## **Gregor Mendel's Genetic Experiments**

### A Statistical Analysis after 150 Years

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#### Abstract

Gregor Mendel is generally acknowledged not only as the founder of genetics but also as the author of the first mathematical result in biology. Although his education had been questioned for a long time, he was profoundly educated in botany as well as physics and in those parts of mathematics (combinatorics, probability theory) applied in his later pea plants experiments. Nevertheless, there remain debates in statistical literature about the reasons why are Mendel's results in such a too good accordance with expected values [22, 28]. The main aim of this paper is to propose new two-stage statistical models, which are in a better accordance with Mendel's data than a classical model, where the latter considers a fixed sample size.

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Institute of Computer Science CAS, Address: Pod Vodárenskou věží 2, 182 07 Praha 8, CR E-mail: kalina@cs.cas.cz If Mendel realized his experiments following such two-stage algorithm, which cannot be however proven, the results would purify Mendel's legacy and remove the suspicions that he modified the results. Mendel's experiments are described from a statistical point of view and his data are shown to be close to randomly generated data from the novel models. Such model is found as the most suitable, which is remarkably simpler according to the model of [28], while the new model yields only slightly weaker results. The paper also discusses Mendel's legacy from the point of view of biostatistics.

#### Keywords

Genetics, history of science, biostatistics, design of experiments

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### **1** Introduction

Gregor Mendel is generally acknowledged not only as the founder genetics, but also as the author of the first mathematical result in biology. Although his education had been questioned for a long time, he was profoundly educated in botany as well as physics and in those parts of mathematics (combinatorics, probability theory) applied in his later pea plants experiments. Nevertheless, there remain debates in statistical literature about the reasons why are Mendel's results in such a too good accordance with expected values [22, 28]. The main aim of this paper is to propose new two-stage statistical models, which are in a better accordance with Mendel's data than a classical model, where the latter considers a fixed sample size. If Mendel realized his experiments following such two-stage algorithm, which cannot be however proven, the results would purify Mendel's legacy and remove the suspicions that he modified the results.

Section 2 of this paper summarizes important facts about Mendel's life. His pea plants experiments are overviewed in Section 3. Also the founder of the mathematical statistics at the beginning of the 20th century were involved in their first interpretations, which is recalled in Section refkap:odpor. A statistical section 5 with an original analysis of Mendel's data is motivated by an attempt to find such design of experiments, which would be in a good accordance with Mendel's data. A newly proposed two-stage model is remarkably simpler according to the model of [28], while the new model yields only slightly weaker results. Finally, the paper also discusses Mendel's legacy from the point of view of biostatistics.

#### 2 Mendel's biography

Gregor Mendel (20.7. 1822 - 6.1. 1884) is justly acknowledged as the founder of genetics and one of the most important biologists of all times. This sections describes Mendel's life in a much shorter way than in available monographs [11, 16, 25], but we do not neglect that Mendel acquired a profound education in mathematics and physics. It is necessary to point out in connection with Mendel's CV that prejudices against Mendel still survive in lay public or in popularization works (e.g. [18]), questioning his education or purpose of his experiments. No discussion is devoted to such prejudices here, because they have been already disproved by a series of arguments standing of proven facts or following from a historical context.

Mendel was born as Johann Mendel in a Germanspeaking Roman Catholic family in today's Silesian village Hynčice and was baptized in the church of St. Peter and Paul in Dolní Vražné, while both villages are nowadays part of the municipality Vražné. His parents were poor peasants and his father devoted himself to breeding fruit trees. Jan Schreiber awakened a deep interest in science education in the young Mendel. Schreiber was not only a priest in Dolní Vražné but also Mendel's teacher in Hynčice, where he taught natural science according to the spirit of Comenius. Mendel continued his studies in Lipník nad Bečvou, later in Opava at a secondary school oriented on science and finally in Olomouc at the Philosophical Institute of the university.

In 1843, Mendel joined St. Thomas' Augustinian Abbey in Old Brno, where he was ordained as a priest in 1847 and accepted a monastic name Gregor. The abbey can be denoted as a progressive education center filled with enlightenment thoughts, where monks devoted themselves to science and humanity. This was the vision of the abbot Cyril Napp (1792–1867), who was a renowned expert on breeding fruit trees himself and aimed at finding young monks with an interest science. The abbey possessed large fields and pastures, where the monks performed also sheep breeding experiments.



