHLH）蛋白和WD40蛋白组成的复合体（MBW）负

责[70-72]，目前已在葡萄[73]、苹果[74]、梨[75]和桃[76]中鉴定出该复合体的MYB成员。Xi等[77]比较红杏与白杏的代谢谱，发现红杏积累更多的矢车菊素、花青素-3-*O*-芸香苷和芍药素，这些花色苷是导致红杏呈红色的主要因素，加权基因共表达网络分析（WGCNA）鉴定出红色花色苷积累相关的R2R3-MYB转录因子PaMYB10以及7个结构基因，而白杏超表达*PaMYB10*促进果皮的红色着色，证实*PaMYB10*参与杏的红色花色苷生物合成；红杏套袋后*PaMYB10*表达下调，说明*PaMYB10*受光照调控。Wang等[78]运用HPLC-MS研究发现花青素*O*-丙二酰基己苷在无花果紫皮表型的形成中具有重要作用，RNA-seq结合系统发育分析和序列比对，发现绿皮无花果编码MYB的序列可能存在转座子插入现象，导致MBW中的R2R3-MYB转录因子受到抑制，造成类黄酮生物合成途径上编码查尔酮合酶到UDP葡萄糖-类黄酮3-*O*-糖基转移酶的基因均下调，以及花青素*O*-丙二酰基己苷等花色苷不能合成。Li等[79]报道类黄酮生物合成途径在猕猴桃果肉色泽调控中也有重要作用，*AaMYB*、*AabHLH*和*AaHB2*可能作为转录因子作用于*aF3H*、*AaLDOX*和*AaUFGT*的启动子，诱导基因表达以及天竺葵素等黄酮类化合物合成，促进果肉变红。除了黄酮类化合物，类胡萝卜素也参与果实的色泽形成[80-81]。基于HPLC-MS和qRT-PCR的研究已确定番木瓜果肉的类胡萝卜素种类及相关调控基因[82-83]，而类胡萝卜素在番木瓜果肉和果皮中积累机制差异仍不确定。最近，Shen等[84]通过代谢组和转录组关联分析，发现幼果期番木瓜果皮的类胡萝卜素代谢途径含α分支，该分支受编码番茄红素环化酶的*LCYE*等基因调控，可调节番茄红素到叶黄素的代谢反应，而果肉中*LCYE*不表达，导致果肉类胡萝卜素代谢缺失α分支，这可能是番木瓜果肉主要积累番茄红素而果皮主要积累叶黄素和β-类胡萝卜素的原因。

果树的田间管理不当常引起果实的生理性病害，降低果实的外观品质。柑橘果皮粗糙生理障碍（RD）是温州蜜柑典型的品质障碍，挂果率低或外源激素施用过多造成的源库比过大会引起RD[85-86]，但温州蜜柑的RD启动机制尚不明确。Lu等[87]通过非靶向和靶向代谢组检测以及转录组测序进一步解析温州蜜柑产生RD的分子机制，发现RD幼果果皮中参与赤霉素信号转导途径的bHLH转录因子表达显著上调，糖、有机酸和氨基酸代谢均改变，淀粉水解输出的过量葡萄糖导致细胞分裂旺盛，最终造成果皮的无序发育。柑橘、苹果、鳄梨、荔枝等果实都有裂果现象[88]，该生理性病害严重影响果实外观品质和贮藏品质。在荔枝裂果方面，前人研究发现钙能改变果实细胞壁的结构，从而影响果实裂果[89]。最近，Wang等[90]比较易裂型‘白糖罂’、抗裂型‘白糖罂’和抗裂型‘妃子笑’的代谢组和转录组，KEGG通路富集表明荔枝裂果与植物激素信号转导途径有关，脱落酸、乙烯和茉莉酸生物合成增加，生长素和油菜素甾醇生物合成减少，是‘白糖罂’荔枝裂果的原因。

2　基于双组学的果实环境响应机制研究

果实生长、发育和成熟期间经历各种环境变化，环境因子的刺激会诱导果树植物体内的信号传递，改变果实细胞的转录调控，最终以改变代谢水平等方式实现果实对环境的响应[29]。

温度是重要的环境因子。其中，低温造成的冷害可改变果实细胞膜的脂质成分及结构，引起细胞代谢紊乱，如过氧化氢酶和过氧化物酶活性降低，以及大量活性氧的生成[91-92]。最近，双组学研究系统地解析了受冷害圣女果的初级代谢调控网络，在碳水化合物代谢中，受冷害果实编码ATP-柠檬酸合成酶和异柠檬酸脱氢酶的基因表达上调，导致三羧酸循环中柠檬酸、顺式琥珀酸和琥珀酸的积累，说明细胞呼吸增强；氨基酸代谢中，丙氨酸氨基转移酶和支链氨基酸转氨酶基因的高表达，引起丙氨酸和亮氨酸含量增加；脂肪酸代谢中，酰基去饱和酶和油酰载体蛋白硫酯酶相关基因表达下调，饱和脂肪酸向不饱和脂肪酸转化的反应受抑制，可能影响细胞膜通透性[93]。非靶向代谢组和RNA-seq研究发现，冷害低抗性苹果在低温下γ-氨基丁酸和谷氨酸合成活跃，编码苯丙氨酸解氨酶的基因表达上调，促进下游的酚类代谢、C6醛类挥发性物质代谢和脂氧合酶应激反应，冷害高抗性苹果在低温下异戊二烯/油菜素类固醇生物合成和三萜类生物合成增强，果实倾向积累法尼醇酰酯和异戊二烯[94-95]。低温在果实的花青素合成中也有重要作用[96]，血橙中的R2R3MYB转录因子*CsRuby1*可响应低温诱导果实的花青素合成[97]。Huang等[98]发现紫柚果肉也存在*CgRuby1*，但

