

Covid 19 vaccination analysis

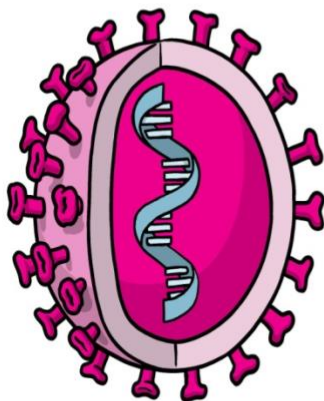
This article is part of a series of explainers on vaccine development and distribution. Learn more about vaccines – from how they work and how they're made to ensuring safety and equitable access

As of December 2020, there are over 200 vaccine candidates for COVID-19 being developed. Of these, at least 52 candidate vaccines are in human trials. There are several others currently in phase , which will enter phase III in the coming months (for more information on the clinical trial phases, see part three of our Vaccine Explained series).

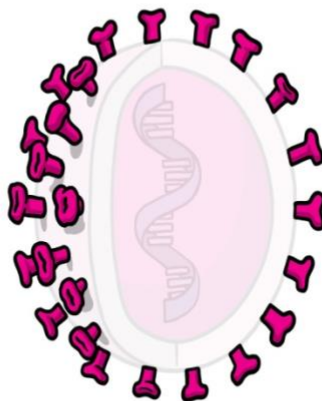
Why are there so many vaccines in development?

Typically, many vaccine candidates will be evaluated before any are found to be both safe and effective. For example, of all the vaccines that are studied in the lab and laboratory animals, roughly 7 out of every 100 will be considered good enough to move into clinical trials in humans. Of the vaccines that do make it to clinical trials, just one in five is successful. Having lots of different vaccines in development increases the chances that there will be one or more successful vaccines that will be shown to be safe and efficacious for the intended prioritized populations.

There are three main approaches to making a vaccine:



Using a whole virus
or bacterium



Parts that trigger
the immune system

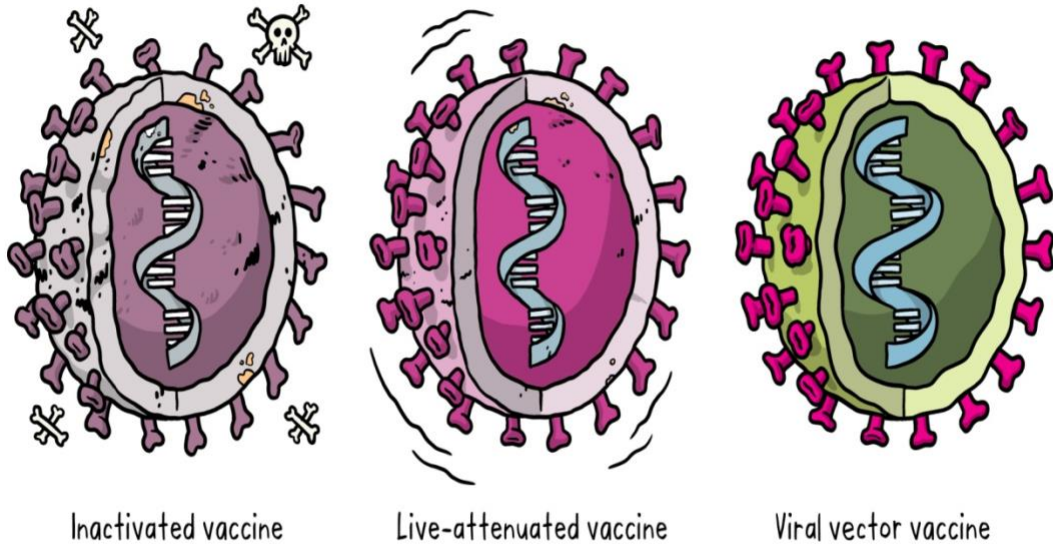


Just the
genetic material

The different types of vaccines

There are three main approaches to designing a vaccine. Their differences lie in whether they use a **whole** virus or bacterium; just the **parts** of the germ that triggers the immune system; or just the **genetic material** that provides the instructions for making specific proteins and not the whole virus.

