On the use of the Pfizer and the Moderna COVID-19 mRNA vaccines in children and adolescents

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This expertise on the use of the Pfizer and Moderna COVID-19 vaccines in children and adolescents is divided into three sections, which will deal with the following questions, in order:

1. Is vaccination of children and adolescents against COVID-19 necessary?
2. Are the Pfizer and Moderna COVID-19 vaccines effective?
3. Are the Pfizer and Moderna COVID-19 vaccines safe?

The arguments presented in Section 1 pertain to all COVID-19 vaccines, whereas those in Sections 2 and 3 apply specifically to the Pfizer and Moderna COVID-19 vaccines.

Section 1 will show that vaccination of adolescents COVID-19 is unnecessary, because

- in this age group the disease is almost always mild and benign;
- for the rare clinical cases that require it, treatment is readily available;
- immunity to the disease is now widespread, due to prior infection with the virus (SARS-CoV-2) or with other coronavirus strains; and
- asymptomatic adolescents will not transmit the disease to other individuals who might be at greater risk of infection.

Section 2 will demonstrate that the claims of efficacy the manufacturers (Pfizer and Moderna) attach to their vaccines—namely, 95% efficacy in adults, and 100% in adolescents—are

- misleading, because these numbers pertain to *relative*, not *absolute* efficacy, the latter being less than 1%;
- specious, because they refer to an arbitrarily defined, clinically meaningless evaluation endpoint, whereas no efficacy at all has been demonstrated against mortality;
- most likely altogether fraudulent.

Section 3 will show that the safety profile of the Pfizer and Moderna COVID-19 vaccines is catastrophically bad. It will be discussed that

- Pfizer, Moderna and the EMA have systematically neglected evidence from preclinical animal trials that clearly pointed to grave dangers of adverse events;
- the Pfizer and Moderna COVID-19 vaccines have caused thousands of deaths within less than a year of their introduction;
- The agencies that granted emergency use authorization for this vaccine committed grave errors and omissions in their assessments of known and possible health risks.

- In addition to already manifest adverse events, recent evidence shows unambiguously that the mRNA vaccines can be copied into DNA within human host cells and then integrate into the cellular DNA. This implies grave risks both for the vaccinees themselves, such as cancer and autoimmune disease, and for their offspring.

The only possible conclusion from this analysis is that the use of these vaccines in children adolescents cannot be permitted, and that its ongoing use in any and all age groups ought to be stopped immediately.

1 Vaccination of children adolescents against COVID-19 is unnecessary

1.1 What does the available evidence show? There are several lines of evidence that show vaccination of children and adolescents against COVID-19 to be unnecessary.

1.1.1 The case fatality rate of COVID-19 in the general population is low. The vast majority of all persons infected with COVID-19 recovers after minor, often uncharacteristic illness. According to world-leading epidemiologist John Ioannidis [1, 2], the infection fatality rate of COVID-19 is on the order of 0.15% to 0.2% across all age groups, with a very strong bias towards old people, particularly those with co-morbidities. This rate does not exceed the range commonly observed with influenza, against which a vaccination of children and adolescents is not considered urgent or necessary.

1.1.2 COVID-19 has a particularly low prevalence and severity in children and adolescents. In the U.S. and as of April 2020, those younger than 18 years accounted for just 1.7% of all COVID-19 cases [3, 4]. Within this age group, the most severe cases were observed among very young infants [4]. This is consistent with the lack in infants of cross-immunity to COVID-19, which in other age groups is conferred by preceding exposure to regular respiratory human coronaviruses. Among slightly older children, a peculiar multisystem inflammatory syndrome was observed in early 2020 [5]; conceivably, these patients, too, were still lacking cross-immunity. Note, however, that some authors consider a post-infectious hypersensitivity mechanism more likely [6]; this would suggest a significant risk of adverse reactions to vaccination in such children also.

Similar findings were reported from China, with less than 1% of cases occurring in children younger than 10 years and another 1% in those 10 to 19 years of age [7]. Moreover, in this age group, disease tends to be very mild [4]. Thus, children and adolescents are at particularly low risk of harm from COVID-19 infection. Vaccination of of children and adolescents is therefore unnecessary.

1.1.3 COVID-19 can be treated. Numerous experienced physicians have collaborated on establishing effective treatment guidelines for clinically manifest COVID-19 [8]. Treatment options are available both for the early stage of the disease, at which emphasis is placed on inhibiting viral replication, and for the later stage, at which anti-inflammatory treatment is paramount. Two drugs that have been used successfully at the early stage are hydroxychloroquine and ivermectin. Both drugs have been, and continue to be, in use against a variety of other diseases. Ivermectin, for example, is considered safe enough to be used not only for treating manifest scabies—a parasite infection of the skin that is unpleasant but not severe—but even prophylactically in asymptomatic contacts of scabies-infected persons [9]. Considering that ivermectin reduces SARS-CoV-2 virus replication in cell culture by a factor of approximately 5000 [10], its favourable clinical effects are not at all surprising.

Ivermectin is also widely used in the treatment of tropical parasitic diseases such as onchocerciasis (river blindness), and for this reason it is on the WHO's list of essential medicines. Yet, with COVID-19, the WHO sees fit to warn against the use of this very same well-known and safe drug outside of clinical trials [11]. This policy cannot be rationally justified, and it has quite appropriately been overridden by national or regional health authorities and ignored by individual physicians worldwide.

The availability of effective treatment voids the rationale for the emergency use of vaccines on any and all age groups, including also adolescents.

1.1.4 Many people are by now immune to SARS-CoV-2. Due to the many inherent flaws and shortcomings of the diagnostic methods in common use [12–14], it is impossible to accurately determine the proportions of those who have already been infected with SARS-CoV-2 and those who have not. However, there are indications that the proportion of those who have been infected and acquired natural immunity is high:

- In a study conducted in early 2021, approximately 60% of randomly selected test persons from British Columbia have detectable antibodies against multiple SARS-CoV-2 proteins (personal communication by Stephen Pelech, University of British Columbia), indicating past infection with the virus—as opposed to vaccination, which would induce antibodies to only one (the spike) protein.
- Comparable numbers were more recently reported by Alejo et al. [15]: specific antibodies to the SARS-CoV-2 spike protein were detected in 99% of those with a confirmed history of COVID-19, in 55% who believed they had had COVID-19 but were never tested, and in 11% with no suspected history of the clinical disease.
- Protective immunity—possibly due to cross-immunity induced by respiratory coronaviruses other than SARS-CoV-2—likely exists in many individuals with no SARS-CoV-2 spike-specific antibodies, largely mediated by T-cells [16]. In this context, a recent study from the UK showed some very striking results [17]. The investigators experimentally inoculated 36 volunteers intranasally with a high dose of SARS-CoV-2. Even though all of these subjects had been pre-screened for having had no history of COVID-19 and no vaccination, only 18 subjects of the 36 became infected (and two more subjects were excluded due to pre-existing antibodies being detected post-hoc). This suggests that, even among those without a history and without specific antibodies, natural immunity is widespread.

Past COVID-19 infection has been found to protect very reliably from reinfection [18], and strong specific humoral and cellular immunity is detected in almost all recovered individuals, and also in those who remained asymptomatic throughout the infection [19]. Thus, a large proportion of individuals in all age groups, including adolescents, already have specific, reliable immunity to COVID-19. As mentioned above, most of those who do not have such specific immunity nevertheless are protected from severe disease by cross-immunity [20, 21]. This immunity will be particularly effective in healthy children and adolescents and young adults.

Individuals with specific immunity or sufficient cross-immunity will not derive any meaningful benefit from undergoing an experimental vaccination [22]. Indiscriminate vaccination regardless of pre-existing natural immunity cannot be rationally justified.

1.1.5 Asymptomatic transmission of COVID-19 is not relevant. An oft-cited rationale for vaccinating individuals who are not themselves at risk of severe disease is the need to induce

"herd immunity:" the few who are at high risk should be protected by preventing the spread of the virus in the general population.

A subtext of this rationale is the idea of "asymptomatic spread"—persons who have been infected but who show no signs of it other than a positive PCR test are assumed to transmit this infection to other susceptible individuals. If we accept the idea of such asymptomatic spread, then preventative mass vaccination might indeed appear as the only means of reliable protection of those at risk.

It has, however, been unambiguously determined that such asymptomatic transmission is not epidemiologically significant. In a large-scale study, which involved almost 10 million Chinese residents, no new infections could be traced to persons that had tested positive for SARS-CoV-2 by PCR, but who did not exhibit any other signs of infection [23]. This agrees with several studies that compared PCR to virus isolation in cell culture among patients with acute COVID-19 disease. In all cases, growth of the virus in cell culture ceased as symptoms subsided, or very shortly thereafter, whereas PCR remained positive for weeks or months afterwards [24, 25]. It was accordingly proposed to use cell culture rather than PCR to assess infectiousness and to determine the duration of isolation [25].

These findings indicate that restricting contact of persons at risk with those who show, or very recently showed, symptoms of acute respiratory disease would be effective and sufficient as a protective measure. Indiscriminate mass vaccinations of persons who are not themselves at risk of severe disease are therefore not required to achieve such protection.

2 The Pfizer and Moderna COVID-19 vaccines lack efficacy

2.1 What does the evidence show? Pfizer and Moderna persistently tout the 95% efficacy of their vaccines, based on the clinical trials that formed the basis of the emergency approvals granted by the FDA [26, 27] and the European Union [28, 29]. In Pfizer's [30] and Moderna's [31] more recent studies on adolescents, the claimed efficacy has been raised to no less than 100%. However, these claims cannot be taken at face value.

2.1.1 Absolute vs. relative efficacy. In Pfizer/BioNTech's first reported clinical trial, 43,548 participants underwent randomization, of whom 43,448 received injections. The experimental vaccine (BNT162b2) was administered to 21,720 persons, and 21,728 received placebo. Across both groups, a total of 170 COVID-19 "cases" was recorded, of which 162 occurred in the placebo group, whereas 8 were observed in the BNT162b2 group. Based on these figures—$^{8}/_{162} \approx 5\%$—Pfizer proceeded to claim 95% efficacy. Clearly, however, this efficacy is only a *relative* value—in absolute terms, less than 1% of the placebo group developed COVID-19, and therefore less than 1% of the vaccine group was protected from it.

The situation is similar with the subsequent, smaller test carried out on 12-15 years old adolescents [30]. Here, the vaccine group comprised 1131 individuals, whereas the placebo group included 1129 persons. In the latter group, 16 individuals were subsequently diagnosed with COVID-19, whereas no such cases occurred in the vaccine group. True to form, Pfizer/BioNTech converted this absolute efficacy of 1.4% to a relative one of 100%; only the latter value is highlighted in the abstract of the published study.

With Moderna's vaccine, the picture is essentially the same. In the first reported clinical trial, the experimental vaccine was administered to 14,134 persons, and 14,073 received placebo. Across both groups, a total of 95 COVID-19 "cases" was recorded, of which 90 occurred in the

placebo group, whereas 5 cases were observed in the vaccine group. Accordingly, Moderna presented this as evidence of 94.5% efficacy. However, less than 0.6% of the placebo group developed COVID-19, and therefore less than 0.6% of the vaccine group was protected from it. In their subsequent study on 12-17 years old adolescents [31], the vaccine group comprised 2163 individuals, whereas the placebo group included 1073 persons. In the latter group, a grand total of four (4) individuals were subsequently diagnosed with COVID-19; none of these cases were severe. No COVID-19 cases were detected in the vaccine group. True to form, Moderna converted this absolute efficacy of 0.37% to a relative one of 100%.

2.1.2 Negative impact of the Pfizer and Moderna COVID-19 vaccines on overall morbidity in adolescents. In Pfizer's cited vaccine study on adolescents, a "case" of COVID-19 was determined as follows:

> *The definition of confirmed COVID-19 included the presence of ≥ 1 symptom (i.e., fever, new or increased cough, new or increased shortness of breath, chills, new or increased muscle pain, new loss of taste or smell, sore throat, diarrhea, vomiting) and being SARS-CoV-2 NAAT-positive [=PCR-positive] during, or within 4 days before or after, the symptomatic period (either at the central laboratory or at a local testing facility and using an acceptable test).*

Thus, a single symptom from a laundry list of non-characteristic symptoms, plus a positive finding from an unreliable PCR test [12–14], was deemed sufficient to establish the diagnosis. While the study goes on to list several clinical criteria of severe disease, it gives no indication that any test persons actually suffered any of those. It can therefore be assumed that very few non-severe, and no clinically severe cases of COVID-19 occurred in the entire test population.

In stark contrast to these numbers pertaining to the disease from which the vaccination is supposed to protect, side effects from the vaccination were exceedingly common. Apart from injection site pain occurring in a high percentage of the vaccine group (79% to 86%), fatigue (60% to 66%) and headache (55% to 65%) abounded. Severe fatigue and headache were reported by several percent of the test persons. Severe headache, in particular, may be associated with underlying thrombotic events (see Section 3.2.3). It is therefore clear that, if we consider both COVID-19 and vaccine adverse effects, overall morbidity was far greater in the vaccinated than in the placebo group.

Much the same observations apply to the Moderna study on adolescents [31], too—as already noted, none of four COVID-19 cases in the control group were severe, whereas significant side effects were even more common than in the Pfizer study.

2.1.3 Unlikely claims and outright contradictions in Pfizer's evidence on efficacy. We saw above that the reported efficacy of Pfizer's vaccine is very modest when expressed in absolute terms. Even this low efficacy, however, cannot be accepted at face value. This is apparent from the assessment reports prepared by the FDA [26] and the EMA [28].

