

Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak

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In its largest outbreak, Ebola virus disease is spreading through Guinea, Liberia, Sierra Leone, and Nigeria. We sequenced 99 Ebola virus genomes from 78 patients in Sierra Leone to ~2,000x coverage. We observed a rapid accumulation of interhost and intrahost genetic variation, allowing us to characterize patterns of viral transmission over the initial weeks of the epidemic. This West African variant likely diverged from Middle African lineages ~2004, crossed from Guinea to Sierra Leone in May 2014, and has exhibited sustained human-to-human transmission subsequently, with no evidence of additional zoonotic sources. Since many of the mutations alter protein sequences and other biologically meaningful targets, they should be monitored for impact on diagnostics, vaccines, and therapies critical to outbreak response.

Ebola virus (EBOV; formerly Zaire ebolavirus), one of five ebolaviruses, is a lethal human pathogen, causing Ebola virus disease (EVD) with an average case fatality rate of 78% (1). Previous EVD outbreaks were confined to remote regions of Middle Africa; the largest, in 1976, had 318 cases (2) (Fig. 1A). The current outbreak started in February 2014 in Guinea, West Africa (3) and spread into Liberia in March, Sierra Leone in May, and Nigeria in late July. It is the largest known EVD outbreak and is expanding exponentially with a doubling period of 34.8 days (Fig. 1B). As of August 19th, 2,240 cases and 1,229 deaths have been docu-

mented (4, 5). Its emergence in the major cities of Conakry (Guinea), Freetown (Sierra Leone), Monrovia (Liberia), and Lagos (Nigeria) raises the specter of increasing local and international dissemination.

In an ongoing public health crisis, where accurate and timely information is crucial, new genomic technologies can provide near real-time insights into the pathogen's origin, transmission dynamics, and evolution. We used massively parallel viral sequencing to understand how and when EBOV entered human populations in the 2014 West African outbreak, whether the outbreak is continuing to be fed by new transmissions from its natural reservoir, and how the virus changed, both before and after its recent jump to humans.

In March 2014, Kenema Government Hospital (KGH) established EBOV surveillance in Kenema, Sierra Leone, near the origin of the 2014 outbreak (Fig. 1C and fig. S1) (6). Following standards for field-based tests in previous (7) and current (3) outbreaks, KGH performed conventional PCR-based EBOV diagnostics (8) (fig. S2); all tests were negative through early May. On May 25, KGH scientists confirmed the first case of EVD in Sierra Leone. Investigation by the Ministry of Health and Sanitation (MoHS) uncovered an epidemiological link between this case and the burial of a traditional healer who had treated EVD patients in Guinea. Tracing led to 13 additional cases—all females who attended the burial. We obtained ethical approval from MoHS, the Sierra Leone Ethics and Scientific Review Committee, and our U.S. institutions to sequence patient samples in the U.S. using approved safety standards (6).

We evaluated four independent library preparation methods and two sequencing platforms (9) (table S1) for our first batch of 15 inactivated EVD samples from 12 patients. Nextera library construction and Illumina sequencing provided the most complete genome assembly and reliable intrahost single nucleotide variant (iSNV, frequency >0.5%) identification (6). We used this combination for a second batch of 84 samples from 66 additional patients, performing two independent replicates from each sample (Fig. 1D). We also sequenced 35 samples from suspected EVD cases that tested negative for EBOV; genomic analysis identified other known pathogens, including Lassa virus, HIV-1, enterovirus A and malaria parasites (fig. S3).

In total, we generated 99 EBOV genome sequences from 78 confirmed EVD patients, representing over 70% of the EVD patients diagnosed in Sierra Leone in late May to mid June; we employed multiple

extraction methods or timepoints for 13 patients (table S2). Median coverage was >2,000x, spanning more than 99.9% of EBOV coding regions (Fig. 1, D and E, and table S2).

We combined the 78 Sierra Leonean sequences with 3 published Guinean samples (3) (correcting 21 likely sequencing errors in the latter (6)) to obtain a dataset of 81 sequences. They reveal 341 fixed substitutions between the 2014 EBOV and all previously published EBOV (35 nonsynonymous, 173 synonymous, 133 noncoding), with an additional 55 single nucleotide polymorphisms (SNPs) (fixed within individual patients) within the West African outbreak (15 nonsynonymous, 25 synonymous, 15 noncoding). Notably, the Sierra Leonean genomes differ from PCR probes for five separate assays used for EBOV and pan-filovirus diagnostics (table S3).