Figure 1: Gregor Mendel (1822–1884).

Mendel needed to pass a rigorous exam in order to promote from his position of a substitute teacher to the fully qualified one. Therefore, he went to Vienna in 1850 to undertake the exam in physics and botany. The head of the commission for the physics part of the exam was Andreas von Baumgartner and one of the members was Christian Doppler (1803–1853). Mendel was able to pass only because Baumgartner was a man of broader knowledge who preferred logical thinking to memorizing [1, 16]. However, members of the other commissions were rather pedants, which had the consequence of Mendel's failing at the whole exam. This was perhaps influenced by his being a self-learner. At any case, Napp sent a letter to Baumgartner with a question about the course of the exam. He obtained the response that Mendel made a convincing impression and as a self-learner showed his talent [1]. Then, Napp sent Mendel to study in Vienna. Mendel spent two years there (1851–1853) in a newly created scientifically oriented study program.

In Vienna, Mendel's teachers were the leading personalities and scientists in botany, physics and geology. Thus, his intellectual horizon could become much wider. He studied also at Doppler, who was the director of the newly established Institute of Experimental Physics. Mendel became acquainted in combinatorics [11], particularly with permutations and combinations in lectures in physics (and especially in meteorology). He learned also basics of probability theory and simple (but at that time not yet formalized) principles of statistical thinking [2, 5]. Mendel's second attempt for the rigorous exam in 1856 ended without success again, particularly because of botany. There are good reasons to believe however than Mendel knew the most recent scientific results in botany better than his too conservative examiners [25].

After returning to Brno, Mendel could continue teaching botany and mainly physics at various schools, while he was known as an excellent, enthusiastic and comprehensible teacher. At the same time, he could develop an intensive program on experimental plant breeding with the aim to explain laws of origin and development of hybrids. The abbot Napp, this forgotten hero in the history of genetics, let an expensive greenhouse be built for Mendel in the garden of the abbey in 1854. Mendel realized his experiments intensively here in 1856–1863; they will be described later in Section 3. Apparently, Mendel designed a detailed plan of the experiments already in Vienna [24]. He was also acknowledged as the qualified teacher even without the exam in 1856.

The modest and introvert Mendel did not cause any controversies in the abbey, he followed liberal religious stands [10] and did not even participate in the national disputes among Czechs and Germans. Both groups jointly proposed him to become the new abbot after Napp's death in 1867. As the abbot, Mendel tenaciously defended interests of the abbey against pressures from the anticlerical government.

Some sources [11, 26] claim that Mendel in his old age had no more time for pea experiments, which thus remained unfinished, and that he was isolated, lonesome and bitter and lost his personal prestige. Such sources seem to be derived from the very first Mendel's biographies (e.g. [12]), which were focused mainly on the biological problems and ignored a broader context. On the other hand, other sources [10] claimed Mendel to acquire a remarkable reputation in the society as well as inner peace. Because he himself considered the experiments to be finished, he was able to devote much time to meteorology, beekeeping and experiments with breeding decorative plants and fruit trees [21, 25]. Finally, he passed away in 1884 in connection to his chronic kidney disease.

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### 3 Mendel's experiments

Mendel spent 8 years with intensive experiments with pea plants. They were apparently performed with the aim to empirically verify principles of heredity, while he was able to understand them theoretically in a correct way already at that time from the points of view of both biology and mathematics [3]. The experiments were performed according to a clear vision and following a theory, which was elaborated prior to the experiments. Mendel so much loved the experiments that he would not allow them to any his assistant [21] and the big greenhouse served only Mendel and only pea plants. He started by selecting varieties suitable for the experiments and invented also a new methodology for heredity research. In very simple conditions, he was able to cross and investigate over 12000 pea plants. Mendel was able to gather a huge amount of experimental data thanks to his (we can say mathematical) thoroughness and precision [10].

Mendel presented his selected results to a community of experts on botany and breeding in Brno twice during 1865. He made the impression of a great experimenter, who was perceived as unfortunately spoiled by mathematics, because he devoted the talk to randomness and probability evaluations. Even in spite of it, he was offered a possibility to publish his summarizing results. Thus, his only paper on heredity [19] was published in 1866. It did not however arouse any attention and was practically ignored so that the core his discovery was lost for one whole generation of Mendel's contemporaries.

