

# Genetic Analysis of the Maingene + Polygene of Soluble Sugar in Eggplant

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## Abstract

In this study, three high-generation inbred lines of eggplant 19-37, eggplant 19-38 and 19-31 were used to prepare two hybrid combinations for selfing and backcrossing, respectively, and six generations of P1, P2, F1, F2, B1 and B2 were established. When the fruit reached edible maturity, the soluble sugar content of eggplant fruit was determined by anthrone-sulfuric acid colorimetry, and the genetic law of soluble sugar was studied by the main gene + polygene mixed genetic model analysis. The results showed that the F2, B1 and B2 segregation populations of soluble sugar in eggplant hybrid combinations were in line with continuous variation and normal distribution, which was in line with the genetic law of multi-gene control. After analysis, it was concluded that the genetic characteristics of soluble sugar in the two combinations were suitable for the B-1 model, namely, the additive-dominant-epistatic model of two pairs of main genes. The B2 population of the two combinations was subject to a high genetic rate of main genes, and the F2 population of the two combinations was subject to a relatively large environmental impact, indicating that it was not suitable for early selection and suitable for late selection. The results can provide theoretical basis for quality inheritance and new variety breeding of eggplant.

## Keywords

Eggplant; Soluble sugar; Heredity; Major gene; Polygene

Eggplant (*Solanum melongena* L., also known as fallen su, rousu, Kunlun purple melon, and eggplant, belongs to the Solanaceae family, *Solanum* genus. Eggplant has excellent adaptability and is one of the most popular staple vegetables worldwide. It is also one of the main vegetable species in China, cultivated over a large area in both open fields and protected facilities, and plays a key role in vegetable production. Eggplant is rich in various nutrients, including various organic compounds and trace minerals. Soluble sugars are a key nutritional indicator of fruits and vegetables, serving as the primary form of plant metabolism and energy storage, as well as the main photosynthetic product. They regulate plant growth, development, and morphology, and are closely related to various aspects of plant growth, development, respiratory metabolism, yield formation, and quality [1] and [2].

Research on soluble sugars in eggplant has primarily focused on correlation and differential analysis. [3] Correlation analysis between botanical and quality traits of eggplant revealed that, for different botanical traits, longer storage time correlated with lower soluble sugar content in eggplant fruits. [4] Differential analysis of soluble sugar content in parthenocarpic and pollinated eggplant fruits revealed that soluble sugar content in unpollinated fruit was similar to that in pollinated fruit, with little difference between the two. Limited research has been conducted on the heritability of soluble sugars in eggplant. This study used three eggplant inbred lines as test materials, creating F1 hybrid combinations that were selfed and backcrossed to generate six generations: P1, P2, F1, F2, B1, and B2. The aim of this study is to investigate the genetic patterns of soluble sugars in eggplant, providing theoretical support and practical guidance for the breeding of new eggplant varieties.

## 1. Results and Analysis

### 1.1 Statistical analysis of soluble sugars in separated generations

of six generations of two combinations (Tables 1 and 2) revealed that the mean and coefficient of variation for F2, B1, and B2 were all greater than those of the parents, indicating heterosis and significant segregation variability in the offspring. The coefficient of variation for the F2 generation of combination 1 (Eggplant 19-37  $\times$  Eggplant 19-38) was 32.65%, significantly greater than that of the parents, and the segregation variability in the backcross offspring was significant. The coefficient of variation for the F2, B1, and B2 generations of combination 2 (Eggplant 19-37  $\times$  Eggplant 19-31) was 20.67 %, 39.73 %, and 36.90 %, also significantly greater than that of the parents, indicating significant segregation variability and requiring further analysis.

### 1.2 Determination of the optimal model

This study used the maximum log-likelihood method to calculate the maximum log-likelihood and AIC values for 24 genetic models of soluble sugars across six generations in two combinations (Tables 3 and 4). Based on the principle of minimizing the AIC value, the B-1 model in combination one had the lowest AIC value of 38.2892, making it the likely optimal model. The B-2 model was also closely matched and selected as a candidate model. Similarly, the B-1 model in combination two had the lowest AIC value of 1608.237, making it the likely optimal model. The C-0 model, with a similar AIC value of 1656.552, was selected as a candidate model.

The fitness test of the two combined models (Table 5, Table 6) U 1 2 U 2 2 U 3 2 (uniformity test), nW 2 (Smirnov test) and Dn (Kolmogorov test) were used to select the optimal genetic model. In combination one, the B-2 model had one parameter with a  $P < 0.05$ , while the B-1 model had no parameter with a  $P < 0.05$ . In combination two, three parameters of the C-0 model showed significant differences, while no parameters in the B-1 model showed significant differences. Based on the principle of selecting the model with the least number of statistical values reaching a significant level in the alternative model suitability test [5], the B-1 model was selected as the optimal model for both combinations one and two.