Deep-sequence coverage allowed identification of 263 iSNVs (73 nonsynonymous, 108 synonymous, 70 noncoding, and 12 frameshift) in the Sierra Leone patients (6). For all patients with multiple time points, consensus sequences were identical and iSNV frequencies remained stable (fig. S4). One notable intrahost variation is the RNA editing site of the glycoprotein (GP) gene (fig. S5A) (10–12), which we characterize in patients (6).

Phylogenetic comparison to all 20 genomes from earlier outbreaks suggests the 2014 West African virus likely spread from Middle Africa within the last decade. Rooting the phylogeny using divergence to other ebolavirus genomes is problematic (Fig. 2A and fig. S6) (6, 13). However, rooting the tree on the oldest outbreak reveals a strong correlation between sample date and root-to-tip distance, with a substitution rate of 8×10^{-4} /site/year (Fig. 2B and fig. S7) (13). This suggests that the lineages of the three most recent outbreaks all diverged from a common ancestor at roughly the same time c. 2004 (Fig. 2C and Fig. 3A), supporting the hypothesis that each outbreak represents an independent zoonotic event from the same genetically diverse viral population in its natural reservoir.

Genetic similarity across the sequenced 2014 samples suggests a single transmission from the natural reservoir, followed by human-to-human transmission during the outbreak. Molecular dating places the common ancestor of all sequenced Guinea and Sierra Leone lineages around late February 2014 (Fig. 3B), three months after the earliest suspected cases in Guinea (3); this coalescence would be unlikely had there been multiple transmissions from the natural reservoir. Thus, in contrast to some previous EVD outbreaks (14), continued human-reservoir exposure is unlikely to have contributed to the growth of this epidemic in areas represented by available sequence data.

Our data suggest the Sierra Leone outbreak stemmed from the introduction of two genetically distinct viruses from Guinea around the same time. Samples from 12 of the first EVD patients in Sierra Leone, all believed to have attended the funeral of an EVD case from Guinea, fall into two distinct clusters (clusters 1 and 2) (Fig. 4A and fig. S8). Molecular dating places the divergence of these two lineages in late April (Fig. 3B), pre-dating their co-appearance in Sierra Leone in late May (Fig. 4B), suggesting the funeral attendees were most likely infected by two lineages then circulating in Guinea, possibly at the funeral (fig. S9). All subsequent diversity in Sierra Leone accumulated on the background of those two lineages (Fig. 4A), consistent with epidemiological information from tracing contacts.

Patterns in observed intrahost and interhost variation provide important insights about transmission and epidemiology. Groups of patients with identical viruses or with shared intrahost variation show temporal patterns suggesting transmission links (fig. S10). One iSNV (position 10,218) shared by twelve patients is later observed as fixed within 38 patients, becoming the majority allele in the population (Fig. 4C) and defining a third Sierra Leone cluster (Fig. 4, A and D, and fig. S8). Repeated propagation at intermediate frequency suggests that transmission of multiple viral haplotypes may be common. Geographic, temporal, and

epidemiological metadata supports the transmission clustering inferred from genetic data (Fig. 4, D and E, and fig. S11) (6).

The observed substitution rate is roughly twice as high within the 2014 outbreak as between outbreaks (Fig. 4F). Mutations are also more frequently nonsynonymous during the outbreak (Fig. 4G). Similar findings have been seen previously (15) and are consistent with expectations from incomplete purifying selection (16–18). Determining whether individual mutations are deleterious, or even adaptive, would require functional analysis; however, the rate of nonsynonymous mutations suggests that continued progression of this epidemic could afford an opportunity for viral adaptation (Fig. 4H), underscoring the need for rapid containment.

As in every EVD outbreak, the 2014 EBOV variant carries a number of genetic changes distinct to this lineage; our data do not address whether these differences are related to the severity of the outbreak. However, the catalog of 395 mutations, including 50 fixed nonsynonymous changes with 8 at positions with high levels of conservation across ebolaviruses, provide a starting point for such studies (table S4).

