THE HYBRIDIZATION WORK OF MENDEL, 102 YEARS AFTER STARTING THE CONTROVERSY

El Trabajo de Hibridación de Mendel, 102 Años después del Inicio de la Controversia

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ABSTRACT

This research was carried out in order to verify by simulation Mendel's laws and seek for the clarification, from the author's point of view, the Mendel-Fisher controversy. It was demonstrated from: the experimental procedure and the first two steps of the Hardy-Weinberg law, that the null hypothesis in such experiments is absolutely and undeniably true. Consequently, repeating hybridizing experiments as those showed by Mendel, it makes sense to expect a highly coincidence between the observed and the expected cell frequencies. By simulation, 30 random samples were generated with size equal to the number of observations reported by Mendel for his single trait trial, in this case, seed shape; assuming complete dominance, with genes A and a; likewise, it was simulated the results for the experiment with two traits, segregating in separate chromosomes, in this case seed shape, as before, and albumen color, with genes B and b, both *loci* with complete dominance. In the case of a single trait, the data only showed evidence for rejecting the null hypothesis (H_o) in 1/30 samples, with (P<0.05). In the case of the 30 samples of the two traits experiment, (H_o) was rejected only on 3/30 times, when it was set α = 0.05. In both simulations there was a high correspondence between the observed and expected cell frequencies, which is simply due to the fact that (H_o) is true, and under these conditions, that is what would to expect. It was concluded, that Mendel had no reason to manipulate his data in order to make them to coincide with his beliefs. Therefore, in experiment with a single trait, and in experiments with two traits assuming complete dominance, segregation ratios are 3:1; and 9:3:3:1, respectively. Consequently, Mendel's laws, under the conditions as were described are absolutely valid and universal.

Key words: Mendel's laws, controversy Fisher-Mendel.

RESUMEN

El propósito de esta investigación fue verificar por simulación las leyes de Mendel y contribuir al esclarecimiento de la controversia Fisher-Mendel. Para ello, se demuestra a partir de: el procedimiento experimental y los dos primeros pasos de la ley de Hardy-Weinberg que la hipótesis nula, en tales experimentos es, sin lugar a dudas absolutamente cierta. En consecuencia, al repetir experimentos de híbridos tal como los planteó Mendel, lo más lógico es esperar una alta coincidencia entre las frecuencias observadas y las esperadas. Mediante simulación, se generaron 30 muestras aleatorias con tamaño igual al número de observaciones reportadas por Mendel para un sólo carácter, en este caso, la forma de la semilla, asumiendo dominancia completa, con alelos *A* y *a.* Así mismo, se simularon los resultados del experimento con dos caracteres, segregando en cromosomas independientes, en este caso la forma de la semilla y el color del albumen, este último con alelos *B* y *b*; asumiendo dominancia completa en ambos *loci*. Para el caso de un carácter, los resultados sólo muestran evidencia para rechazar la hipótesis nula (H_o) en 1/30 muestras, con (P<0,05). En el caso del experimento con dos caracteres, (H_o) fue rechazada en 3/30, oportunidades; cuando se estableció α=0,05. Se observó una alta correspondencia entre las frecuencias observadas y las esperadas, lo cual es debido al hecho de que la (H_o) es verdadera, y en esas condiciones es lo que es de esperar. Se concluye que Mendel no tenía razón alguna, para manipular los resultados con el propósito de hacerlos coincidir con sus creencias. Por lo tanto en experimentos con uno y dos caracteres, y dominancia completa, las proporciones de segregación son 3:1 y 9: 3: 3: 1, respectivamente. En consecuencia, las leyes de Mendel, en las condiciones como las describe son absolutamente válidas y universales.

Palabras clave: Leyes de Mendel, controversia Fisher-Mendel.

Recibido: 01 / 07 / 2013 . Aceptado: 21 / 11 / 2013.

INTRODUCTION

In 1865, an Austrian monk, with knowledge of Biology, Mathematics and Physics, presented a paper that was published a year later [12], at the conference, he recounts the experiences collected over a period of approximately eight years, on plant hybridization [3]. That work, is a jewel of research methodology, according to the criteria of one of the re-discoverers of the work, who argues that he was tempted to leave his research, because he was getting the same results and the same conclusions [4]. The experiments were made in a sequential order, in order to achieve goals, to confirm hypotheses, which lead to repeat experiments, to establish new goals and in short, to build on a theory based on certainty, and someone stated that the success was because Mendel included his mathematical skills in order to decipher the mystery of inheritance [16].