**Table 1. Statistical analysis of soluble sugar content in eggplant combination generation 1-6**

Generation	Minimum value	Maximum value Max	Range	Mean	Coefficient of variation/% CV (%)
P 1	0.836	1.210	0.974	1.190	15.60%
P 2	0.832	1.436	0.604	0.971	12.23%
F 1	0.804	1.377	0.573	1.030	17.56%
F 2	0.552	2.918	2.566	1.755	32.65%
BC 1	0.673	1.492	0.819	1.108	17.81%
BC 2	0.858	1.992	1.134	1.441	19.74%

**Table 2. Statistical analysis of soluble sugar content in the second and sixth generations of eggplant combinations**

Generation	Minimum value	Maximum value Max	Range	Mean	Coefficient of variation/% CV (%)
P 1	0.751	1.228	0.477	1.190	14.80%
P 2	0.906	1.535	0.629	1.102	13.57%
F 1	1.484	2.641	1.157	2.044	12.40%
F 2	1.552	2.731	1.179	1.978	20.67 %
BC 1	0.496	2.392	1.896	1.229	39.73%
BC 2	0.758	2.437	1.679	1.452	36.90%

**Table 3. Maximum log-likelihood and AIC values of the genetic model for soluble sugar in eggplant combinations**

Model	Max-likelihood values	AIC	Model	Max-likelihood values	AIC
A-1	-22.8451	53.6903	D-0	-15.6833	55.3666
A-2	-91.9235	189.847	D-1	-20.1924	58.3848
A-3	-100.9799	207.9597	D-2	-34.1316	84.2632
A-4	-56.3956	118.7912	D-3	-39.7299	95.4598
B-1	-9.1446	38.2892	D-4	-22.9648	61.9295
B-2	-17.2077	46.4154	E-0	-10.4418	56.8836
B-3	-113.426	234.852	E-1	-16.4107	62.8214
B-4	-92.6904	191.3807	E-2	-20.7698	63.5396
B-5	-100.0192	208.0384	E-3	-19.5084	57.0169
B-6	-100.98	207.9599	E-4	-25.7839	67.5677
C-0	-25.0772	70.1543	E-5	-39.7273	97.4545
C-1	-45.0562	104.1124	E-6	-39.7271	95.4543

**Table 4. Maximum log-likelihood and AIC values of the genetic model for two soluble sugars in eggplant combinations**

Model	Max-likelihood values	AIC	Model	Max-likelihood values	AIC
A-1	-859.9357	1727.871	D-0	-818.2764	1660.553
A-2	-860.2671	1726.534	D-1	-831.0874	1680.175
A-3	-859.9361	1725.872	D-2	-830.4933	1676.987
A-4	-857.7317	1721.463	D-3	-830.4933	1676.987
B-1	-794.1188	1608.237	D-4	-830.4934	1676.987
B-2	-858.8303	1729.661	E-0	-816.455	1668.91
B-3	-861.7616	1731.523	E-1	-819.8765	1669.753
B-4	-860.2434	1726.487	E-2	-830.4936	1682.987
B-5	-859.2278	1726.456	E-3	-824.2733	1666.547
B-6	-860.0166	1726.033	E-4	-830.4933	1676.987
C-0	-818.2762	1656.552	E-5	-832.4191	1682.838
C-1	-830.5756	1675.151	E-6	-830.4933	1676.987

## 2. Conclusion and Analysis

The major gene plus multigene multigenerational joint analysis method has been applied to quantitative trait genetic studies in a variety of crops. Genetic analysis of crop yield and quality traits has been conducted, for example [6], using a six-generation joint analysis method to analyze eight traits related to corn yield using hybridization of two cultivars. Studies of peanut fat and protein traits [7] revealed genetic models of PG-AD and MX1 -AD- ADI, respectively. Genetic analysis of phenotypic traits in plants has also been conducted, for example [8], which investigated the inheritance of stigma in different genic male sterile rice varieties. Studies of the genetic model of hypocotyl length in cucumber seedlings at elevated temperatures, compared to normal temperatures, revealed different genetic effects at different temperatures. This analysis method can also be used to study the inheritance of plant color traits. A colorimeter or chlorophyll or anthocyanin measurement can be used to assign values as quantitative traits for research. For example, [8] used a colorimeter to measure the flower color phenotypic values of pink rose hybrid offspring and analyzed the genetic laws of the flower color of the hybrid offspring. [11] conducted a six-generation genetic analysis

by measuring the relative chlorophyll content in the same leaf position of eggplant plants.

