苹果片在干制条件下的蛋白质组学分析

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摘要 [目的]研究苹果片在干制条件下及复合护色剂处理后的蛋白质水平变化。[方法]采用 Label free 技术分析了苹果片在干制条件下及复合护色剂处理后果肉中蛋白质组学的变化。[结果]一共检测到 319 个差异蛋白上调,590 个下调,分别参与了多个不同的代谢途径。其中,催化活性 catalytic activity(48 个差异表达蛋白)、氧化还原过程 oxidation-reduction process(18 个差异表达蛋白)、应激反应 response to stress(17 个差异表达蛋白)等多个途径的蛋白差异表达明显。KEGG 富集分析结果显示,共有 2 个基因通路显著富集,在氧化磷酸化 Oxidative phosphorylation 中有 5 个蛋白参与显著富集;在代谢通路 Metabolic pathways 中有 11 个蛋白参与显著富集。这 2 个途径与抗氧化、褐变酶合成途径有关。[结论]该研究首次在苹果片干制条件下及复合护色剂处理后采用蛋白质组学的方法分析差异蛋白的表达变化,为复合护色剂在实践中果蔬护色提供科学依据。

关键词 复合护色剂;苹果片;干制;蛋白质组学;表达分析;GO 富集分析
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Proteomic Studies in Apple Slices during Drying

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Abstract [Objective] To investigate proteins expression in complex colour-protective reagents treated apple slices during drying. [Method] We analyzed proteomic change in apple slices treated with complex colour-protective reagents during drying using Label free technology. [Result]319 differential proteins were upregulated, 590 differential proteins were downregulated. They involved into different metabolism pathways, respectively. Among them, differential proteins expression in catalytic activity (48 proteins), oxidation-reduction process (18 proteins), response to stress (17 proteins) pathways became very obvious. KEGG enrichment analysis showed that two gene pathways were obviously enriched. 5 proteins involved into Oxidative phosphorylation pathway enrichment. 11 proteins involved into metabolic pathways enrichment. The two pathways were related to antioxidation and enzymes browning procedures. [Conclusion] Proteomic change in complex colour-protective reagents treated apple slices during drying was first reported. This study provided a science support to application of complex colour-protective reagents in fruits and vegetables browning inhibition.

Key words Complex colour-protective reagents;Apple slices;Drying;Proteomics;Expression analysis;GO enrichment analysis

苹果是一种非常适合于工业化生产的水果,新鲜苹果经分级、清洗、整修、去皮、切分、保鲜、包装等处理,供消费者立即食用或餐饮业使用。色泽是判断加工苹果非常重要的一个指标,切割苹果的主要质量问题是褐变。由于在加工过程(如去皮、切分等)中破坏了多酚氧化酶(PPO)和酚类物质在细胞内通过一系列膜系统的区域化分布,因而酶和底物的酚类物质在有氧气的条件下相互接触导致酶促褐变的发生,从而严重影响苹果的颜色、风味、营养和品质,因此防止加工苹果的氧化褐变尤为重要[1-2]。苹果褐变的主要原因是其组织内的酚类物质在多酚氧化酶的作用下氧化为醌类,而醌类物质会进一步聚合而形成黑色素,进而发生酶促褐变[3]。

蛋白质组是指由一个基因组、一个细胞或组织所表达的所有蛋白质[4-5]。蛋白质组学是以蛋白质组为研究对象的新的研究领域,其目的在于阐明生物体全部蛋白质的表达模式及功能模式,包括蛋白质的表达、翻译后的修饰、蛋白结构、蛋白与蛋白之间相互作用等,由此获得蛋白质水平上的关于疾病发生、细胞代谢等过程的整体而全面的认识[6-7]。苹果片干制是保存苹果的一种重要方法,然而在干制过程中,果肉极易发生褐变,使其商品价值大大降低,为此,研制了一种能有效降低果肉褐变的复合护色剂。笔者通过蛋白组学分析技术分析了干制苹果片在护色前后蛋白的差异表达,为揭示复合护色剂抑制苹果片果肉褐变的机制提供科学依据。

1 材料与方法

1.1 材料 试验材料红富士苹果购自太谷县。

1.2 方法

1.2.1 样品处理。洗净苹果,将苹果切成 1 mm 的薄片,均等分成 2 份,其中 1 份放置于空气中 4 h,另 1 份浸泡于复合护色液中 4 h,将 2 份苹果放置于 45 ℃烘箱中烘至恒重。

