

**STATISTICAL INVESTIGATION OF SELECTION IN F<sub>2</sub> ON THE BASIS OF X<sup>2</sup> METHOD IN SOLVING ISSUES RELATED TO MENDEL'S LAWS**

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**DOI: 10.5958/2249-7315.2022.00203.9**

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**ABSTRACT**

*The article aims to determine the level of accuracy of the expected theoretical result in the process of processing or creating problems on G. Mendel's laws using a statistical method. In the pea (*Pisum sativum*) plant, the genes were analyzed in a statistically independent way using the x<sup>2</sup> method to separate the genes in F<sub>2</sub>.*

**KEYWORDS:** *Pisum Sativum, Statistical Method, X<sup>2</sup> Method, Fisher Table, Phenotype, Genotype, Dominant, Heterozygous, Recessive.*

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**INTRODUCTION**

Today, of course, the Natural Sciences stand on the basis of the development of the world industry and technologies. The cultivation, processing of natural products, the preparation of useful products for mankind from them is an urgent profession. This sphere is also one of the priority areas in our country. In particular, according to the resolution of the president of the Republic of Uzbekistan dated August 12, 2020 PP-4805, a number of priority tasks of the state program "Year of Science, Education and digital economy" were set in the direction of development of chemical and Biological Sciences in our country, increasing the quality of education and science results in these areas.

It was emphasized in this decision that there should be an inalienable linkage, effective communication and cooperation between secondary special, professional, higher education, research institutions and production enterprises in the field of Personnel Training and use of the results of science, at the same time, the quality of teaching chemistry and Biology subjects in secondary schools does not meet today's requirements. As a result of these shortcomings, it can be noted that at present, students are faced with some difficulties in finding solutions to the issues related to the laws of Mendel in the entrance tests of biology to higher educational institutions in our country. In the process of solving genetic issues for applicants, school and academic Lyceum students preparing for entrance tests to higher educational institutions, there is a lack of theoretical practical skills. Especially in the formation of questions in Science Olympiads in our country, attention is often paid to molecular biology, molecular genetics, population genetics, medical genetics, human genetics and other areas of genetics. The number of organisms that are given in genetic matters, the generations that are being formed, is theoretically taken approximately. Given these, we would like to note that the number of such derived theoretical, approximate generations is not always correct. As proof of our opinion, the method of statistical examination of the separation of signs in F<sub>2</sub> using the x<sup>2</sup> method was analyzed on the example of independent heredity of genes in the plant of peas (*Pisum sativum*).

**LITERATURE REVIEW AND METHODOLOGY**

As it is known, according to the third law of G.Mendel, genes in the body are inherited in an

independent state. But in some cases, this information will not be relevant to all genes, since some genes can also be inherited by attaching to chromosomes. The heredity of genes was independently identified in the plant of peas (*Pisum sativum*) by G.Mendel. Based on the experiments conducted by G.Mendel, it was found that if the color of the legume fruit of peas (*Pisum sativum*) is yellow, it is dominant, if green; it is recessive, if the color of the fruit is smooth, it is dominant, if curled, and it is recessive and will be inherited independently. [1].

We can note that the data on the morphometric measurements of plants attracted scientists. They included seasonal changes in the dynamics of population, divergence of some species in the evolutionary process from a number of scientific sources [2, 3, and 4]. However, statistical analysis on hereditary processes of genes in plants in an independent state was not carried out.