To aid in relief efforts and facilitate rapid global research, we immediately released all sequence data as generated. Ongoing epidemiological and genomic surveillance is imperative to identify viral determinants of transmission dynamics, monitor viral changes and adaptation, ensure accurate diagnosis, guide research on therapeutic targets, and refine public-health strategies. It is our hope that this work will aid the multidisciplinary, international efforts to understand and contain this expanding epidemic.

In memoriam: Tragically, five co-authors, who contributed greatly to public health and research efforts in Sierra Leone, contracted EVD in the course of their work and lost their battle with the disease before this manuscript could be published. We wish to honor their memory.

References and Notes

1. J. H. Kuhn, L. E. Dodd, V. Wahl-Jensen, S. R. Radoshitzky, S. Bavari, P. B. Jahrling, Evaluation of perceived threat differences posed by filovirus variants. *Biosecur. Bioterror.* **9**, 361–371 (2011). [Medline doi:10.1089/bsp.2011.0051](https://doi.org/10.1089/bsp.2011.0051)
2. J. Burke, Ebola haemorrhagic fever in Zaire, 1976. *Bull. World Health Organ.* **56**, 271–293 (1978). [Medline doi:10.1056/NEJMoa1404505](https://doi.org/10.1056/NEJMoa1404505)
3. S. Baize *et al.*, Emergence of Zaire Ebola virus disease in Guinea—Preliminary report. *N. Engl. J. Med.* 10.1056/NEJMoa1404505 (2014). [doi:10.1056/NEJMoa1404505](https://doi.org/10.1056/NEJMoa1404505)
4. WHO, (2014), www.who.int/csr/don/archive/disease/ebola/en/
5. O. Reynard, V. Volchkov, C. Peyrefitte, Une première épidémie de fièvre à virus Ebola en Afrique de l'Ouest. *Med. Sci.* **30**, 671–673 (2014). [doi:10.1051/medsci/20143006018](https://doi.org/10.1051/medsci/20143006018)
6. See supplementary materials on Science Online.
7. J. S. Towner, T. K. Sealy, T. G. Ksiazek, S. T. Nichol, High-throughput molecular detection of hemorrhagic fever virus threats with applications for outbreak settings. *J. Infect. Dis.* **196** (suppl. 2), S205–S212 (2007). [Medline doi:10.1086/520601](https://doi.org/10.1086/520601)
8. M. Panning, T. Laue, S. Olschlager, M. Eickmann, S. Becker, S. Raith, M. C. Courbot, M. Nilsson, R. Gopal, A. Lundkvist, A. Caro, D. Brown, H. Meyer, G. Lloyd, B. M. Kummerer, S. Gunther, C. Drosten, Diagnostic reverse-transcription polymerase chain reaction kit for filoviruses based on the strain collections of all European biosafety level 4 laboratories. *J. Infect. Dis.* **196** (suppl. 2), S199–S204 (2007). [Medline doi:10.1086/520600](https://doi.org/10.1086/520600)
9. C. M. Malboeuf, X. Yang, P. Charlebois, J. Qu, A. M. Berlin, M. Casali, K. N. Pesko, C. L. Boutwell, J. P. DeVincenzo, G. D. Ebel, T. M. Allen, M. C. Zody, M. R. Henn, J. Z. Levin, Complete viral RNA genome sequencing of ultra-low copy samples by sequence-independent amplification. *Nucleic Acids Res.* **41**, e13 (2013). [Medline doi:10.1093/nar/gks794](https://doi.org/10.1093/nar/gks794)
10. A. Sanchez, S. G. Trappier, B. W. Mahy, C. J. Peters, S. T. Nichol, The virion glycoproteins of Ebola viruses are encoded in two reading frames and are expressed through transcriptional editing. *Proc. Natl. Acad. Sci. U.S.A.* **93**,