1.2.2 蛋白质提取。蛋白质提取按照参考文献[8]的方法进行。

1.2.3 蛋白质酶解。蛋白质酶解按照参考文献[8]的方法进行。

1.2.4 色谱质谱检测流程。检测用 LTQ orbitrapVelos 液质联用仪配备戴安 ultramate 3000 nano – UPLC 进行分析,上机量 10 μL,首先进入保护柱(C18 PepMap100,300 μm × 1 mm,5 μm,100 Å),随后进入分析柱(AcclaimPepMap C18,15 cm × 75 μm,2 μm,100 Å,Dionex)以流速 0.2 μL/min 进行分析。质谱参数:阳离子模式,CID 碰撞模式,120 000 分辨率,质量范围 350 ~ 1 800,NCE 为 35%,前 top15 离子强度用于 MS/MS 分析。

1.3 分析方案 Orbitrap 原始数据定性定量方法:对获得的 Label free 蛋白质原始数据. raw,用 Label free 定性定量软件 maxquant(1.5.0.12)结合搜库定性软件 Andromeda,对每个样本进行定性定量,参考蛋白质数据库为 uniprot(收录了共

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34 361 条记录)。具体的定性和检索方法按照参考文献[8]的方法进行。

2　结果与分析

2.1　差异蛋白表达分析　定性定量分析可以识别到 1 797 个蛋白(unique peptide≥1)。最终获得的差异蛋白总数为 909 个,其中下调总数为 590 个,上调总数为 319 个[8]。

2.2　差异蛋白 GO 富集分析　Gene Ontology 显著性富集分析以 GO term 为单位,找出与基因组的所有表达基因背景相比,在差异表达基因中显著性富集的 GO term。检验 P 值,将用 $P \leqslant 0.05$ 的 GO term 定义为在差异表达基因中显著富集的 GO term。通过 GO 功能显著性富集分析能确定差异表达基因行驶的主要生物学功能。其中 BP 为 biological process(生物学过程)、MF 为 Molecular Function(分子功能)、CC 为 Cellular Component(细胞组件)。用 GO 数据库注释将差异蛋白,分析差异蛋白在本体论水平上的功能富集,结果显示,差异蛋白分别在 Biological process、Cellular component 和 Molecular function 这 3 个水平上有显著富集。其中差异蛋白表达数≥10 的有催化活性 catalytic activity(48 个差异表达蛋白)、氧化还原过程 oxidation-reduction process(18 个差异表达蛋白)、应激反应 response to stress(17 个差异表达蛋白)、碳水化合物代谢过程 carbohydrate metabolic process(13 个差异表达蛋白)、羧酸代谢过程 carboxylic acid metabolic process(11 个差异表达蛋白)、酮酸代谢过程 oxoacid metabolic process(11 个差异表达蛋白)、有机酸代谢过程 organic acid metabolic process(11 个差异表达蛋白)、非生物刺激反应 response to abiotic stimulus(10 个差异表达蛋白)。通过注释信息可知在果肉干制过程中代谢活力整体上功能集中在催化过程和氧化还原过程(表 1、图 1)。