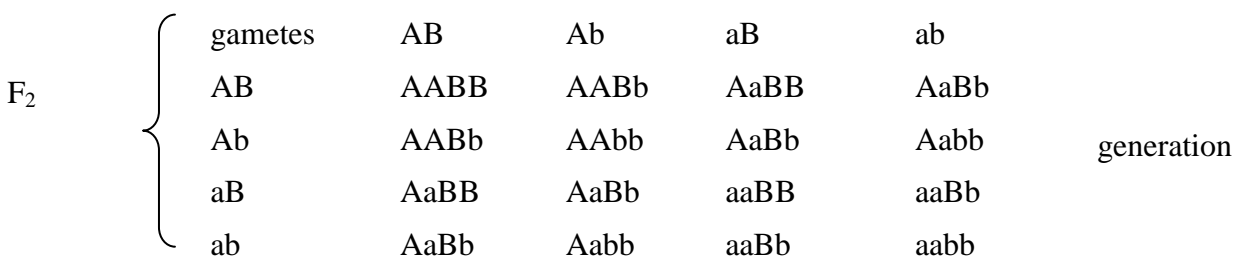
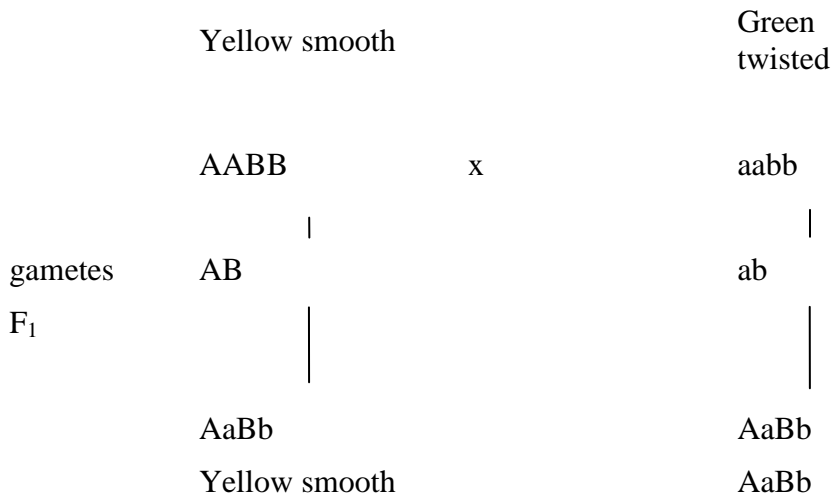
However, mathematical-statistical analysis was carried out in B.Lakin’s style [1].

**RESULTS AND DISCUSSION**

The third law of M.Mendel was carried out by the method of polyhybrid crossing. The scientist observed in his experiments that green twisted peas with yellow smooth peas are mutually crossed, and in F1 a yellow smooth, green twisted organism is formed.

We can express the experience as follows:

- Yellow-                 A\_
- Green-                 aa
- Smooth-                B\_
- Twisted -              bb



The ratio of phenotype in this experiment is as follows:

A_B_	9	Yellow smooth
A_bb	3	Yellow green
aaB_	3	Green smooth
aabb	1	Green twisted

If, for the purpose of determining the genotype of F1 hybrid, an analytical (backcross) crossing is carried out, theoretically, 4 generations of different phenotypes are formed: yellow smooth, yellow green, green smooth and green twisted, that is, it can be as follows.

F <sub>b</sub>	yellow smooth		green twisted	
P	AaBb	x	aabb	
gametes	AB	Ab	aB	ab
ab	AaBb	Aabb	aaBb	aabb
	yellow smooth	yellow green	green smooth	green twisted

According to G.Mendel's law, such a result can be obtained as a result of an analytical crossing, after analytical crossing, hybrids similar to the parent genotype and phenotype are obtained. This is due to the fact that the genes independently spread to gametes.

The ratio of phenotype in this experiment is as follows:

A_B_	1	Yellow smooth
A_bb	1	Yellow green
aaB_	1	Green smooth
aabb	1	Green twisted

On the phenotype, when the F2 generations of organisms with a full dominant heredity on a pair of signs are analyzed 3:1, on genotype 1:2:1 ratio, two character pairs on the analysis of the F2 generation than on selection phenotype 9:3:3:1: on genotype 1;2;1;2;4;2;1;2;1: (1;2;1)<sup>2</sup>, is observed. In such cases, we can see the theoretical result obtained by statistical analysis. To check the theoretically obtained result, the theoretically expected result is compared with the result obtained in the experiment. If the data obtained in the experiment correspond to the theoretically expected result, then in this case the theoretically obtained result will be considered correct. If, however, the information obtained in the experiment theoretically does not correspond

to the expected result, then in these cases, the theoretically obtained result turns out to be absolutely erroneous.