Mendel, without much technical or theoretical resources distinguish from its predecessors, he simplified the problem by reducing it to a minimum, being careful in detail with the experimental error. That work laid the foundations of genetics, but was virtually ignored by his contemporaries, because according to Keines [10], it was only quoted in two theses, two authors whose books one of them is quoted in two other texts; likewise, it appeared in an encyclopedia, it was quoted three times in the German journal Flora, and in the memories of the Viennese Academy of Science. However, for some, the scientific community was not interested, or simply did not understand the work [14]. In 1900, three researchers, working independently re-discovered the work, one of them Correns [4], which with its conclusions is perhaps the one that gives the first indication of the accuracy of Mendel's results.

At a conference at the University of Cambridge in 1911, Sir Ronald Aylmer Fisher, a geneticist and a remarkable man, who laid the foundation of modern statistics stated: *"it is interesting that all of Mendel's original results fall within the limits of probable error",* suggesting also that Mendel, could *"unconsciously put in place dubious plants favoring his hypothesis"* [7]. This initiates the dispute. In 1936 Fisher published another article in detail, which again casts doubt on Mendel's results; he computed chi-square tests for each of Mendel's experiments, adding their values. Then, he added the degrees of freedom [6], which is correct according to the statistical theory [24], but with severe criticism because of the way he did from other points of view [13, 25], particularly he combined: segregation experiments with one, two and three pairs of genes; experiments for checking segregation of the dominant forms; experiments for gamete segregation; which can certainly have different variances. Subsequently, Fisher found the probability of exceeding the observed deviations; the chi-square statistic was 41.6056 for the 84 joint results reported by Mendel [12], which translates to a probability of 0.99993 to exceed the observed deviations. Fisher said that the results were manipulated or best yet, Mendel had an assistant who knew very well what he envisioned.

The attention of Fisher [6] was called because of all experiments, the results do not provide evidence to reject the null hypothesis (H_o), Fisher did not think that the reason for such a coincidence, had to be sought in the nature of the experiment and the experimental plan, this because of Correns' previous observation [4].

Pilgrim [18] is one of the researchers who has defended the honesty of Mendel, according to him, the latter, did nothing else but to publish his results with impeccable fidelity, and argued that it is a discredit to science have not recognized him during his lifetime furthermore, it is unfortunate to slander him. Later [19], he stated that the null hypothesis is correct, but without explaining why, he did a good job on simulation, but felt in the discussion of the coincidence of the results. This is the researcher who has closed to the solution of the problem; he stated that if genetic studies were analyzed by using χ^2 tests, the high probability values are not unusual, if the results are consistent with the null hypothesis, he concluded that χ^2 test is not appropriate to detect data counterfeit and that there is no reason to question Mendel's honesty. Recently it was published a review about the dispute, in which, it was concluded that the data was not manipulated and even suggested that Fisher could be wrong [11]. In fact, it has been mentioned [16] that the reasons for Fisher [6], to argue distortions are unfounded.

Later, Hartl and Fairbanks [9], analyzing the problem and agreed that there is no basis for alleging falsifying data in Mendel's work, they wanted that Fisher's allegation of deliberate falsification, can be set side, because in-depth analysis, it was shown that cannot be supported by convincing evidence. Recently, an investigation led to the conclusion that there is sufficient evidence of the introduction of systematic unconscious of some bias, and they showed a model that fits Mendel's data, without contradict Fisher's results [21]. However, most researchers in the topic, are still looking at the wrong place. This controversy persists until now; there are some that have taken Fisher's previous remarks for comment on Mendel´s results without conducting any analysis [2], which can only laid more confusion and uncertainty.

The purpose of this research was to demonstrate, based on Mendel's experimental procedure, and the Hardy-Weinberg (HW) law, the truth of the H_o. Additionally, by using the theory of the χ^2 test for goodness of fit, checking by simulation under the condition that H_o is true, that the natural is to expect a high coincidence between the evidence provided by the data and what is to be expected by theory.