Previous studies on eggplant soluble sugar content have primarily analyzed differences under external conditions. However, there are numerous studies examining the genetic patterns of soluble sugar in other fruits. For example, [12] conducted genetic analysis of soluble sugar content in the center and periphery of watermelon fruit. The results showed that different soluble sugar types had different genetic models, and that the genetic models for the same sugar content in different parts were not necessarily the same, but all were quantitative traits inherited through a combination of major genes and multiple genes, similar to the results of this study. [13] A six-generation population constructed by crossbreeding tomato varieties with different sugar contents was analyzed for soluble sugar content in the fruit. The genetic model was found to be MX1 - AD- ADI, with polygenic effects predominating. [14] Six generations of crossbreeding and backcrossing of high-fructose and low-fructose cucumber fruits were analyzed for genetic patterns. The results showed that the genetic pattern was controlled by a pair of additive-dominant major genes plus additive-dominant-epistatic polygenes, with major genes predominating.

**Table 5. Suitability test of the genetic model of eggplant combination- soluble sugar**

Model	Generation	U 1 2	U 2 2	U 3 2	n W 2	D n
B-1	P 1	0.7325 (0.3921)	0.6846 (0.408)	0 (0.996)	0.1008 (>0.05)	0.0666 (>0.05)
	F 1	0.3085 (0.5786)	0.1945 (0.6592)	0.1499 (0.6986)	0.0791 (>0.05)	0.0674 (>0.05)
	P 2	0.3029 (0.5821)	0.2724 (0.6017)	0.0019 (0.9651)	0.1164 (>0.05)	0.0625 (>0.05)
	B 1	0.016 (0.8993)	0.0916 (0.7622)	0.5195 (0.4711)	0.0689 (>0.05)	0.0229 (>0.05)
	B 2	0.007 (0.9117)	0.0165 (0.8978)	0.0071 (0.9327)	0.0553 (>0.05)	0.0214 (>0.05)
	F 2	0.0664 (0.7966)	0.1287 (0.7198)	0.1907 (0.6624)	0.05 (>0.05)	0.0246 (>0.05)
B-2	P 1	6.3365 (0.0118)	7.5187 (0.0061)	1.4857 (0.2229)	0.6648 (< 0.05)	0.062 (>0.05)
	F 1	3.7516 (0.0528)	3.9056 (0.0481)	0.1628 (0.6866)	0.4214 (>0.05)	0.0738 (>0.05)
	P 2	0.1332 (0.7152)	0.0635 (0.8011)	0.1646 (0.6849)	0.0734 (>0.05)	0.0696 (>0.05)
	B 1	0.5224 (0.4698)	0.6433 (0.4225)	0.1672 (0.6826)	0.0874 (>0.05)	0.0189 (>0.05)
	B 2	0.3375 (0.5613)	0.1962 (0.6578)	0.2285 (0.6326)	0.1092 (>0.05)	0.036 (>0.05)
	F 2	0.2968 (0.5859)	0.4714 (0.4923)	0.4051 (0.5245)	0.0848 (>0.05)	0.0311 (>0.05)

Note: U 1 2 U 2 2 U 3 2 (homogeneity test); nW 2 (Smirnov test); Dn (Kolmogorov test); the number before the bracket is the statistical value, the numbers in the brackets after U 1 2, U 2 2, and U 3 2 are the probability levels, and the numbers in the brackets after nW 2 and Dn are the significance criteria.

