The MVA-NP+M Influenza Vaccine *did* work. It may help defeat COVID.

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Many scientists are developing COVID-19 vaccines. However, we need effective influenza vaccines as well. Otherwise, a second wave of COVID will be a double whammy.

Here I show that the results of Davenport *et al* [1] are significantly better than reported in the original study.

Experiment 1

Method and Results

I used the 6-gene profile data from Davenport *et al* [1] and subtracted the mean of 11 vaccinated participants from the mean of 11 unvaccinated participants. The results are shown below:

<i>Gene Name</i>	<i>Unvaccinated minus Vaccinated group</i>
CCL2	.701
LAMP3	.561
MT1G	.642
OAS3	.933
RTP4	.376
SEPT4	.446

Fisher's Exact Test = .012

Experiment 2

Method and Results

I used a 19-gene profile from Muller *et al* [2] with the data of [1] and obtained the following results:

<i>Gene Name</i>	<i>Unvaccinated minus Vaccinated group</i>
CCL2	.701
CCL8	.630
CXCL10	.269
HERC5	.481
IFI27	.204
IFI44	.346
IFI44L	.658
IFI6	.423
IFIT1	.390
IFIT3	.493
ISG15	.723
LAMP3	.561
OAS3	.933
OASL	.258
OTOF	.777
RSAD2	.735
SERPING1	.398
SPATS2L	.574
USP18	.395

It may be seen that the Unvaccinated participants had higher symptom scores than Vaccinated participants on each gene expression measure. Getting a positive number every time, instead of a negative one, is equivalent to flipping a coin and getting 19 heads in a row.

Fisher's Exact Test = .0000019073

Discussion

Davenport *et al* [1] concluded that they “did not detect a difference in the gene expression profile between vaccinated and unvaccinated individuals.”

Clearly, the new objective 19-gene profile from [2] *did* detect a difference.

It did so, even though this profile was derived from a different sample of participants, who had been challenged by H1N1 instead of H3N2 influenza.

Interestingly, the vaccinated group included a participant (Study ID = D) who developed moderate to severe subjective flu symptoms.

Research is underway to understand how to get the MVA-NP+M1 vaccine to work also with individuals like participant D.

Meanwhile, the faster this vaccine is developed, the fewer people will die because they catch *both* influenza *and* COVID-19 in the second wave.

References

- [1] Davenport EE, Antrobus RD, Lillie PJ, Gilbert SC, Knight JC. Transcriptomic profiling facilitates classification of response to influenza challenge. *J Mol Med*. 2015; 93:105-14. doi: 10.1007/s00109-014-1212-8.
- [2] Muller J, Parizotto E, Antrobus RD, Francis J, Bunce C, Stranks A, Nicols M, McClainM, Hill AVS, Ramasamy A, Gilbert SC. Development of an objective gene expression panel as an alternative to self-reported symptom scores in human influenza trials. *J Transl Med*. 2017; 15:134. doi: 10.1186/s12967-017-1235-3.