The whole-microbe approach



The whole-microbe approach

Inactivated vaccine

The first way to make a vaccine is to take the disease-carrying virus or bacterium, or one very similar to it, and inactivate or kill it using chemicals, heat or radiation. This approach uses technology that's been proven to work in people – this is the way the flu and polio vaccines are made – and vaccines can be manufactured on a reasonable scale.

However, it requires special laboratory facilities to grow the virus or bacterium safely, can have a relatively long production time, and will likely require two or three doses to be administered.

Live-attenuated vaccine

A live-attenuated vaccine uses a living but weakened version of the virus or one that's very similar. The measles, mumps and rubella (MMR) vaccine and the chickenpox and shingles vaccine are examples of this type of vaccine. This approach uses similar technology to the inactivated vaccine and can be manufactured at scale. However, vaccines like this may not be suitable for people with compromised immune systems.

Viral vector vaccine

This type of vaccine uses a safe virus to deliver specific sub-parts – called proteins – of the germ of interest so that it can trigger an immune response without causing disease. To do this, the instructions for making particular parts of the pathogen of interest are inserted into a safe virus. The safe virus then serves as a platform or vector to deliver the protein into the body. The protein triggers the immune response. The Ebola vaccine is a viral vector vaccine and this type can be developed rapidly.

The subunit approach

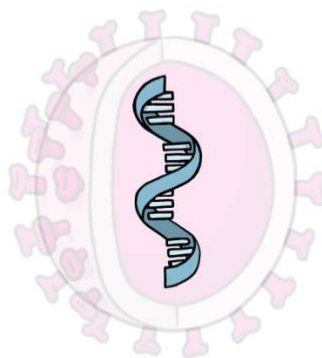
The subunit approach



Only uses the very specific parts (the subunits) of a virus or bacterium that the immune system needs to recognize.

A subunit vaccine is one that only uses the very specific parts (the subunits) of a virus or bacterium that the immune system needs to recognize. It doesn't contain the whole microbe or use a safe virus as a vector. The subunits may be proteins or sugars. Most of the vaccines on the childhood schedule are subunit vaccines, protecting people from diseases such as whooping cough, tetanus, diphtheria and meningococcal meningitis.

The genetic approach (nucleic acid vaccine)

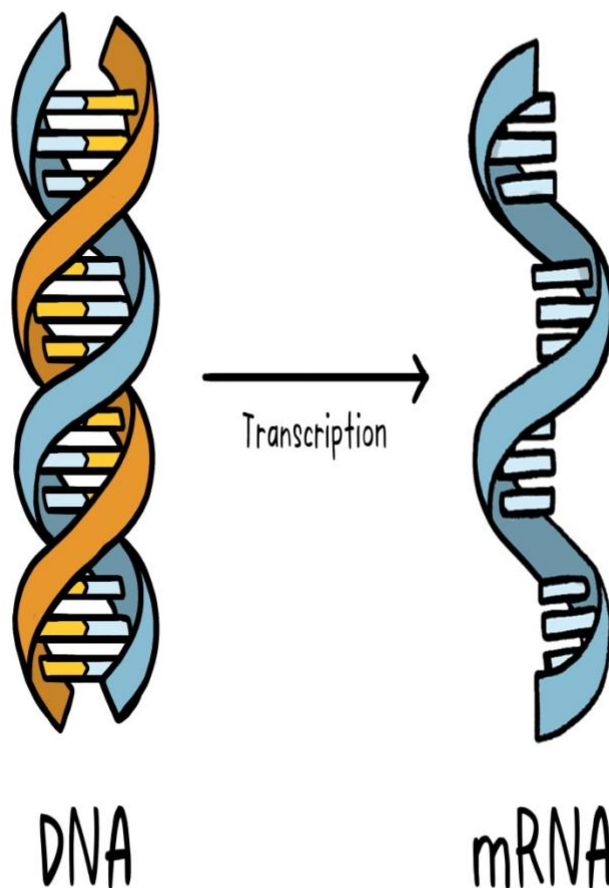


Uses the genetic material for specific proteins - the DNA or RNA.