- 3602–3607 (1996).
11. V. E. Volchkov, S. Becker, V. A. Volchkova, V. A. Ternovoj, A. N. Kotov, S. V. Netesov, H. D. Klenk, GP mRNA of Ebola virus is edited by the Ebola virus polymerase and by T7 and vaccinia virus polymerases. *Virology* **214**, 421–430 (1995). [Medline doi:10.1006/viro.1995.0052](#)
 12. V. A. Volchkova, O. Dolnik, M. J. Martinez, O. Reynard, V. E. Volchkov, Genomic RNA editing and its impact on Ebola virus adaptation during serial passages in cell culture and infection of guinea pigs. *J. Infect. Dis.* **204** (suppl. 3), S941–S946 (2011). [Medline doi:10.1093/infdis/jir321](#)
 13. G. Dudas, A. Rambaut, Phylogenetic analysis of Guinea 2014 EBOV Ebolavirus outbreak. *PLOS Curr. Outbreaks* **6**, 10.1371/currents.outbreaks.84ee5ce43ec9dc0bf0670f7b8b417d (2014). [doi:10.1371/currents.outbreaks.84ee5ce43ec9dc0bf0670f7b8b417d](#)
 14. J. Kuhn, C. H. Calisher, Eds., *Filoviruses: A Compendium of 40 Years of Epidemiological, Clinical, and Laboratory Studies* (Springer, New York, 2008).
 15. M. J. Schreiber, E. C. Holmes, S. H. Ong, H. S. Soh, W. Liu, L. Tanner, P. P. Aw, H. C. Tan, L. C. Ng, Y. S. Leo, J. G. Low, A. Ong, E. E. Ooi, S. G. Vasudevan, M. L. Hibberd, Genomic epidemiology of a dengue virus epidemic in urban Singapore. *J. Virol.* **83**, 4163–4173 (2009). [Medline doi:10.1128/JVI.02445-08](#)
 16. J. O. Wertheim, S. L. Kosakovsky Pond, Purifying selection can obscure the ancient age of viral lineages. *Mol. Biol. Evol.* **28**, 3355–3365 (2011). [Medline doi:10.1093/molbev/msr170](#)
 17. S. Y. Ho, M. J. Phillips, A. Cooper, A. J. Drummond, Time dependency of molecular rate estimates and systematic overestimation of recent divergence times. *Mol. Biol. Evol.* **22**, 1561–1568 (2005). [Medline doi:10.1093/molbev/msi145](#)
 18. E. C. Holmes, Patterns of intra- and interhost nonsynonymous variation reveal strong purifying selection in dengue virus. *J. Virol.* **77**, 11296–11298 (2003). [Medline doi:10.1128/JVI.77.20.11296-11298.2003](#)
 19. J. R. Kugelman, M. S. Lee, C. A. Rossi, S. E. McCarthy, S. R. Radoshitzky, J. M. Dye, L. E. Hensley, A. Honko, J. H. Kuhn, P. B. Jahrling, T. K. Warren, C. A. Whitehouse, S. Bavari, G. Palacios, Ebola virus genome plasticity as a marker of its passaging history: A comparison of in vitro passaging to non-human primate infection. *PLOS ONE* **7**, e50316 (2012). [Medline doi:10.1371/journal.pone.0050316](#)
 20. S. Günther, M. Asper, C. Röser, L. K. Luna, C. Drosten, B. Becker-Ziaja, P. Borowski, H. M. Chen, R. S. Hosmane, Application of real-time PCR for testing antiviral compounds against Lassa virus, SARS coronavirus and Ebola virus in vitro. *Antiviral Res.* **63**, 209–215 (2004). [Medline doi:10.1016/j.antiviral.2004.05.001](#)
 21. G. Grard, R. Biek, J. J. Muyembe Tamfum, J. Fair, N. Wolfe, P. Formenty, J. Paweska, E. Leroy, Emergence of divergent Zaire ebola virus strains in Democratic Republic of the Congo in 2007 and 2008. *J. Infect. Dis.* **204** (suppl. 3), S776–S784 (2011). [Medline doi:10.1093/infdis/jir364](#)
