Large genome models used to design new viruses

The same, yet different

In some ways, these designed viruses were quite similar to the original ΦX174, but in other ways they were quite distinct.

For the “the same” perspective, the most effective viruses in the group of 285 tended to look a lot like the original. The overall fraction of viable viruses was only 16 out of the 285 outputs tested (5.6 percent). But if you looked only at the outputs that were most similar to the original ΦX174 (those with 98 percent sequence similarity and up), viability rose to 46 percent. So, if you don’t look a lot like a normal ΦX174, chances are good that you’re not going to work as a virus at all.

Most of the viable viruses had the same set of genes found in the original. None of them had even a single change in the stretch of DNA where the duplication of the virus’s genome starts.

All of that is in keeping with past studies that have shown that making even a single base change that alters just one amino acid in one of the proteins made from the virus’s genome had, on average, a 20 percent chance of inactivating the virus entirely. ΦX174 doesn’t just fear change; it’s typically murdered by it. Accordingly, the changes suggested by the AI produced a population of viable viruses that, on average, looked a lot like the original.

But, as individuals, the viruses were fairly distinct. One of

them lost one of the viral proteins entirely, compensating for its loss with changes elsewhere in the genome. Another added an entirely new gene. Many had genes that were either longer or shorter than the original. One even replaced one of the ΦX174 genes with a gene from a very distantly related virus.

The researchers did an interesting analysis based on the idea that any one amino acid change had a 20 percent chance of inactivating the virus. Doing the math, they say that any viruses with less than 25 changes have only a 2.3 percent chance of being viable. Of the 300 or so viruses the AI output, five viruses fell in that range, and three of them were viable. At above 25 individual amino acid changes, the chances of producing a viable virus are essentially zero. Yet nearly a quarter of the AI-suggested viruses that had more than 25 changes were viable, including two that had over 50 amino acid alterations.

https://arstechnica.com/science/2026/08/large-genome-models-used-to-design-new-viruses/