The text of the whole paper [19], which was also repeatedly translated to various languages, has the experiments and measured data as its central topic. Mendel does not formulate genetic laws in a general form. This is why the paper gives a rather complicated impression at first glance. At second glance, or during repeated reading, a today's reader may already understand Mendel's thoughts, which is however to a large extent a consequence of our understanding of elementary genetic laws. In Mendel's times, the paper must made a blurry impression. Mendel denoted variables by letters like it is common in contemporary algebra. However, when he considered counts and probabilities in the paper, he did not use contemporary mathematical terminology, which was not defined at that time. He either defined his own concepts or tried to circumscribe them in an idiosyncratic fashion.

From the mathematical point of view, Mendel identified that the ratio 3:1 of e.g. green and yellow unripe legumes in reality corresponds to the ratio 1:2:1, where the green color is dominant and the ratio corresponds to green legumes with genotype AA, green Aa and yellow aa, respectively. Perhaps it is the very grasping the mathematical structure of the results and these abstract thoughts that reveal Mendel most clearly as a man of genius.

Mendel's results in meteorology, in which he published 9 papers, represent an independent topic. Indeed, he was far ahead his time also in meteorology [20]. His description

and explanation of causes of strong wind effects, which also destroyed his greenhouse, is remarkable. Towards the end of his life, Mendel devoted much time to a thorough weather measurement and his hand-written reports from 1879–1883 constitute the basis of regular meteorological observations in Brno.

# 4 Statistics as a deteriorating circumstance

Mendel's only paper on heredity was rediscovered only in 1900 in a way which was denoted as a fairy-tale [5]. Soon, Mendel became a target of questioning results, pseudoscientific interpretations as well as fanatic attacks against his personal reputation. Thus, he was to a large extent considered as a controversial or naïve amateur, dilettante or uneducated person, who was able to come to important discoveries only by a mere chance and good luck behind the walls of the abbey. Also important statisticians of the beginnings of the 20th century contributed to such assessment of Mendel's legacy.

One of main Mendel's critics was Karl Pearson (1857– 1936), who was the first professor of statistics in the world [15]. In the Biometrika journal, he criticized Mendel. He considered his results absurd and the statistical arguments half-bogus [4]. He founded the statistical school of biometricians, who attacked Mendel's results for being extremely close to expected values by means of the Pearson's  $\chi^2$  goodness-of-fit test. While biometricians believed that heredity (i.e. genetic variability) is continuous, another school denoted as Mendelists opposed them with the idea of a discrete heredity. William Bateson (1861–1926), their leading personality and biologist, believed Mendel's statistical results, but he did not understand the statistical arguments and even considered statistics in biology to be senseless and useless [17].

The controversy of both schools was ended by Ronald A. Fisher, a leading biostatistician and biologist, who confirmed Mendel's idea of a discrete heredity. Although the result was a practical victory of Mendelists, Fisher was at the same time able to reconcile both groups. Fisher admired Mendel with humility [5, 14] and also used his data to illustrate some of the novel statistical methods (e.g. proposed in [7]), although he was deeply convinced about Mendel's falsifying the data.

Let us remark that Mendel's legacy was not allowed to be commemorated in Czechoslovakia after 1948 until 1960s [32], not only because of his clerical background, but also with the justification that Mendel exploited statistical reasoning [30].

Currently, there continue debates of experts attempting to explain why are Mendel's results biased towards expected values. Various scientific papers (e.g. [21, 27, 28]) have recently tried to rehabilitate Mendel. One of the arguments is based on the idea that he could have performed the experiments according to a more complex design. So far, there have appeared no remarkable arguments against it. The following section proposes new possible models. Numerical simulations are used to find out if Mendel's original data are in accordance with these newly proposed designs.

# 5 Two-stage models for Mendel's experiments

In literature, there have been intensive discussions attempting to find explanation for a too good accordance between Mendel's data and expected values. In such context, expected values are those which would have been obtained in ideal experiments without any nuisance external effects under the assumption that the randomness may not influence the results in any extreme manner [27, 29]. Such explanation remains however unknown also as a consequence of lacking knowledge of the detailed organization of all Mendel's experiments as well as of lacking preliminary results. Statistical attempts for such explanation include proposed two-stage models of [13, 28], which assume Mendel to decide for more experiments if the results do not yield a sufficiently remarkable confirmation of the theoretical model. There is no indication that Mendel used a two-stage design but this is not impossible. One more reason for it is a lack of outlying measurements (outliers) in the data [22]. In this section, a new two-stage model is proposed and compared with the model of [28] by means of numerical simulations. Also, a method for finding an optimal constant, on which the model depends, is proposed.