 22. G. P. Kobinger, A. Leung, J. Neufeld, J. S. Richardson, D. Falzarano, G. Smith, K. Tierney, A. Patel, H. M. Weingartl, Replication, pathogenicity, shedding, and transmission of Zaire ebolavirus in pigs. *J. Infect. Dis.* **204**, 200–208 (2011). [Medline doi:10.1093/infdis/jir077](#)
 23. T. Hoenen, S. Jung, A. Herwig, A. Groseth, S. Becker, Both matrix proteins of Ebola virus contribute to the regulation of viral genome replication and transcription. *Virology* **403**, 56–66 (2010). [doi:10.1016/j.virol.2010.04.002](#)
 24. J. A. Blow, C. N. Mores, J. Dyer, D. J. Dohm, Viral nucleic acid stabilization by RNA extraction reagent. *J. Virol. Methods* **150**, 41–44 (2008). [Medline doi:10.1016/j.jviromet.2008.02.003](#)
 25. A. R. Trombley, L. Wachter, J. Garrison, V. A. Buckley-Beason, J. Jahrling, L. E. Hensley, R. J. Schoepp, D. A. Norwood, A. Goba, J. N. Fair, D. A. Kulesh, Comprehensive panel of real-time TaqMan polymerase chain reaction assays for detection and absolute quantification of filoviruses, arenaviruses, and New World hantaviruses. *Am. J. Trop. Med. Hyg.* **82**, 954–960 (2010). [Medline doi:10.4269/ajtmh.2010.09-0636](#)
 26. J. D. Morlan, K. Qu, D. V. Sinicropi, Selective depletion of rRNA enables whole transcriptome profiling of archival fixed tissue. *PLOS ONE* **7**, e42882 (2012). [Medline doi:10.1371/journal.pone.0042882](#)
 27. X. Adiconis, D. Borges-Rivera, R. Satija, D. S. DeLuca, M. A. Busby, A. M. Berlin, A. Sivachenko, D. A. Thompson, A. Wysoker, T. Fennell, A. Gnirke, N. Pochet, A. Regev, J. Z. Levin, Comparative analysis of RNA sequencing methods for degraded or low-input samples. *Nat. Methods* **10**, 623–629 (2013). [Medline doi:10.1038/nmeth.2483](#)
 28. L. Jiang, F. Schlesinger, C. A. Davis, Y. Zhang, R. Li, M. Salit, T. R. Gingeras, B. Oliver, Synthetic spike-in standards for RNA-seq experiments. *Genome Res.* **21**, 1543–1551 (2011). [Medline doi:10.1101/gr.121095.111](#)
 29. R. C. Edgar, MUSCLE: Multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* **32**, 1792–1797 (2004). [Medline doi:10.1093/nar/gkh340](#)
 30. P. Cingolani, A. Platts, L. Wang, M. Coon, T. Nguyen, L. Wang, S. J. Land, X. Lu, D. M. Ruden, A program for annotating and predicting the effects of single nucleotide polymorphisms, SnpEff: SNPs in the genome of *Drosophila melanogaster* strain w1118; iso-2; iso-3. *Fly* **6**, 80–92 (2012). [Medline doi:10.4161/fly.19695](#)
 31. A. Stamatakis, T. Ludwig, H. Meier, RAxML-III: A fast program for maximum likelihood-based inference of large phylogenetic trees. *Bioinformatics* **21**, 456–463 (2005). [doi:10.1093/bioinformatics/bti191](#)
 32. F. Ronquist, J. Huelsenbeck, MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* **19**, 1572–1574 (2003). [doi:10.1093/bioinformatics/btg180](#)
 33. A. J. Drummond, M. A. Suchard, D. Xie, A. Rambaut, Bayesian phylogenetics with BEAUti and the BEAST 1.7. *Mol. Biol. Evol.* **29**, 1969–1973 (2012). [Medline doi:10.1093/molbev/mss075](#)
 34. M. Hasegawa, H. Kishino, T. Yano, Dating of the human-ape splitting by a molecular clock of mitochondrial DNA. *J. Mol. Evol.* **22**, 160–174 (1985). [Medline doi:10.1007/BF02101694](#)