Sudden onset of immunity on day 12 after the first injection. A key illustration that occurs in both reports compares the cumulative incidence of COVID-19 among the vaccinated and the placebo group. This graph, which is shown as Figure 9 in the EMA report, is here reproduced in Figure 1A. Up to day 12 after the first injection, the cumulative incidences in the two groups track each other closely. After day 12, however, only the placebo group continues to accumulate

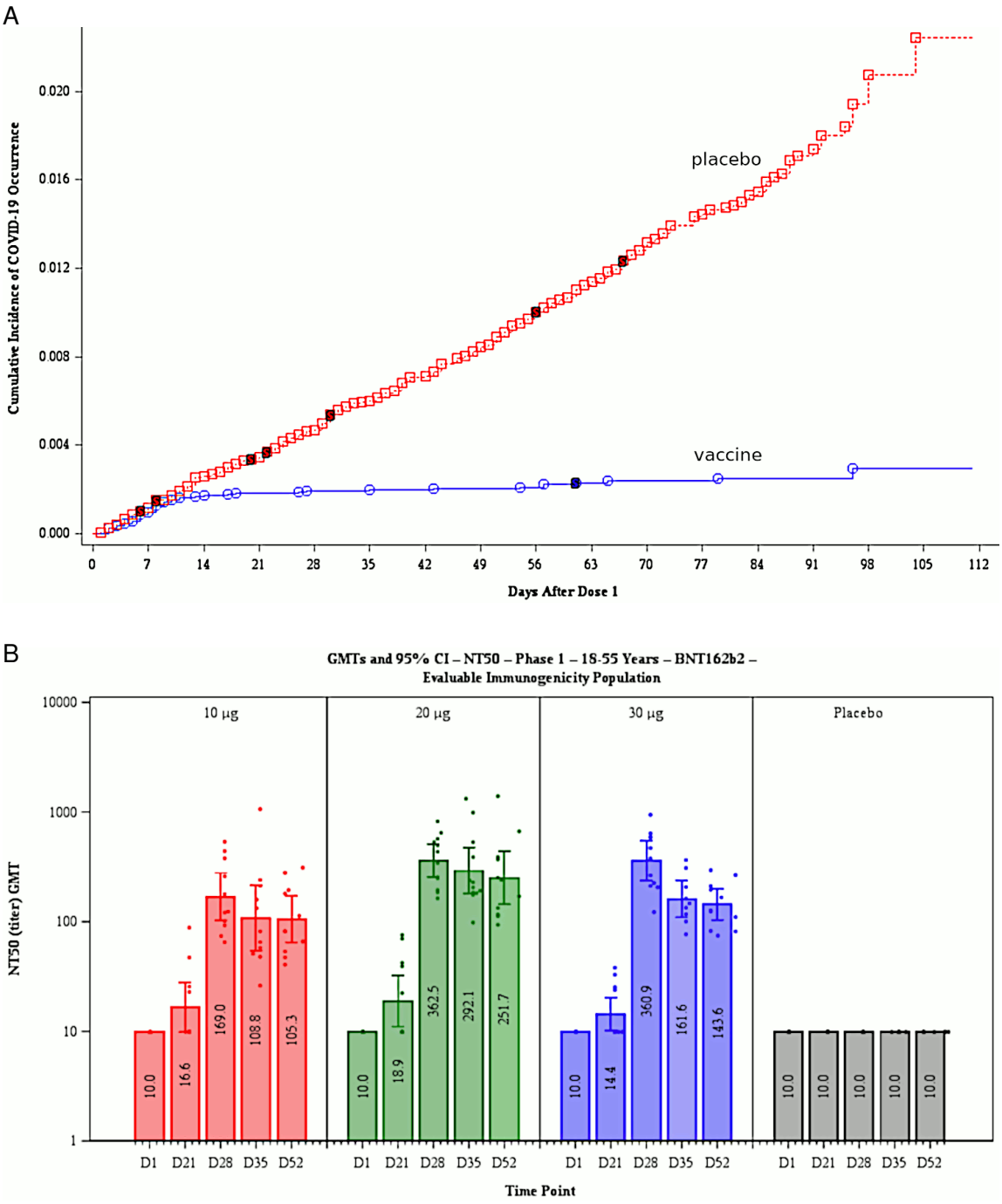


Figure 1 Reproduction of Figure 9 (A; cumulative incidence of COVID-19 among vaccinated and placebo groups) and of Figure 7 (B; neutralizing antibody titres on various days after the first injection) from the EMA assessment report [28]. Note the logarithmic y axis in B. See text for discussion.

further new cases at a steady pace, whereas the slope of the graph drops to almost zero in the vaccine group.

This remarkable observation suggests that immunity sets in very suddenly and uniformly on day 12 exactly among the vaccinated. Since the second injection occurred 19 or more days after the first one, this would imply that one injection is enough to establish full immunity.

Table 1 Subjects without evidence of infection in vaccine and placebo groups at various time points in the clinical trial. Data excerpted from Table 4 in [28]. See text for discussion.

	Vaccine	Placebo
No evidence of infection before dose 1	93.1%	93.0%
No evidence of infection prior to 14 days after dose 2	85.6%	85.0%
Difference (= infection between day 0 and day 14 after dose 2)	7.5%	8.0%

This conclusion, however, is not stated, and in fact Pfizer does not report any data at all on test persons who received one injection only.

A sudden onset of full immunity on day 12 after the first exposure to the antigen is not at all a biologically plausible outcome. Typically, immunity develops more slowly and gradually; and such a pattern is in fact reported for this very same vaccine (Pfizer COVID-19 vaccine) in Figure 7 of the EMA report, reproduced here as Figure 1B. The figure shows the increase of neutralizing antibodies to SARS-CoV-2 as a function of time after the first injection of the vaccine.

The induction of neutralizing antibodies is the declared purpose of the Pfizer vaccine. Generally speaking, antibodies are protein molecules produced by our immune system when it encounters *antigens*—macromolecules that do not occur within our own bodies. These antigens are often part of infectious microbes, including viruses. An antibody binds to a specific feature on the surface of its antigen; this feature is called the *epitope* of the antibody in question.

In the context of virus infections, antibodies can be neutralizing or non-neutralizing. A neutralizing antibody recognizes an epitope that is essential for the function of the virus, for example because this epitope must make contact to a *receptor* molecule on the surface of the host cell which the virus must enter in order to replicate. A non-neutralizing antibody simply happens to recognize a surface feature (epitope) that plays no essential role in the infectiousness of the virus.

Considering the foregoing, we should expect that the blood level of neutralizing antibodies should reflect the degree of clinical immunity to the virus. This is, however, not at all what we see in Figure 1B. On day 21 after the first injection, that is, a full 9 days after the purported sudden onset of full clinical immunity, the amount of neutralizing antibodies in the blood has barely risen above the background level. The maximal level of neutralizing antibodies is observed only on day 28 after the first injection, at which time most test persons would already have had their second injection. The time course of cellular (T-cell) immunity was not reported, but in the absence of proof positive to the opposite it can be assumed to resemble that of the antibody response.

It is very difficult to reconcile the two contrasting observations of sudden onset of full clinical immunity on day 12, but neutralizing antibodies appearing only weeks later. Yet, neither the EMA reviewers nor those of the FDA appear to have been interested in the problem.

The Pfizer documentation contradicts itself on COVID-19 incidence after vaccination. Table 1 lists the percentages of subjects in the vaccine group and the placebo group who showed no evidence of SARS-CoV-2 infection on day 0 (before the first dose) and on day 14 after the second dose, respectively. From the differences between the two time points, we can work out that 7.5%

Table 2 Incidence of COVID-19 among subjects not previously infected but vaccinated, or previously infected but not vaccinated. Data excerpted from Tables 6 and 7 in [26]. See text for discussion.

	Vaccine			Placebo		
	Total	Cases	Incidence (%)	Total	Cases	Incidence (%)
All subjects	19965	9		20172	169	
Initially negative	**18198**	**8**	**0.044**	18325	162	
Previously infected	1767	1		**1847**	**7**	**0.38**

of the subjects in the vaccine group and 8% in the control group converted from negative to positive—that is, became infected—between the two time points.

According to [26], the second dose was administered approximately 21 days after the first, although all subjects who received it between days 19 and 42 after the first injection were included in the evaluation. If we take day 35 after the first injection as the approximate time point of the comparison, we see from Figure 1A that the cumulative incidence between day 0 and day 35 is more than twice higher in the placebo group than in the vaccine group; but from Table 1, we see that it is almost the same. Moreover, with both groups the numbers are substantially higher in the table than in the figure.

These two sets of data cannot possibly be reconciled; one must be false. Since, as discussed, the sudden onset of immunity implied by Figure 1A lacks any biological plausibility, it is most likely that it is this data set which was fabricated.

Pfizer's data imply that the vaccine protects from COVID more effectively than does prior infection with the virus. We can also scrutinize Pfizer's reported data in order to compare the immunity conferred by the vaccine to that induced by prior natural infection with the virus. The relevant data are summarized in Table 2. The reported 8 cases of COVID-19 among vaccinated persons who had initially tested negative for the virus amount to an incidence of 0.044%. Pfizer also reports 7 cases among persons who had initially tested positive but were not vaccinated. Since this group is considerably smaller, those 7 cases translate into an almost ninefold higher incidence (0.38%).

It is common knowledge that vaccines will at best approach, but not surpass the immunity conferred by the corresponding natural infection. Very robust immunity after prior natural infection with SARS-CoV-2 has recently been reported [18]; in that study, not a single case of COVID-19 was observed among 1359 individuals who had remained unvaccinated. Robust immunity after infection is also confirmed by comprehensive laboratory investigations [19]. A very recent study from Israel directly compared protection from reinfection by natural immunity and by vaccination, respectively, and found that the former was clearly superior [32]. We note that Israel mostly uses the Pfizer vaccine. Therefore, the above analysis corroborates yet again that the trial results reported by Pfizer cannot be trusted. That neither the FDA nor the EMA picked up on any of these inconsistencies does not instil confidence in the thoroughness and integrity of their review processes.

Allegations of irregularities in Pfizer's clinical trials by contractors. Several individuals who had carried out contract work for Pfizer in the clinical trials spoke to the British Medical Journal

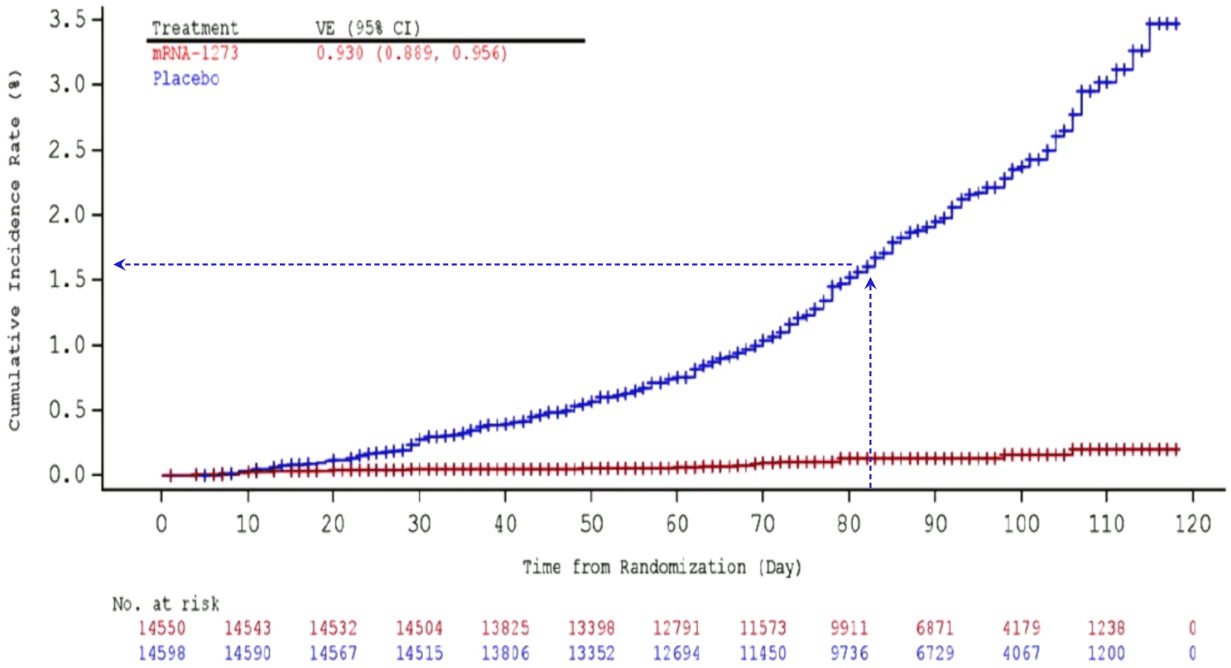


Figure 2 Reproduction of Figure 18 of the EMA assessment report [29]; arrows added by the authors of this document. The figure is said to show the cumulative incidence of COVID-19 cases among vaccinated and placebo groups in the clinical study on the Moderna COVID-19 vaccine. See text for discussion.

about irregularities such as poor laboratory management, delayed and intentionally falsified data entry, and altogether missing follow-up examinations on symptomatic patients [33]. One of them summed it up as follows: "I don't think it was good clean data . . . It's a crazy mess."

2.1.4 Unlikely claims and contradictions in Moderna's evidence on efficacy. Close scrutiny of the EMA assessment report on the Moderna COVID-19 vaccine [29] Moderna's reveals a similar pattern of exaggeration and inconsistencies.

Contradictory claims about COVID-19 incidence in clinical trials. The text of the EMA document maintains that in all 90 "cases" of COVID occurred in the placebo arm of the study. On the other hand, the study also shows a graph that is said to represent the cumulative incidence of COVID in both the vaccine and the placebo group (Figure 2). At the bottom of this graph, we see the number of individuals at risk of becoming COVID "cases" at various time points after their assignment to either group; from Table 20 in [29], we can infer that this time point coincides with the first injection. The number of those at risk decreases with time; for example, 9,911 persons in the vaccine group, and 9,736 in the placebo group, were followed during the trial for 80 days or more and were therefore at risk of contracting COVID on day 80. We can estimate that this number would have dropped to 9,000 on or about day 82. Therefore, if all 90 COVID cases had been diagnosed on day 82, then the cumulative incidence should on this day be 1%. However, the dashed arrows drawn atop the graph indicate that the depicted value on this day is approximately 1.6%.