The difference between the data obtained in experiments and the result obtained theoretically can be different. In some cases, the difference can be small or random, in some cases; a large or clearly correct output is also possible. Therefore, it is worthwhile to determine the theoretical results obtained and expected in the experiment according to statistics. More and more  $\chi^2$  techniques are used in identifying such problems. This method was invented in 1900 by the English mathematician K.Pirson. This method can be used as follows [1].

To do this, you will need a table, and the table will consist of two sections, that is, the amount of data and individes. Individes, according to the amount of phenotypic Classes formed:

- 1) Dominant sign;
- 2 ) recessive sign;
- 3) The total is divided into individuals.

In the Data section, the selection (p) obtained in the experiment, under which the expected ratio and theoretically the expected selection (q) are written.

The most commonly used plant in matters is pisum sativum yellow smooth plants, taking approximate numbers as a result of the crossing with the green twisted plants, we see that the experiment yields a degree of accuracy.

**Experiment 1.** For example, in F2, 875 yellow smooth, 305 yellow twisted, 270 green smooth and 95 green twisted plants were formed. Let's assume that in the experiment a total of 1545 plants were obtained, when filling out the graph of the expected ratio in such cases, it is written that 9 is below the number 875; 3 is below the number 305, 3 is below the number 270, 1 is below the number 95. Because when AABB x AABB genotyped organisms are interrelated, the number of generations obtained in F2 will be a total of 16 units, and according to the phenotype 9; 3; 3; 1 ratio, while on the genotype 1;2;1;2;4;2;1;2;1: genotypic ratio in appearance (1;2;1) selection occurs in 2 proportions.

Theoretically, if all organisms in F2 have 1545 units, the expected separation is 875 units of yellow smooth, 305 units of yellow twisted, 270 units of green smooth and 95 units of green twisted plants are formed. Now, in the next row below in the table, the difference between the result obtained in the experiment and the theoretically expected result is written  $d=p-q$ .

As a result of our observation, it is  $875-869=+6$ ;  $305-290=+15$ ;  $270-290=-20$ ;  $95-96=-1$  equal to. To equalize the signs of the value d, we raise it to a square. During the experiment,  $d^2$  36; 225; 400; 1 is formed. To determine  $\chi^2$ , we divide the  $d^2$  that comes out according to each phenotypic class into theoretically expected phenotypic data (q). In the example presented it is formed  $36:869=0,0414$ ;  $225:290=0,7758$ ;  $400:290=1,379$ ;  $1:96=0,0104$ . All the results obtained to determine  $\chi^2$  are calculated by adding,  $0,0414+0,7758+1,379+0,0104 =2,2066$  if we sum up the information obtained, then we see that  $\chi^2=2,2066$  is formed (Table 1) [1].

**TABLE 1 (1900, K.PIRSON)**

Data		Result (p)	Expected ratio	Theoretically expected (-q)	Difference - $d^2=p-q$	$d^2$ - square of difference	$d^2 /q$ ratio	
Number of plants	Yellow smooth	875	9	869	+6	36	0,0414	$\chi^2=2,2066$
	Yellow twisted	305	3	290	+15	225	0,7758	

Green smooth	280	3	290	-10	400	1,379
Green twisted	95	1	96	-1	1	0,0104

The essence of the  $\chi^2$  method is that with its help it will be possible to determine whether the difference between the observed and expected results is random or inevitable. It is done with the help of a R.Fisher's table. In the vertical column on the left side of the table are the degrees of freedom, above which are shown the different probabilities on the horizontal. Determination of the value of  $\chi^2$  at various degrees of freedom (Table 2) [1].

