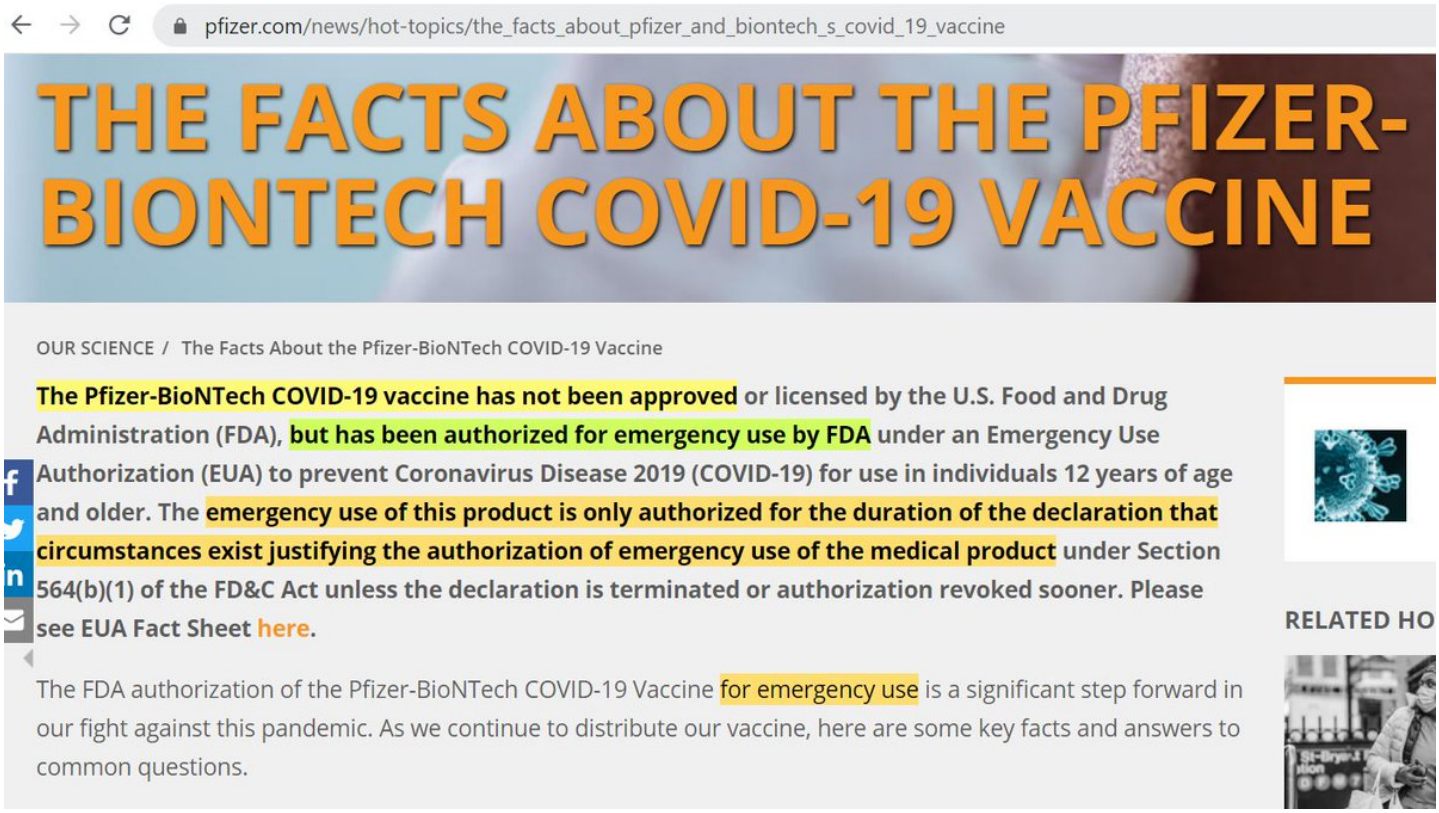
Twitter Thread by Conspiracy Mill

Conspiracy Mill
@conspiracymill

If I were to point out that Pfizer's investigational medicines have not been approved by FDA I might get my account suspended, or have my content censored.

