

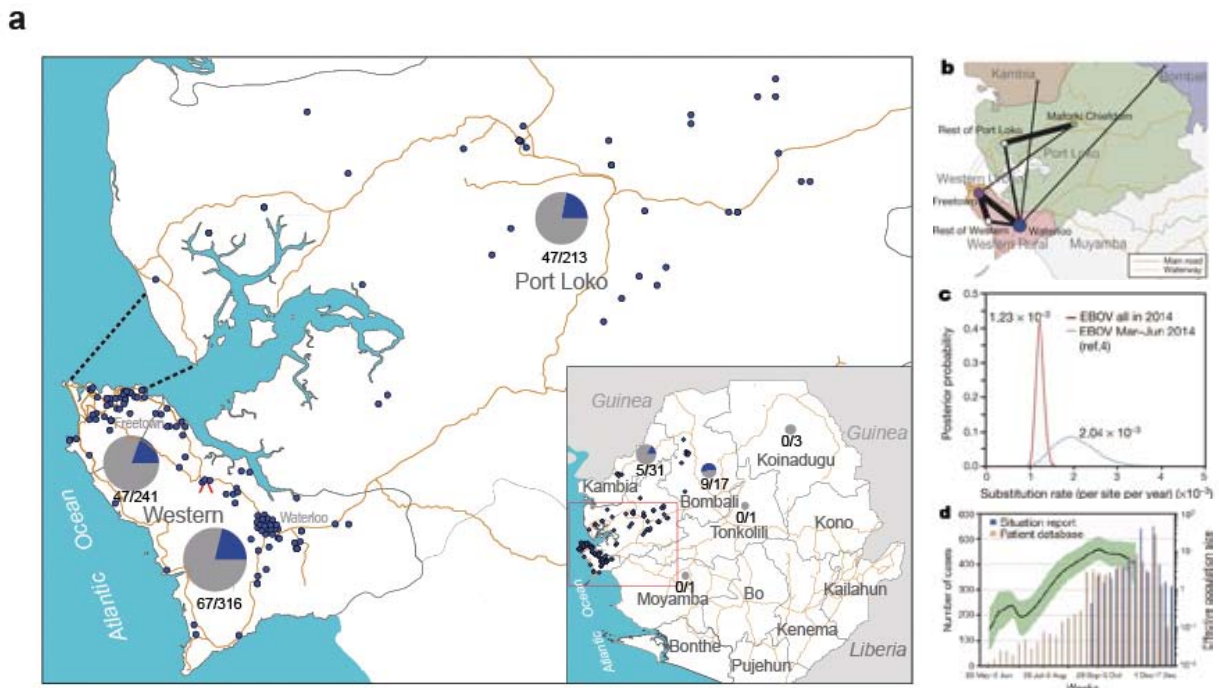
Ebola Mutation Slower than Thought

By SONG Jianlan (Staff Reporter)

The new variation of Ebola virus (EBOV) is not mutating at an accelerated rate, but a steady one, reports a group of Chinese scientists in a paper published in *Nature* on May 14. This result is drawn from an analysis of 175 genome sequences collected from five severely stricken districts in Sierra Leone from September to November 2014. The team reveals sharply increased phylogenetic and genetic diversity in this new variation, but no sign of rapid mutation as reported in previous research. Inferred from the latest data, this might help ease the worries about its virulent evolution, shedding new light on vaccine development and therapeutic strategies for this ongoing epidemic.

First identified in March 2014, EBOV is believed to be the culprit of an independent outbreak and the subsequent human-to-human transmission in West Africa. It infected more than 25,000 people and claimed a death toll of over 10,000, according to a situation report released by the World Health Organization on April 1, 2015, marking the biggest and most serious outbreak so far.