MATERIAL AND METHODS

This research was carried out at the office of the Animal Breeding Academic Unit, of the Veterinary Medicine and Husbandry Faculty of the Universidad Michoacana de San Nicolás de Hidalgo (UMSNH). The results of the experiment were used with a single character, seed form, with alleles A and a,

and phenotypes round (AA or Aa) and rough (aa). For the case of two traits, it was added cotyledon color, with alleles B and b, and phenotypes yelow (BB or Bb) and green (bb). By using the functions RANUNI (seed) and ROUND (variable) of the Statistical Analysis System (SAS) [22], there were generated 30 samples, with sample sizes 7324 and 556, for the first and second experiment, respectively, which corresponded to the sample sizes of Mendel's experiments. The SAS RANUNI function generates random values from a uniform distribution on the continuous interval [0,1], Thereafter, with the ROUND function, there were assigned the values 0 or 1 to the gametes carrying the recessive or dominant genes, respectively, the "seeds" used for the random generator were: for the first experiment (1) and (32) while for the second were: (7), (11) in the first *locus*, and (3), (14) in the second. Finally, genotypes were obtained by combining male and females gametes sources. It was found that the function correctly generate gametes, running goodness of fit χ^2 analysis, to test the null hypothesis: "The allele frequencies of *A* and *a* are equal in the F_1 generation", this is: H_o: 0,5: 0,5 with the SAS FREQ procedure [22].

For the first experiment it was performed a goodness of fit test, considering the null hypothesis: "The phenotypic frequencies in the F_2 were 3:1", that is H_o: 0.75: 0.25. Finally in the second experiment, it was also fitted a goodness of fit test, to check the null hypothesis: "The phenotypic frequencies in the experiment were 9:3:3:1", this is: H_o: 0.5625: 0.1875: 0.1875: 0.0625. The values of the probabilities computed by Fisher, were obtained with the sentence prob = 1-CDF ('chisq', χ^2_{calc}, df), which gives the probability $prob > \chi^2_{calc}$.

Further, it was confirmed the veracity of the hypothesis, based on two aspects: first, the methodology used by Mendel in his experiments, and second, on the basis of the principle governing the dynamics of genes in populations [5, 23].

RESULTS AND DISCUSSION

The null hypothesis is true

In Mendel's experimental plan, it was made abstraction of what for each character was irrelevant, and he focused on the study of only alternative forms, as a result, the problem was reduced to a minimum. The transcendental point was, that the parental generation, in each character was homozygous for the two alternative forms, which thus could produce only a single type of gametes, as a result, the F_1 specimens, which were used for the deductions, were 100% heterozygous and therefore could only produced two types of gametes but at identical rates. The random mating process is equivalent to the random union of gametes being produced by the F_1. Therefore it is to expect a genotypic segregation pattern of 1:2:1, which in turn, assuming complete dominance translates into a 3:1 phenotypic segregation in the F_2 generation [8, 12].

In population genetics there is a principle that governs the dynamics of genes, which is known as the Hardy-Weinberg law [5, 23], the derivation of this law involves three steps, which are strongly explained [23]. It is only needed the first two steps of the deduction, to show that H_o is true, which is equivalent to the statement stated in the previous paragraph.

First step: demonstration of frequencies of gametes produced by the genotypes. The homozygous parental forms can only produce one type of gametes (unless there is mutation, which is excluded), either, $A \rightarrow p = 1.0$ for the first parent and $\alpha \rightarrow q = 1.0$ for the second parent. The heterozygous individuals produce two types of gametes, but no matter the number of such individuals the frequency of each gamete is ½.

Second step, requires the random mating of parents, but that is equivalent to random union of gametes produced by them, if all individuals are heterozygous (which was Mendel's experimental approach); accompanying whatever symbol that was used to represent the alleles in the first row and column of a Punnett square, it should be placed ½ for each allele, as the frequency of each gamete, this will lead to the genotypic segregation: $\frac{1}{4}AA:\frac{1}{2}A\alpha:\frac{1}{4}\alpha\alpha$, and if the dominance is complete, phenotypic segregation ratios must be ¾ round ($0.25AA$ + $0.50A\alpha$) and ¼ rough $0.25\alpha\alpha$. For the case of two *loci*, a similar reasoning, with a bit more work would lead to phenotypic ratios 9:3:3:1, if complete dominance and genes are transmitted independently. With this, it was concluded that in both cases, the null hypothesis is correct.