表 1　差异蛋白 GO 富集统计

Table 1　GO enrichment statistics of differential protein

GO 编号 GO ID	GO 注释信息 Term	注释上所有 GOterm 的差异蛋白总数 Count	P	基因编号 Genes No.
GO:0031408	Oxylipin biosynthetic process	5	1.60E－08	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000923670
GO:0031407	Oxylipin metabolic process	5	1.90E－08	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000923670
GO:0019252	Starch biosynthetic process	3	3.30E－06	MDP0000095637,MDP0000247496,MDP0000272992
GO:0006108	Malate metabolic process	4	3.70E－06	MDP0000132833,MDP0000174740,MDP0000384593,MDP0000599133
GO:0006633	Fatty acid biosynthetic process	6	4.10E－05	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000330776,MDP0000923670
GO:0006950	Response to stress	17	5.30E－05	MDP0000052608,MDP0000142814,MDP0000146698,MDP0000154668,MDP0000162904,MDP0000174018,MDP0000174740,MDP0000195614,MDP0000211088,MDP0000259661,MDP0000285074,MDP0000295542,MDP0000300274,MDP0000330776,MDP0000479436,MDP0000698024,MDP0000816297
GO:0051365	Cellular response to potassium ion starvation	2	0.000 11	MDP0000146698,MDP0000300274
GO:0072330	Monocarboxylic acid biosynthetic process	6	0.000 12	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000330776,MDP0000923670
GO:0043473	Pigmentation	2	0.000 16	MDP0000174748,MDP0000243196
GO:0043648	Dicarboxylic acid metabolic process	4	0.000 16	MDP0000132833,MDP0000174740,MDP0000384593,MDP0000599133
GO:0005982	Starch metabolic process	3	0.000 16	MDP0000095637,MDP0000247496,MDP0000272992
GO:0006631	Fatty acid metabolic process	6	0.000 17	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000330776,MDP0000923670
GO:0009607	Response to biotic stimulus	8	0.000 20	MDP0000052608,MDP0000142814,MDP0000162904,MDP0000174018,MDP0000195614,MDP0000259661,MDP0000295542,MDP0000330776
GO:0010035	Response to inorganic substance	8	0.000 21	MDP0000174740,MDP0000211088,MDP0000261821,MDP0000285074,MDP0000330776,MDP0000479436,MDP0000698024,MDP0000709748
GO:0006952	Defense response	8	0.000 36	MDP0000052608,MDP0000142814,MDP0000162904,MDP0000174018,MDP0000195614,MDP0000259661,MDP0000295542,MDP0000330776
GO:0009415	Response to water	5	0.000 42	MDP0000211088,MDP0000285074,MDP0000330776,MDP0000479436,MDP0000698024
GO:0008610	Lipid biosynthetic process	7	0.000 66	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000299402,MDP0000330776,MDP0000923670
GO:0032787	Monocarboxylic acid metabolic process	7	0.000 67	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000330776,MDP0000823956,MDP0000923670
GO:0006970	Response to osmotic stress	6	0.000 75	MDP0000052608,MDP0000174740,MDP0000285074,MDP0000300274,MDP0000330776,MDP0000816297
GO:0005975	Carbohydrate metabolic process	13	0.000 89	MDP0000095637,MDP0000127542,MDP0000140483,MDP0000162904,MDP0000174537,MDP0000174740,MDP0000177786,MDP0000247496,MDP0000252855,MDP0000272992,MDP0000330776,MDP0000823956,MDP0000832632

