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辣椒青熟期紫黑色果皮的主基因+多基因混合遗传分析

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摘要:【目的】果皮颜色是辣椒的重要农艺性状之一。旨在探究青熟期紫色辣椒果色遗传规律,为辣椒新品种选育和紫色辣椒呈色机制提供理论依据。【方法】研究以C152(青熟期紫黑色果皮)为母本、A37(青熟期绿色果皮)为父本,构建 P_1 、 P_2 、 F_1 、 F_2 4个世代遗传群体。细化青熟期果皮颜色分类,调查统计发育正常、达到商品成熟度的对椒果皮颜色。对所得数据进行正态分布检验,并联合分析4个世代获得遗传模型,计算各遗传模型的MLV值和有关成分分布参数,将MLV值转换为AIC值,选取遗传模型中AIC值最小的5个模型作为备选模型,对备选模型进行适合性检验,并获得统计量,选取显著统计量最少的备选模型作为最佳遗传模型,计算最佳遗传模型的一阶遗传参数,并由群体方差和有关成分分布方差估计出最佳遗传模型的二阶遗传参数。【结果】统计结果显示, F_1 代为浅紫黑色,介于母本的紫黑色和父本的绿色之间,且更偏向于母本。 F_2 群体中颜色过渡丰富,性状变异呈连续状态。正态性检验结果表明,所得数据的中位数与众数为4,平均值为4.097,变异系数为49.38%,果色性状的峰度为-1.117,偏度为-0.321,两者绝对值在1.96之间,符合正态分布。一阶遗传参数中主基因加性效应值为2.542 8、显性效应值为0.535 2,主基因的显性度为0.220 1。二阶遗传参数结果表明,群体表型的总方差为0.562 6,主基因遗传方差为3.529 9,多基因的遗传方差与遗传力均为0。群体的主基因遗传率为86.25%。【结论】辣椒青熟期果皮颜色紫黑色对绿色为不完全显性,紫黑色果皮受到一对加性-显性主基因+加性-显性-上位性多基因控制,主基因的加性效应与显性效应皆为正向,且加性效应强于显性效应。紫黑色果皮表现出极高的遗传力,性状决定受遗传因素较大。

关键词:辣椒;青熟期果色;主基因+多基因;遗传分析

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A mixed genetic analysis of major gene plus polygene for purplish-black pericarp at mature-green stage in pepper

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Abstract: [Objective] Pericarp skin color is one of the important agronomic traits of chili peppers. In order to investigate the genetic pattern of peel color and provide a theoretical basis for the selection and breeding of new varieties of purple peppers at the green stage of ripening, a study was conducted to determine the mechanism of color expression in purple peppers. [Method] C152 (purplish-black pericarp at green ripening stage) was used as the female parent and A37 (green pericarp at green ripening stage) was used as the male parent in this study. Genetic populations were constructed for four generations, P_1 , P_2 , F_1 , and F_2 . A more precise classification was conducted for peppers at the green ripening stage, the peel color was investigated and counted for those peppers that developed normally and reached commercial maturity. Normal distribution was tested for the obtained data, different genetic models were obtained by joint analysis among the four different generations, Maximum Likelihood Value (MLV) of the respective genetic models and parameters of the distribution of the components of interest were computed, MLV were converted into Akaike's information criterion (AIC) values. The five models with the smallest AIC values in the genetic model were selected as the alternative models. The fitness test of the alternative models was conducted and the statistics were obtained. The alternative model with the least significant statistics was selected as the optimal genetic model. The first-order genetic parameters of the optimal genetic model were calculated, and the second-order genetic parameters of the optimal genetic model were estimated from the population variance and the distribution variance of the relevant components. [Result] The findings showed that the F_1 generation was light purple black, which is between the purple black of the female parent and the green of the male parent, and it was more biased towards the female parent. Color transitions were abundant in the F_2 population and the trait variation was continuous. The results of normality test showed that the median and the multitude of the obtained data were 4, the mean was 4.097, the coefficient of variation was 49.38%, the kurtosis of the fruit color trait was -1.117, the skewness was -0.321, and the absolute values of the two were in the range of 1.96, which was in line with the normal distribution. In the first order genetic parameters, the additive effect value of the main gene was 2.542 8, dominant effect value was 0.535 2 and dominance degree of the main gene was 0.220 1. The results of the second order genetic parameters showed that the total variance of the population phenotypes was 0.5626, the genetic variance of the main genes was 3.529 9, and the genetic variance of the polygenes and the heritability were 0. The heritability of the main genes in the population was 86.25%. [Conclusion] Purplish-black is incompletely dominant to green in green-ripe peppers; purplish-black pericarp is controlled by a pair of additive-dominant primary genes plus additive-dominant-superior polygenes, and the additive and dominant effects of the primary genes are both positive, and the additive effect is stronger than the dominant effect. Purplish-black pericarp shows a extremely high level of heritability, and the trait decision was influenced by genetic factors.