 35. Z. Yang, Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: Approximate methods. *J. Mol. Evol.* **39**, 306–314 (1994). [Medline doi:10.1007/BF00160154](#)
 36. M. S. Gill, P. Lemey, N. R. Faria, A. Rambaut, B. Shapiro, M. A. Suchard, Improving Bayesian population dynamics inference: A coalescent-based model for multiple loci. *Mol. Biol. Evol.* **30**, 713–724 (2013). [Medline doi:10.1093/molbev/mss265](#)
 37. A. J. Drummond, S. Y. Ho, M. J. Phillips, A. Rambaut, Relaxed phylogenetics and dating with confidence. *PLOS Biol.* **4**, e88 (2006). [Medline doi:10.1371/journal.pbio.0040088](#)
 38. G. Baele, P. Lemey, S. Vansteelandt, Make the most of your samples: Bayes factor estimators for high-dimensional models of sequence evolution. *BMC Bioinform.* **14**, 85 (2013). [doi:10.1186/1471-2105-14-85](#)
 39. M. A. Ferreira, M. C. O'Donovan, Y. A. Meng, I. R. Jones, D. M. Ruderfer, L. Jones, J. Fan, G. Kirov, R. H. Perlis, E. K. Green, J. W. Smoller, D. Grozeva, J. Stone, I. Nikolov, K. Chambert, M. L. Hamsheer, V. L. Nimgaonkar, V. Moskvina, M. E. Thase, S. Caesar, G. S. Sachs, J. Franklin, K. Gordon-Smith, K. G. Ardlie, S. B. Gabriel, C. Fraser, B. Blumenstiel, M. Defelice, G. Breen, M. Gill, D. W. Morris, A. Elkin, W. J. Muir, K. A. McGhee, R. Williamson, D. J. MacIntyre, A. W. MacLean, C. D. St. M. Robinson, M. Van Beck, A. C. Pereira, R. Kandaswamy, A. McQuillin, D. A. Collier, N. J. Bass, A. H. Young, J. Lawrence, I. N. Ferrier, A. Anjorin, A. Farmer, D. Curtis, E. M. Scolnick, P. McGuffin, M. J. Daly, A. P. Corvin, P. A. Holmans, D. H. Blackwood, H. M. Gurling, M. J. Owen, S. M. Purcell, P. Sklar, N. Craddock, Collaborative genome-wide association analysis supports a role for ANK3 and CACNA1C in bipolar disorder. *Nat. Genet.* **40**, 1056–1058 (2008). [Medline doi:10.1038/ng.209](#)
 40. M. Mehedi, D. Falzarano, J. Seebach, X. Hu, M. S. Carpenter, H. J. Schnittler, H. Feldmann, A new Ebola virus nonstructural glycoprotein expressed through RNA editing. *J. Virol.* **85**, 5406–5414 (2011). [Medline doi:10.1128/JVI.02190-10](#)
 41. T. R. Gibb, D. A. Norwood Jr., N. Woollen, E. A. Henchal, Development and evaluation of a fluorogenic 5' nuclease assay to detect and differentiate between Ebola virus subtypes Zaire and Sudan. *J. Clin. Microbiol.* **39**, 4125–4130 (2001). [Medline doi:10.1128/JCM.39.11.4125-4130.2001](#)
 42. J. M. Morvan, V. Deubel, P. Gounon, E. Nakoune, P. Barriere, S. Murri, O. Perpete, B. Selekon, D. Coudrier, A. Gautier-Hion, M. Colyn, V. Volekhov, Identification of Ebola virus sequences present as RNA or DNA in organs of terrestrial small mammals of the Central African Republic. *Microbes Infect.* **1**, 1193–1201 (1999). [Medline doi:10.1016/S1286-4579\(99\)00242-7](#)
 43. A. Sanchez, T. G. Ksiazek, P. E. Rollin, M. E. Miranda, S. G. Trappier, A. S. Khan, C. J. Peters, S. T. Nichol, Detection and molecular characterization of Ebola viruses causing disease in human and nonhuman primates. *J. Infect. Dis.* **179** (suppl. 1), S164–S169 (1999). [Medline doi:10.1086/514282](#)
 44. M. Weidmann, E. Mühlberger, F. T. Hufert, Rapid detection protocol for