Pfizer is allowed to say it tho. Maybe they have to.
https://t.co/ip7Y2K9bll
https://t.co/FRIhUqWntb #CrimesAgainstHumanity



What's this? According to Pfizer's current public documentation, there is still insufficient data to "inform vaccine-related risks in pregnancy."

Someone better tell that to CDC. ■

"Tho the spike shares an amino acid sequence with placenta, they're different, & distinct.■" ■

6. **What can you share about the Pfizer-BioNTech COVID-19 Vaccine in pregnant women?**

Available data on the Pfizer-BioNTech COVID-19 Vaccine administered to pregnant women are insufficient to inform vaccine-associated risks in pregnancy.[1] If you are pregnant, discuss your options with your healthcare provider.

7. **Does the Pfizer-BioNTech COVID-19 Vaccine cause infertility?**

It has been suggested that COVID-19 vaccines will cause infertility because of a shared amino acid sequence in the spike protein of SARS-CoV-2 and a placental protein. Although the SARS-CoV-2 spike protein shares an amino acid sequence with a placental protein, the two proteins are immunologically different and distinct.[5]

In an animal study in which the Pfizer-BioNTech COVID-19 Vaccine was administered prior to and during gestation, no vaccine-related adverse effects on female fertility, fetal development, or postnatal development were reported.[1] If you are pregnant, or planning to become pregnant, discuss your options with your healthcare provider.

What's that little ■ there?

Oh, it's the "Exaptation of Retroviral Syncytin for Development of Syncytialized Placenta, Its Limited Homology to the SARS-CoV-2 Spike Protein and Arguments against Disturbing Narrative in the Context of COVID-19 Vaccination" https://t.co/uJ1c5USYGk

Exaptation of Retroviral Syncytin for Development of Syncytialized Placenta, Its Limited Homology to the SARS-CoV-2 Spike Protein and Arguments against Disturbing Narrative in the Context of COVID-19 Vaccination

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"Arguments against Disturbing Narrative," huh. ■

I wonder which "disturbing narrative" they might be talking about.

Maybe this one. ■■■■
https://t.co/Zy2x0bfs3V

> This says that the coronavirus spike looks the same to the body as placenta. So contracting coronavirus or getting the vaccine would cause the body to remember placenta as coronavirus, & shred it accordingly.
>
> And they're acting like the low birth rates in 2020 are a big mystery. https://t.co/xWGJhFUO8x
>
> — Conspiracy Mill (@conspiracymill) December 3, 2020

That is disturbing. I hope they have some good arguments against it. Let's take a look.

Not looking particularly convincing so far tbh. ■

6. Hypothetical Role of Syncytin-1 in Fertilization

The syncytin-1 is also present in the human gametes and, although there are no functional studies, hypothetically it may be involved in the gamete fusion during fertilization (**Figure 3**).

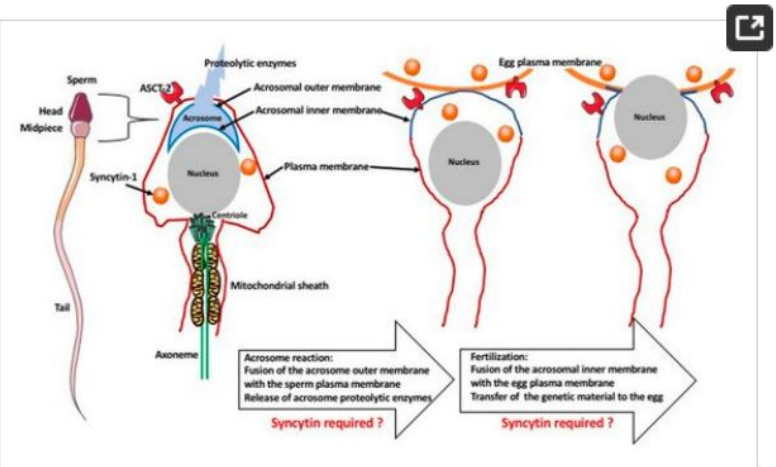

Figure 3. Membrane fusion during fertilization.