接下表

续表 1

GO 编号 GO ID	GO 注释信息 Term	注释上所有 GOterm 的差异蛋白总数 Count	*P*	基因编号 Genes No.
GO:0019752	Carboxylic acid metabolic process	11	0.001 02	MDP0000132833,MDP0000154668,MDP0000169311,MDP0000174168,MDP0000174740,MDP0000186011,MDP0000330776,MDP0000384593,MDP0000599133,MDP0000823956,MDP0000923670
GO:0043436	Oxoacid metabolic process	11	0.001 22	MDP0000132833,MDP0000154668,MDP0000169311,MDP0000174168,MDP0000174740,MDP0000186011,MDP0000330776,MDP0000384593,MDP0000599133,MDP0000823956,MDP0000923670
GO:0006082	Organic acid metabolic process	11	0.001 24	MDP0000132833,MDP0000154668,MDP0000169311,MDP0000174168,MDP0000174740,MDP0000186011,MDP0000330776,MDP0000384593,MDP0000599133,MDP0000823956,MDP0000923670
GO:0044262	Cellular carbohydrate metabolic process	6	0.001 70	MDP0000095637,MDP0000174537,MDP0000247496,MDP0000272992,MDP0000330776,MDP0000823956
GO:0009628	Response to abiotic stimulus	10	0.001 77	MDP0000052608,MDP0000146698,MDP0000174740,MDP0000211088,MDP0000285074,MDP0000300274,MDP0000330776,MDP0000479436,MDP0000698024,MDP0000816297
GO:0044255	Cellular lipid metabolic process	7	0.002 26	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000299402,MDP0000330776,MDP0000923670
GO:0055114	Oxidation-reduction process	18	0.002 28	MDP0000132833,MDP0000133306,MDP0000154668,MDP0000169311,MDP0000174168,MDP0000174740,MDP0000186011,MDP0000188052,MDP0000197462,MDP0000207799,MDP0000261821,MDP0000283457,MDP0000285427,MDP0000384593,MDP0000599133,MDP0000818359,MDP0000874667,MDP0000923670
GO:0009651	Response to salt stress	5	0.002 61	MDP0000052608,MDP0000174740,MDP0000285074,MDP0000300274,MDP0000330776
GO:0009414	Response to water deprivation	4	0.002 70	MDP0000211088,MDP0000285074,MDP0000330776,MDP0000479436
GO:0043086	Negative regulation of catalytic activity	2	0.002 72	MDP0000145032,MDP0000162904
GO:0043269	Regulation of ion transport	2	0.002 72	MDP0000300274,MDP0000330776
GO:0006869	Lipid transport	3	0.002 78	MDP0000221771,MDP0000285074,MDP0000304369
GO:0046686	Response to cadmium ion	4	0.003 36	MDP0000174740,MDP0000211088,MDP0000261821,MDP0000709748
GO:0010876	Lipid localization	3	0.003 72	MDP0000221771,MDP0000285074,MDP0000304369
GO:0065009	Regulation of molecular function	3	0.004 01	MDP0000145032,MDP0000162904,MDP0000330776
GO:0016053	Organic acid biosynthetic process	6	0.005 42	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000330776,MDP0000923670
GO:0046394	Carboxylic acid biosynthetic process	6	0.005 42	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000330776,MDP0000923670
GO:0051049	Regulation of transport	2	0.005 78	MDP0000300274,MDP0000330776
GO:0044092	Negative regulation of molecular function	2	0.006 05	MDP0000145032,MDP0000162904
GO:0032879	Regulation of localization	2	0.007 85	MDP0000300274,MDP0000330776
GO:0010038	Response to metal ion	4	0.009 28	MDP0000174740,MDP0000211088,MDP0000261821,MDP0000709748
GO:0044711	Single-organism biosynthetic process	11	0.009 37	MDP0000095637,MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000207799,MDP0000247496,MDP0000272992,MDP0000299402,MDP0000330776,MDP0000923670
GO:0005985	Sucrose metabolic process	2	0.009 50	MDP0000174537,MDP0000330776
GO:0009501	Amyloplast	3	2.30E-07	MDP0000095637,MDP0000247496,MDP0000272992
GO:0005856	Cytoskeleton	8	3.10E-07	MDP0000264119,MDP0000299245,MDP0000408630,MDP0000423104,MDP0000437009,MDP0000474142,MDP0000497445,MDP0000582937
GO:0009524	Phragmoplast	4	6.90E-06	MDP0000408630,MDP0000437009,MDP0000474142,MDP0000497445
GO:0003779	Actin binding	9	2.80E-12	MDP0000264119,MDP0000299245,MDP0000408630,MDP0000423104,MDP0000437009,MDP0000474142,MDP0000497445,MDP0000573939,MDP0000582937
GO:0008092	Cytoskeletal protein binding	9	5.20E-08	MDP0000264119,MDP0000299245,MDP0000408630,MDP0000423104,MDP0000437009,MDP0000474142,MDP0000497445,MDP0000573939,MDP0000582937
GO:0004373	Glycogen(starch)synthase activity	3	1.30E-06	MDP0000095637,MDP0000247496,MDP0000272992
GO:0016615	Malate dehydrogenase activity	4	5.00E-06	MDP0000132833,MDP0000174740,MDP0000384593,MDP0000599133
GO:0051213	Dioxygenase activity	5	1.10E-05	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000923670