**TABLE 2 (FISHER)**

Degrass of freedom N=n-1	Probability						
	0,99	0,95	0,80	0,50	0,10	0,05	0,01
1	0,000157	0,0393	0,642	0,455	1,642	3,841	6,635
2	0,101	0,103	0,446	1,386	3,219	5,991	9,210
3	0,115	0,352	1,005	2,366	4,642	7,815	11,341
4	0,297	0,711	1,649	3,357	5,989	9,488	13,277
5	0,554	1,145	2,343	4,351	7,289	11,070	15,086
6	0,872	1,635	3,070	5,348	8,558	12,592	16,812
7	1,239	2,167	3,822	6,346	9,803	14,067	18,475
8	1,646	2,733	4,594	7,344	11,030	15,507	20,090
9	2,088	3,325	5,380	8,348	12,242	16,919	21,666
10	2,558	3,940	6,179	9,342	13,442	18,307	23,209

The value of the degree of freedom will be equal to  $n=n-1=4-1=3$ , the number of N-phenotypic classes, the degree of freedom is equal to  $n=3$ , since 4 phenotypic classes are formed in F2 in monohybrid crossing. Probabilities: determining the value of a transaction depends on for what purpose experiments are conducted. In medicine, more 0,01% probability is used, in our example it is sufficient to use 0,05% probability. 0,05 probability means that from 100 realities on 95 we correctly deduce the hypothesis put forward. So, the degree of freedom is equal to 3, the probability is equal to 0,05, in the table Fisher is equal to 7,815. If the  $\chi^2$ -amount calculated from our side is smaller than the value given in the table 2,2066, then  $2,2066 < 7,815$  means that the difference between the result obtained in the experiment and the theoretically expected result in accordance with the zero hypothesis is not inevitable, that is, 9;3;3;1 corresponds to the ratio. The magnitude of  $\chi^2$  from the value specified in the table indicates that the forward hypothesis is irrelevant, which means that the zero hypothesis is incorrect. Now we get acquainted with an example confirming the zero hypotheses and its relevance.

**Experiment 2.** The breeder crossed two breeds of mulberry silkworm. They differed from each other in the following signs. The first butterfly produces green larvae and they hatch into yellow cocoons, while the second butterfly gives birth to striped larvae and they hatch into white cocoons. F1, the larvae of the offspring are striped, wrapped in yellow cocoons. In F2, 6385 yellow cocoon larvae, 2145 white larvae, 2099 yellow larvae, 691 white larvae a greenish larva was obtained. Determine the number of striped colored larvae that wrap around a white cocoon of the genotype digomozygote.

This issue is also related to polyhybrid crossing, and the number of generations given in F2 is approximate. We check the accuracy of the number of generations given based on the Pearson table.

yellow cocoon - AA  
 white cocoon - aa  
 green larva - BB  
 striped larva - bb

	AABB	x	Aabb
gametes	AB		Ab
F <sub>1</sub>	AaBb		AaBb

F <sub>2</sub> generation	gametes	AB	Ab	aB	Ab
	AB	AABB	AABb	AaBB	AaBb
	Ab	AABb	AAbb	AaBb	Aabb
	aB	AaBB	AaBb	aaBB	aaBb
	ab	AaBb	Aabb	aaBb	Aabb

Phenotypic ratio

	6385	A_B_	9	Yellow cocoon, green larva
	2145	A_bb	3	Yellow cocoon , striped larva
The data section	2099	aaB_	3	White cocoon, green larva
contains the experimental	691	aabb	1	White cocoon , striped larva

separation (p), the expected ratio, and the theoretically expected separation (q) will be written below of it.