Cases diagnosed before day 82 would have occurred among a larger number of individuals at risk, which should have lowered the cumulative incidence on day 82. Furthermore, the curve continues to rise after day 82, which implies that some of the altogether 90 cases occurred at

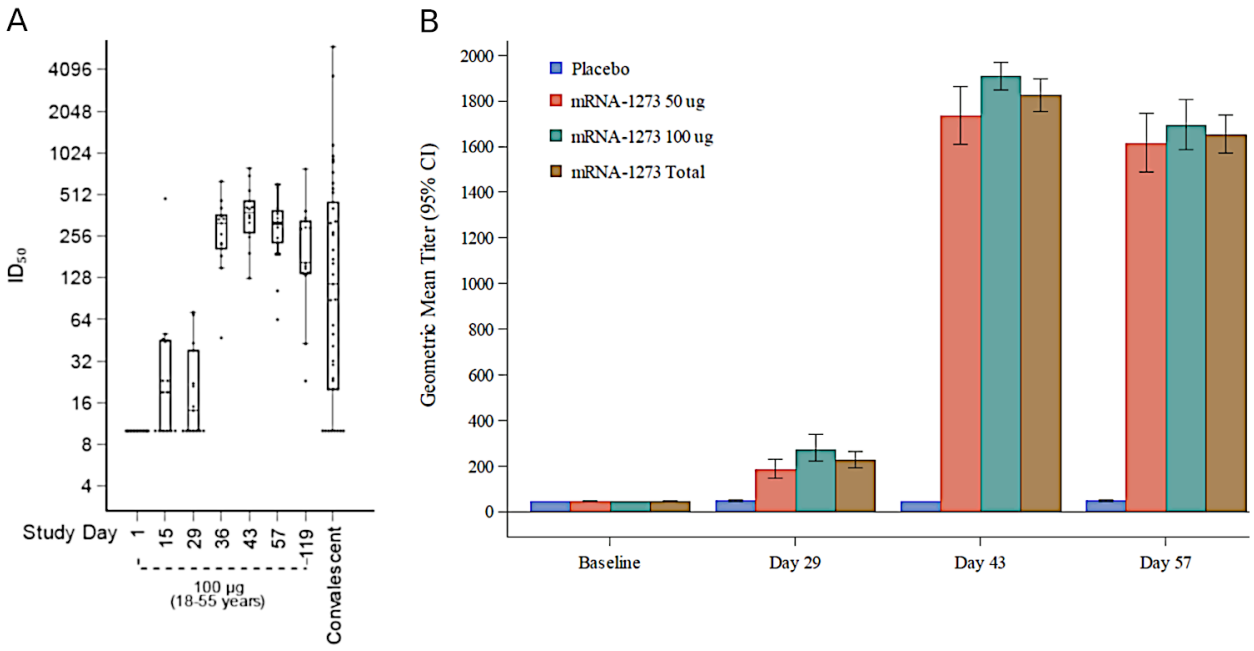


Figure 3 Neutralizing antibodies at various time points after vaccination. A: Box plot of pseudovirus neutralization titres (adapted from Figure 7 of [29]. Note that on days 15 and 29 multiple samples remain below the detection limit; only on day 36 are neutralizing antibodies detected in all samples. Note also multiple negative samples among convalescent individuals. B: Geometric means of neutralizing antibodies. Adapted from Figure 16 of the EMA report. All data pertain to the age group between 18 and 55 years.

a later time. This should further reduce the cumulative incidence observed on day 82. Thus, while the available information does not permit us to quantify the discrepancy exactly, we can say that it is substantial. That the EMA reviewers did not catch this rather obvious problem does not instil confidence in the thoroughness of their assessment process.

Early vs. late onset of immunity. According to Figure 2, new COVID cases accumulated at the same pace within the placebo group and the vaccine group until day 12 or 13. Thereafter, they diverge, indicating the onset of immunity in the vaccinated; and the uniformly low increase with time of the cumulative incidence among the vaccinated suggests that the maximum extent of immunity was attained within a very short time period. Such an early onset of immunity is not expected after the first exposure to an antigen; instead, it is typical of a memory reaction. The occurrence of memory reactions would fit with the many observations of cross-immunity reported in other studies (see Section 1.1.4 above). However, Moderna's own data indicate that only some, but not all test persons showed a memory response; on days 15 and 29 after the first injection, the titres of neutralizing antibodies remained low overall, and in what appears to be about half of the individuals below the detection limit (see Figure 3A). Nor can Moderna's reported data on T-cell-mediated immunity account for the rapid onset of clinical immunity: Figure 4 shows that any activation of T-cells is weak and is observed only on day 43, that is, after the second injection. This applies in particular to CD8 cells, which are crucial effectors of cellular antiviral immunity. Thus, an obvious discrepancy exists between the early onset of the claimed clinical immunity and the delayed responses observed in immunological laboratory

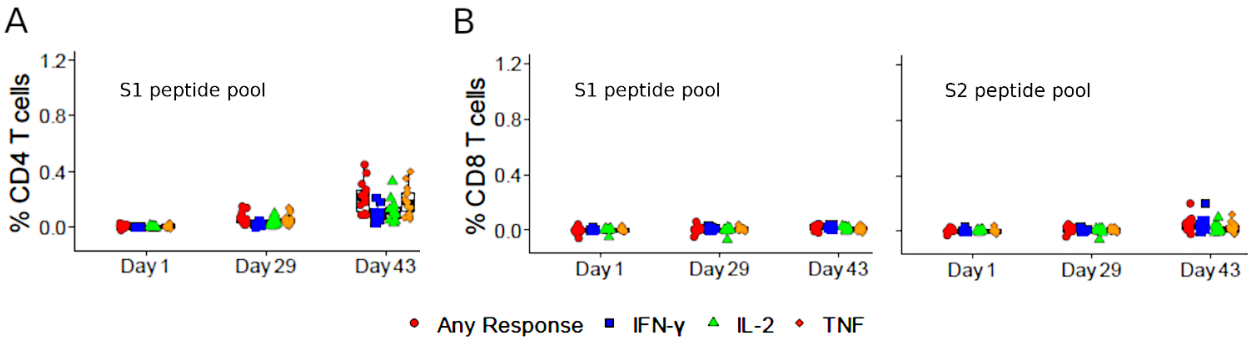


Figure 4 T-cell activation by the Moderna COVID-19 vaccine. CD4 and CD8 cells were isolated at various time points after the first injection and stimulated in vitro with peptide pools representing the S1 or the S2 fragments of the spike protein and stained for expression of IFN-γ, IL-2, and TNF. A: activation of CD4 cells. Adapted from Figure 10 of [29]. B: activation of CD8 cells. Adapted from Figures 11 and 12 of the EMA report. All data pertain to vaccine doses of 100 µg and the age group between 18 and 55 years.

studies. Had the EMA review been conducted with due diligence, this discrepancy would not simply have been passed over.

2.2 What evidence is lacking to make the case? We had already noted the specious and contrived character of the endpoint used in Pfizer's and Moderna's clinical trials—namely, the counting of a COVID-19 "case" based on nothing more than a positive PCR result, together with one or more items from a list of mostly uncharacteristic clinical symptoms. We must therefore ask if the vaccine provides any benefits that are more substantial than the claimed—but, as discussed above, most likely fabricated—reduction in the count of such trivial "cases."

2.2.1 Prevention of severe disease and mortality. Page 48 of the FDA report on the Pfizer COVID-19 vaccine [26] sums up this question as follows:

> *A larger number of individuals at high risk of COVID-19 and higher attack rates would be needed to confirm efficacy of the vaccine against mortality.*

Moderna's study on adults [29] reports that 30 cases of "severe disease" occurred in the placebo group, and none in the vaccine group. The report states that

> *The majority of the severe cases were adjudicated as such based on SpO_2 [blood oxygen saturation] below the defining threshold of 93% for varying duration. Whereas reassuring for efficacy across varying disease severity, the cases overall seem mostly mild, which is a limitation of the dataset.*

The normal range of arterial blood saturation with O_2 is 95 to 100%; therefore, the use of a cut-off as high as 93% to diagnose a "severe" case seems questionable. It is noteworthy that only nine of these "severe" cases were hospitalized, and only two required admission to the intensive care unit (one of these two patients died). Thus, the number of truly severe cases possibly prevented by the vaccine is very small at best. The single fatal case does not suffice to prove efficacy against death.

No fatalities at all occurred in the cited study on adolescents [31]; and we already noted that this study does not report any cases of severe disease either. Therefore, in this specific age group, too, neither a meaningful benefit nor an emergency are in evidence.

We note that the collective findings not only answer the posed question in the negative, but it also disposes of the entire pretext for granting emergency use authorization for these experimental vaccines. If in studies that involve some 30,000 or even 40,000 individuals the number of fatal outcomes is too small to permit the detection of any benefit of the vaccine, then surely no "emergency" exists that would justify the very grave risks, and meanwhile manifest harm, associated with the extraordinarily rushed introduction of these and other COVID-19 vaccines.

No fatalities at all occurred in the cited studies on adolescents [30, 31]; and we already noted that these studies do not report any cases of severe disease either. Therefore, in this specific age group, too, neither a meaningful benefit of vaccination nor an emergency are in evidence.

2.2.2 Effectiveness for those at high-risk of severe COVID-19. Here, the FDA report on the Pfizer COVID-19 vaccine has this to say:

> *Although the proportion of participants at high risk of severe COVID-19 is adequate for the overall evaluation of safety in the available follow-up period, the subset of certain groups such as immunocompromised individuals (e.g., those with HIV/AIDS) is too small to evaluate efficacy outcomes.*

The report shirks the question of risk reduction among those with more common predisposing conditions, such as for example chronic heart or lung disease. Naturally, the clinical study on adolescents [30] is completely barren in this regard. Overall, no evidence has been adduced by Pfizer's clinical studies to prove clinical benefit in those at high risk of severe COVID-19.

2.2.3 Effectiveness against long-term effects of COVID-19 disease. The FDA report's verdict is as follows:

> *Additional evaluations will be needed to assess the effect of the vaccine in preventing long-term effects of COVID-19, including data from clinical trials and from the vaccine's use post authorization.*

In other words, the clinical trials provided no such evidence.

2.2.4 Reduction of transmission. On this topic, the FDA report offers only that

> *. . . additional evaluations including data from clinical trials and from vaccine use post-authorization will be needed to assess the effect of the vaccine in preventing virus shedding and transmission, in particular in individuals with asymptomatic infection.*

In plain language, there is no evidence that transmission is reduced, and in fact the trials were simply not even designed to prove or disprove such an effect.

2.2.5 Duration of protection. The FDA on the Pfizer COVID-19 vaccine report correctly states (on page 46) that

> *as the interim and final analyses have a limited length of follow-up, it is not possible to assess sustained efficacy over a period longer than 2 months.*

Even if we choose to believe that any efficacy at all has been demonstrated pertaining to the two-month study period, such a short duration of protection does not justify the risks associated with vaccination. Regarding the Moderna COVID-19 vaccine, the EMA report states [29, p. 110]:

It is presently not known if the vaccine protects against asymptomatic infection, or its impact on viral transmission. The duration of protection is not known.

The clinical trials indeed made no provisions for determining any effect on transmission; and the duration of protection (if any) could of course not be ascertained within such a short time. However, as noted above, the failure of the vaccine in the real world has since become apparent (see Section 2.3.4).

2.2.6 Inadequate efforts to determine the optimal dose. Figure 1B shows that the level of neutralizing antibodies by the Pfizer COVID-19 vaccine is virtually the same with vaccine (mRNA) doses of 20 µg and 30 µg, respectively. This raises the question why the higher dose was employed throughout—and not only with adults, on whom these data were obtained, but also with children as young as 12 years, whose lower body weights should suggest a dose reduction. Furthermore, the data in Figure 1A suggest that full immunity is induced already by the first dose; application of the second dose does not change the pace at which new cases accrue in the vaccine group, and therefore apparently has no effect on immunity. This would imply that a one-dose regimen should have been evaluated, which would reduce the overall likelihood of adverse events.

Moderna tested several different doses of the Moderna COVID-19 vaccine (10, 25, 50 100, and 250 µg). The EMA report does not lay out all findings with all dose groups, but it does show that there is very little difference in the levels of neutralizing antibodies with 50 and 100 µg, respectively (see Figure 3B); and the same applies to T-cell activation after doses of 25 or 100 µg (see Figures 10 to 12 in the EMA report). All of these findings suggest that lower dose regimens would provide levels of immunity very similar to that of the 100 µg dose that was ultimately selected. (Of note, a dose of 30 µg was selected for the Pfizer mRNA vaccine, which is very similar in nature to Moderna's vaccine.) Thorough and comprehensive dose-finding studies should therefore have been carried out. This is of particular significance with children.

Furthermore, the graph shown in Figure 2 shows no decrease in cumulative incidence among the vaccinated after 30 to 50 days. Accordingly, the second injection, which was administered on or about day 28 after the first, has no detectable effect on clinical immunity. This observation should have prompted the evaluation of a single-dose regimen, since omitting the second injection could significantly reduce the incidence of adverse events. However, on page 109 of the EMA report [29], we read:

No definitive conclusion on clinical efficacy after one dose can be drawn based on the very short time window between the two doses and consequently very few cases.

In other words, no separate trial group was established to evaluate the efficacy of a single-dose regimen.

2.2.7 Summary. The clinical trials carried out by Pfizer and Moderna contain no proof of any meaningful benefit conferred by the vaccine with respect to any clinically relevant endpoints. This applies to all tested age groups, and in particular also to adolescents. Some evidence on the efficacy of the vaccines in the real world will be considered in the next section.

2.3 Can the current types of COVID-19 vaccines be expected to effectively stop infection and transmission? While scrutinizing the documentation supplied by the manufactures is important, we should also look at the question of vaccine efficacy from a more fundamental van-

tage point. Generally speaking, there are several different possible rationales for vaccination. In decreasing order of stringency, the aim may be that vaccinated persons

1. be completely protected from becoming infected;
2. have a significantly reduced probability of becoming infected;
3. be completely protected from a severe clinical course of the infection;
4. have a significantly reduced probability of a severe clinical course.

Quite obviously, vaccination can only stop the transmission of a virus such as SARS-CoV-2 if efficacy rises at least to level 2; and moreover, the probability of infection must be reduced to such an extent that it becomes feasible, with a high enough vaccination rate of the population, to push the *basic reproductive number* to a value below 1. This parameter represents the number of new cases caused, on average, by transmission of the virus from a single established case. When it comes to mandating vaccination "for the sake of others," then we only need to consider the vaccines' efficacy against transmission, and we can set aside the question of whether they can prevent severe disease.

Next, we can ask what general rules govern the duration of immunity against respiratory viruses, and what these rules imply for vaccination against SARS-CoV-2. We know from experience that natural immunity against some viruses lasts a lifetime. The best examples are childhood diseases such as measles, rubella, and also chickenpox, even though the latter can stage a resurgence later in life, which in most cases takes the form of shingles. On the other hand, people are often infected with type A influenza virus multiple times in the course of their lives. How can we understand this discrepancy?

2.3.1 Genetic variability of viruses. A key determinant of the duration of natural immunity is the rate of genetic variation of the virus in question. Like any other life form, viruses are subject to genetic mutations, which in turn are subject to natural selection. Those mutations which increase fitness—in case of a virus, the ability to infect human hosts with immunity to the non-mutated strain of the virus—will be retained, whereas those which decrease fitness will be weeded out.

Both measles virus and influenza virus have single-stranded RNA genomes, and therefore in principle have high rates of mutation. Nonetheless, measles virus shows very low genetic variability. Apparently, this virus reached an optimum of fitness a long time ago; and accordingly, only very few of the mutations that arise anew are beneficial to the virus and are therefore retained. This very low rate of change implies that immunity acquired in early childhood will recognize the virus and protect us from it throughout life.

In contrast, genetic change in influenza viruses shows a rather different pattern. With this virus, we distinguish two different kinds of mutational events, respectively referred to as *antigenic shift* and *antigenic drift*. In an antigenic shift event, entire genes are swapped between two distantly related strains of influenza virus, which usually have different but overlapping host species ranges. Through this genetic *reassortment*, an influenza virus strain that is infectious for humans can acquire a major antigenic determinant from another virus strain that only occurs in animal species. This swap would occur within an animal host, often a pig, that can be infected by both strains.

