

Source: [\[KBhBIO101Viruses\]](#)

# 1 | Viral Genetic Mutations

## 1.1 | Genetic Shift

Whole segments of genome exchange abruptly as two flu viruses infect the same cell to create a new strand. There are two mechanisms by which happens — ( #ASK ) the **crossing-over mechanism** and **genome segment reassortment**

### 1.1.1 | Crossing-over

Self-mixing of #ask #ask #ask of either polyprotein sections or ozaki fragments (I think the latter)

### 1.1.2 | genome segment reassortment

(I think that's where two viruses coinfect the same cell, causing cross-talk in swapping segments)

## 1.2 | Genetic Drift

This usually occurs due an error in a polymerase-driven process, where single/groups of nucleotides flip slowly over time due to mistakes in [\[KBhBIO101RNAReplication\]](#).

The former is an environment-dependent process, where the latter is able to be modeled as it is due to predictable transcription mistake.

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1.3 | Mutation w.r.t. [\[KBhBIO101TypesOfViruses\]](#)

## Viral genome size vs. mutation rate

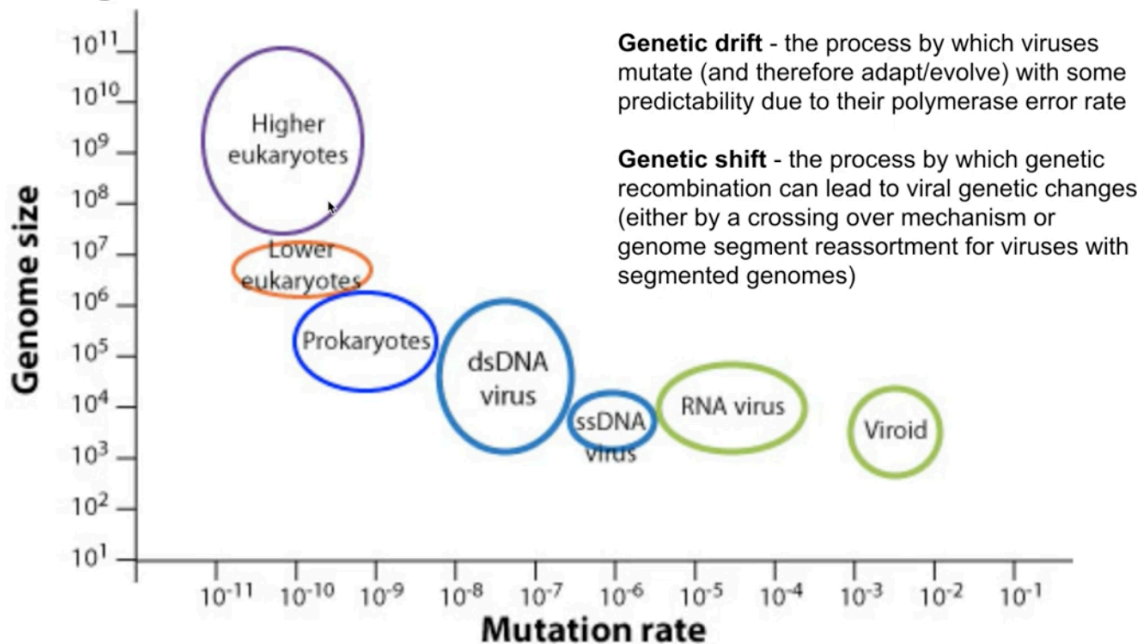


Figure 1: Screen Shot 2020-10-12 at 11.24.39 PM.png

- **RNA viruses** could mutate more because it does not have checks
- **More complex+largest viruses** (DNA viruses) harder to mutate