The nature of a goodness of fit χ^2 test

In these tests, the important thing is H_o, [17]. The procedure is to calculate the test statistic χ^2_{calc}, calculating the squared deviations of the observed and expected values of the cells, divided by what is expected on each of the κ classes, then adding the resulting values. The H_o is rejected if the calculated χ^2_{calc} value exceeds a critical value tabulated $\chi^2_{(1-\alpha)}$ for a distribution with $k-1$ degrees of freedom. In this context then, if there is much discrepancy between the observed and the expected cell frequencies, the tendency is to reject H_o, otherwise, if the discrepancy between the observed and the expected tends to be small, in which case, the evidence produced by the data does not provide enough support to reject H_o. This explanation is crucial, for this investigation, because many researchers have focused their attention of the controversy on it.

Therefore, with the demonstration of the veracity of H_o and as indicated in the previous paragraph in relation to the decision rule, it is not even required, the simulation, because if H_o were correct, it is natural to expect that most the results in any experiment of this nature, should have the tendency for the results to provide no evidence to reject H_o, as noted by Pilgrim [19], indeed, if that were true, in a high proportion of the experiments, the values of the test statistic should be low and not contradictory to H_o. In a very few opportunities the re-

searcher might expect to reject H_o. Consequently probability values should have the tendency to be high; this will suffice to explain Fisher's uncertainty [6].

Checking for the correct functioning of the RANUNI function

For this purpose, it was calculated a χ^2 goodness of fit test, for the hypothesis H_o: 0.50: 0.50 for the segregation of the two alleles in each sex, with the data from the 30 samples of the single trait experiment. In Appendix 1 it is showed the segregation and the proportions of gametes carrying both alleles for the female and the male parents respectively. Also it is included the results of the χ^2 test. In none of the cases, there was disagreement with the theory and it was concluded that the random generator worked properly, gamete frequencies were very close to 0.50 in both sexes.

Analysis of the results of Mendel's single trait experiments

Results of the first Mendel's seven experiments are reproduced in TABLE I, there are also included the results of a χ^2 test for the goodness of fit, for checking the null hypothesis H_o: 0.75: 0.25; by using the FREQ procedure of SAS [22].

For these cases and assuming complete dominance it would be expected according to the law of segregation that phenotypic proportions were, 3 dominant: 1 recessive. The dominant forms ranged from a minimum of 73.79% to a maximum of 75.89%. On the other hand, the recessive forms ranged from minimum of 24.11% to a maximum of 26.03%, which suggest a high coincidence between the observed and the expected results in each of these experiments, this translates into very low values of the χ^2 test statistic and hence to obtain high probability values. It was observed that the dominant and recessive forms deviate very little from the theoretical expectations, these discrepancies can only be attributed to random chance, which in biology is inevitable. However, the deviation is minimal, as to be mismatched, with the theory. The experimental procedure is for sure, the crucial point on Mendel's results, by knowing the difference between accuracy and precision [1].

In row eight, column six of TABLE I, it is showed the sum of the seven χ^2_{calc} values. It is almost the same as reported previously [6], and it would be obtained the same probability if the results were rounded at two significant digits. The procedure used by Fisher [6] is correct, in the full extent [17, 24, 25]. But the authors disagree in the form that it was used, adding the values of all of Mendel's experiments [13, 25]. This approach focuses on the nature, of the experiments, as it was noted previously. Under these circumstances, it is logical to assume that in what he was adding, may have problems in variance homogeneity, and for which Fisher [6] has received severe criticism from the scientific community [11, 18, 25]. Fisher was an excellent geneticist, with notable contributions to the evolution and in fact was the founder of modern statistics, so it is very difficult to contradict him. It is probably because of his highness that many researchers have relied on his shoulders, to doubt about Mendel reputation, especially those who did not test anything [2].