**Table 6 Suitability test of the genetic model of two soluble sugars in eggplant combination**

Model	Generation	U 1 2	U 2 2	U 3 2	n W 2	D n
B-1	P 1	0.0857 (0.7697)	0.0196(0.8888)	0.3302 (0.5656)	0.0684 (>0.05)	0.1667 (>0.05)
	F 1	2.0399 (0.2255)	1.1516 (0.2832)	0.1612 (0.6881)	0.1933 (>0.05)	0.4273 (>0.05)
	P 2	1.4689 (0.799)	0.071 (0.791)	0.006 (0.941)	0.055 (>0.05)	0.161 (>0.05)
	B 1	0.4865 (0.4855)	0.3541 (0.5518)	0.1031 (0.7481)	0.151 (>0.05)	0.1227 (>0.05)
	B 2	0.5975 (0.4395)	0.4097 (0.5221)	0.2378 (0.6258)	0.0601 (>0.05)	0.09 (>0.05)
	F 2	0.0246 (0.8755)	0.1509 (0.6977)	0.896 (0.3438)	0.0709 (>0.05)	0.0896 (>0.05)
C-0	P 1	0.0028 (0.958)	0.0407 (0.8402)	0.3629 (0.5469)	0.0636 (>0.05)	0.1916 (>0.05)
	F 1	0.0152 (0.9019)	0.002 (0.988)	0.2891 (0.5908)	0.059 (>0.05)	0.1834 (>0.05)
	P 2	0 (0.9998)	0.005 (0.9437)	0.0791 (0.7785)	0.0817 (>0.05)	0.2918 (>0.05)
	B 1	0.185 (0.6671)	0.227 (0.5346)	0.6696 (0.4132)	0.1673 (>0.05)	0.1212 (>0.05)
	B 2	0.6581 (0.4172)	3.1864 (0.0743)	0.183 (0.669)	0.1479 (>0.05)	0.193 (>0.05)
	F 2	0.1103 (0.7398)	0.1967 (0.6574)	15.9859 (0)	0.7014 (<0.05)	0.287 (<0.05)

Note: U12 U22 U32 (homogeneity test); nW2 (Smirnov test); Dn (Kolmogorov test); the statistic before the brackets is the value, the numbers in brackets after U12 , U22 , and U32 are the probability levels, and the numbers in brackets after nW2 and Dn are the significance criteria.

This study used green round eggplant and white short-barreled eggplant as female parents and purple long eggplant as male parent to cross two eggplant combinations, generating six generations: P1, P2, F1, F2, B1, and B2. The genetic models of these combinations were compared and analyzed. The results revealed that the genetic models of the two eggplant hybrids were identical, with two pairs of major genes exhibiting additive-dominant-epistatic relationships. The genetics of the F2 populations from both combinations were significantly affected by the environment, making them unsuitable for early seed selection. The B2 populations from both combinations had a higher heritability of the major genes, ranging from 84.86% to 90.99%. The differences in the genetic models and parameters for soluble sugars obtained in this experiment contribute to the analysis of the genetic patterns of soluble sugars in eggplant.

### 1.3 Parameter estimation of genetic models

the two combined B - 1 models were estimated using the least squares method, and the first-order and second-order genetic parameters of the two models were obtained (Table 7, Table 8). Analysis of the first-order and second-order genetic parameters of the optimal genetic model of the combination showed that the additive effect of the first major gene was -0.2189, the dominance effect of the first major gene was -0.2957, and the dominance of the first major gene,  $h^2$ , was 1.3508. The additive effect of the second major gene was 0.0839, the dominance effect of the second major gene was -0.2184, and the dominance of the second major gene was -2.6031. The additive interaction effect of the two major genes was -0.3653, the additive-dominant interaction effect of the two major genes was -0.331, the additive-dominant interaction effect of the two major genes was 0.2272, and the dominant interaction effect of the two major genes was 0.7333. The heritability of the major genes for soluble sugar ( $h^2$ ) in the B 1, B 2, and F 2 segregating generations was 83.9 %, 84.86 %, and 49.15%, respectively. %, and the environmental efficiency ( $1-h^2$ ) was 16.1 %, 15.14 % and 50.85 %, indicating that the inheritance of soluble sugar content in B 1 and B 2 fruits was greatly affected by the two pairs of major genes. The soluble sugar content of F 2 generation was mainly inherited by the two pairs of genes and was greatly affected by environmental factors. It was suitable for late selection in breeding and was less affected by the environment.

first -order and second-order genetic parameters of the optimal genetic model of combination two showed that the additive effect of the first major gene was -0.3425, the additive effect of the second major gene was -0.3425, the dominance effect of the first major gene was 246.0474 , the dominance effect of the second major gene was 40.1116, the dominance of the first major gene was 1.3508 , the dominance of the second major gene was -2.6031, the additive interaction effect of the two major genes was -4.7684, the additive-dominant interaction effect of the two major genes was -1.5712, the dominant-additive interaction effect of the two major genes was -207.5069, and the dominant-dominant interaction effect of the two major genes was -290.0822. The heritability of the major genes for soluble sugar ( $h^2$ ) in the B 1, B 2, and F 2 segregating generations was 32.52 %, 90.99%, and 99.89 %, respectively. 34.96 %, and the environmental efficiency ( $1-h^2$ ) was 67.48 %, 9.01 % and 65.04 %, indicating that the inheritance of soluble sugar content in fruit of B 2 generation was greatly affected by two pairs of major genes, and B 1 and F 2 generations were greatly affected by environmental factors. They were suitable for early selection of varieties in breeding and were less affected by the environment.