The genetic approach (nucleic acid vaccine)

Unlike vaccine approaches that use either a weakened or dead whole microbe or parts of one, a nucleic acid vaccine just uses a section of genetic material that provides the instructions for specific proteins, not the whole microbe. DNA and RNA are the instructions our cells use to make proteins. In our cells, DNA is first turned into messenger RNA, which is then used as the blueprint to make specific proteins.

A nucleic acid vaccine delivers a specific set of instructions to our cells, either as DNA or mRNA, for them to make the specific protein that we want our i



immune system to recognize and respond to.

The nucleic acid approach is a new way of developing vaccines. Before the COVID-19 pandemic, none had yet been through the full approvals process for use in humans, though some DNA vaccines, including for particular cancers, were undergoing human trials. Because of the pandemic, research in this area has progressed very fast and some mRNA vaccines for COVID-19 are getting emergency use authorization, which means they can now be given to people beyond using them only in clinical trials

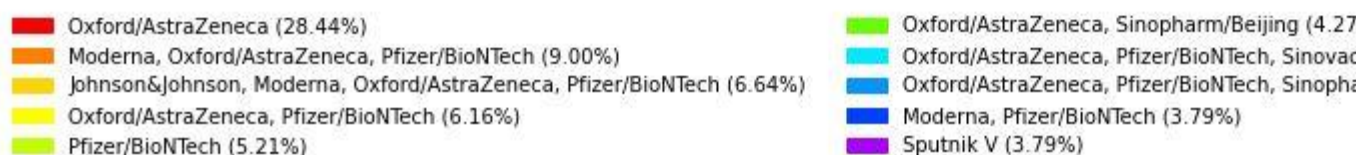
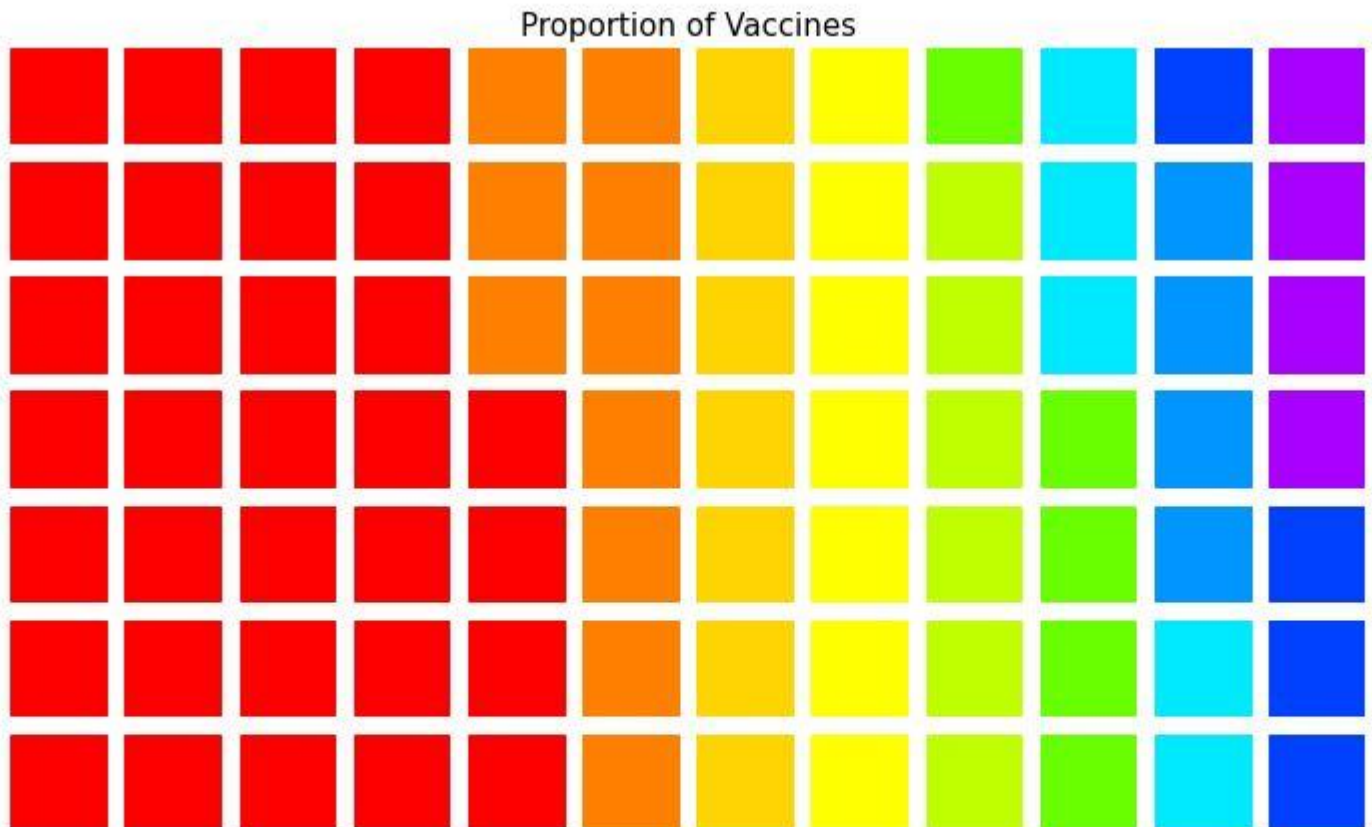
Program

```
import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
import matplotlib.pyplot as plt
import seaborn as sns
import plotly.express as px
from plotly.offline import download_plotlyjs,init_notebook_mode,plot,iplot
import plotly.graph_objects as go
import plotly.figure_factory as ff
from plotly.colors import n_colors
from wordcloud import WordCloud,ImageColorGenerator
init_notebook_mode(connected=True)
from plotly.subplots import make_subplots
from pywaffle import Waffle
import warnings
warnings.filterwarnings("ignore")
top10 = new_df['vaccines'].value_counts().nlargest(10)
top10
data = dict(new_df['vaccines'].value_counts(normalize = True).nlargest(10)*100)