In order to illustrate his findings, Mendel [12] introduced to his colleagues the results of what was observed in ten plants: In TABLE II, it was showed the results and the χ^2_{calc} goodness of fit test, for each of the plants, this was done to corroborate the match between the observed and the expected according to the theory, and also to compare Fisher's calculations [6], likewise, the $prob > \chi^2_{calc}$ are shown.

Once again, the match between observed and expected frequencies is such that in none of the plants, the results provided evidence as to reject H_o. consequently all of them segregated on the basis of a 3:1 ratio. If the same analysis, were performed on the extreme cases identified by Mendel, it surely would provide evidence as to reject H_o. About this point, Wright [25] strongly suggested that these results should not be incorporated in the analysis. We assume that Wright's thinking was based upon the inference that they could come from crosses that did not represent the true experiment, or most

TABLE I
RESULTS OBSERVED BY MENDEL IN THE SEVEN INDIVIDUAL EXPERIMENTS (*Pisum sativum*)

	Dominants		Recessives		χ^2	$prob > \chi^2$
Character	*f*	%	*f*	%		
Seed form	5474	74.74	1850	25.26	0.2629	0.6081
Seed color	6022	75.06	2001	24.94	0.0150	0.9025
Seed cover	705	75.89	224	24.11	0.3907	0.5319
Legume form	882	74.68	299	25.32	0.0635	0.8010
Legume color	428	73.79	152	26.21	0.4506	0.5040
Flower position	651	75.87	207	24.13	0.3497	0.5543
Stem length	787	73.97	277	26.03	0.6065	0.4361
Σ					2.1389	0.9518
Total	14949	74.90	5010	25.10	0.1096	0.7406

TABLE II
RESULTS OBSERVED BY MENDEL FOR FORM AND COLOR OF SEEDS IN THE SINGLE TRAIT EXPERIMENTS

	Phenotype		χ^2	*prob* > χ^2	Phenotype		χ^2	*prob* > χ^2
U.E	Round	Rough			Yellow	Green		
1	45	12	0.4737	0.4913	25	11	0.5926	0.4414
2	27	8	0.0857	0.7697	32	7	1.0342	0.3092
3	24	7	0.0968	0.7557	14	5	0.0175	0.8946
4	19	10	1.3908	0.2383	70	27	0.4158	0.5190
5	32	11	0.0078	0.9298	24	13	2.0270	0.1545
6	26	6	0.6667	0.4142	20	6	0.0513	0.8208
7	66	24	0.7679	0.3827	32	13	0.3630	0.5469
8	22	10	0.6667	0.4142	44	9	1.8176	0.1776
9	28	6	0.9804	0.3221	50	14	0.3333	0.5637
10	25	7	0.1667	0.6831	44	18	0.5376	0.4634
Σ							7.1899	0.7074
Total	336	101	0.8308	0.3621	355	123	0.1367	0.7116

probably by experimental errors, such as those that could be introduced by bugs.

Simulation results of the experiment with a single trait

Results of the experiment for the shape of the seed (round and rough), for the thirty samples of size 7324, were presented in TABLE III. In sample 1, as an example the risk of committing a type I error is high and it is concluded that there is no evidence in the data as to reject H_o. If it was observed sample ten, the H_o should be reject. In addition, as an extreme case, in sample twelve, the agreement between the expected and observed was absolute and χ^2_{calc} is consequently zero and the conclusion was that there is no evidence to reject H_o in favor of H_o, but once again, this was due to chance. In the thirty samples generated only in 1/30, support evidence for rejecting H_o, with α = 0.05, with sample nineteen, we might have some doubt but H_o can only be rejected at (P<0.10), which was too high in the opinion of the authors.

These results were those that would be expected, since, as it was demonstrated before, H_o is true. This had been previously established in 1986 [19], who pointed out that the coincidence is due to the fact that H_o, was true, but unfortunately the author, did not explain the reasons, as to why, the null was true. He did focus on the analysis from a statistical point of view and did not stop to think on the reason for the coincidence. Following this, yet still appeared some publications [9, 11, 21] on the same discussion, including an analysis from a philosophical point of view, which have even suggested, the search for other sources of error [20].

Once Mendel ensured the veracity of the results for a single trait, he proceeded to further investigate what happened when, two traits were included simultaneously. For this, purpose an experiment was planned with two traits; this led him to discover the law of independent transmission, for pairs of genes that are in separate chromosomes.