We work with results of Mendel's 84 experiments. The number of pea plants, for which Mendel collected the data, ranges between 19 and 8023 in various experiments. Particularly, we explain the two-stage models on one experiments devoted to flower color. He hypothesized that purple and white flower appear in the population exactly in the ratio 3:1. This corresponds to the probability  $\pi_0 = 3/4$ for purple. Mendel plants n = 8023 pea plants. Consequently, he observed purple flowers (dominant trait) exactly for X = 6022 plants. We consider X as a realization of a random variable with a binomial distribution  $Bi(n, \pi_0)$ , where the appearance of the dominant trait is denoted as a success. The expected value for the number of successes equals  $n\pi_0 = 6017.25$ . Other Mendel's experiments are considered in an analogous way leading to binomial distributions with different values of  $\pi_0$ , namely 1/2, 2/3, or 3/4.

Pires and Branco [28] claimed that Mendel could have used a two-stage design based on the  $\chi^2$  test for the binomial distribution. The whole approach will be described in a rather more complicated way now in order to allow for comparisons of different models. Let us first introduce the notation  $(X, n, \pi_0)$  for the triple of values, where X is a random variable following the binomial distribution  $\operatorname{Bi}(n, \pi_0)$ . The model (design) will be described by Algorithm 1, where  $\chi^2(X, n, \pi_0)$  denotes the value of the  $\chi^2$  statistic for testing the null hypothesis  $H_0$ :  $\pi = \pi_0$  against the alternative hypothesis  $H_1$ :  $\pi \neq \pi_0$ , i.e.

$$\chi^2 = \frac{(X - n\pi_0)^2}{n\pi_0(1 - \pi_0)}.$$
(1)

Algorithm 1 The two-stage model of [28].
<b>Input:</b> $n_1 \in \mathbb{N}, n_2 \in \mathbb{N}, c_1 \in [0, 1], \pi_0 \in (0, 1)$
<b>Output:</b> Number of observations <i>n</i> , number of successes
X, corresponding $p$ -value $p$
Perform $n_1$ measurements (i.e. on $n_1$ plants)
$X_1 :=$ number of successes among $n_1$ measurements
$p_1 := p$ -value corresponding to $\chi^2(n_1, X_1, \pi_0)$
$ \mathbf{if}  p_1 \geq c_1  \mathbf{then} \\$
$n := n_1, X := X_1, p := p_1$
else
Perform $n_2$ measurements and denote the number of
successes as $X_2$
$p_2 := p$ -value corresponding to $\chi^2(n_2, X_2, \pi_0)$
$n := n_i, X := X_i$ and $p := p_i$ , where $i = \arg \max p_i$
over $i \in \{1, 2\}$
end if

Such approach, when the measurement is performed either once or twice, is denoted as two-stage. The classical approach, performing all measurements at once with a fixed sample size, is denoted as one-stage. We already proposed an alternative two-stage algorithm in the paper [13], where however only values from the second block of measurements is used (i.e. if the second block is performed), ignoring the whole first block. The new model is proposed in Algorithm 2, exploiting the notation

$$Z = \frac{|X - n\pi_0|}{n}.\tag{2}$$

Algorithm 2 New two-stage model.
Input: $n_1 \in \mathbb{N}, n_2 \in \mathbb{N}, c_2 \ge 0$
<b>Output:</b> Number of observations <i>n</i> , number of successes
X, corresponding $p$ -value $p$
Perform $n_1$ measurements
$X_1 :=$ number of successes among $n_1$ measurements
$p_1 := p$ -value of the $\chi^2$ test for $(n_1, X_1, \pi_0)$
if $Z < c_2$ then
$n := n_1, X := X_1, p := p_1$
else
Perform $n_2$ measurements and denote the number of
successes as $X_2$
$p_2 := p$ -value of the $\chi^2$ test for $(n_2, X_2, \pi_0)$
$n := n_i, X := X_i$ and $p := p_i$ , where $i = \arg \min Z_i$
over $i \in \{1, 2\}$
end if

Performing the experiments using Algorithm 2 neither require the computation of the  $\chi^2$  statistic nor of the *p*-value. Because both were unknown in Mendel's times, the approach based on Algorithm 1 seems much more intuitive. We included computations of the *p*-values only artificially in order to allow comparisons which of the models

is the best for explaining Mendel's data. We will generate random data from Algorithm 1 with various  $c_1$  and from Algorithm 2 with various  $c_2$ . Simulated data will be generated from the binomial distribution with the same values of n and  $\pi_0$  as in Mendel's experiments.