接下表

续表 1

GO 编号 GO ID	GO 注释信息 Term	注释上所有 GOterm 的差异蛋白总数 Count	*P*	基因编号 Genes No.
GO:0003939	L-iditol 2-dehydrogenase activity	2	3.00E－05	MDP0000188052,MDP0000874667
GO:0004470	Malic enzyme activity	3	5.10E－05	MDP0000132833,MDP0000384593,MDP0000599133
GO:0004471	Malate dehydrogenase(decarboxylating)(NAD+)activity	3	5.10E－05	MDP0000132833,MDP0000384593,MDP0000599133
GO:0016616	Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	6	5.40E－05	MDP0000132833,MDP0000174740,MDP0000188052,MDP0000384593,MDP0000599133,MDP0000874667
GO:0004674	Protein serine/threonine kinase activity	6	7.10E－05	MDP0000052608,MDP0000216765,MDP0000300274,MDP0000320149,MDP0000330776,MDP0000816297
GO:0016702	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	4	9.40E－05	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000923670
GO:0016701	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	4	0.000 23	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000923670
GO:0016614	Oxidoreductase activity, acting on CH－OH group of donors	6	0.000 24	MDP0000132833,MDP0000174740,MDP0000188052,MDP0000384593,MDP0000599133,MDP0000874667
GO:0048037	Cofactor binding	8	0.000 66	MDP0000132833,MDP0000174748,MDP0000197462,MDP0000243194,MDP0000243196,MDP0000261821,MDP0000384593,MDP0000599133
GO:0050662	Coenzyme binding	7	0.000 70	MDP0000132833,MDP0000174748,MDP0000243194,MDP0000243196,MDP0000261821,MDP0000384593,MDP0000599133
GO:0016491	Oxidoreductase activity	17	0.000 86	MDP0000132833,MDP0000133306,MDP0000154668,MDP0000169311,MDP0000174168,MDP0000174740,MDP0000174748,MDP0000186011,MDP0000188052,MDP0000197462,MDP0000207799,MDP0000261821,MDP0000283457,MDP0000384593,MDP0000599133,MDP0000874667,MDP0000923670
GO:0035251	UDP-glucosyltransferase activity	4	0.001 05	MDP0000095637,MDP0000174537,MDP0000247496,MDP0000272992
GO:0046527	Glucosyltransferase activity	4	0.001 09	MDP0000095637,MDP0000174537,MDP0000247496,MDP0000272992
GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups	6	0.00126	MDP0000152370,MDP0000166457,MDP0000214714,MDP0000388537,MDP0000428199,MDP0000637737
GO:0003824	Catalytic activity	48	0.002 08	MDP0000052608,MDP0000095637,MDP0000127542,MDP0000132833,MDP0000133306,MDP0000140483,MDP0000145032,MDP0000152370,MDP0000154668,MDP0000162904,MDP0000166457,MDP0000169311,MDP0000170162,MDP0000170302,MDP0000174168,MDP0000174537,MDP0000174740,MDP0000174748,MDP0000177786,MDP0000186011,MDP0000188052,MDP0000197462,MDP0000207799,MDP0000214714,MDP0000216765,MDP0000243194,MDP0000243196,MDP0000247496,MDP0000252855,MDP0000261821,MDP0000272992,MDP0000283457,MDP0000299402,MDP0000300274,MDP0000320149,MDP0000330776,MDP0000384593,MDP0000388537,MDP0000428199,MDP0000461555,MDP0000599133,MDP0000637737,MDP0000709748,MDP0000816297,MDP0000823956,MDP0000832632,MDP0000874667,MDP0000923670
GO:0016746	Transferase activity, transferring acyl groups	6	0.002 65	MDP0000152370,MDP0000166457,MDP0000214714,MDP0000388537,MDP0000428199,MDP0000637737
GO:0008289	Lipid binding	4	0.002 67	MDP0000052608,MDP0000221771,MDP0000285074,MDP0000304369
GO:0051287	NAD binding	3	0.002 97	MDP0000132833,MDP0000384593,MDP0000599133
GO:0019899	Enzyme binding	3	0.003 17	MDP0000146698,MDP0000302895,MDP0000330776
GO:0008194	UDP-glycosyltransferase activity	4	0.005 21	MDP0000095637,MDP0000174537,MDP0000247496,MDP0000272992
GO:0016758	Transferase activity, transferring hexosyl groups	6	0.006 42	MDP0000095637,MDP0000170162,MDP0000174537,MDP0000247496,MDP0000272992,MDP0000461555
GO:0003746	Translation elongation factor activity	2	0.009 72	MDP0000162037,MDP0000312975
GO:0031408	Oxylipin biosynthetic process	5	1.60E－08	MDP0000154668,MDP0000169311,MDP0000174168,MDP0000186011,MDP0000923670

2.3　差异基因的 pathway 富集分析　KEGG(Kyoto Encyclopedia of Genes and Genomes)是系统分析基因功能、基因组信息数据库,它有助于研究者把基因及表达信息作为一个整体网络进行研究。KEGG 的一个数据库是 GENES,另一个数据库是 LIGAND。KEGG 提供的整合代谢途径(pathway)查询十分出色,包括碳水化合物、核苷、氨基酸等的代谢及有机物的生物降解,不仅提供了所有可能的代谢途径,而且对催化各步反应的酶进行了全面的注解,包含有氨基酸序列、PDB库的链接等。