For the case of two traits, there are modified patterns of Mendel's inheritance, for example under genetic interaction with recessive epitasis, the classic phenotype segregation pattern 9: 3: 3: 1, changes to 9: 3: 4. However, there will be nine genotypes in the F_2 in proportions 1: 2: 1: 2: 4: 2: 1: 2: 1, it is the mode of genetic action that changes the phenotypic segregation pattern [8]. If someone analyze the cases of linkage in *Drososphila melanogaster*, it is know that in the male of this species there is not recombination during in *meiosis*; therefore only parental forms are found, due to complete linkage. However, in the female *meiosis*, there is recombination and females form four types of gametes, but the proportions of these will vary from the expected, depending on the frequency of recombination [15], by way of an example, Morgan mated females of long wings and gray body, to black males with rudimentary wings, the F_1 was as expected of gray body and long wings. But when he mated the F_1 females to black males with rudimentary wings, he obtained 83% of parental forms and 17% of recombinant forms. Identical results were obtained in the test cross, when he formed the F_1 using black body and long wings females mated to gray body and vestigial wings males. Moreover, he showed different segregation ratios in the parental and the recombinant forms for various traits. For the cases in which the *loci* are located on the same chromosome but separated by a distance such that there occurs recombination in 100% of the tetrads during *meiosis*, the characters will be transmitted, as if they were on separate chromosomes [23], according to the Mendel's principle.

Simulation results of the two traits experiment

In TABLE IV it is showed the simulation results for the two traits selected by Mendel, in his experiment. Thirty random samples of size 556 were generated. In the last row are the results obtained by Mendel, with a χ^2_{calc} test statistic of 0.4700, for which the value of *prob* > χ^2_{calc} is 0.92540, without evidence as to reject H_o. In this simulation, setting the prob-

TABLE III
SIMULATION OF THE 3:1 SEGREGATION FOR SEED FORRM ON MENDEL'S EXPERIMENT

	Dominants		Recessives		χ^2	*prob* > χ^2
Sample	*f*	%	*f*	%		
1	5550	75.78	1774	24.22	2.3659	0.1240
2	5527	75.46	1797	24.54	0.8418	0.3589
3	5530	75.51	1794	24.49	0.9969	0.3181
4	5517	75.33	1807	24.67	0.4194	0.5172
5	5471	74.70	1853	25.30	0.3524	0.5527
6	5503	75.14	1821	24.86	0.0728	0.7873
7	5536	75.59	1788	24.41	1.3424	0.2459
8	5512	75.26	1812	24.74	0.2629	0.6081
9	5517	73.33	1807	24.67	0.4194	0.5172
10	5393	73.63	1931	26.37	7.2820	0.0070
11	5543	75.68	1781	24.32	1.8202	0.1773
12	5493	75.00	1831	25.00	0	1.00
13	5449	74.40	1875	25.60	1.4098	0.2351
14	5500	75.10	1824	24.90	0.0357	0.8502
15	5504	75.15	1820	24.85	0.0881	0.7666
16	5477	74.78	1847	25.22	0.1864	0.6659
17	5433	74.18	1891	25.82	2.625	0.1054
18	5446	74.36	1878	25.46	1.6086	0.2047
19	5423	74.04	1901	25.96	3.5682	0.0589
20	5489	74.95	1835	25.05	0.0117	0.9140
21	5489	74.95	1835	25.05	0.0117	0.9140
22	5492	74.99	1832	25.01	0.0007	0.9785
23	5494	75.01	1830	24.99	0.0007	0.9785
24	5517	75.33	1807	24.67	0.4194	0.5172
25	5533	75.57	1789	24.43	1.2845	0.2571
26	5470	74.69	1854	25.31	0.3852	0.5348
27	5508	75.20	1816	24.80	0.1638	0.6856
28	5437	74.20	1887	27.76	2.3826	0.1307
29	5494	75.01	1830	24.99	0.0007	0.9785
30	5503	75.14	1821	24.86	0.0728	0.7873
Global	164752	74.98	54968	25.02	0.0351	0.8515
Mendel	5474	74.74	1850	25.26	0.2629	0.6081

ability of Type I error to α = 0.05, H_o can only be rejected in 3/30 opportunities. There is once again, a huge coincidence between the observed and expected values according to the theory.