低温不能诱导*CgRuby1*表达以及花青素合成，说明*CsRuby1*和*CgRuby1*的调控机制不同，进一步研究发现血橙中*CsRuby1*启动子上游包含一个典型的长末端重复序列（LTR）反转座子*Tcs1*插入，LTR的顺式元件能与MYB转录因子结合而诱导花青素合成，而*CgRuby1*启动子缺失LTR导致低温诱导不能促进紫柚果肉花青素合成。

在光照方面，苹果[99]、梨[100]、荔枝[101]的研究表明R2R3MYB转录因子能响应光信号促进果实花青素积累。代谢组学研究发现套袋血橙和套袋紫柚的果皮花青素3-葡萄糖苷和花青素3-（6”-丙二酰基）葡萄糖苷明显减少，证实光在诱导血橙和紫柚果皮积累花色苷方面的重要作用，套袋处理强烈抑制*Cs-Ruby1*和*CgRuby1*的表达，序列多态性比较表明，血橙和紫柚果皮都是通过*Ruby1*启动子上的光响应顺式元件调控花青素合成的[98]。

CO_2作为气体环境因子可影响果实细胞能量代谢、乙醇积累和果胶代谢，改善果实的质地和贮藏品质[102-103]。双组学研究进一步解析草莓果实响应高浓度CO_2的细胞反应，发现碳水化合物代谢中编码转化酶抑制因子的基因下调，促进蔗糖向己糖转化，合成细胞防御所需的代谢物，果胶酯酶相关基因下调，抑制甲酯化果胶的降解，增加草莓果实的硬度[104]。果实对氧气浓度的变化也高度敏感，研究发现涉及ERF转录因子的氧传感机制参与了果实响应缺氧环境的调控[105-106]，而最近的双组学研究解析了参与果实缺氧响应的其他代谢途径。Brizzolara等[107]发现缺氧下苹果的γ-氨基丁酸分支途径被抑制，果实积累缺氧应激相关的γ-氨基丁酸，2-酮戊二酸关联的双加氧酶基因被激活，说明初级代谢转向三羧酸循环；次生代谢中苯丙烷途径转录改变，将丙酸合成转向甲基赤藓糖醇磷酸途径；在植物激素信号转导方面，向果实细胞运输的生长素减少，脱落酸生物合成增强。

3 基于双组学的植物免疫互作机制研究

微生物侵染会引发果树复杂的防御机制。基于RNA-seq的研究已基本揭示果实对死体营养型微生物、活体营养型微生物和半活体营养型微生物防御反应的启动机制[108]，而最近联合转录组学和代谢组学的研究将果实防御微生物侵染的生物过程进一步完善，为该领域的研究开辟新视野[109]。

真菌侵染果实会改变果实的新陈代谢，造成果实品质劣化，而果实通过积累抗菌代谢物和形成物理防御屏障两种类型的抗性机制防御真菌侵染[110-111]。拟青霉病作为一种柑橘病害可诱导柑橘果实的植物激素代谢、类苯丙烷生物合成等次生代谢[112-113]。最近，Tang等[114]运用GC-MS和RNA-seq研究‘鲍威尔’脐橙受指状拟青霉侵染后的防御反应，发现指状拟青霉诱导增强了脐橙初级代谢中的蔗糖水解、糖酵解和三羧酸循环，造成果实可溶性糖的大量消耗以及品质劣化，而脐橙通过增强ERF、WRKY和MYB转录因子以及编码过氧化物酶和NBS-LRR等应激基因的转录，激活茉莉酸和乙烯途径，以及积累鼠李糖和肌醇，抑制指状拟青霉的侵染。He等[115]为了探究脐橙抗病突变体对真菌的防御机制，通过整合脐橙果实的代谢组和转录组构建了一个基因组规模代谢模型（GEM），发现突变体中脂肪酸通路重定向，导致茉莉酸的生物合成和信号传导途径被刺激而参与防御反应。枣果实黑斑病是由链格孢霉引起的病害，而水杨酸[116]和β-氨基丁酸[117]能诱导果实的防御反应而减轻黑斑病的侵害。Yuan等[118]研究链格孢霉侵染枣果实的生物过程，该菌的侵染会诱发枣果病斑外依次形成绿环和红环，病斑的发展往往终止于红环区域，RNA-seq和超高效液相色谱-质谱（UPLC-MS）分析表明，绿环和红环区域中茉莉酸生物合成的α-亚麻酸代谢增强，参与苯丙烷类途径和木质素生物合成反应活跃，木质素的积累可能增加果实细胞壁厚度而抑制真菌的传播。在致病疫霉侵染番茄果实的研究中，Rodenburg等[119]将寄主与微生物的代谢组和转录组整合成GEM，该GEM涉及4 303种代谢物、4 578个基因和4 695个生化反应，结果表明致病疫霉的硫胺素焦磷酸形成依赖于番茄的硫胺素生物合成途径，侵染后期，致病疫霉由活体营养阶段转向死体营养阶段，氨基酸生物合成、糖酵解和三羧酸循环逐渐减缓。在苹果根皮苷合成核心基因*MdUGT88F1*对苹果发育和抗腐烂病的作用机制研究中，Zhou等[120]通过*MdUGT88F1*超表达和RNAi得到两种转基因系苹果，超表达品系总二氢查尔酮无明显变化，而RNAi品系的根皮苷显著降低，表现出矮化表型，这与木质素代谢途径上香豆酸和肉桂酰的衍生物减少造成木质素含量降低有密切关系，RNAi品系转录组