Keywords: pepper; fruit color during green ripening period; major gene plus polygene; genetic analysis

【研究意义】辣椒(*Capsicum annum* L.)作为一种常见蔬菜,不仅是人们膳食中必需的新鲜蔬菜和调味品,也是一种重要的工业原料。从辣椒中提取的辣椒红素和辣椒玉红素,作为自然源的食品添加剂和增色剂,在食品、化工和农业等方面都有着重要的用途^[1]。植物生长发育与自身产生的色素密不可分,色素为叶子、花以及果实提供颜色,以吸引传粉者和种子散布者^[2]。各种各样的颜色也是花卉、水果、蔬菜的主要消费性状^[3]。赋予果实颜色的色素还与营养、风味和健康有关^[4]。【前人研究进展】决定辣椒果皮颜色的色素主要为叶绿素类、类胡萝卜素类和类黄酮类等。在辣椒果实发育过程中,青熟期果实的绿色主要由叶绿素主导。类胡萝卜素主要与完熟期红、橙、黄色的果实有关。青熟期紫色和紫黑色辣椒则是由于花青素在叶、花和果实中的积累导致^[5]。花青素是由类黄酮生物合成途径衍生而来的水溶性次生代谢产物,是辣椒中主要的类黄酮类色素。研究表明,黑色果实中花青素的含量远高于紫红色果实^[6]。然而,

在辣椒果实的发育过程中,花青素的积累是临时的,因为它只出现在青熟期,并不存在于完熟期的果实中,所以青熟期为紫色的辣椒往往随着花青素的代谢在完熟期转变成其他颜色。在辣椒发育过程中,叶绿素、类胡萝卜素、花青素等色素物质处于动态变化之中,各色素之间彼此影响、共同作用,形成了一个复杂的调节网络,共同调控辣椒果实的颜色,使辣椒在青熟期和完熟期表现出多样的色彩类型。常见的颜色转变类型有:绿转红、黄、橙、橄榄绿、棕,白转红、橙黄,或依旧为白色,紫转红、橙;黄转红,或依旧保持黄色,黑转红、橙等。由于丰富多样的果色表型,也使得辣椒已经成为果色相关研究的一种模式植物^[7]。

【本研究切入点】果色是影响辣椒外观品质的重要因素,也是评价果实外观和商品品质的标准之一。市场上出售的鲜食辣椒多为青熟期果实,然而,目前关于辣椒果实颜色的研究主要集中在成熟果实上,对青熟期辣椒果实的研究尚浅。已报道的与辣椒果实颜色相关基因数量较少。紫色辣椒作为稀有种质资源,可以为育种者提供优质的种质资源,增加辣椒的遗传多样性。【拟解决的关键问题】本研究旨在利用主基因+多基因混合分析法研究青熟期辣椒紫黑色果皮的遗传规律,为紫黑色果皮相关基因的定位提供参考,并为今后辣椒新品种选育和紫色辣椒呈色机制提供理论依据。