During fertilization, there is a fusion between the sperm and the egg membrane (oolemma). The syncytin-1 and its receptor (ASCT-2) are present in the sperm and oocytes/eggs. Sperm is surrounded by the plasma membrane. The sperm head contains the nucleus and the acrosome, which is surrounded by the outer and inner membrane and contains proteolytic enzymes. The midpiece region of the sperm contains centriole, which forms the axoneme (microtubules), which in turn is surrounded by a sheath of mitochondria. After recognition of egg presence, the sperm undergoes an acrosome reaction that fuses the outer acrosomal membrane with the sperm plasma membrane.

"The empirical bioinformatic studies showed that the protein pairs which share 8 amino acid identities, but not > 35% identity over 80 amino acid stretches, are not cross-reactive. [75]"

"empirical bioinformatic studies" ■

"are not"■

Maybe we'd better have a look at [75]. ■

Figure 4. The comparison between amino acid sequences of human syncytin-1 and the spike protein of SARS-CoV-2.

The Blast comparison of these two sequences does not show any similarities. However, the search for the similarity between 5-amino acid stretches (marked in yellow) shows two 2-amino acid identities (marked in red). Such very limited similarity is very unlikely to cause cross-reactivity between anti-SARS-CoV-2 antibodies and the human syncytin-1 protein.

The empirical bioinformatic studies showed that the protein pairs which share 8 amino acid identities, but not > 35% identity over 80 amino acid stretches, are not cross-reactive [75]. Although there are no published clinical data on the safety of the COVID-19 vaccine for pregnancy, placentation, and fertility, there are very strong indications that pregnant women should be the first candidates for preventative measures, such as COVID-19 vaccination [76,77]. Pfizer/BioNTech are conducting animal studies on the effects of the COVID-19 vaccine on pregnancy, and unpublished reports indicate that the vaccine is safe. Moderna performed similar studies using a rat model and concluded that there were no adverse effects on female reproduction, fetal development, or postnatal development. During the Pfizer/BioNTech vaccine clinical trials, 23 women became pregnant and so far no adverse effects have been reported [78]. Both the Centers for Disease Control and Prevention (CDC) and The American College of Obstetricians and Gynecologists (ACOG) recommend that the COVID-19 vaccine should not be withdrawn from pregnant and lactating women [79,80]. Further evaluation of potential impacts of COVID-19 vaccines on fertility, placentation, pregnancy and general health of mother and newborn is required. However, on the basis of the very low sequence similarity between human syncytin-1 and the SARS-CoV-2 S protein, it is considered to be unlikely that any S protein-specific SARS-CoV-2 vaccine would generate an immune response which is cross-reactive with syncytin 1 and this way affect fertility and pregnancy.

11. Conclusions

Human syncytin-1 plays a role in human placentation. Syncytin-1 has a retroviral origin and is slightly similar to the spike protein expressed on the surface of SARS-CoV-2. The similarity between sycytin-1 and SARS-CoV-2 spike protein is very limited. It is very unlikely that any spike protein-specific SARS-CoV-2 vaccine would generate an immune response which is cross-reactive with syncytin 1 and affect fertility and pregnancy.

75 ■ https://t.co/2R3MDN3UM3

Everything we've read down this Pfizer rabbit hole is based on this, apparently.

pubmed.ncbi.nlm.nih.gov/19874602/

› Clin Mol Allergy. 2009 Oct 29;7:9. doi: 10.1186/1476-7961-7-9.