filoviruses. *J. Clin. Virol.* **30**, 94–99 (2004). [Medline doi:10.1016/j.jcv.2003.09.004](#)

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Supplementary Materials

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Materials and Methods

Supplementary Text

Figs. S1 to S11

Tables S1 to S4

Supplementary files S1 to S4

References (19–44)

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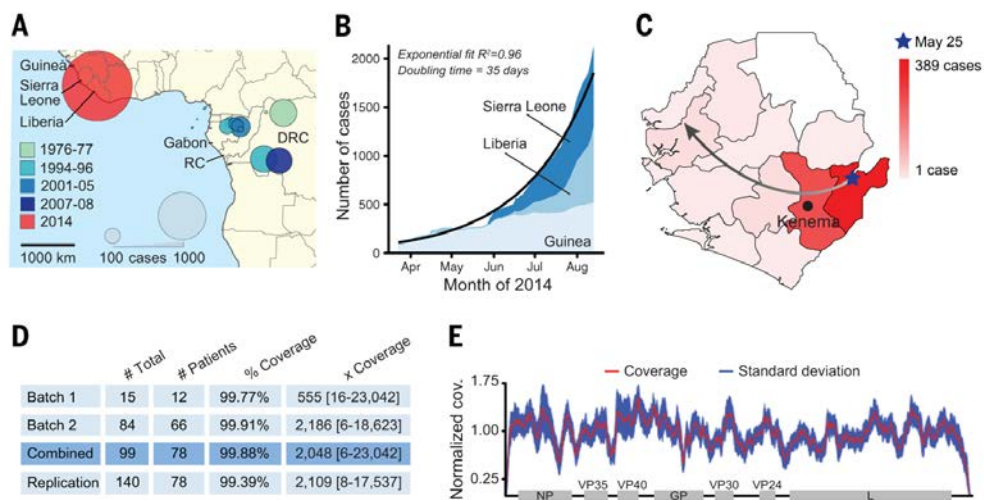


Fig. 1. Ebola outbreaks, historical and current. (A) Historical EVD outbreaks, colored by decade. Circle area represents total number of cases (RC = Republic of the Congo; DRC = Democratic Republic of Congo). (B) 2014 outbreak growth (confirmed, probable and suspected cases). (C) Spread of EVD in Sierra Leone by district. The gradient denotes number of cases and the arrows depict likely direction. (D) EBOV samples from 78 patients were sequenced in two batches, totaling 99 viral genomes (Replication = technical replicates (6)). Mean coverage and median depth of coverage with range are shown. (E) Combined normalized (to the sample average) coverage across sequenced EBOV genomes.