Analysis based on earlier specimens indicated an evolutionary rate much faster than previous epidemics, and hence aroused widespread concerns that this virus might become more virulent or deadlier when spreading. Meanwhile it also triggered disputes in the scientific community, as the tempo of evolution has great impact on



Geographic distribution and evolutionary dynamics of 2014 EBOV. a, geographical distribution of 823 EBOV samples and 175 newly sequenced genomes. b, the phylogeographic linkage of 2014 EBOV in Sierra Leone. c, nucleotide substitution rate of 2014 EBOV. d, growth of the effective population size of 2014 EBOV. (Source: Tong YG, *et al*, *Nature* 2015, doi:10.1038/nature14490; Image and legend by courtesy of Prof. GAO)

vaccine development and therapeutic research. However only very limited viral information is available for further studies and verification since July 2014, when this extremely dangerous epidemic went into a rapid growth. To some extent, the evolutionary dynamics revealed in this research could fill this gap.

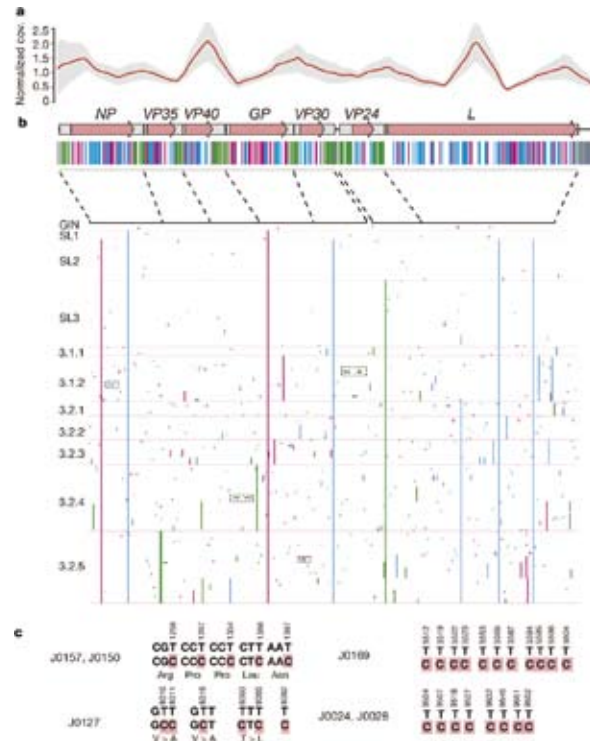
Upon request of Sierra Leone Government, Chinese Government sent a mobile laboratory testing team to this country in September 2014, joining forces from Chinese Center for Disease Control and Prevention (CCDCP), the Academy of Military Medical Sciences, Chinese Academy of Medical Sciences and the Chinese Academy of Sciences (CAS). CAS Member Prof. GAO Fu (George F. Gao), Vice Director of CCDCP and a professor at the Institute of Microbiology, CAS (IMCAS) worked as the co-leader of the team, and also designed and supervised the research.

During their adventure, the joint team conducted medical examinations for over 3,000 people and successfully extracted 175 specimens of EBOV from over 800 Ebola-positive individuals; and subsequently performed full-genome sequencing of the specimens.

Now comparing the datasets from this round of sequencing and those from an earlier research, the team were able to interpret how the virus might have evolved and transmitted.

In their analysis of these valuable datasets, the researchers identified multiple novel lineages, but an evolutionary rate (indicated by substitution rate of mutations) approximately the same as what observed between previous epidemics.

The virus might have evolved very fast at the onset phase; the researchers infer, but slowed down at the later



The researchers report steady, rather than accelerated genomic variations of the 2014 EBOV, based on an analysis of the latest data. (Source: Tong YG, *et al*, *Nature* 2015, doi:10.1038/nature14490; Image by courtesy of Prof. GAO)

phases of its evolutionary trajectory.

Given the sharp increase in its genetic diversity, however, the researchers suggest that extensive surveillance of EBOV still necessary in Sierra Leone, Guinea and Liberia, to better understand the viral evolution and transmission dynamics of ongoing outbreaks.

For more information please refer to:

Tong YG, Shi WF and Liu D, *et al*. (2015) Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone, *Nature*, doi: 10.1038/nature14490.
Hayden, E. C. (2015) Latest Ebola data rule out rapid mutation, *Nature*, doi: 10.1038/nature.2015.17554.