1 材料与方法

1.1 试验材料

如表 1 所示,以青熟期果皮颜色为紫黑色的辣椒(C152)做母本、绿色辣椒(A37)做父本,试验材料由甘肃农业大学园艺学院蔬菜育种实验室提供,2021 年春季配制杂交组合 C152×A37,收获杂交种子 F₁。2021 年秋季种植 F₁ 代,自交后收获种子得到 F₂ 代。2022 年在甘肃农业大学园艺学院兰州试验基地塑料大棚种植 4 个世代群体 P₁₁(C152)、P₂₁(A37)、F₁、F₂,两个亲本各 5 株,F₁ 共 5 株,F₂ 共 442 株,常规化管理所有试验材料。

表 1 试验材料及其果皮颜色
Tab.1 Test materials and their properties

材料名称 Accessionns	时期 Stages	方法 Method	颜色 Color
C152	青熟期	目测法	紫黑色
A37			绿色

1.2 青熟期果皮颜色调查方法

依据《辣椒种质资源描述规范和数据标准》,发育正常、达到商品成熟度的对椒果面颜色为青熟果色,发育正常、达到生理成熟度的对椒果面颜色为老熟果色^[8]。按照该标准,对青熟期果皮颜色进行分类并加以改进,具体分类情况和标准颜色如表 2 所示。调查统计发育正常、达到商品成熟度的对椒果皮颜色,每株至少观察 3 颗以上果实。

表 2 青熟期 F₂ 代果皮颜色调查统计
Tab.2 Investigation and statistical table of peel color in F₂ generation during the green maturity period

性状 Character	时期 Stages	方法 Method	分类 Classification	代号 Code	株数 Number of plants
青熟期果皮颜色 Peel color during green ripening period	青熟期	目测法	浅绿色	1	95
			绿色	2	22
			深绿色	3	7
			浅紫色	4	131
			紫色	5	43
			浅紫黑色	6	96
			紫黑色	7	48

1.3 数据分析

应用植物数量性状主基因+多基因混合遗传模型,使用章元明教授团队研制的R软件包SEAv2.0^[9],对P₁、P₂、F₁、F₂群体的青熟期对椒果色进行4个世代联合分析,获得不同的遗传模型。计算各遗传模型的极大似然函数值(MLV,maximum likelihood method)和有关成分分布参数,从而将MLV转换为AIC值(Akaike's information criterion),依据Akaike提出的最大熵规则^[10],从遗传模型中选取AIC值最小的5个模型作为备选模型。进一步对5个备选模型进行均匀性检验、Smirnov检验和Kolmogorov检验^[11]并获得统计量,选取显著统计量最少的备选模型作为最佳遗传模型,采用最小二乘法估计出最佳遗传模型的一阶遗传参数,由群体方差和成分分布方差估计出最佳遗传模型的二阶遗传参数^[12-13]。

2 结果与分析

2.1 P₁、P₂、F₁、F₂ 4个世代表型特征

如表3所示,共获得5株紫黑色的P₁,5株绿色的P₂,父母本果皮颜色对比强烈、差异明显。F₁代为浅紫黑色,介于母本的紫黑色和父本的绿色之间,且更偏向于母本。F₂群体中除了绿色、紫黑色、浅紫黑色之外,还出现了浅绿色、深绿色、浅紫色和紫色。

表3 4个世代的表型统计
Tab.3 Phenotypes were counted between four generations

世代 Generation	颜色代号/Color code							株数 Number of plants
	1	2	3	4	5	6	7	
P ₁	0	0	0	0	0	0	5	5
P ₂	0	5	0	0	0	0	0	5
F ₁	0	0	0	0	0	5	0	5
F ₂	95	22	7	131	43	96	48	442

2.2 F₂群体数据分析

统计F₂分离群体的表型(图1),并进行正态性检验(表4),结果显示,中位数与众数为4,平均值为4.097,变异系数为49.38%,果色性状的峰度为-1.117,偏度为-0.321,两者绝对值在1.96之间,符合正态分布,表明该性状是一个典型的数量性状,可应用主基因+多基因混合遗传模型分离分析法进行研究。