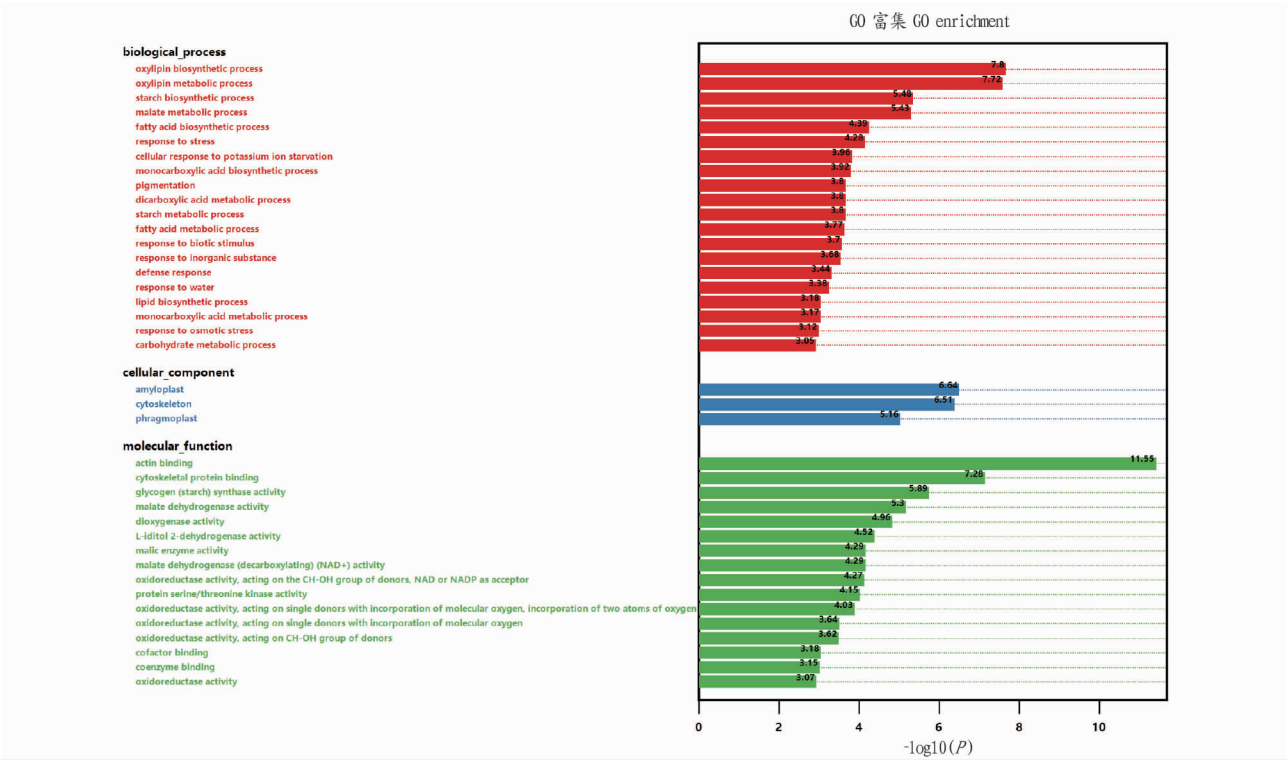

图 1 GO 富集柱状图分析

Fig. 1 Histogram analysis of GO enrichment

KEGG 是进行生物体内代谢分析、代谢网络研究的强有力工具。

用 KEGG 数据库注释差异蛋白,分析差异蛋白在 KEGG 代谢通路中的富集,对差异蛋白进行富集分析,取 $P<0.05$ 为最终差异的代谢通路。结果显示,共有 2 个基因通路显著富集,在氧化磷酸化 Oxidative phosphorylation 中有 5 个蛋白参与显著富集;在代谢通路 Metabolic pathways 中有 11 个蛋白参与显著富集。这 2 个途径与抗氧化、褐变酶合成途径有关,说明在果片干制过程中的褐变酶与抗氧化酶蛋白可能参与褐变代谢相关酶的生成或抑制过程。这个结果与 GO 富集分析结果一致(表 2、图 2)。