It is now necessary to measure the distance between Mendel's data and simulated data from Algorithms 1 and 2. Individual *p*-values are random variables and the aim is not to compare them themselves, but the whole set of 84 *p*-values. It is worth noting that values of  $\chi^2$  or Z themselves depend on the sample sizes and thus are not suitable as distance measures. Indeed, the task is to find a suitable measure of distance between two distributions or a loss function expressing the loss of a particular twostage model compared to Mendel's observed data. We consider the measures

$$M_1 = \sum_{i=1}^{84} |p_{(i)}^1 - p_{(i)}^M| \quad \text{and} \quad M_2 = \sum_{i=1}^{84} |p_{(i)}^2 - p_{(i)}^M|, \quad (3)$$

to be suitable, where

- $(p_1^M, \dots, p_{84}^M)^T$  = vector of *p*-values of the  $\chi^2$  test for 84 Mendel's experiments,
- $(p_1^j, \ldots, p_{84}^j)^T$  = vector of *p*-values of the  $\chi^2$  test for randomly generated data from Algorithm *j*, where  $j \in \{1, 2\}$  and  $c_j$  is given.

• 
$$p_{(1)}^M \leq \ldots \leq p_{(84)}^M$$
 = arranged values  $p_1^M, \ldots, p_{84}^M$ ,

•  $p_{(1)}^j \leq \ldots \leq p_{(84)}^j$  = arranged values  $p_1^j, \ldots, p_{84}^j$  for  $j \in \{1, 2\}.$ 

Naturally,  $M_1$  depends on selected  $c_1$  and  $M_2$  depends on  $c_2$ . We will perform the random generation 1000-times and averaged values of  $M_1$  and  $M_2$  will be considered.



Figure 2: Comparison of data generated from Algorithm 1 with Mendel's data, depending on the choice of  $c_1$ . The comparison is performed by means of the measure  $M_1$ .

Figure 2 shows computed values of the measure  $M_1$  depending on the choice of  $c_1$ . The values  $c_1 = 0$  corresponds to the one-stage model. If  $c_1 = 1$ , the maximum of both *p*-values is considered. We can see, and it is revealed also by other more detailed analysis, that Algorithm 1 is the closest to Mendel's data for c = 0.2, which corresponds to the optimal value c = 0.201 of [28]. The improvement compared to the one-stage model is remarkable.



Figure 3: Comparison of data generated from Algorithm 2 with Mendel's data, depending on the choice of  $c_2$ . The comparison is performed by means of the measure  $M_2$ .

Figure 3 shows computed values of the measure  $M_2$  depending on the choice of  $c_2$ . The interpretation of the figure is different from Figure 2. The value  $c_2 = 0$  now corresponds to the minimum of two values of Z, while a sufficiently large  $c_2$  (not limited from above) corresponds to the one-stage model. The optimal value of  $c_2$  in Algorithm 2 is  $c_2 = 0.08$ .

Table 1: Added value of two-stage models compared to the one-stage model. The numbers are values of a distance measure between the two-stage model and Mendel's data divided by the distance measure between two one-stage model and Mendel's data.

Algorithm	Ratio
1	0.42
2	0.45
3	0.51
4	0.70

We performed additional computations for other twostage models, which lead only a slight improvement compared to the one-stage model. These include Algorithm 3, which differs from Algorithm 2 only in  $X := X_1 + X_2$  in case that  $Z < c_2$ . Algorithm 4 differs from Algorithm 2 only in  $X := X_2$  in case that  $Z < c_2$ . Table 1 shows the relative ratio of improvement of individual models compared to the one-stage model. For example, Algorithm 1 allows to reach (with the optimal value of  $c_1$ ) only 42 % of the value of  $M_1$  attainable with the one-stage model (with c = 0). Very similar results are obtained if a quadratic distance measure between two vectors instead of (3) is used.