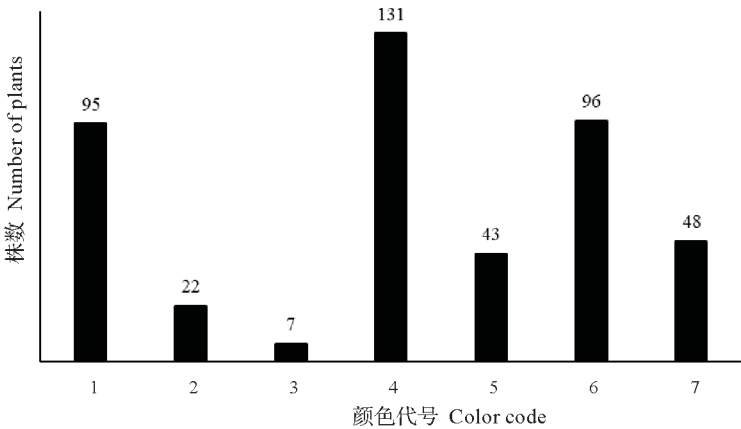


图1 F₂分离群体表型统计
Fig.1 Phenotypic statistics of F₂ segregated population

表4 F₂分离群体数据分析
Tab.4 The data analysis of F₂ segregated population

平均值 Mean	标准误差 SE	中位数 Median	众数 Mode	标准差 SD	方差 Variance	变异系数/% CV	峰度 Kurtosis	偏度 Skewness	最小值 Min	最大值 Max	观测数 Observations
4.097	0.096	4	4	2.023	4.093	49.38	-1.117	-0.321	1	7	442

2.3 青熟期紫绿辣椒主基因+多基因遗传模型分析

利用植物数量性状主基因+多基因混合遗传分析法,对 P_1 、 P_2 、 F_1 、 F_2 4 个世代群体进行联合分析,如表 5 所示,共获得 5 类 24 种遗传模型。分析极大对数似然值和 AIC 值,选取 AIC 值最小的 5 个模型作为备选模型,分别为 MX1-AD-AD、MX1-AD-ADI、MX2-AD-AD、MX2-ADI-AD 和 MX2-ADI-ADI, AIC 值分别为 2 423.950 8、2 400.716 3、2 420.311、2 402.812 3 和 2 404.830 5。5 个备选遗传模型的 AIC 值比较接近,进一步对其进行适合性检测(均匀性检验、Smirnov 检验和 Kolmogorov 检验,5 个统计量分别为 U_1^2 、 U_2^2 、 U_3^2 、 W^2 和 D_n),并选择适合性检验统计量达到显著水平个数最少的模型作为最佳遗传模型。如表 6 所示,各候选遗传模型的适合性检验统计量与该模型的差异均达到显著性水平,且模型 MX1-AD-ADI 和 MX2-ADI-ADI 的适合性检验统计量达到显著水平个数均为 9,结合 AIC 值最小原则,选择 MX1-AD-ADI 作为最佳遗传模型。即青熟期紫-辣椒遗传符合一对加性-显性主基因+加性-显性-上位性多基因混合遗传模型。

表 5 青熟期紫色辣椒的 24 种遗传模型的极大似然值 (MLV) 和 AIC 值
Tab.5 Maximum likelihood value (MLV) and AIC values of 24 genetic models for purple pepper during the green maturity period

模型 Model	极大对数似然值 MLV	AIC 值 AIC value	模型 Model	极大对数似然值 MLV	AIC 值 AIC value
1MG-A	-1 639.797 9	3 289.595 8	MX1-AD-ADI	-1 192.358 1	2 400.716 3
1MG-AD	-1 280.334 2	2 572.668 5	MX1-AEND-AD	-1 299.116 1	2 610.232 1
1MG-AEND	-1 603.888 7	3 217.777 5	MX1-EAD-AD	-1 247.275 9	2 506.551 8
1MG-EAD	-1 585.839 9	3 181.679 7	MX2-A-AD	-1 221.270 1	2 448.540 1
2MG-A	-1 639.846 8	3 289.693 6	MX2-AD-AD	-1 205.155 5	2 420.311
2MG-AD	-1 239.467 6	2 492.935 1	MX2-ADI-AD	-1 192.406 1	2 402.812 3
2MG-ADI	-1 216.173	2 454.345 9	MX2-ADI-ADI	-1 190.415 3	2 404.830 5
2MG-AED	-1 588.311 7	3 186.623 4	MX2-AED-AD	-1 220.871 4	2 447.742 9
2MG-EA	-1 639.847 2	3 287.694 4	MX2-EAED-AD	-1 222.319	2 448.637 9
2MG-EEAD	-1 596.908 6	3 201.817 2	MX2-EEAD-AD	-1 236.812	2 477.624
MX1-A-AD	-1 221.270 1	2 454.540 1	PG-AD	-1 299.119 7	2 608.239 3
MX1-AD-AD	-1 204.975 4	2 423.950 8	PG-ADI	-1 290.372 7	2 592.745 4