表 2 差异蛋白 KEGG pathway 富集统计

Table 2 KEGG pathway enrichment statistics of differential protein

KEGG 代谢通路数据库中的注释信息 #Term	ID	注释上所有 KEGG 代谢通路的差异基因总数 Input number	背景数 Background number	*P*	输入的 DEP 基因号 Input
Oxidative phosphorylation	mdm00190	5	17	0.010 395	J7MFY4|J7MFW9|J7MPW8|J7MB93|J7MB90
Metabolic pathways	mdm01100	11	84	0.030 559	Q8RVK7 | J7MPW8 | J7MFY4 | J7MFW9 | I1U4K5 | K4HV56 | S4UKU5 | S4UKU7 | K4HW86|J7MB90|J7MB93
Linoleic acid metabolism	mdm00591	3	12	0.067 261	S4UL91|S4UKU5|S4UKU7
Fructose and mannose metabolism	mdm00051	2	5	0.070 494	C7A7X8|K4HV56
Starch and sucrose metabolism	mdm00500	2	8	0.133 576	K4HW86|K4HV56
alpha-Linolenic acid metabolism	mdm00592	2	8	0.133 576	S4UKU5|S4UKU7
Biosynthesis of secondary metabolites	mdm01110	6	59	0.239 149	G1E6S8 | Q8RVK7 | I1U4K5 | K4HV56 | S4UKU5|S4UKU7
Isoquinoline alkaloid biosynthesis	mdm00950	1	5	0.333 696	I1U4K5
Amino sugar and nucleotide sugar metabolism	mdm00520	1	5	0.333 696	K4HV56
Tyrosine metabolism	mdm00350	1	5	0.333 696	I1U4K5
Plant-pathogen interaction	mdm04626	1	9	0.492 967	Q6LBM2
Flavonoid biosynthesis	mdm00941	1	15	0.664 708	G1E6S8
Plant hormone signal transduction	mdm04075	2	39	0.767 559	A0A076JU29|A0A076JYZ8
Oxidative phosphorylation	mdm00190	5	17	0.010 395	J7MFY4|J7MFW9|J7MPW8|J7MB93|J7MB90
Metabolic pathways	mdm01100	11	84	0.030 559	Q8RVK7 | J7MPW8 | J7MFY4 | J7MFW9 | I1U4K5 | K4HV56 | S4UKU5 | S4UKU7 | K4HW86|J7MB90|J7MB93
Linoleic acid metabolism	mdm00591	3	12	0.067 261	S4UL91|S4UKU5|S4UKU7

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5.6　植物景观配置　在进行植物配置时，以景观、生态、互生、共生的生态理念为指导，根据植物的生长习性、时相变化或者季相变化，构成植物空间，做到四季常绿，形成园区景观化、园林化，构建丰富多彩、五彩缤纷的美丽环境。

5.7　建筑风格设计　园区建筑的布置采用生态学的观点，结合客家文化，客家建筑元素的特点，将节能、节水设计理念融入建筑风格中，形成特有的生态农业观光园的建筑风格。

6　结语

生态农业观光园是一个特色型、生态型、文化型、科技型的综合现代农业示范区。它的建设可以挖掘、继承、发扬乡村的优秀传统文化，创造现代化农村形象，发展现代乡愁，深化旅游开发，保护生态环境。上犹梅水生态农业观光园开发建设对于促进城乡一体化、加快社会主义新农村建设具有时代意义，可为农业持续发展提供源源不断的动力，为我国赣南地区的农业发展提供一种新的模式，为赣南农业发展和研究提供了新的思路。

参考文献

[1] 刘坤. 生态农业观光园规划设计研究[D]. 保定：河北农业大学，2012.

[2] 赵其国. 现代生态农业与农业安全[J]. 生态环境，2003，12(3)：253－259.

[3] 马勇，舒伯阳. 区域旅游规划：理论·方法·案例[M]. 天津：南开大学出版社，1998：109－112.

[4] 钟喜林，罗致迪，姜媛. 江西赣州“绿源休闲农业产业园”生态景观营造研究[J]. 安徽农业科学，2012，40(32)：15771－15773.

[5] 黄丽霞，杨振华，李琴，等. 基于生态保护与文化传承的大足石刻农业观光园规划探讨[J]. 西南师范大学学报(自然科学版)，2017，42(5)：76－82.

[6] 钟喜林，钟晓红. 河岸生态园林景观营造研究：以江西省龙南县河岸生态园林景观营造为例[J]. 安徽农业科学，2011，39(24)：14862－14864.