On the one hand, then, the lack of pre-existing immunity to this newly acquired animal-derived antigen in the human population will permit the *reassortant* virus strain to spread very

effectively and cause a new pandemic wave. On the other hand, the animal-derived antigen will not be well-adapted to human hosts. This means that spontaneous mutations that occur within this newly acquired gene will have a relatively high likelihood of being adaptive and therefore retained. The result will be a rapid accumulation of incremental changes to the protein's antigenic properties. These cumulative changes constitute the antigenic drift. The pace of antigenic drift is fast enough to threaten obsolescence of last year's flu shot in every new flu season.

The question then arises which of these two paradigms applies to SARS-CoV-2, the coronavirus strain which causes COVID-19. On the one hand, its genome does not have the peculiar (segmented) structure which facilitates the wholesale swapping of genes (reassortment) observed with influenza virus strains. On the other hand, the very recent "emergence" of SARS-CoV-2 in the human population means that many of its genes should have a large scope for incremental optimization, and accordingly for rapid antigenic drift.[1] Two years into the COVID-19 pandemic, this expectation has clearly been borne out by the emergence of several SARS-CoV-2 variants in quick succession (see Section 2.3.3 below).

2.3.2 Vaccine-induced vs. natural immunity. Typically, the duration and reliability of immunity conferred by vaccination will at best approach, but not exceed the natural immunity which arises after infection with the corresponding pathogenic virus itself. This is illustrated in a study by Bianchi et al. [39], who directly compared serum antibody titres between persons that had been vaccinated against measles and others with a history of the disease itself. Moreover, multiple studies on highly vaccinated populations have found a certain rate of "breakthrough" measles infections that led to local outbreaks; see for example [40–43].

With influenza, the general recommendation to take booster injections every year implies very low expectations for the duration of vaccine-mediated immunity. By analogy, then, we should expect a similar trajectory with SARS-CoV-2—rapid obsolescence of the vaccines as new variants arise.

2.3.3 SARS-CoV-2 variants in Italy. During the year 2021, three major SARS-CoV-2 variants emerged in Italy, according to whole genome sequencing data curated by a research consortium at the Scripps Institute [44]. The time course of these changes is shown in Figure 5. The Alpha variant arose in early 2021. In mid 2021, it was displaced by Delta, which was dislodged in turn in December 2021 by the Omicron variant. The latter currently continues to be responsible for most new cases. This situation is very similar in other parts of the world. Thus, for practical purposes, we could focus on vaccine efficacy against Omicron alone, but Delta will be considered below as well.

2.3.4 Recent studies on the efficacy of COVID vaccines. Data published by Israel's health ministry during the summer of 2021 indicated that COVID was equally likely to occur in vaccinated and unvaccinated persons, which suggests that the true efficacy at the time was not 95% but rather close to 0%. The same is evident from a CDC report by Brown et al. that examined a cluster of COVID infections which occurred in Barnstable County, Massachusetts during July

[1] Readers may be aware of the controversy surrounding the true origin of SARS-CoV-2. While for a long time the predominant narrative was that the virus arose naturally in a species of bats [34] or possibly in pangolins [35], a thorough analysis of the genome sequences of SARS-CoV-2 and of related virus strains indicates unambiguously that the virus is in fact of artificial origin [36–38]. Without going into further detail, we only note here that the conclusion of SARS-CoV-2's large scope for incremental optimization holds regardless of which of the two competing narratives is correct.

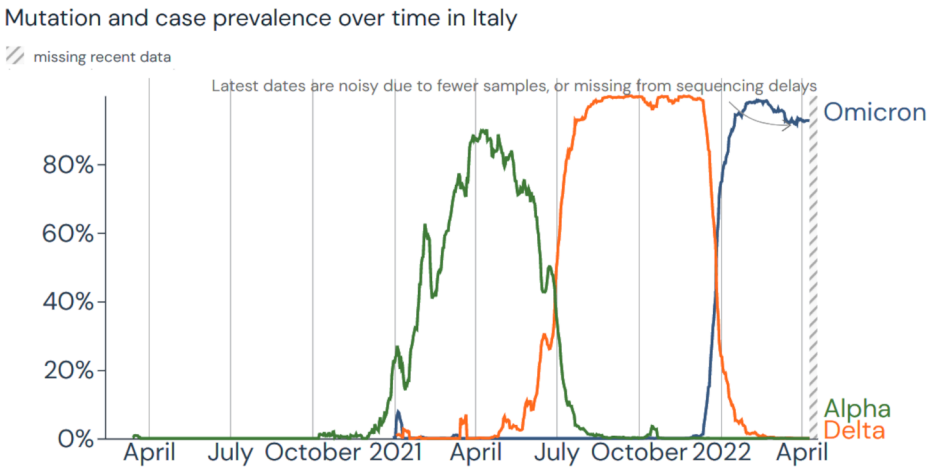


Figure 5 Distribution of variants of SARS-CoV-2 in Italy, during 2021 and 2022, according to sequencing data. Plot obtained from [44] on April 18, 2022. The Delta variant displaced the Alpha variant in mid 2021 but was itself displaced by the Omicron variant in the course of December 2021. Omicron has since remained dominant.

2021 [45]. Both vaccinated and unvaccinated persons were affected. The data from this study are summarized in Table 3. The relative risk of hospitalization stated in the table is based on a total of only 5 cases and therefore is not statistically robust. We note, however, that this low number of hospitalized cases indicates a rather low disease severity overall. Of particular interest in this connection is that most of these cases appear to have been due to the Delta variant, which was identified in 89% of those 133 cases where the viral RNA was characterized by genomic sequencing.

Brown et al. do not state whether the Delta variant was overrepresented among the "breakthrough" cases in vaccinated persons; thus, the limited data provided in this study do not rule out the possibility that the vaccine might have been somewhat more effective with the original Wuhan strain of SARS-CoV-2 or with the Alpha variant. Be that as it may, however—as we noted above, it has become clear that SARS-CoV-2 is subject to rapid antigenic drift. Even if we assume that the vaccines had been active against the Wuhan strain or early variants, their obsolescence due to antigenic drift within mere months of their introduction would suffice to make them useless in practice.

Brown et al. state that all of their reported cases were "associated with large public gatherings," which suggests that most of the affected persons were in a reasonable state of health before contracting the infection. Other studies have reported vaccine "breakthrough" cases of infection both among the healthy [46] and among those with pre-existing neurological disease [47]. Overall, the study indicates that the vaccines are failing.

Further evidence of the vaccines' lack of efficacy is provided by a statistical overview of 68 countries, in which the incidence of COVID-19, within the week before September 3, 2021, was correlated to the vaccination rate of the population [48]. The results are summarized in Figure 6. The vaccination rate ranges from 0% to 80%; thus, if vaccination could indeed reduce the spread of the disease, this should be evident in the graph. Instead, we see that the incidence of COVID-19 actually goes up with the vaccination rate; but the correlation is very week. Overall, it is clear that this large-scale comparison fails to show any protective effect of vaccination.

Table 3 COVID infections detected among vaccinated and unvaccinated persons in Barnstable County, Massachusetts between July 5th and 26th 2021. Data from [45].

	Cases % (n)	Population %	Relative risk
Unvaccinated	26% (123)	31%	0.85
Pfizer vaccine	34% (159)	39%	0.88
Moderna vaccine	28% (131)	26%	1.07
Johnson & Johnson vaccine	12% (56)	4.8%	2.47
Any vaccine	74% (346)	69%	1.07
Hospitalized (any vaccine)	80% (4)	—	(1.29)

Very recently, Beattie reported a comparative "big data" analysis on how COVID-19 morbidity and mortality changed in altogether 145 countries after the onset of vaccinations, compared to a "basket" of countries in which vaccination rates were negligibly low [49]. He found that mortality showed a significant decrease in 13 countries, but increased significantly in 115 countries; similarly, infection rates decreased significantly in 16 countries but increased significantly in 105 others. Changes were not significant in the remaining countries. Of note, Beattie's study includes data up to November 2021, and therefore should include a large number of infections with the Delta but likely not yet significant case numbers of the Omicron variant.

2.3.5 Vaccine efficacy against the Delta and Omicron variants. In Section 2.3.4, we already discussed several studies that fail to detect any real world efficacy; these studies were recent enough to comprise the Delta variant. Some other studies, however, report some reduction in susceptibility to infection with the Delta variant after vaccination. Ng et al. [50] carried out a retrospective study in Singapore to trace infections and outcomes among 1024 contacts of 301 PCR-confirmed index cases; of these 1024 contacts, the majority (753) were exposed to an index case that had been identified as Delta. The rate of infection was approximately twice higher among unvaccinated than among vaccinated contacts, which would indicate an efficacy against infection of approximately 50%. Secondary infections were not significantly affected by the vaccine status of the index case, which means absence of effectiveness against transmission. Very similar findings, but with somewhat higher infection rates among both vaccinated and unvaccinated secondary contacts, were reported in a prospective study from England [51].

As noted above, the Delta variant has very recently been displaced in many or most countries, including Italy, by the Omicron variant. Omicron is even more highly mutated than Delta [52, 53] and therefore less likely to be protected against by the existing vaccines. Two very recent studies cover vaccine efficacy against both of these variants [54, 55]. Both find significant efficacy against Delta, but much weaker and rapidly fading efficacy against Omicron—in fact, Buchan et al. [55] report that efficacy against Omicron turns *negative* at 60 days after the second injection, and Hansen et al. [54] find the same after 90 days. Since Omicron is now the dominant variant worldwide, none of the mutually incompatible data sets on vaccine efficacy against the Delta variant should at present form the basis of decisions on mandating vaccinations.

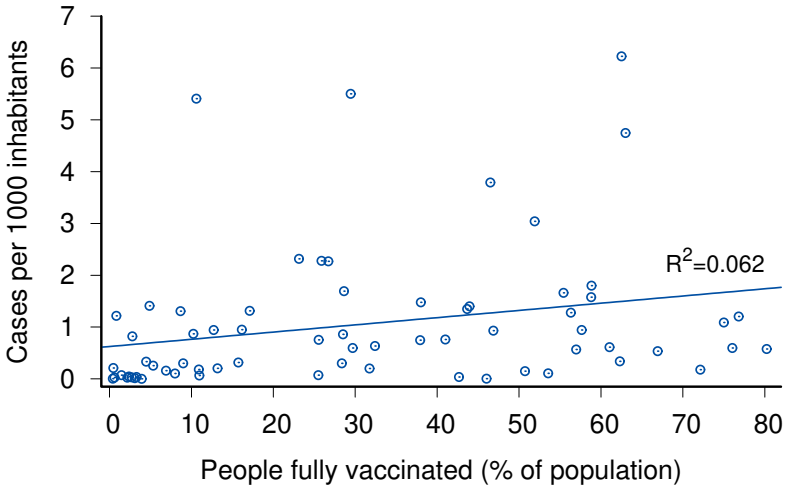


Figure 6 COVID-19 cases per 1000 residents versus vaccination rate of the population by country. Each data point represents one country of 68 overall. Cases were counted within the week ending on or shortly before September 3rd, 2021 [48].

2.3.6 Mucosal vs. systemic immunity. Thus far, we have discussed properties of the SARS-CoV-2 virus itself which limit the prospects for lasting immunity through vaccination. In addition to these, we must also ask whether the strategy adopted with the existing vaccines is really suitable for inhibiting infection and transmission.

Airborne viruses that invade the mucous membranes of the respiratory tract can be countered by the immune system right then and there, or, should they manage to breach the mucosal barrier, within the bloodstream and the tissues inside the body. The mucosal defence consists largely of secretory antibodies (of the IgA isotype), whereas the systemic immune response involves various types of non-secretory antibodies (IgM, IgG, IgA), cytotoxic T-cells, and some other types of effector cells.

The mucosal and systemic subsystems of the immune system are complementary—neither can fully compensate for the other. Secretory IgA is essential for suppressing the local propagation of a virus within the mucous membranes, whereas systemic immunity guards against the spread of such an initially local infection through the bloodstream. It is important to note that secretory IgA will be induced efficiently only by local application of the antigen to the mucous membranes, but not by intramuscular or subcutaneous injection [56, 57]. A careful recent study on MERS, which like COVID-19 is caused by a coronavirus, has confirmed this yet again [58]. Below is a trenchant quote from the earlier review paper by McGhee et al. [56]:

> *It is surprising that despite our current level of understanding of the common mucosal immune system, almost all current vaccines are given to humans by the parenteral route. Systemic immunization is essentially ineffective for induction of mucosal immune responses. Since the majority of infectious microorganisms are encountered through mucosal surface areas, it is logical to consider the induction of protective antibodies and T cell responses in mucosal tissues.*

Even though this statement was made already three decades ago, nothing has changed in practice—the same flawed approach of intramuscular injection has remained predominant in medical practice, and it has been adopted yet again with the "modern" COVID-19 vaccines. It

is therefore unsurprising that these vaccines have very unconvincing efficacy against infection with SARS-CoV-2. Intranasal vaccines have attracted substantial development effort, but they are not generally used. This holds true fo influenza [59], measles [60] and also for COVID-19. In summary, the intramuscular application of the COVID-19 vaccines must be assumed to contribute to their feeble and rapidly waning efficacy against infection and transmission.

2.3.7 Conclusion. In summary, the evidence indicates that the current vaccines are unable to stop the spread of COVID-19. With respect to previously prevalent Delta variant, some disagreement exists in the literature as to whether vaccine efficacy against transmission was low or entirely lacking. Regarding the currently predominant Omicron variant, the limited available literature indicates essentially a total failure of the vaccines.

3 The Pfizer and Moderna COVID-19 vaccines lack safety

3.1 What does the evidence show? The clinical trials for the Pfizer and Moderna COVID-19 vaccines, as well as for the other COVID-19 vaccines, were rushed through in a very short time; this has meant that proper precautions to ensure their safety were not taken. However, animal experiments carried out before the start of clinical testing already gave reason to expect severe toxicity. Unfortunately, this expectation has been abundantly borne out in practice since the beginning of mass vaccinations.

3.1.1 Preclinical data from animal experiments indicate potential for grave harm. All gene-based COVID-19 vaccines, including the Pfizer and Moderna COVID-19 vaccines, cause the expression in vivo of one specific protein of SARS-CoV-2—namely, the so-called spike protein, which is located on the surface of the virus particle. The spike protein mediates the virus particle's initial attachment to the host cell and also its subsequent entry into the cell. The key idea behind the Pfizer and Moderna mRNA vaccines is as follows:

1. a synthetic mRNA that encodes the spike protein is complexed with a mixture of neutral and cationic (positively charged) synthetic lipids, which cluster together in lipid nanoparticles (LNPs);
2. after injection, the LNPs facilitate the uptake of the mRNA into host cells, where the mRNA will cause the expression (synthesis) of the spike protein;
3. the spike protein will appear on the surface of the host cells and induce an immune reaction to itself.