On the whole, the computations and figures show that the idea of a two-stage approach is definitely not meaningless. Algorithm 1 corresponds to Mendel's data better than Algorithm 2, but this superiority is practically negligible. On the other hand, Algorithm 2 gives a more likely impression for its simplicity from the points of view of interpretation and computation. Algorithms 3 and 4 are less reliable for describing Mendel's data.

# 6 Mendel's legacy from the point of view of biostatistics

Mendel was the first to explain the substance of heredity. He developed the methodology for the study of heredity, which has been used until now, and strongly influenced current genetic engineering [32]. He belongs also to the most important theoretical biologists as the founder of genetics. At his time, nobody would expect that general genetic laws could be derived by means of (possibly large) experiments on an only plant. Also pea plants were too ordinary for such far-reaching experiments. Nowadays, genetic laws are denoted by Mendel's name and their correctness was theoretically proven after the discovery of DNA. Mendel has been also acknowledged as the founder of bioinformatics thanks to his discovery of the substance of hereditary bioinformation. His understanding the gene as an algebraic unit truly represents a jump to the 21th century [30].

Mendel was also the first to exploit combinatorics, probability theory and mathematics in general in biology. This was a revolutionary step already by understanding very significance and influence of randomness in heredity. He explained that randomness is manifested as a discrete variable, which allowed him to derive probabilities for the genotype and phenotype of the offsprings. He had contributed to constructing modern biology on statistical thinking even before mathematical statistics started its existence. Botany experts of that time perceived it as a contamination of their science, but we can view statistics as an inseparable part of current biological or biomedical research. Mendel used only a naïve definition of probability and intuitive inductive thinking [5], which was sufficient for the particular statistical comparison of his results with expected values. In spite of his contribution to the development of biostatistics, Mendel is not generally acknowledged as its founder.

Mendel influenced also sophisticated design of experiments, which belongs to statistics as its integral part. He organized the experiments in an unprecedented way although the design seemed obscure to his contemporaries. The design required to consider and evaluate an enormous number of plants within the experiments. Fisher [6] derived statistical formulas for their analysis and we nowadays understand the whole procedure, which is now known as factorial design, as natural, intuitive and standard. It is worth mentioning that the statistical concept of factorial design comes from Mendel's notion of factors (in German *die Faktoren*) for genes. This concept was later adopted by Fisher for variables measured in any (not only genetic) experiment.

Mendel is also denoted as the progenitor of Mendelian randomization, which obtain increasing popularity in analytical epidemiological studies [23, 31]. If the influence of various factors (affected by environment and/or genetics) on the treatment of patients is investigated, randomized control studies have to face a number of practical limitations. It is for example impossible to perform a randomization of the genotype, which is given by a random combination of genes of a particular patient's parents, but is already fixed at the time of the study, because the randomization of alleles was performed by the nature itself at the time of conception. Another hardly imaginable requirement on a strict randomization would be to push a patient to become a smoker or alcoholic for the purpose of the study.

The Mendelian randomization is a procedure stemming directly from the second Mendel's law, which is able to replace the machinery of randomized clinical trials. From the statistical point of view, the method represents a correction for a systematic error (confounding) in the design of the study. It is namely common that patients selected for a clinical study have a better (or in the contrary worse) prognosis compared to patients treated with conventional methods. The principle of the method is statistical and consists in approaching a particular genetic variant as a natural instrumental variable, while hypothesis testing or estimating the effect is performed by means of the instrumental variable estimator, which is a popular procedure mainly in econometrics.

It will be never more possible to prove without doubt if Mendel modified his experimental data and performed an intentional scientific misconduct or not. This cannot be decided even by means of a statistical analysis. This paper however contributes to the discussions if the data could really arise without his falsifications. Numerous works in scientific journals have in recent years attempted to rehabilitate Mendel from the accusations of modifying or even creating the results. Their arguments come from different fields of genetics, breeding, history, ethics and even psychology, philosophy or theology [21, 24]. According to such recent arguments, our whole knowledge about Mendel shows his intentional modifications of results to be highly improbable [21]. In fact, it were rather Mendel's critics who performed experiments violating ethics or credibility principles, such as eugenicists or the Soviet biologist T.D. Lysenko (1898–1976) [8]. Thus it seems that Gregor Mendel, the respectable and exemplar priest, can finally come out from all the controversies and accusations as a moral authority and man of the noblest character [10].

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