Labeling the columns for the total row of TABLE IV for the four phenotypes as A, B, C and D, so that A+B+C+D=T, with T being the grand total. The segregation for the round shape form would be obtained from (A+B)/T, likewise, the rough shape form, could be obtained from (C+D)/T (ignoring cotyledon color), as it were a single trait experiment. Similarly, for the other trait, the yellow cotyledon form, may be obtained from (A+C)/T, finally, the green form from (B+D)/T. (ignoring seed shape). In both cases, segregation ratios were closed to the 3:1 segregation pattern. This reflection is because Fisher [6], examined carefully Mendel's experimental procedure. He pointed out that Mendel had two choices: the first, to proceed with one character at a time, in his point of view, the longer and more expensive; second, to experiment simultaneously with several characters and then analyze the results individually. Surely, Mendel took the first option, because for the time, there was no idea of the nature of inheritance, and he was only complicating the experimental procedure, as it was solving previous hypothesis. In fact, for the law of segregation, only seven experiments were performed, dedicating a lot of his precious time, for the demonstration of the segregation of

TABLE IV
SIMULATION OF MENDEL'S TWO TRAITS EXPERIMENT FOR CHEKING THE 9:3:3:1 SEGREGATION

	Phenotypes									
	*A_B_*		*A_bb*		*aaB_*		aabb		χ^2	*prob* > χ^2
Sample	f	%	f	%	f	%	f	%		
1	333	59.89	106	19.06	87	15.65	30	5.40	4.8441	0.1836
2	312	56.12	99	17.81	108	19.42	37	6.65	0.5468	0.9085
3	305	54.86	95	17.09	119	21.40	37	6.65	3.2454	0.3553
4	300	53.96	109	19.60	109	19.60	38	6.83	1.2566	0.7995
5	300	53.96	102	18.35	108	19.42	46	8.27	4.3453	0.2265
6	316	56.83	112	20.14	100	17.99	28	5.04	2.0943	0.5531
7	317	57.01	101	18.17	87	15.65	51	9.17	10.6123	0.0140
8	321	57.73	111	19.96	95	17.09	29	5.22	2.4269	0.4887
9	303	54.50	129	23.20	86	15.47	38	6.83	9.6787	0.0215
10	308	55.40	110	19.78	103	18.53	35	6.29	0.4061	0.9390
11	312	56.12	97	17.45	110	19.78	37	6.65	0.9688	0.8088
12	309	55.58	102	18.35	119	21.40	26	4.68	4.3837	0.2229
13	309	55.58	105	18.88	107	19.24	35	6.29	5.3749	0.1463
14	322	57.91	117	21.04	89	16.01	28	5.04	5.3749	0.1463
15	309	55.58	105	18.88	104	18.71	38	6.83	0.3549	0.9494
16	311	55.94	115	20.68	96	17.27	34	6.12	1.7884	0.6177
17	316	56.83	104	18.71	99	17.81	37	6.65	0.4444	0.9309
18	302	54.32	109	19.60	113	20.32	32	5.76	1.5380	0.6735
19	313	56.29	111	19.96	102	18.35	30	5.40	1.1351	0.7686
20	319	53.37	91	16.37	113	20.32	33	5.94	2.6315	0.4520
21	278	50.00	129	23.20	105	18.88	44	7.91	12.2046	0.0067
22	309	55.58	109	19.60	106	19.36	32	5.76	0.5084	0.9170
23	298	53.60	109	19.60	113	20.32	36	6.47	1.6914	0.6388
24	318	57.19	103	18.53	103	18.53	32	5.76	0.3357	0.9532
25	311	55.94	111	19.06	96	17.27	38	6.83	1.4037	0.7047
26	310	55.76	108	19.42	104	18.71	34	6.12	0.1759	0.9814
27	319	58.99	91	16.37	102	18.35	35	6.29	2.4780	0.4793
28	316	56.83	104	18.71	98	17.63	38	6.83	0.7130	0.8701
29	317	57.01	97	17.45	121	21.76	21	3.78	8.6938	0.0337
30	328	58.99	91	16.37	102	18.35	35	6.29	2.4780	0.4793
Total	9341	56.00	3298	19.17	3102	18.60	1039	6.23	1.9924	0.5740
Mendel	315	56.65	108	19.42	101	18.17	32	5.76	0.4700	0.9254

the F_2 dominant forms, and the gametes types produced by F_1. which today can be solved with a single test cross. In contrast, the experiment with two characters was performed only twice. However, that was well justified, for the lack of prior theoretical foundations on inheritance. Subsequently, He further complicated the problem, including three characters.