The immune reaction to the spike protein will comprise both antibodies, which may or may not be neutralizing (see Section 2.1.3), and T-lymphocytes (T-cells). Some of these T-cells are cytotoxic (also known as T-killer cells); their function is to kill virus-infected body cells.

While this vaccination strategy may look good on paper, it has a number of drawbacks and risks. These arise both from the lipid mixture and from the spike protein, both of which have known toxic activities.

Toxic and procoagulant activities of the spike protein. Severe clinical COVID-19 disease is often accompanied by a pathological activation of blood clotting [61]. The central role of the spike protein in this complication is recognized [62]. Notably, there are at least two different mechanisms for triggering blood coagulation:

1. If the spike protein is expressed within vascular endothelial cells—the innermost cell layer of the blood vessels—then an immune reaction to the spike protein can destroy these cells.

The resulting vascular lesion will activate blood clotting. This immune reaction can involve cytotoxic T-cells, but also antibodies that trigger the complement system and other immune effector mechanisms.

2. Spike protein molecules may undergo proteolytic cleavage, and one of the products (the S1 fragment) may be released from the cell. S1 fragments that are formed within the circulation, or which enter it after being synthesized elsewhere in the body, can directly bind to blood platelets (thromboycytes) and activate them. This will again set off blood clotting.

The second mechanism is significant because it does not involve an immune reaction; therefore, it can be triggered right away even in those persons who have no pre-existing immunity. The first mechanism will be most effective in those who already have immunity to the spike protein, due to either infection with the virus or a previous injection of vaccine. Note that the underlying mechanism of cell damage will also operate in other tissues—any cell in the body that expresses the spike protein will thereby become a target for the immune system.

Since the Pfizer and Moderna COVID-19 vaccines induce the synthesis of active, and therefore potentially toxic, spike protein, it is important to understand how this protein with be distributed within the body. Toxicity might be limited if the vaccine, and therefore the synthesis of the spike protein, remained confined to the site of injection, within the muscle tissue but outside the circulation. On the other hand, if the vaccine were to enter the bloodstream, then one would have to expect expression of the spike protein within the blood vessels and toxicity through the activation of blood clotting.

Distribution of the vaccine in animal experiments. As it turns out, the vaccine does indeed appear in the bloodstream very rapidly after intramuscular injection. In experiments which Pfizer reported to the Japanese health authorities [63, 64], rats were injected with a mock vaccine sample. This material was was chemically similar to the Pfizer COVID-19 vaccine, but it contained an mRNA molecule that encoded an easily traceable, non-toxic model protein (luciferase) rather than the SARS-CoV-2 spike protein. The lipid mixture used to form the LNPs was the exact same as with the Pfizer COVID-19 vaccine. One of the lipids in this mixture was radioactively labelled, which permitted the distribution of the sample within the body to be traced and quantified sensitively and accurately. Several remarkable observations were made:

1. The radioactive lipid appeared rapidly in the bloodstream. The blood plasma concentration peaked after 2 hours; but even at only 15 minutes into the experiment, the plasma level had already reached 45% of that maximal value.
2. Very high levels of the radioactive lipid accumulated in the liver, the spleen, the adrenal glands, and the ovaries.
3. Comparatively low levels accumulated in the central nervous system (the brain and the spinal cord).
4. Expression of the model protein encoded by the mRNA was studied only in the liver, where it was readily detected.

Mechanism of uptake into the circulation after intramuscular injection. Considering that the complex consisting of mRNA with bound LNPs has a rather large molecular size and therefore cannot cross an intact capillary barrier, we may wonder how the vaccine managed to enter the bloodstream so rapidly. This occurs most likely through lymphatic transport. The fluid within the interstitial space is continuously drained through the lymphatic system; all lymph fluid

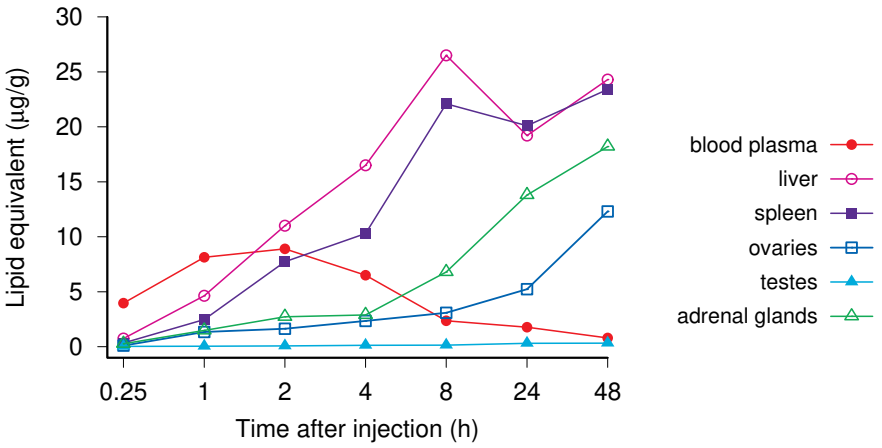


Figure 7 Organ distribution in rats of a model mRNA vaccine with the same lipid composition as the Pfizer COVID-19 vaccine. Plot generated from data in Table 2.6.5.5B of [64]. The blood level rises quickly and then falls as the vaccine accumulates in various organs. The vaccine was measured using radioactively labelled cholesterol (unlabelled cholesterol is a regular ingredient of the vaccine lipid nanoparticles). The data represent vaccine content in µg of vaccine lipid per gram of tissue or blood plasma. Note the high concentrations in liver, spleen, adrenal glands, and ovaries.

ultimately enters the bloodstream through the thoracic duct. Particles which are too large for traversing the capillary barrier can ultimately reach the circulation by way of this lymphatic drainage.

The SARS-CoV-2 spike protein, together with activation of the complement system, has been implicated in the causation of injury to small blood vessels in COVID-19 infections [65, 66]. Similar injury must be expected after vaccination near the injection site. The resulting leakiness of the capillaries should accelerate plasma exudation and lymphatic drainage. In addition, it may also permit some of the vaccine particles to enter the bloodstream directly.

Other indications of LNP toxicity. The proposed breakdown of the capillary barrier by the LNPs implies a cytotoxic effect on the endothelial cells, which form the only cellular element of the capillary walls. Cytotoxic effects of the LNPs are also evident from damage to muscle fibres at the injection site [28, p. 49] and to liver cells [28, p. 46]. Note that these data, too, were obtained with the model mRNA encoding the presumably non-toxic luciferase enzyme. Therefore, these cytotoxic actions are not due to any direct action of the spike protein. An immunological component of the cell damage cannot be completely ruled out, but it is likely not dominant in this case, since luciferase, unlike spike protein, is not transported to the cell surface.

Mechanisms of accumulation in specific organs. The high rates of accumulation of the vaccine in the liver and the spleen suggest uptake by macrophage cells, which abound in both organs and are generally in charge of clearing away unwanted debris. The accumulation in the adrenal glands, the ovaries, and again the liver suggests a role of lipoproteins in cellular uptake within these organs. Lipoproteins are complexes of lipids and specific protein molecules (apolipoproteins) that function as lipid carriers in the bloodstream. It is known that artificial lipid nanoparticles (LNPs) like those used in the COVID mRNA vaccines can acquire a shell—a

"corona"—of the body's own apolipoprotein molecules, after which these particles will be taken up into body cells in the same way as native lipoproteion [67]

The liver has a central role in lipid and lipoprotein metabolism generally, whereas the adrenal glands and the ovaries take up lipoproteins to acquire cholesterol, which they then convert to their respective steroid hormones. Such a role of lipoproteins in the transport and cellular uptake of lipid nanoparticles is in fact accepted [68]. We must therefore expect that other organs with a high rate of lipoprotein uptake will be similarly affected. This includes in particular the placenta, which like the ovaries produces large amounts of steroid hormone (progesterone), and the lactating mammary glands, which acquire cholesterol contained in lipoproteins for secretion into the breast milk.

Correlation of lipid uptake and mRNA expression. In the experimental study in question, the liver and the spleen were also shown to express the mRNA that is associated with the LNPs [63, 64]. As stated above, the mRNA used in this study encoded the firefly enzyme *luciferase*, which is the very protein that enables these animals to glow in the dark. Mammalian tissues expressing this enzyme will also become luminescent, in proportion to the amount of luciferase protein which they synthesize.

Measurements of this luminescence are not very sensitive, though, which was most likely the reason why Pfizer detected it only with the liver and spleen (as well as near the injection site) but not with smaller organs such as the ovaries and adrenal glands. However, in the absence of proof positive to the opposite, we must assume that the correlation between efficient LNP uptake and mRNA expression that applies to the liver will also hold with other organs. If the cargo mRNA encodes the spike protein, then these organs will be exposed to the toxicity of the spike protein, and to the immune reaction against it, in proportion to the level of LNP and mRNA uptake.

Potential risks to fertility and to the breastfed newborn. A high level of spike protein expression in the ovaries raises the prospect of significant damage to that organ, with possible consequences for female fertility. Uptake of the vaccine by mammary gland cells opens two possible pathways of toxicity to the breastfed child: firstly, the expression of spike protein and its secretion into the breast milk, and secondly, the wholesale transfer of the vaccine into the milk. The mammary glands are *apocrine*, which means that they pinch off and release fragments of their own cytoplasm into the milk; thus, anything that has reached the cytoplasm might also reach the breast milk. In this connection, we note that both the VAERS database and the EU drug adverse events registry (EudraVigilance) report fatalities in breastfed newborns after vaccination of their mothers.

The manufacturers failed to investigate risks evident from preclinical studies. With the exception of fertility, which can simply not be evaluated within the short period of time for which the vaccines have been in use, all of the risks discussed above have been substantiated since the vaccines have been rolled out—all are manifest in the reports to the various adverse event registries (see Section 3.2). We must stress again that each of these risks could readily be inferred from the cited limited preclinical data, but were not followed up with appropriate in-depth investigations. In particular, the clinical trials did not monitor any laboratory parameters that could have provided information on these risks, such as those related to blood coagulation (e.g. D-dimers/thrombocytes), liver damage (e.g. γ-glutamyltransferase), and myocarditis (troponin).

Table 4 COVID-19 vaccine-related adverse events and deaths reported to EudraVigilance for the four major vaccine manufacturers, as of March 6, 2022 [69].

Manufacturer	Adverse events	Deaths	Deadly events
Pfizer	861,135	19,548	2.3%
AstraZeneca	467,760	8,638	1.8%
Moderna	264,297	11,592	4.4%
Johnson & Johnson	54,910	2,729	5.0%
Total	1,648,102	42,507	2.6%

3.1.2 Contaminations arising from the manufacturing process. The commercial scale manufacturing process of the Pfizer COVID-19 vaccine gives rise to several contaminations that may compromise vaccine safety and effectiveness. For brevity, we will here mention only two such contaminants.

Contaminating bacterial DNA. The mRNA is produced in vitro using a DNA template, which in turn is obtained from bacterial cells. While steps are taken to remove this DNA afterwards, they are not completely effective, which is acknowledged in the EMA report (pages 17 and 40). Contaminating DNA injected with the vaccine may insert into the genomes of host cells and cause potentially harmful mutations. Bacterial DNA also non-specifically promotes inflammation.

Lipid impurites. The EMA report also observes impurities originating from the synthesis of the lipid ingredients of the vaccine (page 24):

> *Lipid-related impurities have been observed in some recently manufactured finished product batches, correlated with ALC-0315 lipid batches. The quality of ALC-0315 excipient is considered acceptable based on the available data on condition that specific impurities in the finished product will be further evaluated.*

Considering that the synthetic lipid referred to as ALC-0315 has never before been used on humans, there is no sound empirical basis for deciding on "acceptable" levels of impurities. Furthermore, it appears that the contaminating species have not even been identified. EMA's arbitrary blanket approval of unknown contaminants of an unproven vaccine ingredient is completely unacceptable.

The same applies to Moderna as well—their lipids, too, were found to contain various unidentified and unquantified contaminants [29, p. 23], and the cationic lipid SM-102 had not received previous approval for use in humans.

3.2 Adverse events after the onset of vaccinations. Since the introduction of the vaccines, numerous adverse events have been reported to registries around the world. We will here focus on two registries, namely, the U.S. vaccine adverse events reporting system (VAERS) and the EU monitoring system for drug adverse events (EudraVigilance).

3.2.1 Total cases and fatalities reported to EudraVigilance and VAERS. Table 4 summarizes the numbers of adverse events for each of the four COVID vaccines deployed in the countries of the European Union. We see very high numbers of incidents and fatalities across the board. Pfizer has managed to rack up the highest body count because their vaccine is the most widely

Table 5 Adverse events (total and deadly) reported to VAERS as of December 7th, 2021, by age group, for the Pfizer vaccine as well as for all COVID-19 vaccines combined. Data retrieved from OpenVAERS [70].

	Pfizer			All		
Age (years)	Total events	Deaths	Deadly (%)	Total events	Deaths	Deadly (%)
0–9	1,358	4	0.3	1,522	5	0.3
10–19	25,135	52	0.2	37,959	70	0.2
20–29	41,574	94	0.2	82,291	195	0.2
30–39	63,068	167	0.3	123,359	340	0.3
40–49	61,632	226	0.4	121,121	509	0.4
50–59	59,148	494	0.8	122,001	1,070	0.9
60–69	48,457	1,038	2.1	112,634	2,152	1.9
70–79	31,448	1,560	5.0	77,212	3,004	3.9
≥ 80	18,639	2,974	16.0	38,815	4,871	12.5
Total	350,459	6,609	1.9	716,914	12,216	1.7

used. The Moderna vaccine takes the second spot; it is also remarkable for its high percentage of reported events which are fatal.

The totals are somewhat lower but overall still appallingly high in the American VAERS database. With VAERS, we can also obtain the case numbers and fatalities by age group. These data are summarized in Table 5, separately for the Pfizer vaccine and for all COVID vaccines combined (also including Pfizer). Deadly events occur in all age groups, but the elderly are more often affected.[2]

It is impossible to know what percentage of all fatalities that occur shortly after vaccination will actually be reported to VAERS or EudraVigilance. Comparison between different European countries suggest that reporting is very incomplete. For example, Iceland and the Netherlands report one adverse event for every 112 and 77 vaccine injections, respectively, whereas that number is 534 for Germany, 8,367 for Slovakia, and 36,851 for Poland.

We note that the total of the COVID vaccine fatalities in VAERS already exceeds that reported for all other vaccines combined, over the entire 30 year period that this reporting system has been in existence. It is therefore clear that these vaccines are far and away the most deadly ones in history—quite predictably so, and all for a disease whose case fatality rate does not exceed that of influenza [72] and is negligible in otherwise healthy persons [73, 74].