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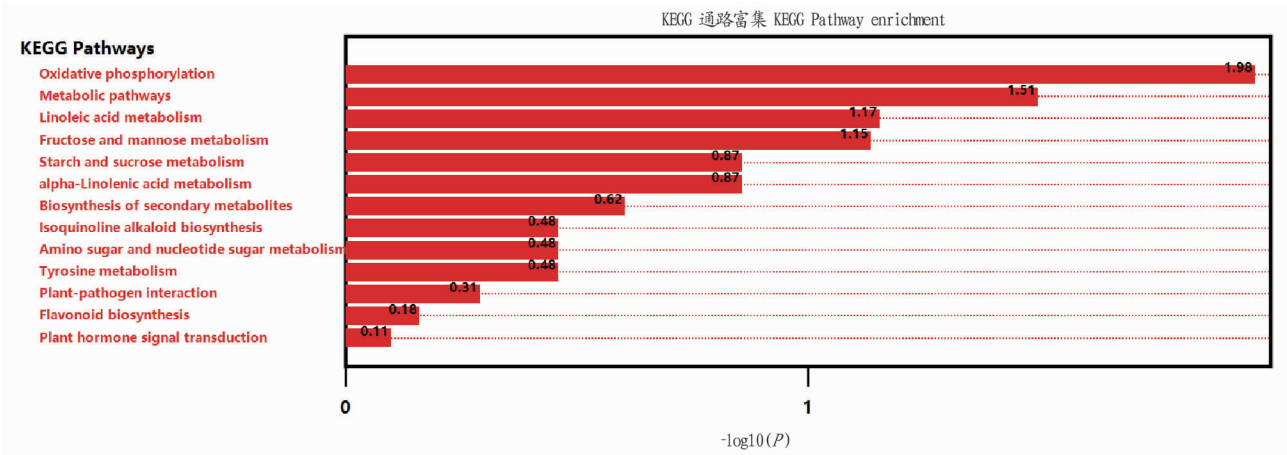

图 2　KEGG 富集柱状图分析

Fig. 2　Histogram analysis of KEGG enrichment

3　结论

苹果片经复合护色剂处理后，经干制后取样分析，结果表明，差异蛋白在 Biological process、Cellular component 和 Molecular function 这 3 个水平上均有显著富集。其中差异蛋白表达数≥10 的有催化活性 catalytic activity(48 个差异表达蛋白)、氧化还原过程 oxidation-reduction process(18 个差异表达蛋白)、应激反应 response to stress(17 个差异表达蛋白)等。KEGG 分析表明，共有 2 个基因通路显著富集。

参考文献

[1] PERSIC M，MIKULIC-PETKOVSEK M，SLATNAR A，et al. Chemical composition of apple fruit，juice and pomace and the correlation between phenolic content，enzymatic activity and browning[J]. LWT-Food science and technology，2017，82：23－31.

[2] HEMACHANDRAN H，ANANTHARAMAN A，MOHAN S，et al. Unraveling the inhibition mechanism of cyanidin-3-sophoroside on polyphenol oxidase and its effect on enzymatic browning of apples[J]. Food chemistry，2017，227：102－110.

[3] SUKHONTHARA S，KAEWKA K，THEERAKULKAIT C. Inhibitory effect of rice bran extracts and its phenolic compounds on polyphenol oxidase activity andbrowning in potato and apple puree[J]. Food chemistry，2016，190：922－927.

[4] DU L N，SONG J，PALMER L C，et al. Quantitative proteomic changes in development of superficial scald disorder and its response to diphenylamine and 1-MCP treatments in apple fruit[J]. Postharvest biology and technology，2017，123：33－50.

[5] CHANG C L. Proteomic identification of a potential sex biomarker for 2 fruit fly species at pupal stage[J]. Journal of Asia-pacific entomology，2017，20：125－131.

[6] D'AMBROSIO C，ARENA S，ROCCO M，et al. Proteomic analysis of apricot fruit during ripening[J]. Journal of proteomics，2013，78：39－57.

[7] SÁNCHEZ-BEL P，EGEA I，SÁNCHEZ-BALLESTA T T，et al. Understanding the mechanisms of chilling injury in bell pepper fruits using the proteomic approach[J]. Journal of proteomics，2012，75(17)：5463－5478

[8] 李新明，郭志利，李群，等. 无硫复合护色剂处理的干制苹果片中差异蛋白表达的分析[J]. 安徽农业科学，2017，45(28)：71－73.