In Appendix 2, it was attempted to reproduce the results for seed shape reported by Mendel for 100 and 100,000 samples in order to discern, how likely it was to get exactly the same results. Those results are which would be expected. In the 100 samples, in four of the trials the result was zero matches, the others were between 1 and 2 matches. In the case of 100,000 samples, they ranged from a minimum of 887 to a maximum of 951 matches. In both cases, the expected claims of the exact coincidence [1] of an experiment are very low, unless working with a small number of observations.

The authors had given principles of genetic and usually when they facilitate the basis of the population genetics chapter, inform the students, the reasons, from his point of view, as to why Mendel could not fail in their deductions, which are those that we demonstrate in this paper. With the conviction, then, that after 102 years of the origin of the dispute, it has be-

come apparent without any doubt, the strong honesty of Mendel, and we hope that this is the end point, of something that only is sowing uncertainty and bad examples to new generations [9]. The veracity of Mendel deductions were initially identified by one of the researchers cited as one of those who rediscovered these principles and who claimed that the differences between his research and Mendel's results were only in nomenclature [4]. The experiments should be analyzed in the way they were planned; χ^2 tests only were available, almost when the principles were re-discovered. In any refereed journal it is not required for the researchers to publish their data. The researchers at most present in their papers: usually tables with measures of central tendency, a measure of dispersion and the sample size; a graph which in most opportunities, is probably best represented by an equation or a frequency distribution, as appropriate. Fisher, has earned a deep respect, but Mendel also deserves admiration, for many of us, Mendel's work suggested the basis for the research methodology.

CONCLUSIONS

It is noted that estimates of Fisher and other researchers, are accurate from the point of view of the calculation of the test statistic and the odds, but there is doubt in the appropriateness of its use under the conditions as they were carried out along this controversy.

It was proved by deduction from the experimental technique and H-W law, that the null hypotheses are true, and therefore, in an infinite repetition of such experiments, the most obvious, is to obtain low values for the test statistic and there is a high probability that the results do not provide evidence to reject the null hypothesis.

Likewise, it is checked by simulation, using the uniform distribution that segregation ratios of a locus with complete dominance, under random mating of F_1 specimens is 3:1, on the other hand, when considering two independent *loci*, under the same conditions in both loci, segregation ratios in the progeny should 9:3:3:1, with a high coincidence between observed and expected frequencies.

Mendel's laws are universal, and used today in the study of the behavior of genes in populations. It should be understood that *"science works not because what is reported is <<true>> but because it works."* Mendel's laws are an abstraction of reality, not an exact repetition of it.

ACKNOWLEDGMENTS

Authors want to recognize the Veterinary Medicine Faculty of LUZ, UMSNH and UCOLA for their support. We also will thank reader's advice of any error or omission. Scripts to reproduce the simulation are available upon request, for teaching purposes. For those who have had some degree of uncertainty in the reading of previous works, noting the controversy, we will want to share opinions.

APPENDIX 1

SIMULATION OF THE FREQUENCY OF GAMETES CONTAININ THE DOMINANT AND RECESSIVE ALLELES

	A		α		χ^2	*prob* > χ^2
Gametes	*f*	%	*f*	%		
Male	109800	49.97	109920	50.03	0.0655	0.7979
Female	109748	49.95	109972	50.05	0.2284	0.6327

APPENDIX 2

SIMULATION OF THE NUMBER OF MATCHES OF THE SEDD'S FORMS IN MENDEL'S EXPERIMENTS

		Number of trials	
Seeds		100	100000
p	*q*	Matches	Matches
1	32	0	928
7	4	1	910
3	11	0	911
6	5	2	922
1	16	0	928
7	23	1	910
4	67	1	887
43	27	2	951
3	45	0	911
99	31	2	942

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