3.2.2 Heart attacks and myocarditis or pericarditis by age group. It is generally accepted that, in COVID-19 disease, the spike protein of the virus triggers vascular lesions and blood clotting [66, 75, 76]. A prominent clinical manifestation of blood clotting is myocardial infarc-

[2]We should note here that a major chasm has opened between the numbers of adverse events reported by the official VAERS website and by the OpenVAERS website [70], respectively. OpenVAERS builds and maintains its own database using records periodically downloaded from VAERS itself. Apparently, VAERS has been systemically deleting records from its database [71]. This report relies on the data supplied by OpenVAERS.

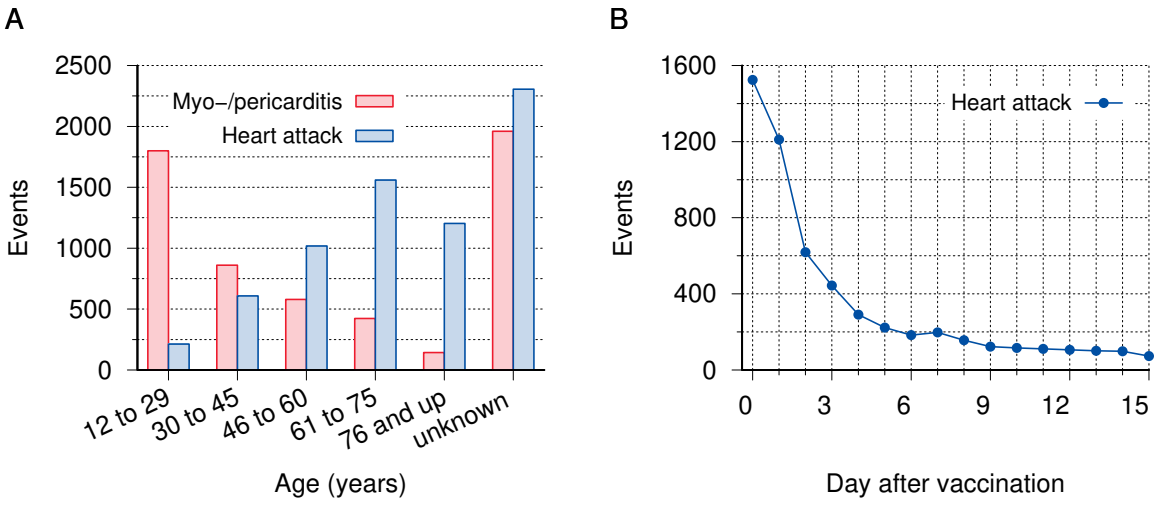


Figure 8 Myocarditis/pericardits and heart attacks reported to VAERS for all COVID vaccines combined, as of September 10th, 2021 [78]. A: Disease cases by age group. B: Reported cases of heart attack by day after vaccination.

tion (heart attack). Another form of cardiac involvement, also connected to the spike protein but purely inflammatory rather than related to clotting, is myocarditis [77].

Since all of the COVID vaccines induce the production of active spike protein, they, too, must be expected to cause heart attacks and myocarditis; and in fact both VAERS and EudraVigilance document a large number of cases. In Figure 8A, the cases of these diseases reported to VAERS have been grouped by age. The incidence of heart attack rises with age, which is expected. Note, however, that even in the youngest age group, there are as many as 213 cases; this is highly irregular. Panel B of the same figure groups the reported heart attacks according to time elapsed since vaccine injection. Of all heart attacks reported, 49% occurred within one day of the vaccination, and 84% within one week. This close correlation in time very strongly points to causation by the vaccine.

From panel A, it is evident that the age distribution of myocarditis/pericarditis is practically a mirror image of that of heart attacks—it is highest in the youngest age group and drops continuously with age. Myocarditis in particular is a very serious condition in its own right; it can be fatal in the acute phase and is likely to leave behind some measure of lifelong functional impairment. Thus, overall, all age groups are at substantial risk to suffer grave harm to their cardiovascular health from the vaccines.

3.2.3 Other severe events related to disrupted blood clotting. Aside from myocardial infarctions, the litany of diagnoses in both databases that indicate pathological activation of blood clotting is almost endless—strokes, thromboses in the brain and in other organs, pulmonary embolism; but also thrombocytopenia and bleeding, which result from excessive consumption of thrombocytes and of coagulation factors in disseminated intravascular coagulation. Clotting disorders caused many of the fatalities summarized above; in other cases, they caused severe acute disease, which will in many cases leave behind severe disability.

3.2.4 Miscarriages. As of December 3rd, 2021, VAERS contained 2,437 case reports of miscarriage among vaccinated pregnant women; of these, 1,786 concern the Pfizer vaccine. While it is difficult to ascertain what percentage of these miscarriages must be attributed to vaccination—

Table 6 Clinical outcomes of vaccination adverse event reports received and processed by Pfizer as of February 28th, 2021. Data from Table 1 in [81].

Case outcome	Number of cases
Fatal	1,223
Recovered with sequelae	520
Not recovered at the time of report	11,361
Recovered/Recovering	19,582
Unknown	9,400
Total	42,086

the CDC claimed to have addressed this question [79], but had to admit in an erratum that this study was completely botched [80]—we must note that most of the cases in VAERS and in EudraVigilance were reported by healthcare professionals, who evidently considered a connection to the vaccine at least plausible.

This high number of reports alone would be reason enough to pause the vaccinations and investigate. We must also note that pregnant women had been excluded from the clinical trials on the Moderna vaccine, as well as on the other COVID vaccines. Continuing vaccination without proper investigation in the face of mounting indications of harm is completely irresponsible.

3.2.5 Other severe reactions. Severe reactions also include seizures and other neurological symptoms, particularly related to motor control, and severe systemic inflammation with damage to multiple organs. Again, in many of these patients, long-lasting or even permanent residual damage is highly likely.

3.2.6 Pfizer ignores the evidence of grievous harm in its own adverse event database. The non-profit organization *Public Health and Medical Professionals for Transparency* obtained, through a FOIA request, Pfizer's first post-marketing report to the FDA, which includes adverse event reports received by Pfizer directly [81]. The report explicitly acknowledges that the filing of such reports is voluntary and incomplete, and that therefore "the spontaneous reporting system should be used for signal detection rather than hypothesis testing."

With that in mind, one should think that a number of 1,223 fatalities reported within slightly more than two months of the vaccine roll-out should amount to a "detectable signal" even in the minds of hard-boiled pharma executives. However, in the conclusion of the report, we read:

> *Review of the available data for this cumulative PM [post-marketing] experience, confirms a favorable benefit : risk balance for BNT162b2. Pfizer will continue routine pharmacovigilance activities . . .*

It is plain that neither Pfizer nor the FDA consider a body count of 1,223 within only two months of the vaccine roll-out enough of a "signal" to halt the program or at least inform and consult with the public. Furthermore, we must assume that regulators other than the FDA also received Pfizer's pharmacovigilance report from and likewise failed to warn the public of their home countries. This situation is unprecedented.

3.3 Missing evidence. We saw above that significant positive indications of risk were neglected in the clinical trials and subsequent rushed emergency approval of the Pfizer vaccine, with unfortunate yet predictable outcomes. Equally damning is the list of omissions—potential risks that should have been investigated in preclinical or clinical trials but never were.

3.3.1 Proper pharmacokinetics. Section 3.1.1 described some data provided by Pfizer pertaining to the distribution of a surrogate vaccine. While these studies did provide important and useful information, it must be noted that the expression of the spike protein instead of the presumably inert luciferase enzyme might affect the distribution due to its interference with vascular integrity, including at the blood brain barrier, and with blood clotting. EMA and other regulators should have insisted that such experiments be carried out and documented.

Moderna reported no studies at all on the pharmacokinetics of the cationic lipid (SM-102) which is contained in their vaccine. Instead, they showed surrogate studies with "SM-86, a close structural analogue" [29, p. 53]. These are not an acceptable substitute. Likewise, proper pharmacokinetic studies on the second synthetic lipid component (PEG2000-DMG) are missing. EMA should have insisted that the distribution and the elimination of both synthetic lipids contained in tne Moderna COVID-19 vaccine (SM-102 and PEG2000-DMG) be fully characterized in animal experiments.

3.3.2 Drug interactions. The EMA report on the Pfizer vaccine states [28, p. 110]:

> *Interaction studies with other vaccines have not been performed, which is acceptable given the need to use the vaccine in an emergency situation.*

Since it is clear that mortality due to COVID-19 is low (see Section 1.1.1) and therefore that no emergency exists, this argument must be rejected as specious.

Immunosuppressive effects of Pfizer and Moderna COVID-19 vaccines are apparent from a drop of blood lymphocyte numbers among those vaccinated, as well as from clinical observations of Herpes zoster (shingles), which arises through the reactivation of persistent varicella-zoster virus [82]. This suggests that the desired immune response to other vaccines simultaneously administered may be impaired.

Furthermore, studies of interactions should not have been limited to vaccines alone, but also been extended to other drugs. One area of concern is the experimentally apparent liver toxicity of Pfizer and Moderna COVID-19 vaccines. The liver is central in the metabolic inactivation and disposal of many drugs; any interference with the function of this organ immediately creates numerous possibilities of adverse drug interactions.

With respect to the Moderna COVID-19 vaccine, he EMA report states [29, p. 119]:

> *Study P301 was not intended to measure drug interactions or the impact of other vaccines being administered in a close temporal relationship to mRNA-1273, based on exclusion criterion 'Has received or plans to receive a non-study vaccine within 28 days prior to or after any dose of IP (except for seasonal influenza vaccine which is not permitted within 14 days before or after any dose of IP).'*

Immunosuppressive effects of the Moderna COVID-19 vaccine are apparent from a drop of blood lymphocyte numbers among those vaccinated, as well as from clinical observations of Herpes zoster (shingles), which arises through the reactivation of persistent varicella-zoster virus [83–85]. This suggests that the desired immune response to other vaccines administered shortly before or after the Moderna vaccine may be impaired. In real life, it is not always

feasible to avoid the application of multiple vaccines within a short time frame. Therefore, this potential immunological interaction should have been studied.

Furthermore, studies of interactions should not have been limited to vaccines alone but also included other drugs, since many potential recipients of the vaccine will be on some kind of permanent medication. One area of particular concern is the experimentally apparent liver toxicity of the Moderna COVID-19 vaccine. The liver has a central place in the metabolic inactivation and disposal of many drugs; any interference with the function of this organ immediately creates numerous possibilities of adverse drug interactions.

3.3.3 Genotoxicity. No studies have been carried out regarding genotoxicity, that is, damage to the human genetic material, which could lead to heritable mutations and cancer. Recent evidence has shown this risk to to be very real; this will be discussed in depth in Section 3.4.

3.3.4 Reproductive toxicity. With both Pfizer and Moderna COVID-19 vaccines, reproductive toxicity was assessed using only one species (rats). Pfizer submitted data on only a small number of animals (21 litters). A greater than twofold increase in pre-implantation loss of embryos was noted, with a rate of 9.77% in the vaccine group, compared to 4.09% in the control group. Instead of merely stating [28, p. 50] that the higher value was "within historical control data range," the study should have stated unambiguously whether or not this difference was statistically significant; and if it was not, the number of experiments should have been increased to ensure the required statistical power. The same applies to the observations of "very low incidence of gastroschisis, mouth/jaw malformations, right sided aortic arch, and cervical vertebrae abnormalities." Overall, these studies are inadequately described and apparently were also inadequately carried out.

The EMA report on the Moderna COVID-19 vaccine contains similarly scanty data and evasive language [29, p. 51]. A low risk of genotoxicity is asserted, from which the inference is drawn that reproductive toxicity will be low as well; however, as we will see in Section 3.4, this optimistic assessment is unjustified.

3.3.5 Autoimmunity. Exposure to the vaccine will lead to cell damage due to the cationic lipids, and also to the immune attack on cells producing the spike protein. From the cells undergoing destruction, proteins and other macromolecules will be released; such material must then be cleared away by macrophages.

When the clearing system is overloaded because of excessive cell damage and apoptosis (cell death), then the accumulation of cellular debris will lead to chronically excessive type I interferon release; this, in turn, will trigger further inflammation. With time, some macromolecules in the debris will become targets for the formation of autoantibodies and the activation of autoreactive cytotoxic T cells—they will begin to function as auto-antigens. This then leads to further tissue damage and the release of more auto-antigens—autoimmune disease will develop. Such an outcome is particularly likely in immunocompromised people or in those who are genetically predisposed to autoimmune disease (e.g. those with the HLA-B27 allele).

The risk of autoimmunity induced by Pfizer and Moderna COVID-19 vaccines could be adequately addressed only in long-term studies; as with fertility or cancer, the very short period of preclinical and clinical testing means that we are flying blind. It should go without saying that all of these risks are particularly grave with children, adolescents, and young adults.

3.3.6 Antibody-dependent enhancement. While antibodies in principle serve to protect us from infections, in some cases they can increase disease severity. This phenomenon is referred to as antibody-dependent enhancement.

The principle. In Section 2.1.3 above, we saw that antibodies may or may not neutralize the virus that elicited them. While in most cases non-neutralizing antibodies are not harmful, with some viruses they can actually make matters worse by facilitating entry of these viruses into host cells. This occurs because certain cells of the immune system are supposed to take up antibody-tagged microbes and destroy them. If a virus particle to which antibodies have bound is taken up by such a cell but then manages to evade destruction, then it may instead start to multiply within this cell. Overall, the antibody will then have enhanced the replication of the virus. Clinically, this antibody-dependent enhancement (ADE) can cause a hyperinflammatory response (a "cytokine storm") that will amplify the damage to our lungs, liver and other organs of our body.

ADE can occur both after natural infection and after vaccination, and it has been observed with several virus families, including Dengue virus, Ebola virus, respiratory syncytial virus (RSV), and HIV [86]. Importantly, ADE also occurs with coronaviruses, and in particular with SARS, whose causative agent is closely related to SARS-CoV-2. Attempts to develop vaccines to SARS repeatedly failed due to ADE—the vaccines did induce antibodies, but when the vaccinated animals were subsequently challenged with the virus, they became more ill than the unvaccinated controls (see e.g. [87]).

SARS-CoV-2 and ADE. The possibility of ADE in the context of natural infection with SARS-CoV-2, as well as of vaccination against it, has been acknowledged [88]. More specifically, ADE due to spike protein antibodies elicited by other coronavirus strains has been invoked to account for the peculiar geographical distribution of disease severity within China [89]. However, the experimental research required to address it remains missing, even after more than one year into the pandemic.

With some experimental SARS vaccines, ADE could be mitigated through the use of inulin-based adjuvants [90]. This approach might be feasible for avoiding ADE with COVID-19 vaccines also, but so far this appears not to have been investigated with any of the existing COVID vaccines.