Value of eight-amino-acid matches in predicting the allergenicity status of proteins: an empirical bioinformatic investigation

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Affiliations + expand

PMID: 19874602 PMCID: PMC2773230 DOI: 10.1186/1476-7961-7-9

Free PMC article

Abstract

The use of biotechnological techniques to introduce novel proteins into food crops (transgenic or GM crops) has motivated investigation into the properties of proteins that favor their potential to elicit allergic reactions. As part of the allergenicity assessment, bioinformatic approaches are used to compare the amino-acid sequence of candidate proteins with sequences in a database of known allergens to predict potential cross reactivity between novel food proteins and proteins to which people have become sensitized. Two criteria commonly used for these queries are searches over 80-amino-acid stretches for >35% identity, and searches for 8-amino-acid contiguous matches. We investigated the added value provided by the 8-amino-acid criterion over that provided by the >35%-identity-over-80-amino-acid criterion, by identifying allergens pairs that only met the former criterion, but not the latter criterion. We found that the allergen-sequence pairs only sharing 8-amino-acid identity, but not >35% identity over 80 amino acids, were unlikely to be cross reactive allergens. Thus, the common search for 8-amino-acid identity between novel proteins and known allergens appears to be of little additional value in assessing the potential allergenicity of novel proteins.

The spike and placenta only share 4 out of 100 pairs of amino acids. So although they look almost identical, they're really just a teeny tiny bit identical.

That's totally okay, right? What harm could four lil amino acids do?

I'm sure they have good evidence that this is fine■

For protein pairs having the shorter protein in each pair from 29 to 79 amino acids in length, 213 pairs having only 8-amino-acid sequence identity were identified. A plot of the length of the shorter protein in each pair versus the cumulative number of pairs yielded a pattern that was well fit by two individual linear regression lines (Figure 2). There was a natural split in the slope of the line at the 39-amino-acid length. When the shorter protein in the pair was less than 39 amino acids long, each amino-acid reduction resulted in >18 new pairs of proteins sharing only 8 identical contiguous amino acids. For proteins from 39 to 79 amino acids in length, removal of each amino acid increased the number of pairs sharing only 8 identical contiguous amino acids by less than 1. When the number of 8-mer-only pairs was adjusted for the number of proteins in each amino-acid-length category that was present in the FARRP database, the number of pairs generated per protein was still over 10-fold higher for the shorter protein class [see Additional file 2]. It is noteworthy that for proteins ≥80 amino acids, the rate of 8-mer-only pairs was only 4 per 100, and for those proteins less than 29 amino acids in length, the rate of 8-mer-only pairs was 539 per 100. For 8-mer-only pairs with the shorter protein containing 39 to 79 amino acids, 31 unique protein pairs were identified [see Additional file 3]. These 31 pairs of proteins consisted of 17 pairs of source organisms due to multiple isoforms of each protein being present in most cases.

Let's break down what 4/100 means.

8x2 base pairs x 4 of 100 amino acids are the same

That means there are 64 identical sequences between spike & syncytin.

Syncytin is integral in the development of placenta, which is integral to reproduction.

And the evidence this is fine?■

"IgE-binding epitopes may consist of short contiguous amino-acid stretches," but it "is believed" that they need more than 64 of them to bind.

Well that's a relief, it is *believed* that this is probably fine.

Remember, this is what Pfizer is basing "different and distinct" on.

It seems reasonable to conclude from these patterns that the major contributor to the observation that shorter proteins generate more 8-mer-only pairs is the decreased capacity of shorter sequences to share >35% identity over 80 amino acids, rather than a greater propensity to share 8 identical contiguous amino acids with other sequences in the database. Expanding further on this hypothesis, we researched the typical full-length amino-acid length of 8-mer-only pairs where the shorter sequence in each pair was from 39 to 79 amino acids in length. In every case, the shorter protein sequence in each pair was only represented by a partial sequence in the FARRP database, and these sequences ranged from 2 to 52% of a typical full-length sequence [see Additional file 3] [16-24]. This observation fit with the expectation that partial amino acid sequences may be insufficient to detect >35% identity over 80 amino acids when in fact such identity might exist if full-length sequences were available.