MG:主基因模型;MX:主基因+多基因混合模型;PG:多基因遗传模型;A:加性效应;D:显性效应;I:互作;N:负向;E:相等。例如:E-1 模型 MX2-ADI-AD,表示 2 对加性-显性-上位性主基因+加性-显性多基因混合遗传模型。下划线标注数值为 AIC 最小值。

MG: Main gene model; MX: Main gene+multi gene hybrid model; PG: Multi gene genetic model; A: Additive effect; D: Dominant effects; I: Interaction; N: Negative direction; E: Equal. For example, the E-1 model MX2-ADI-AD represents a mixed genetic model of 2 pairs of additive dominant epistatic main genes and additive dominant polygenes. The underlined value is the minimum AIC value.

2.4 遗传参数分析

如表 7 所示,由一阶遗传参数可知,主基因的加性效应 d_a 值为 2.547 7,显性效应 h_a 值为 0.560 7,主基因的显性度 $|h_a/d_a|$ 为 0.220 1,为正向不完全显性。主基因的加性效应与显性效应皆为正向,且加性效应强于显性效应。二阶遗传参数结果表明,群体表型的总方差 δ_p^2 值为 0.562 6,主基因遗传方差 δ_{mg}^2 值为 3.529 9,多基因的遗传方差 δ_{pg}^2 与遗传力 h_{pg}^2 均为 0。群体的主基因遗传率为 86.25%,表现出极高的遗传力,性状决定受遗传因素较大。

表 6 备选模型的适合性检验
Tab.6 Suitability testing of alternative models

模型 Model	世代 Generation	U_1^2	U_2^2	U_3^2	${}_nW^2$	D_n	达显著水平个数 Number of significant levels
MX1-AD-ADI	P ₁	21.635(0)*	41.844(0)*	61.782 7(0)*	11.039 9(0)*	0.008 1(1)	9
	P ₂	0.029 6(0.863 5)	9.132 3(0.002 5)*	130.460 8(0)*	9.166 1(0)*	0.100 4(0.153 5)	
	F ₁	0(1)	0.390 6(0.532)	6.25(0.012 4)*	0.416 7(0.273 1)	0.5(0.111 5)	
	F ₂	0.121 6(0.727 3)	0.121 6(0.727 3)	0.100 7(0.751)	1.844 6(0)*	0.053 6(0.151 9)	
MX2-ADI-AD	P ₁	24.892(0)*	44.848 1(0)*	55.718 3(0)*	11.324 5(0)*	0.008 1(1)	12
	P ₂	0.181 4(0.670 2)	10.580 7(0.001 1)*	129.092 1(0)*	9.172 2(0)*	0.098 2(0.171)	
	F ₁	5.042 6(0.024 7)*	4.704 3(0.030 1)*	0.000 5(0.983)	0.836 9(0.000 2)*	0.789 9(0.000 8)*	
	F ₂	0.076 3(0.782 3)	0.076 3(0.782 3)	0.660 6(0.416 4)	1.796 6(0)*	0.048(0.252 3)	
MX2-ADI-ADI	P ₁	22.841 2(0)*	42.978 3(0)*	59.493 2(0)*	11.145 3(0)*	0.008 1(1)	9
	P ₂	0.033 5(0.854 7)	9.152 5(0.002 5)*	129.781 7(0)*	9.162 1(0)*	0.094 9(0.200 7)	
	F ₁	0(1)	0.390 6(0.532)	6.25(0.012 4)*	0.416 7(0.273 1)	0.5(0.111 5)	
	F ₂	0.691 4(0.464 3)	0.157 5(0.691 4)	0.464 3(0.495 6)	1.805 8(0)*	0.048 1(0.250 8)	
MX2-AD-AD	P ₁	26.718 8(0)*	46.456 6(0)*	52.476 7(0)*	11.484 1(0)*	0.008 1(1)	13
	P ₂	0.396 2(13.353 7)	13.353 7(0.000 3)*	128.387 3(0)*	9.220 4(0)*	0.113 6(0.075 1)	
	F ₁	14.301 9(0.002)*	6.244 8(0.012 5)*	21.631 3(0)*	1.608 5(0)*	0.988 2(0)*	
	F ₂	0.919 5(0.249 4)	0.010 2(0.919 5)	0.249 4(0.617 5)	1.820 3(0)*	0.051(0.193)	
MX1-AD-AD	P ₁	26.718 8(0)*	46.456 6(0)*	52.476 7(0)*	11.484 1(0)*	0.008 1(1)	13
	P ₂	0.396 2(13.353 7)	13.353 7(0.000 3)*	128.387 3(0)*	9.220 4(0)*	0.113 6(0.075 1)	
	F ₁	14.301 9(0.002)*	6.244 8(0.012 5)*	21.631 3(0)*	1.608 5(0)*	0.988 2(0)*	
	F ₂	0.919 5(0.249 4)	0.010 2(0.919 5)	0.249 4(0.617 5)	1.820 3(0)*	0.051(0.193)	

