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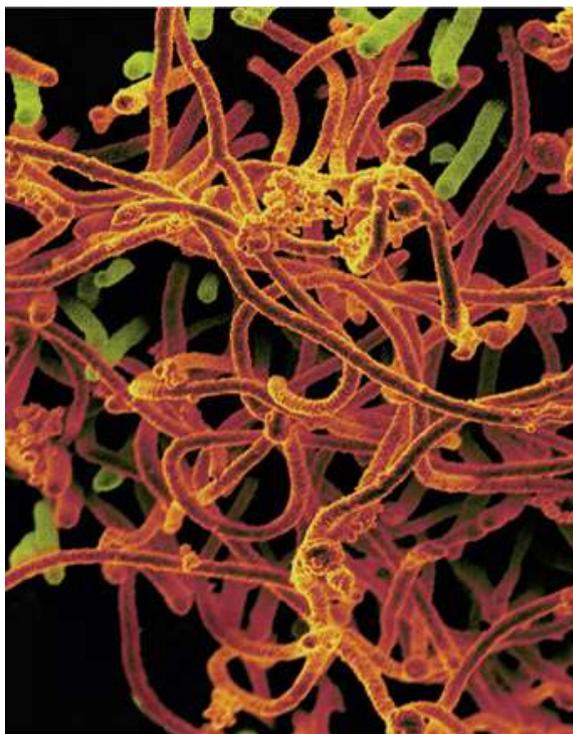


### Mutation rate and genotype variation of Ebola virus from Mali case sequences –review Science DOI: 10.1126/science.aaa5646

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#### Abstrakt

The occurrence of Ebola virus (EBOV) in West Africa during 2013–2015 is unprecedented.



Early reports suggested that in this outbreak EBOV is mutating twice as fast as previously observed, which indicates the potential for changes in transmissibility and virulence and could render current molecular diagnostics and countermeasures ineffective. We have determined additional full-length sequences from two clusters of imported EBOV infections into Mali, and we show that the nucleotide substitution rate ( $9.6 \times 10^{-4}$  substitutions per site per year) is consistent with rates observed in Central African outbreaks. In addition, overall variation among all genotypes observed remains low. Thus, our data indicate that EBOV is not undergoing rapid evolution in humans during the current outbreak. This finding has important implications for outbreak response and public health decisions and should alleviate several previously raised concerns.

*Ebola virus (orange) isolated from a patient in Mali.*

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