分析发现参与肌醇转化为肌醇半乳糖苷的相关基因表达上调，造成肌醇减少以及细胞壁多糖组成异常而影响RNAi品系的生长，而腐烂病病菌降解根皮苷后生成的间笨三酚等毒素会加速苹果组织坏死，因此RNAi品系表现出更高的腐烂病抗性，这些结果证实*MdUGT88F1*的正常表达能维持苹果的正常生长，其下调表达能增强植株腐烂病抗性。

病毒维持生命活动需要活细胞提供营养物质，属于活体营养型或半活体营养型微生物[121]。黄化曲叶病毒（TYLCV）常引起番茄生长迟缓，结实困难[122]。通过基因沉默筛选番茄抗TYLCV基因的研究已确定*LeHT1*等69个抗病基因[123-124]。代谢组学和转录组学进一步解析番茄抗TYLCV的分子机制，发现TYLCV侵染下抗病番茄的初级代谢受到更有序的调控，参与类黄酮合成的基因*CHS*、*CHI*、*F3H*、*F3'H*和*FLS*的表达模式出现变化，同时芸香甙和山萘酚的合成增强，说明类黄酮生物合成在抗病番茄防御TYLCV中发挥作用；*ICS*和*PAL*表达增强，说明抗病番茄通过异分支酸途径和肉桂酸途径合成水杨酸，增加对TYLCV的抗性[125]。此外，双组学研究发现茉莉酸甲酯介导的防御性酰糖生物合成可促进番茄毛状体中酰糖和酚类代谢物的积累，也能增强番茄对TYLCV的抗性[126]。

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代谢组可揭示果树受遗传或外源因素影响后的代谢状态，是构成果树复杂表型的基础；而转录组集合了大量差异表达基因以及众多调控网络的信息，是联系果树基因组的纽带。代谢组学和转录组学联合分析提高了鉴定功能基因的准确性，能更全面、更透彻地解析果树各种生理现象背后复杂的分子功能及调控机制，在系统生物学和功能基因组学研究领域贡献突出。虽然代谢组学和转录组学联合分析在果树研究领域的应用晚于模式植物番茄[127]和拟南芥[128]，但随着近几年代谢组检测准度和灵敏度提高、转录组测序速度和准度优化，果树代谢调控网络的研究取得了较明显的进步，推动了柑橘[49-50]、苹果[47]、梨[59]、桃[66]、葡萄[48]和荔枝[90]等果树在果实品质形成、非生物因素或生物因素响应方面的研究进展。

截至目前，果树代谢组学和转录组学关联分析的研究成果仍不够完善。在代谢组学方面，由于代谢物结构类型的多样性和未知代谢物鉴定的复杂性，多数代谢物的种类仍然未能鉴别[129]。转录组学方面，果树童期长等特点制约了果实相关功能基因的验证，很多基因的功能尚不明确；很多果树尚未完成全基因组测序，缺少参考基因组，需要借助生物信息学方法对基因注释。代谢网络上仍有很多空白位点，需要更多的代谢物、调控基因来填补。在生物信息学方面，代谢物检测和转录本测序产生的庞大数据量会造成信息解读和分析的困难，最大限度地挖掘数据中隐藏的关键信息和验证核心数据是研究的难题。将来，随着代谢物检测分辨率提高以及更多果树全基因组测序的完成，果树转录代谢的动态变化有望得到更精细的解读，从而进一步拓展生物信息数据库，深化代谢组学和转录组学在果树代谢调控网络机制方面的研究，为系统生物学和功能基因组学的下一步研究奠定厚实基础。

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