## 3. Materials and Methods

### 3.1 Test materials

The three parental materials used in this experiment are all independently bred high-generation inbred lines, Eggplant 19-27, Eggplant 19-28 and Eggplant 19-31. Eggplant 19-27 has green fruit, green flesh, and spherical fruit; Eggplant 19-28 has white fruit, white flesh, and short cylindrical fruit; Eggplant 19-31 has purple fruit, green flesh, and long strip fruit.

In 2019, the parental materials were formulated into two hybrid combinations, combination one was eggplant 19-27 × eggplant 19-28, and combination two was 19-28 × eggplant 19-31. In 2020, backcrossing and self - pollination were carried out to obtain 6 generation groups of the two combinations. In March 2021, the 6 generation groups of the two combinations were planted in the field in double rows with a row spacing of 60. cm, plant spacing 45 cm, of which 30 plants were planted for parents P1 and P2, 50 plants were planted for F1, and 120 plants were planted for F2, B1 and B2 respectively, and conventional field management was carried out.

**Table 7. Estimation of genetic parameters of the optimal model for combination - soluble sugar content**

1st order parameter	Estimate	2nd order parameter	Estimate		
			B 1	B 2	F 2
m	1.3833	$\sigma_{mg}^2$	0.1335	0.1436	0.0248
da	-0.2189	$\sigma_{pg}^2$	-	-	-
db	0.0839	h mg 2 (%)	83.9	84.86	49.15
ha	-0.2957	h pg 2 (%)	-	-	-
hb	-0.2148	h 2 (%)	83.9	84.86	49.15
i	-0.3653	1- h 2 (%)	16.1	15.14	50.85
j ab	-0.331				
j ba	0.2272				
l	0.7333				

Note: m: generation mean; da : additive effect of the first major gene; db: additive effect of the second major gene; ha: dominance effect of the first major gene; i : additive  $\times$  additive interaction between two major genes; jab: additive  $\times$  dominance interaction between two major genes; jba : dominance  $\times$  additive interaction between two major genes; l: dominance  $\times$  dominance interaction between two major genes;  $\sigma_{mg}^2$  : major gene variance;  $\sigma_{pg}^2$  : polygenic variance; hmg2 : heritability of the major gene; hpg2 : heritability of the polygenic factor; h2 : heritability of the major gene plus the polygenic factor. 1- h2: ratio of environmental variance to total variance.

**Table 8. Estimation of genetic parameters of the optimal model for combination - soluble sugar content**

1st order parameter	Estimate	2nd order parameter	Estimate		
			B 1	B 2	F 2
m	145.5279	$\sigma_{mg}^2$	302.4501	6344.545	337.376
da	-0.3425	$\sigma_{pg}^2$	-	-	-
db	-0.3425	h mg 2 (%)	32.52	90.99	34.96
ha	246.0474	h pg 2 (%)	-	-	-
hb	40.1116	h 2 (%)	32.52	90.99	34.96
i	-4.7684	1- h 2 (%)	67.48	9.01	65.04
jab	-1.5712				
jba	-207.5069				
l	-290.0822				

Note: m: generation mean; da : additive effect of the first major gene; db: additive effect of the second major gene; ha: dominance effect of the first major gene; i : additive  $\times$  additive interaction between two major genes; jab: additive  $\times$  dominance interaction between two major genes; jba : dominance  $\times$  additive interaction between two major genes; l: dominance  $\times$  dominance interaction between two major genes;  $\sigma_{mg}^2$  : major gene variance;  $\sigma_{pg}^2$  : polygenic variance; hmg2 : heritability of the major gene; hpg2 : heritability of the polygenic factor; h2 : heritability of the major gene plus the polygenic factor. 1- h2: ratio of environmental variance to total variance.

### 3.2 Method for determination of soluble sugar

Eggplant fruits were harvested when they reached edible maturity. One sample was taken from each eggplant plant, and each sample was repeated three times. Part of the fruit was weighed and placed in a dryer for drying, then ground and passed through an 80-mesh sieve. About 0.05 g of dry sample was weighed for each sample, and the soluble sugar content in the eggplant fruit was determined using the anthrone-sulfuric acid colorimetric method and a spectrophotometer.

### 3.3 Statistical analysis methods

The Windows version of the SEA software package [15] was used in the R language environment to analyze the data of the soluble sugar content of eggplant over six generations. The method of major gene + polygene combined analysis over multiple generations [15] was used to determine whether it was controlled by the major gene plus polygene based on the genetic model and meaning of the model code, and to determine the final genetic model.

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