U_1^2 、 U_2^2 、 U_3^2 :均匀性检验统计量; ${}_nW^2$:Smirnov 检验统计量; D_n :Kolmogorov 检验统计量; *: $P<0.05$ 。
 U_1^2 、 U_2^2 、 U_3^2 :Uniformity test statistics, ${}_nW^2$:Smirnov test statistics, D_n :Kolmogorov test statistic, *: $P<0.05$.

表 7 最佳遗传模型(MX1-AD-ADI)的遗传参数估计值
Tab.7 Estimation of genetic parameters for the best genetic model(MX1-AD-ADI)

一阶遗传参数 1st order parameter	估计值 Estimate	二阶参数 2nd order parameter	估计值 Estimate
m	2.563 6	δ_p^2	0.562 6
d_a	2.547 7	δ_{mg}^2	3.529 9
h_a	0.560 7	δ_{pg}^2	0
$ h_a/d_a $	0.220 1	$h_{mg}^2/\%$	0.862 5
		$h_{pg}^2/\%$	0

m :群体均值; d_a :主基因加性效应值; h_a :主基因显性效应值; $|h_a/d_a|$:主基因显性度; δ_p^2 :表型方差; δ_{mg}^2 :主基因方差; δ_{pg}^2 :多基因方差; h_{mg}^2 :主基因遗传率; h_{pg}^2 :多基因遗传率。
 m :Population mean; d_a :Additive effect value of major gene; h_a :Dominant effect value of major gene; $|h_a/d_a|$:Dominance of major genes; δ_p^2 :Phenotypic variance; δ_{mg}^2 :Major gene variance; δ_{pg}^2 :Polygenic variance; h_{mg}^2 :Major genes heritability; h_{pg}^2 :Polygenic heritability.

3 讨论与结论

3.1 讨论

由盖钧铭^[14]提出的植物数量性状主基因+多基因混合遗传模型分析法不仅可以检测数量性状主基因的个数和多基因的存在,还可对基因遗传效应及方差等遗传参数进行估计,已成为植物数量性状遗传解析的重要方法之一。该方法已在多种作物的数量性状遗传上得到应用,如水稻^[15]、烟草^[16]、辣椒^[17]、冬瓜^[18]、蓝花丹^[19]、德国鸢尾^[20]等。本研究调查所得的 F_2 群体表型过渡丰富,呈现连续变异的趋势,群体数据的中位数与众数为4,平均值也接近4,说明数据的集中趋势较高,即大部分植株表现为浅紫色。变异系数为49.38%,说明分离世代群体内存在明显变异,具有极高的遗传多样性。青熟期果色性状数据的峰度和偏度的绝对值均在1.96之间,符合正态分布,是一个典型的数量性状,可应用主基因+多基因混合遗传模型分离分析法进行研究。