#dict(new_df['vaccines'].value_counts(normalize = True) * 100)
vaccine = ['Oxford/AstraZeneca', 'Moderna, Oxford/AstraZeneca, Pfizer/BioNTech',
           'Oxford/AstraZeneca, Pfizer/BioNTech',
           'Johnson&Johnson, Moderna, Oxford/AstraZeneca, Pfizer/BioNTech',
           'Pfizer/BioNTech', 'Sputnik V', 'Oxford/AstraZeneca, Sinopharm/Beijing',
           'Sinopharm/Beijing', 'Moderna, Pfizer/BioNTech',
           'Oxford/AstraZeneca, Pfizer/BioNTech, Sinovac']
fig = plt.figure(
    rows=7,
    columns=12,
    FigureClass = Waffle,
    values = data,
    title={'label': 'Proportion of Vaccines', 'loc': 'center',
          'fontsize':15},
    colors=("#FF7F0E", "#00B5F7",
            "#AB63FA", "#00CC96", "#E9967A", "#F08080", "#40E0D0", "#DFFF00", "#DE3163", "#6AFF00"),
    labels=[f'{k} ({v:.2f}%)' for k, v in data.items()],
    legend={'loc': 'lower left', 'bbox_to_anchor': (0, -0.4), 'ncol': 2,
            'framealpha': 0},
    figsize=(12, 9)
)
fig.show()
data = new_df[['country','total_vaccinations']].nlargest(25,'total_vaccinations')
fig = px.bar(data, x = 'country',y = 'total_vaccinations',title="Number of total
vaccinations according to countries",)
fig.show()
data = new_df[['country','daily_vaccinations']].nlargest(25,'daily_vaccinations')
fig = px.bar(data, x = 'country',y = 'daily_vaccinations',title="Number of daily
vaccinations according to countries",)
fig.show()
```

OUTPUT:

Oxford/AstraZeneca	57
Moderna, Oxford/AstraZeneca, Pfizer/BioNTech	20
Oxford/AstraZeneca, Pfizer/BioNTech	13
Johnson&Johnson, Moderna, Oxford/AstraZeneca, Pfizer/BioNTech	12
Pfizer/BioNTech	12
Oxford/AstraZeneca, Sinopharm/Beijing	8
Sinopharm/Beijing	8
Sputnik V	8
Moderna, Pfizer/BioNTech	6
Oxford/AstraZeneca, Pfizer/BioNTech, Sinovac	6

Name: vaccines, dtype: int64



Number of total vaccinations according to countries

