Ebolavirus has been posing a threat to human health since 1976, when it first appeared, causing severe symptoms and leading to death [1]. While at first the outbreaks were limited to a small number of cases, ranging from 32 to 318, in 2013 an outbreak occurred, that lasted until 2016, with 28646 recorded cases [2]. This was the first outbreak that occurred in west Africa and was also reported in places outside Africa and due to its duration and magnitude it was characterised as the largest Ebola epidemic [1]. During this outbreak there was a concern that ebolavirus is mutating faster, which could increase its virulency, transmissibility and antigenicity [1]. This assumption was based on computational studies that were carried out early during the epidemic and estimated atypically high rates of mutation of the virus, that were almost two times higher than what had been observed until that time [3]. However, later studies that included a larger number of viral sequences sampled over the whole epidemic, found lower mutation rates and disproved this belief [4]. These genome sequencing studies revealed that Ebola Makona, which is the Ebola strain responsible for this outbreak, has a substitution rate between 0.87e-3 and 1.42e-3 [8], that is within the range of substitution rates for RNA viruses, 10e-2 – 10e-5 [9].It has now been proved that those high rate estimations at the beginning of the outbreak were due to the small number of samples and the limitations of the computational methods used, and the fact that evolutionary rates sampled over short periods of time can lead to higher mutation rate estimations as many deleterious mutations have not been weeded out yet by natural selection [4].

In May of 2018 a new Ebola outbreak was reported in DRC, with 3318 cases reported by December of 2019 [5]. Although there are signs that the number of cases is declining, the epidemic continues to spread [5] and because of this it is harder to assess its magnitude and make assumptions about the rate of mutation. Despite the fact that we do not yet have information about the entirety of this outbreak, it has been clear since its beginning that it is one of the largest outbreaks that have occurred [5]. Further studies have shown that the epidemiological features as well as the case fatality ratio are similar to other outbreaks that have previously occurred [6]. Sequencing analysis of early samples revealed that the ebolavirus Tumba, which evolves at a slower rate than other ebolavirus variants, was the cause of this outbreak. Although there were some differences found in the rate of evolution between ebolavirus Tuba and ebolavirus Makona, their intra-outbreak rates were found to be similar [7].

In recent years there have been developments in the field of immunology that allow in depth genomic surveillance of viruses through next-generation sequencing, so sequences can be directly obtained from samples [1]. This, in combination with the use of better computational models, that allow for a more relaxed set-up that doesn’t heavily rely on assumptions, have led to more clear rate estimations [4]. RNA viruses, like Ebola, evolve rapidly and mutations can accumulate over short periods of time, so being able to obtain full length sequences quickly is of great importance for understanding its epidemiology [10,11]. The two previously mentioned Ebola outbreaks were the first outbreaks on which real-time genomic surveillance was applied [8]. During the 2013-2016 Ebola outbreak, Quick et al. created a portable genome sequencing device, that could generate readings within an hour [8]. The analysis of the sequences obtained through this technique gave insightful information about the lineages of Ebola that were responsible for the epidemic, how they arose, when their most common ancestor appeared, how they were related to previous outbreaks and when and where the outbreak first started [1]. Studying the origins of the different lineages gave researches a better understanding of the transmission patterns and whether there was species jumping during the outbreak [1]. Sequencing data were also useful for studying evolutionary rate, as it made it easier to analyse the nucleotide substitutions per site per year and view the number of variable sites within a dataset [1].

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