花青素是一种广泛存在于植物中的天然水溶性色素,与植物组织的颜色密切相关。花青素的生物合成通路已经在拟南芥^[21]、矮牵牛^[22]、玉米^[23]、葡萄^[24]等植物中进行了详细的阐述。在辣椒中,叶、花和青熟果的紫色或黑色主要是由于花青素在这些组织中积累的结果,只考虑色彩有无时,有研究认为单显性基因控制紫色和黑色,且紫色^[25]和黑色^[26]对绿色为显性。也有研究者认为辣椒果实青熟期的黑色和紫色受 $sw1$ (Sulfony white immature fruit color)、 A 和 MoA 等3个基因共同控制^[27]。辣椒果实或组织的紫色调控基因还有 As (Anthocyanin on style)基因、 Asf (Anthocyanin on style and filament)基因和 al 基因^[28]等。尽管不同学者的研究结果存在差异,但都表明辣椒的紫色是由关键基因决定并受多种基因调控,且基因之间存在相互作用。这与本研究结论一致。本研究在调查色彩有无的基础上,考虑了色彩深浅程度,进一步细化了辣椒青熟期紫色果皮的分级。结果表明, F_1 代为更接近母本颜色的浅紫黑色, F_2 群体中除了存在与 P_1 、 P_2 、 F_1 代相同的绿色、紫黑色、浅紫黑色表型外,还出现了浅绿色、深绿色、浅紫色等新的表型,过渡类型丰富。遗传分析表明青熟期辣椒紫黑色果皮受一对主基因+多基因控制,与前人研究的不同之处在于本研究将紫色性状视为数量性状,认为紫色对绿色为不完全显性。此外,本研究还发现存在多种微效基因与主基因共同调控紫色表型,基因之间存在相互作用,其中,主基因加性效应值为2.542 8、显性效应值为0.535 2,主基因的加性效应与显性效应皆为正向,且加性效应强于显性效应。

国内也有学者开展对于紫色辣椒的研究。周燕^[29]将果实紫色视为数量性状,通过色差仪分级,采用数量性状主基因+多基因混合遗传模型多世代联合分析,发现3个紫、绿果杂交组合均受两对加性-显性-上位性主基因+加性-显性多基因控制,主基因的遗传率不低于85.37%,隋益虎^[30]通过构建紫色与绿色辣椒3个杂交组合的6世代群体,用分光光度法测定辣椒叶片花青素相对含量,研究其遗传规律,结果表明辣椒叶片花青素含量的遗传模式符合两对加性-显性-上位性主基因+加性-显性-上位性多基因模型。 F_2 群体主基因遗传率较高,为78.89%~91.47%。然而,丁盼盼^[31]使用紫-绿双亲构建6个世代的遗传分析发现,紫-绿组合辣椒商品成熟期果皮颜色性状符合一对加性主基因+加性-显性混合多基因模型。本研究与丁盼盼^[31]的研究结果相似,有别于周燕^[29]的结论。造成不同结论的原因有:虽然花青素的合成通路在辣椒中一样,但是结构基因和调控基因的表达却不尽相同,组织差异、发育时期等因素造成了基因的差异表达;其次,这些基因之间的相互作用不同,导致了不同表型的出现;再次为表型统计方法和用于遗传分析的世代存在差异;最后还与试验材料所处的生长环境有关。

3.2 结论

研究结果显示辣椒青熟期果实紫黑色对绿色为不完全显性。遗传分析表明辣椒青熟期紫黑果色符合一对加性-显性主基因+加性-显性-上位性多基因模型,主基因加性效应值为2.542 8、显性效应值为0.535 2,主基因遗传率为86.25%。主基因遗传率很高,受多基因和环境的影响较小,新品种的选育适合在早期后代中开展。

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