Pfizer and the regulatory bodies are well aware of the risk of ADE as well. The FDA notes in its briefing document [26, p. 44]:

> *Pfizer submitted a Pharmacovigilance Plan (PVP) to monitor safety concerns that could be associated with Pfizer-BioNTech COVID-19 Vaccine. The Sponsor identified vaccine-associated enhanced disease including vaccine-associated enhanced respiratory disease as an important potential risk.*

Here, the term "vaccine-associated enhanced disease" refers to ADE. EMA has likewise acknowledged that this risk must be investigated further [28, p. 141]:

> *Any important potential risks that may be specific to vaccination for COVID-19 (e.g. vaccine associated enhanced respiratory disease) should be taken into account. The Applicant has included VAED/VAERD as an important potential risk and will further investigate it in the ongoing pivotal study and a post-authorization safety study.*

With respect to the Moderna COVID-19 vaccine, the EMA summarizes the information supplied by the manufacturer as follows [29]126:

> The potential risk of VAED was assessed in non-clinical animal models in mice and non-human primates and raised no concerns based on a Th1 skewed type of immune response ... In the pivotal [clinical] trial, ... 30 cases of severe COVID-19 were reported in the placebo group, while 0 case was reported in the vaccine group, providing no signal for a possible disease enhancement after vaccination with mRNA-1273 [which is contained the Moderna vaccine].

Overall, it is clear that the risk of ADE is recognized in theory but is not addressed in practice. Given the abundant evidence of ADE with experimental SARS vaccines, this is completely irresponsible.

3.4 Genotoxicity of the mRNA vaccines: recent evidence. In the EMA assessment report on the Pfizer COVID-19 vaccine, we find the following succinct statement [28, p. 50]:

> *No genotoxicity studies have been provided. This is acceptable as the components of the vaccine formulation are lipids and RNA that are not expected to have genotoxic potential.*

Apparently, EMA's experts were assuming that RNA in general will not affect the integrity of the host cell genome. The first exception to this rule has been known since 1970, when oncogenic retroviruses were found to carry a reverse transcriptase activity that could copy the viral RNA genome into DNA, which could then insert into the host genome [91, 92]. The realization that eukaryotic cells themselves have similar reverse transcriptase activities came one and a half decades later [93], but it could hardly be considered a novelty in 2020. Thus, in a nutshell, EMA dismissed the genotoxicity risks of the Pfizer and Moderna COVID-19 vaccines based on outdated science.

3.4.1 Genomic insertion of RNA viruses through cellular reverse transcriptase activities. The first studies to demonstrate the existence of mammalian (mouse) DNA sequences that were derived from an RNA virus which was *not* a retrovirus were reported by Klenerman et al. [94] in 1997. The virus in question was Lymphocytic Choriomeningitis Virus. Since this virus does not itself encode a reverse transcriptase enzyme, it followed that the observed partial DNA copies of the viral RNA genome had to have been created through reverse transcription by cellular enzymes. The molecular mechanism was later elucidated in detail by scientists from the same laboratory [95]. It turned out that a *retrotransposon* had accomplished both the reverse transcription of the viral RNA and the insertion of the DNA copy into the cellular genome.

3.4.2 The biological role of cellular retrotransposons. Retrotransposons are mobile genetic elements in the cellular genome that encode the protein apparatus for generating additional copies of themselves. Most of the time, it is the mRNA of the retrotransposon itself that ends up being copied back into DNA and inserted. However, the retrotransposon proteins may occasionally 'lose' their own mRNA template and pick up another RNA molecule instead, which will then undergo reverse transcription into DNA and insertion into the cellular genome (Figure 9).

There are several homologous families of retrotransposons, of which in humans the most active and important one is the LINE-1 family [96–98]. Since the location of new insertions within the genome is largely random [99], the biological outcomes are quite varied. If the insertion occurs within a functional gene, that gene may be disrupted; if insertion occurs in

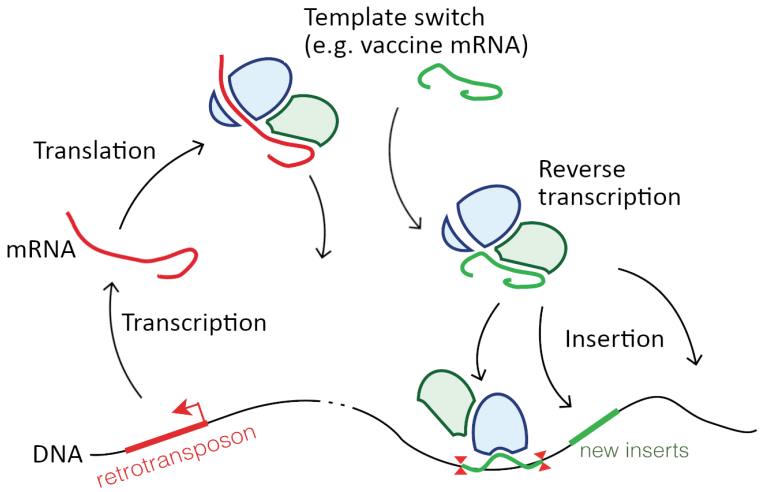


Figure 9 Reverse transcription and genomic insertion of an mRNA molecule by a retrotransposon (graphic adapted from Wikipedia). A retrotransposon, which is part of the cellular DNA, is initially transcribed and translated by the cellular machinery. It encodes two proteins that usually mediate the reverse transcription of the transposon's own mRNA into DNA, and the subsequent insertion of this DNA copy into the cellular DNA. However, occasionally the mRNA template may be replaced by another RNA molecule, e.g. an mRNA vaccine, which will then end up as a DNA copy in the genome.

the vicinity of a functional gene, then the activity of the latter may be regulated upward or downward. Depending on the specific role of the affected gene, the behaviour of the cell may be changed, and cancer or other diseases may result [100, 101].

While retrotransposon activity differs between the types and functional states of our body cells, it is noteworthy that retrotransposons are active in both dividing and non-dividing cells [102] and also in oocytes [103]. We must therefore expect that viral or other foreign RNAs may be inserted by retrotransposons not only into somatic cells, and thereby potentially cause cancer, but also into germline cells, and therefore propagate within the human population.

3.4.3 Genomic DNA sequences derived from non-retroviral RNA viruses. A multitude of RNA viruses other than retroviruses have given rise to partial copies inserted into the genomes of mammals and other vertebrates [104–107]. Similar findings have been made in other eukaryotic organisms such as fungi, plants and protozoa [108–110]. All of these virus-derived sequences must have arisen through some kind of retrotransposition mechanism, which clearly substantiates the above point that retrotransposition can occur in the germline cells of all these species.

While all of the observations cited here pertain to sequences derived from RNA viruses, retrotransposition by LINE-1 is not sequence-specific [111], and there is no reason to exclude the possibility that other RNA sequences, such as for example those of the Pfizer or Moderna mRNA vaccines, would be subject to the same mechanism.

3.4.4 Summary. Even though this had not yet been experimentally demonstrated when EMA released its assessment report [28], there was ample precedent to suggest the *strong possibility* that DNA copies of the vaccine mRNA would be produced and inserted into the cellular genome. Rather than waving away this risk as it did, EMA should have obligated Pfizer to carry out the necessary studies for excluding this risk *before* green-lighting authorization.

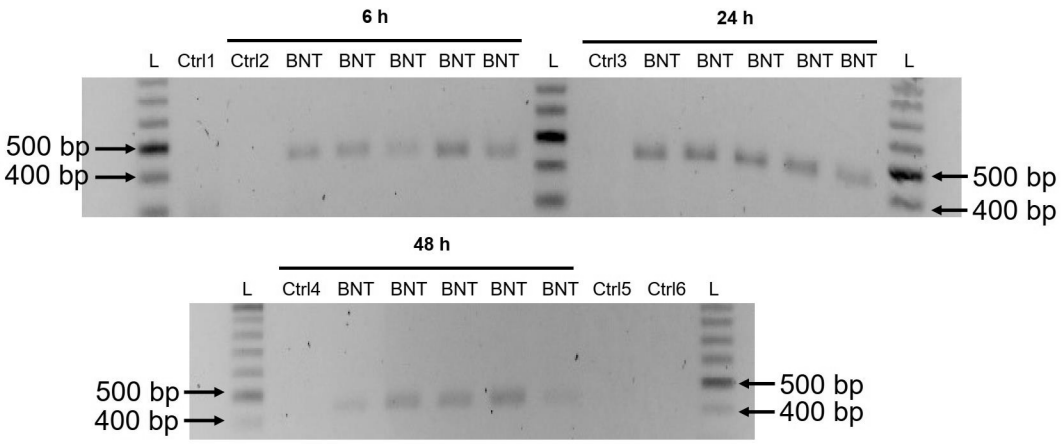


Figure 10 Detection of copies of the Pfizer COVID-19 vaccine mRNA within the cellular DNA of a human liver cell line (taken from Figure 5 in [112]). The cells were exposed to the vaccine for the lengths of time indicated. Cellular DNA was then isolated, and inserted DNA copies of the vaccine mRNA detected by PCR amplification of a fragment 444 base pairs (bp) in length. All samples labelled with 'BNT' had been treated with the vaccine, and they all show a PCR product of the expected length, as is evident from comparison to a DNA fragment length standard ('L'). Samples labelled with 'Ctrl *n*' were controls: Ctrl 1–4 contained DNA from cells not incubated with vaccine, Ctrl 5 contained RNA (not DNA) from vaccine-treated cells, and Ctrl 6 the same but additionally treated with RNAse, which step was also performed in the purification of DNA samples. As expected, none of the control samples contain the PCR product.

3.5 The current state of the evidence. As of this writing, substantial new evidence has accumulated regarding the genetic risks posed by the Pfizer COVID-19 vaccine.

3.5.1 DNA copies of the Pfizer COVID-19 vaccine mRNA are inserted into the host cell genome. Already in 2021, it was demonstrated that partial DNA copies of the genomic RNA of the SARS-CoV-2 virus can insert into the cellular DNA of infected cells [113]. Even though this does not directly relate to the mRNA vaccines, it does show that SARS-CoV-2-derived RNA sequences are not exempt from the general mechanism. Moreover, this study demonstrated that the insertion was mediated LINE-1 retrotransposons.

Of even greater and more immediate relevance is the recent demonstration that the mRNA contained in the Pfizer COVID-19 vaccine itself can integrate into the cells of a human-derived liver cell line [112]. Even though in this initial study the participation of LINE-1 was not rigorously demonstrated, the evidence of the vaccine mRNA's integration into the DNA as such is solid (see Figure 10).

3.5.2 Long-term expression of the spike protein. While it had initially been assumed that expression of the spike protein after vaccination would be of short duration and largely limited to the injection site, it has since become clear that it is neither. A recent study by Röltgen et al. [114] detected both the spike protein and mRNA encoding it within lymph nodes of vaccinated people at 60 days after the most recent injection. Bansal et al. [115] detected the spike protein on exosomes (small cell-derived membrane vesicles) in the circulation even at four months after the most recent injection.

This surprisingly long persistence is difficult to reconcile with the notion that the expression is only driven directly by the injected recombinant mRNA. Of note, the Pfizer COVID-19

vaccine mRNA is modified with 1-methylpseudouridine [28]. It is sometimes asserted that RNA containing 1-methylpseudouridine will be more stable than that which contains regular uridine [116]. However, while the substitution very strongly increases the level of protein expression from the mRNA, its effect on RNA lifetime is rather modest, so that the half-life of both the modified and the unmodified mRNA is on the order of no more than a few days [117, 118]. We must therefore take the possibility very seriously that the gene encoding the spike protein is perpetuated and continuously expressed in vivo by way of DNA insertion.

3.5.3 Distribution of injected vaccine to interior organs via the bloodstream. We have already discussed the distribution pattern of model vaccine studied by Pfizer above (see Section 3.1.1). In the present context, we recall in particular the very high level of accumulation of the vaccine in the ovaries.

3.5.4 Summary. The reverse transcription of the Pfizer COVID-19 vaccine mRNA into DNA and the integration of the DNA copy into the genome of host cells has been directly demonstrated in vitro, and the spike protein's documented long-term persistence in the bodies of vaccinated persons suggests that DNA integration may occur in vivo and perpetuate the expression of the spike protein. Moreover, the ovaries accumulate high levels of the vaccine, which implies that oocytes may be exposed to significant amounts of the recombinant mRNA.

Considering that both the mRNA and the lipid constituents of the Moderna vaccine are very similar to those of Pfizer's, the same risks must be assumed to apply to it as well.

3.6 Known and plausible risks that arise from the recently established genomic insertion of Pfizer COVID-19 vaccine. The results reported by Alden et al. [112], even though preliminary in some respects, pose some very serious questions that can no longer be ignored by the EMA and other regulatory authorities.

3.6.1 Likelihood of DNA insertion occurring in vivo. One remarkable feature in Figure 10 is that the PCR product which signals genomic insertion is observed in each of the DNA samples isolated from vaccine-treated cells. This indicates that one or more insertion events have occurred in each experiment. As noted above, the Pfizer COVID-19 vaccine mRNA—as well as the mRNA in Moderna's vaccine—is modified with 1-methylpseudouridine, which will protect the mRNA from certain degradative pathways [116, 119–121], which may conceivably increase the likelihood of reverse transcription and insertion. This question has apparently not been experimentally elucidated; not having compelled Pfizer to carry out such experiments is another glaring oversight committed by the EMA.

In the depicted experiments, the concentration of vaccine was higher than that which can be expected to occur in vivo. However, in the absence of evidence to the contrary, it is reasonable to surmise that the likelihood of insertion will be the same for each individual mRNA molecule and independent of the number of such molecules within a given cell. Thus, the number of insertion events in vivo would be limited simply by the total amount of mRNA injected; and that amount exceeds the combined amount used in all samples shown in Figure 10.

Even though we do not know how the efficiency of genomic insertion compares between the particular human cell line used by Alden et al. and the various cell types found in the human body, we must expect, at least until proof positive of the opposite is obtained, that some insertion events will occur in many or even all vaccinated persons.

Retrotransposition is particularly common in actively dividing cells, because during cell division the membrane barrier which separates the nucleus from the cytoplasm transiently breaks down; this facilitates the entry of the DNA copy that was generated from the mRNA in question into the nucleus. While most tissues inside the body have lower proliferation rates than cell cultures in vitro, we reiterate that retrotransposition (i.e., genomic insertion) events may occur in non-dividing cells also [102].

3.6.2 Biological consequences of DNA insertion. With the LINE-1 retrotransposon at least, DNA insertions are apparently distributed in a random fashion [99], but they will occur preferentially within or near transcriptionally active genes, since the DNA of inactive genes will be tightly packed into complexes with histone proteins and therefore poorly accessible. The genotoxic effect of an insertion on an active gene can be manifested in several ways.