In F<sub>2</sub>, 6385 yellow cocoons, green larvae, 2145 yellow cocoons, striped larvae, 2099 white cocoons, green larvae and 691 white cocoons, striped larva plants were formed. Assume that a total of 11,320 plants were obtained in the experiment. Under the number 2145 is written 3, under the number 2099 is written 3, and under the number 691 is written 1. Because when AABB x aabb genotype organisms are cross-bred, the total number of offspring obtained in F<sub>2</sub> is 16 and is 9: 3; 3; 1 by phenotype and 1; 2; 1; 2; 4 by genotype; Separation occurs in the genotypic ratio (1; 2; 1) 2 in the form of 2; 1; 2; 1.

While all organisms are 11,320 in F<sub>2</sub>, the theoretically expected separation is 6367 yellow cocoons, green larvae, 2124 yellow cocoons, striped larvae, 2124 white cocoons, green larvae and 708 green twisted plants are formed. Now at the bottom of another row of the table is written the

difference between the result obtained in the experiment and the theoretically expected result  $d = p - q$ .

As a result of our observation, it is equal  $6385 - 6368 = + 17$ ;  $2145 - 2122 = + 23$ ;  $2099 - 2122 = -23$ ;  $691 - 708 = -17$ . We square the sign of the value of  $d$  to equalize it.  $D^2$  289 during the experiment; 529; 529; 289 is formed. (To determine  $x^2$ , we divide the resulting  $d^2$  for each phenotypic class by the theoretically expected phenotypic information ( $q$ ). In the example given, 289: 6368 = 0.04538; 529: 2122 = 0.2492; 529: 2122 = 0.2492; 289: 708 = 0.408. To determine  $x^2$ , all the results obtained are calculated by adding,  $0.04538 + 0.2492 + 0.2492 + 0.408 = 0.95178$ . Then we see that  $x^2 = 0.95178$  is formed (Table 3) [1].

**TABLE 3 (1900, K.PEARSON)**

Data		Result (p)	Expected ratio	Theoretically expected (-q)	Difference – $d=p-q$	$d^2$ - square of difference	$d^2 / q$ ratio	
Number of plants	Yellow smooth	6385	9	6368	+17	289	0,4538	$x^2 = 0,95178$
	Yellow twisted	2145	3	2122	+23	529	0,2492	
	Green smooth	2099	3	2122	-23	529	0,2492	
	Green twisted	691	1	708	-17	289	0,408	

The essence of the  $x^2$  method is that it can be used to determine whether the difference between the observed and expected results is random or inevitable. This is done using the R. Fisher table. The vertical column on the left of the table shows the degrees of freedom and the horizontal above shows the different probabilities. Determining the value of  $x^2$  at different degrees of freedom [1].

The table shows that the amount of  $x^2$  obtained in different families of *Drosophila* varies greatly. In the first case, the difference between the observed and theoretically expected results is large, so the amount of  $x^2$  is large and higher than the 7,815 in the Fisher table (Table 2 Fisher). So zero assumption is wrong. In the second case, the amount of  $x^2$  obtained is smaller than the value obtained from the table ( $0.95178 < 7.815$ ), ie the result obtained corresponds to the ratio 9; 3; 3; 1.

**Note:**

**AA** - dominant

**Aa** - heterozygous

**aa** - recessive

**p** is the obtained result

**q** is the theoretically expected result

**n** is the degree of freedom

**d** is the difference between the result obtained and the theoretically expected result

**F1** is the first generation

**F2** is the second generation

**Fb** - analytical (bekross) confusion

**CONCLUSION**

When solving problems related to Mendel's laws or in the process of creating such problems, it is useful to determine the degree of accuracy of the expected theoretical result using statistical methods. Because it was studied that the expected theoretical result does not correspond to the practical result. In scientific research, too, such processes are sometimes used to obtain theoretical results. In view of similar cases, in the case of Mendel's laws, the analysis of statistical analysis of the separation of traits in F2 in the independent inheritance of genes using the method  $\chi^2$  was clarified.

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