We then examined the FASTA alignments and 8-mer matches for those 8-mer-only hits where both members of the pair were ≥80 amino acids in length. Of the 52 protein pairs identified, 25 pairs did not have an identical stretch of 8 or more contiguous amino acids within the FASTA alignment, suggesting that the identified short amino-acid matches were unrelated to overall structural similarity between the proteins in these pairs [see Additional file 1]. This is important because, even though IgE-binding epitopes may consist of short contiguous amino-acid stretches, the presentation of two epitopes within the overall structure of a protein is believed to be critical in clinical cross reactivity. For example, Klinglmayr et al. (2009)[25] grafted putative short amino-acid epitopes from the apple allergen Mal d 1 into the analogous regions of the homologous birch pollen allergen Bet v 1 (64% similarity) and saw increased IgE reactivity in patients with clinical apple-pollen cross reactivity. These investigators recognized that the conserved 3-dimentional shape and almost identical secondary structure of Mal d 1 and Bet v 1 were required to elicit a response from the transplanted short contiguous amino-acid epitopes. Thus, the absence of significant homology between protein pairs in the region of identical short amino-acid stretches suggests that these stretches are unlikely to function as epitopes capable of clinical cross reactivity. In addition to falling outside of the FASTA alignment, all 25 pairs of proteins in this group consisted of low-complexity matches. Low-complexity amino-acid stretches have an increased likelihood of generating random matches

"Expert opinion rather than experimental evidence." ■

And who are these experts who say this is fine with no evidence?

Dow employees. Dow employees working on transgenic crops.

Based on what?

Pure fucking conjecture.

But go ahead pregnant ladies, CDC says this is fine. ■■

Our empirical results using protein sequences in the FARRP allergen database are consistent with the previous hypothesis that short contiguous amino acid matches provide little additional value in assessing the potential allergenicity of novel proteins. However, more research is needed to establish that the relatively few pairs of proteins meeting only the 8-mer match criterion are not clinically cross reactive. Further consideration of the value of adding short incomplete sequences to the FARRP database is also recommended since such sequences are of little or no value in searches designed to detect domain-wide or global alignments.

Conclusion

Go to:

The current guidelines for conducting allergen homology searches are based on expert opinion rather than experimental evidence [1-3]. Our investigation using the amino-acid sequences of known allergens suggests that short contiguous amino-acid matches alone are a poor predictor of allergenic cross reactivity. The approach taken here may have value in evaluating alternative bioinformatic criteria and may lead to more evidence-based protocols for predicting the cross reactivity between novel proteins and known allergens.

Abbreviations

Go to:

AA: amino acid; FARRP: Food Allergy Research and Resource Program; FASTA: fast all.

Competing interests

Go to:

The authors are employed by Dow AgroSciences LLC which develops and markets agricultural products, including transgenic crops.

Although this document is posted without a date, you know it is the most current, updated info from Pfizer because they note that the EUA is good for "individuals 12 years of age and older," since the FDA only just lowered the age to twelve recently, within the last couple weeks.

OUR SCIENCE / The Facts About the Pfizer-BioNTech COVID-19 Vaccine

The Pfizer-BioNTech COVID-19 vaccine has not been approved or licensed by the U.S. Food and Drug Administration (FDA), but has been authorized for emergency use by FDA under an Emergency Use Authorization (EUA) to prevent Coronavirus Disease 2019 (COVID-19) for use in individuals 12 years of age and older. The emergency use of this product is only authorized for the duration of the declaration that circumstances exist justifying the authorization of emergency use of the medical product under Section 564(b)(1) of the FD&C Act unless the declaration is terminated or authorization revoked sooner. Please see EUA Fact Sheet here.

https://t.co/xbk7s8OdJ1

So they do have to say it. It's like the warning they put on cigarettes.

They've also appended a large pinned warning to the bottom of the page advising people who have had a severe reaction to the first not to get the second. \U0001f928\U0001f914https://t.co/31FbR8YPgKhttps://t.co/2x959nFvDO pic.twitter.com/tpYGX3xHMW

— Conspiracy Mill (@conspiracymill) May 20, 2021