Gene inactivation. Insertion may occur within a gene and disrupt it. This can lead to the loss of important cellular gene products (i.e., proteins) and thus, potentially, to the development of disease including cancer [100, 101]. Insertion may be accompanied by the deletion of large gene fragments [122].

Gene regulation. Transcriptional and epigenetic regulation mechanisms may be affected, thus up- or down-regulating protein expression levels with unpredictable and undesirable results. Indirect regulatory effects may affect even distant genes located on other chromosomes.

Activation of oncogenes. This is a special case of the preceding point, but it is important enough to be highlighted separately. The occurrence of malignancies through DNA integration and activation of cancer-promoting genes (oncogenes) has been demonstrated in clinical trials with a retroviral vector for the genetic treatment of children with SCID-X1 (severe combined immune deficiency) [123]. These malignancies will typically become manifest only several years after the completion of treatment [124]. Therefore, thorough long-term investigations concerning possible genotoxic effects of chromosomal integration are absolutely necessary, in both the pre-clinical and the clinical trial stages, for a valid benefit-risk analysis. This does not apply just with retroviral vectors, but with any recombinant nucleic acid that can end up inserting into the chromosomes of the cell [125].

Autoimmune-like disease. Integration of the spike protein gene into the host cell could lead to permanent expression of this antigen and thus induce chronic autoimmune-like disease.

Germline integration. We noticed above that Pfizer's own experiments indicate a high level of vaccine accumulation in the ovaries. Furthermore, LINE-1 and other retrotransposons are active and cause genomic insertion events in human oocytes [103]. In combination, these findings indicate that the Pfizer COVID-19 vaccine gene sequence may be integrated into the DNA of oocytes, and hence into the human germline. Insertion into male germline cells cannot be ruled out either, even though according to the animal studies the tissue levels of the Pfizer COVID-19 vaccine in the testes are significantly lower than in the ovaries.

Should this indeed come to pass—should the germline cells of vaccinated individuals be rendered transgenic—then the risk of spawning or conceiving transgenic children will not be limited to these individuals only, but it will necessarily be shared by their current or future spouses. In effect, an entire generation of future parents will be exposed to this risk.

3.6.3 Summary. Integration of the mRNA sequences into somatic cells is likely and implies a risk of cancer and of autoimmune disease. Moreover, the risk of germline integration, resulting in transgenic offspring, cannot be denied. These risks must urgently be addressed through in-depth animal studies. Meanwhile, the vaccine authorizations based on EMA's demonstrably inadequate scientific assessment must urgently be revoked.

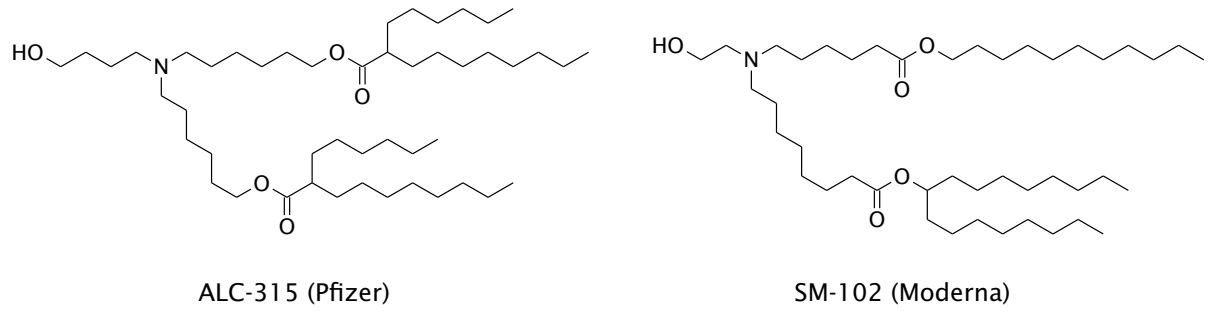
3.7 Genotoxic potential of lipid nanoparticles. While any adverse consequences of genomic insertion would take some time to become manifest as clinical disease, very many severe adverse events have occurred shortly after vaccination and must therefore be ascribed to other pathogenetic mechanisms. The toxicity of the spike protein, as well as the consequences of immune attack on the cells producing it, were already discussed in detail in our previous submission to the court, and they will therefore not be reiterated here. We will only note that the death toll continues to mount, with the latest figures from EudraVigilance having surpassed 42,000 dead [69]. In the following, we will briefly discuss the potential toxicity of the major synthetic lipid contained in the Pfizer COVID-19 vaccine.

The quote from the EMA assessment report given at the beginning of Section 3.4 dismissed not only RNA, but also lipids as possible causes of genotoxicity. With respect to the latter, such a statement is rather curious, since lipids are a very large and somewhat vaguely defined class of compounds, which invalidates any general claims as to their toxicity or the absence thereof. But since we do know the specific lipids contained in the lipid nanoparticles of the Pfizer COVID-19 vaccine, we can consider whether or not they pose a risk of genotoxicity. There are four lipids overall, two of which occur naturally (cholesterol and distearoyl-phosphatidylcholine), whereas the other two are synthetic and had not previously been approved for use in humans. We will focus here on the more abundant one of these synthetic lipids, which is known by the short name ALC-315 (see Figure 11).

3.7.1 Cytotoxic effect of cationic lipids. The first step in the process of vaccine particle uptake is *endocytosis*—the particle enters the cell, but it is initially still trapped within a membrane vesicle that budded off the cell membrane. The crucial step of releasing the mRNA from this vesicle (the endosome) into the cytosol is mediated by a synthetic cationic (positively charged) lipid. In the Pfizer vaccine, that lipid is ALC-315. After their escape into the cytosol, the cationic lipid molecules will continue to disrupt intracellular membranes, including those of the *mitochondria*. These are little organelles within our cells that carry out *cell respiration*—they generate hydrogen and react it with molecular oxygen in order to produce ATP, the most important energy-rich metabolite of the cell. Disruption of mitochondrial metabolism will cause *reactive oxygen species* (ROS) to form. These ROS, in turn, can wreak all kinds havoc inside the cell, including damage to the DNA—hence, they cause genotoxicity.

It should be noted that with any agent that causes genetic damage—this includes ionizing radiation, but also cytotoxic anticancer drugs—there is a risk of cancer and leukæmia, and moreover there is a lifetime limit on the overall dose that can be tolerated. Thus, the prospect of frequently repeated COVID "booster shots," and also that of extending mRNA technology to vaccines against other pathogens or non-infectious diseases, conjures up a very grave public health risk.

3.7.2 Indications of genetic damage due to cationic lipids in Moderna's mRNA vaccine. According to the EMA assessment report on the Pfizer COVID-19 vaccine, this manufacturer did



ALC-315 (Pfizer) SM-102 (Moderna)

Figure 11 Molecular structures of the proprietary cationic lipids contained in the mRNA vaccines produced by Pfizer and by Moderna, respectively. The nitrogen (N) atoms will be partially protonated under intracellular conditions and thereby acquire a positive charge. Oxygen (O) atoms are indicated; unlabelled atoms are carbon, saturated with hydrogen.

not provide any experimental data on the potential cytotoxicity of their lipid mixture (and the EMA committed a grave error in letting them get away with it). In contrast, Moderna, in its own application to the EMA, did supply some experimental data. While Moderna uses a different proprietary cationic lipid (named SM-102), the two lipids are very similar in structure (see Figure 11), and there is no reason to expect a major difference in cytotoxic activity.

In Moderna's animal experiments, *polychromatic* erythrocytes (red blood cells, RBC) were counted, as well as those with *micronuclei.* Polychromatic RBC are those which have only just finished their differentiation inside the bone marrow and disposed of their nuclei. At this stage, they still retain their ribosomal RNA, which causes them to appear bluish rather than red in the Giemsa stain. Changes in the percentage of RBC with this characteristic indicate changes in erythrocyte maturation kinetics. Genotoxic agents can cause both decreases [126] and increases [127] in this parameter. Differences between sexes are expected to be small. Using a luciferase-encoding mRNA packaged into a lipid mixture which contained SM-102, Moderna found a significantly decreased level of erythrocyte polychromasia, but only in male rats. The reported gender difference raises questions about the statistical power of this study.

Using another model mRNA and again a lipid mixture containing SM-102, Moderna found "statistically significant increases in micronucleated erythrocytes ... in both sexes." A so-called micronucleus is a chromosome fragment which was produced by chromosome damage [127, 128] and then left behind in the cytoplasm when the main nucleus was expelled. The micronucleus assay is widely used to assess genotoxicity in vivo [128].

The EMA report on the Moderna vaccine [29] quotes a study done by the company to the effect that the increased abundance of micronucleated RBC might have been due not to genotoxicity, but rather to the impeded clearance of these cells from the bloodstream as a consequence of the vaccine's spleen toxicity. However, no proof of this contention is shown; and the EMA report further states that "a strong increase in Molecular initiating event (MIE) was observed 48 hours after the final administration in the highest dose group in male rats." While no details are given as to the exact nature of the observed MIE, an "increase in molecular initiating events" clearly suggests an actual increase in the rate of formation of genetically damaged cells rather than merely a decrease in their clearance. Certainly, a report as sketchy and opaque as this one does not provide a sound basis for dismissing the risk of genotoxicity and proceeding with approval.

In conclusion, while the data provided by Moderna are incomplete, they strongly suggest that their SM-102 lipid is indeed genotoxic. This agrees with prior observations of genotoxicity associated with similar cationic lipids in liposomes, reviewed for example by Inglut et al. [129]. Unless proof positive to the opposite is provided, it must be assumed that the same also applies to Pfizer's ALC-315 lipid.

3.7.3 Sensitivity of lymphocytes to cytotoxic agents. As noted above, reactive oxygen species also mediate to a large extent the cytotoxic effects of ionizing radiation. A cell type that is particularly sensitive to radiation, but also to metabolically inflicted genetic damage, are the lymphocytes.[3] Since the lymphocytes are the backbone of the adaptive immune system, we must expect that cationic lipid toxicity will cause immunosuppression.

3.7.4 Summary. Apart from the mRNA, the cationic lipid contained in the Pfizer COVID-19 vaccine also poses a risk of genotoxicity. The EMA erred in neglecting this risk and not insisting on its rigorous experimental assessment by the manufacturer.

3.8 EMA's evaluation of the Pfizer and Moderna COVID-19 vaccines did not comply with EU regulations. EMA's evaluation process, as documented in the assessment reports [28, 29], fell short of the rules set out in various EU directives and regulations.

3.8.1 Failure to enforce the submission of mutagenicity studies. The most comprehensive EU directive on the evaluation and approval of new medicines is Directive 2001/83/EC of the European Parliament and of the Council of 2001 [131]. While it has been superseded in parts by later directives, most of its provisions remain in force. This includes in particular Part 3 on toxicological and pharmacological tests. Under the subheading *II. Performance of Tests*, paragraph *D. Mutagenic potential* specifies that studies on mutagenicity are obligatory with any new substance. This provision is general and not limited to any particular category of medicines.

Both of the synthetic lipids and the mRNAs contained in the Pfizer and Moderna COVID-19 vaccines are novel compounds that so far had not been approved for use as part of any other medicine. Thus, in waiving Pfizer's and Moderna's obligation to submit the appropriate studies, the EMA failed to enforce compliance with this binding and specific regulation.

3.8.2 Gene-based vaccines are a form of "advanced therapy." The above-mentioned directive was updated and partly superseded by EC regulation No 1394 in 2007 [132]. This regulation introduces the concept of "advanced therapies" (emphasis added):

> *(1) New scientific progress in cellular and* ***molecular biotechnology*** *has led to the development of* ***advanced therapies****, such as gene therapy . . .*
>
> *(2) Insofar as advanced therapy products are presented as having properties for treating or* ***preventing diseases*** *in human beings, or that they may be used in or administered to human beings with a view to restoring, correcting or modifying physiological functions by* ***exerting principally a*** *pharmacological,* ***immunological or metabolic action*** *. . .*

[3] See in particular the example of adenosine deaminase deficiency, a metabolic disease that causes genotoxic stress to all body cells yet selectively eradicates the lymphocytes, which causes severe combined immunodeficiency (SCID) [130].

The relevance of this definition of "advanced therapies" is that, by virtue of the terms highlighted in the quote, it unequivocally includes gene-based vaccines, even though the subsequently issued directive 2009/120/EC [133] explicitly excludes "vaccines against infectious diseases" from its definition of "gene therapy medicinal products."

3.8.3 Failure to enforce evaluation of risk of genome integration. Another Commission Directive, 2009/120/EC, is concerned entirely with "advanced therapy medicinal products," which as just shown includes the gene-based vaccines. It states that a risk-based approach "may be applied" to determine what kind of studies will be required for approval. In this context, the "level of integration of nucleic acid sequences" into the genome and the risk of oncogenicity are explicitly mentioned.

Section 4 on *specific requirements regarding Module 4*, subheading 4.1 on *all advanced therapy medicinal products,* states that with pharmacological and toxicological testing, rationales for the choice of models and experiments must be given. This arguably implies that rationales for *not* performing certain studies must also be provided—as indeed was done by the EMA in its barren statement that "the components of the vaccine formulation are lipids and RNA that are not expected to have genotoxic potential." Of course, as is clear from both earlier evidence and the experimental demonstration of the vaccine's genome integration, the EMA's reasoning was flawed.

3.8.4 Summary. The EMA has failed in its duty to protect the EU population from the inherent genotoxic risks of the Pfizer and Moderna COVID-19 vaccines. Even without understanding the relevant science at the depth we should expect of it, the EMA could easily have avoided this grave mistake by adhering to the letter of existing EU regulations on medicinal products in general and on "advanced therapies" in particular.

4 Signatures

SIGNED AT Waterloo, Ontario, Canada, on April 18, 2022

Dr. Michael Palmer

SIGNED AT Martinsrade, Schleswig-Holstein, Germany, on April 18, 2022

Prof. Dr. Sucharit Bhakdi

5 Short biographies of the authors

Professor Sucharit Bhakdi, MD, is a Professor Emeritus of Medical Microbiology and Immunology and Former Chair, Institute of Medical Microbiology and Hygiene, Johannes Gutenberg University of Mainz. Dr. Bhakdi has conducted experimental research on numerous topics including the complement system, bacterial toxins, malaria, and atherosclerosis.

Michael Palmer, MD, was until March 2022 an Associate Professor of Biochemistry in the Department of Chemistry at the University of Waterloo, Ontario, Canada. He obtained a board certification in Medical Microbiology and Infectious Disease Epidemiology from the German province of Rhenania-Palatinate while working with Dr. Sucharit Bhakdi at the University of Mainz, Germany. His research has focused on bacterial toxins and lipopeptide antibiotics, and his teaching subjects include medical microbiology, metabolism, and pharmacology.

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