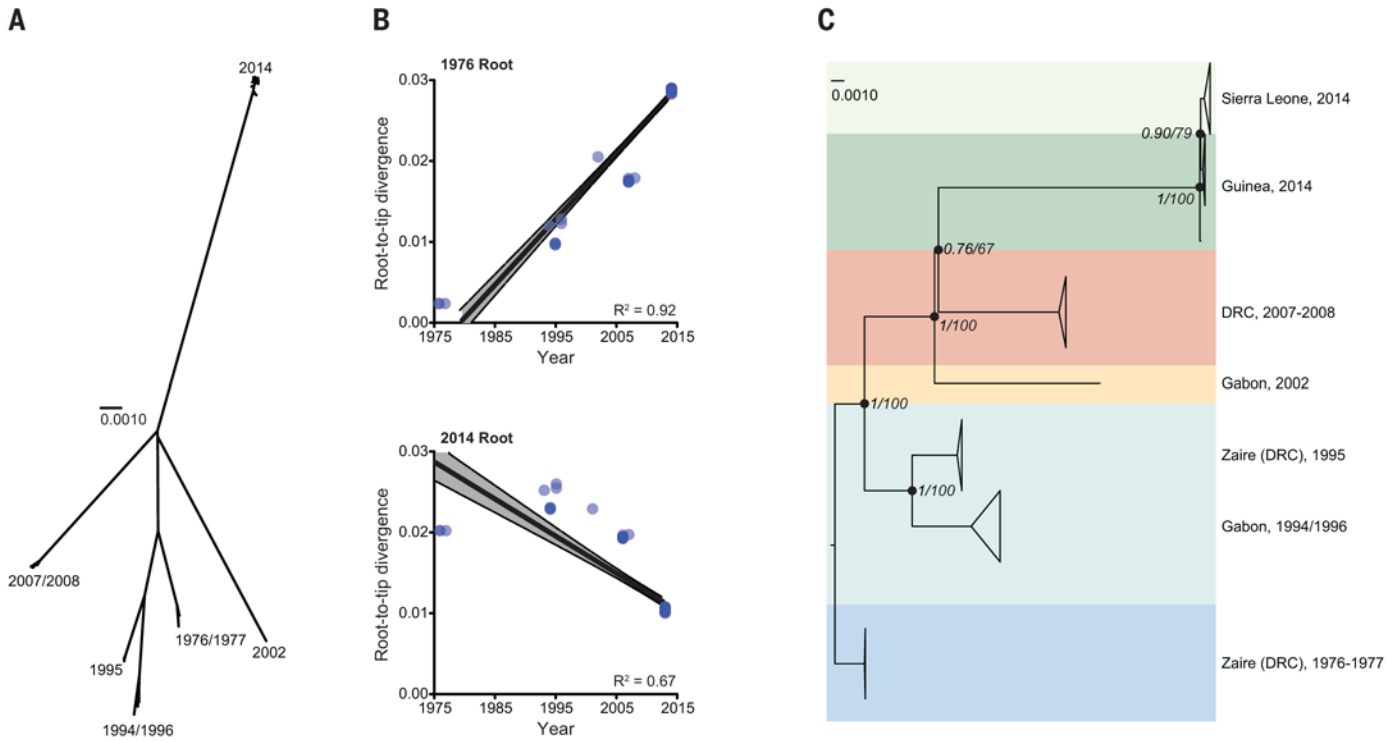


Fig. 2. Relationship between outbreaks. (A) Unrooted phylogenetic tree of EBOV samples; each major clade corresponds to a distinct outbreak (scale bar = nucleotide substitutions/site). (B) Root-to-tip distance correlates better with sample date when rooting on the 1976 branch ($R^2 = 0.92$, top) than on the 2014 branch ($R^2 = 0.67$, bottom). (C) Temporally rooted tree from (A).

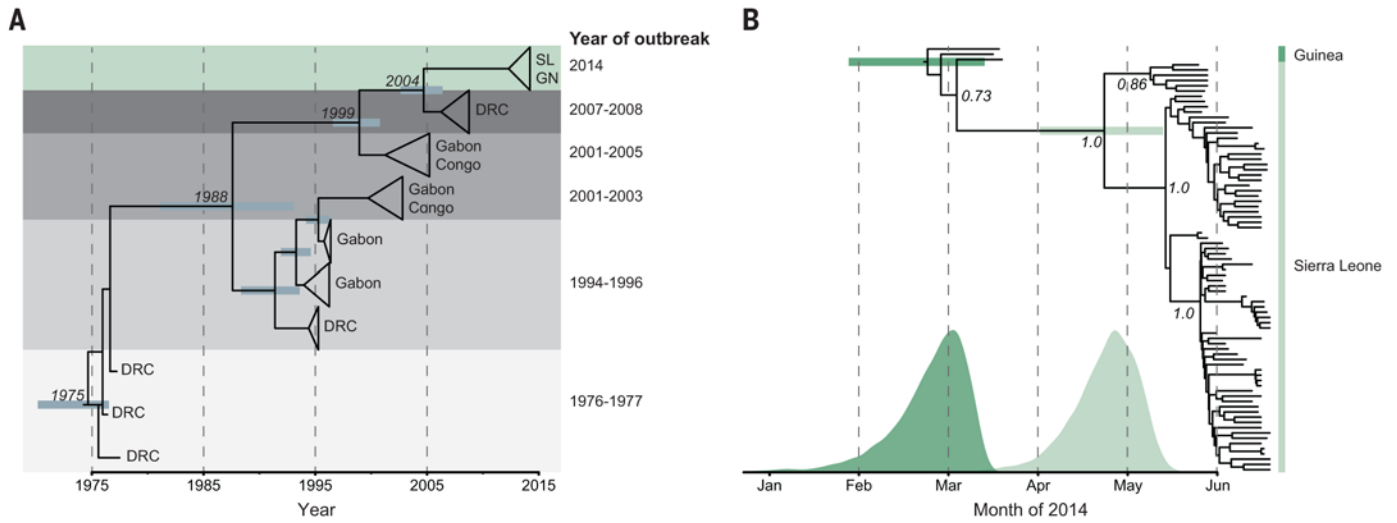


Fig. 3. Molecular dating of the 2014 outbreak. (A) BEAST dating of the separation of the 2014 lineage from Middle African lineages (SL = Sierra Leone; GN = Guinea; DRC = Democratic Republic of Congo; tMRCA: Sep 2004, 95% HPD: Oct 2002 - May 2006). (B) BEAST dating of the tMRCA of the 2014 West African outbreak (tMRCA: Feb 23, 95% HPD: Jan 27 - Mar 14) and the tMRCA of the Sierra Leone lineages (tMRCA: Apr 23, 95% HPD: Apr 2 - May 13); probability distributions for both 2014 divergence events overlaid below. Posterior support for major nodes is shown.

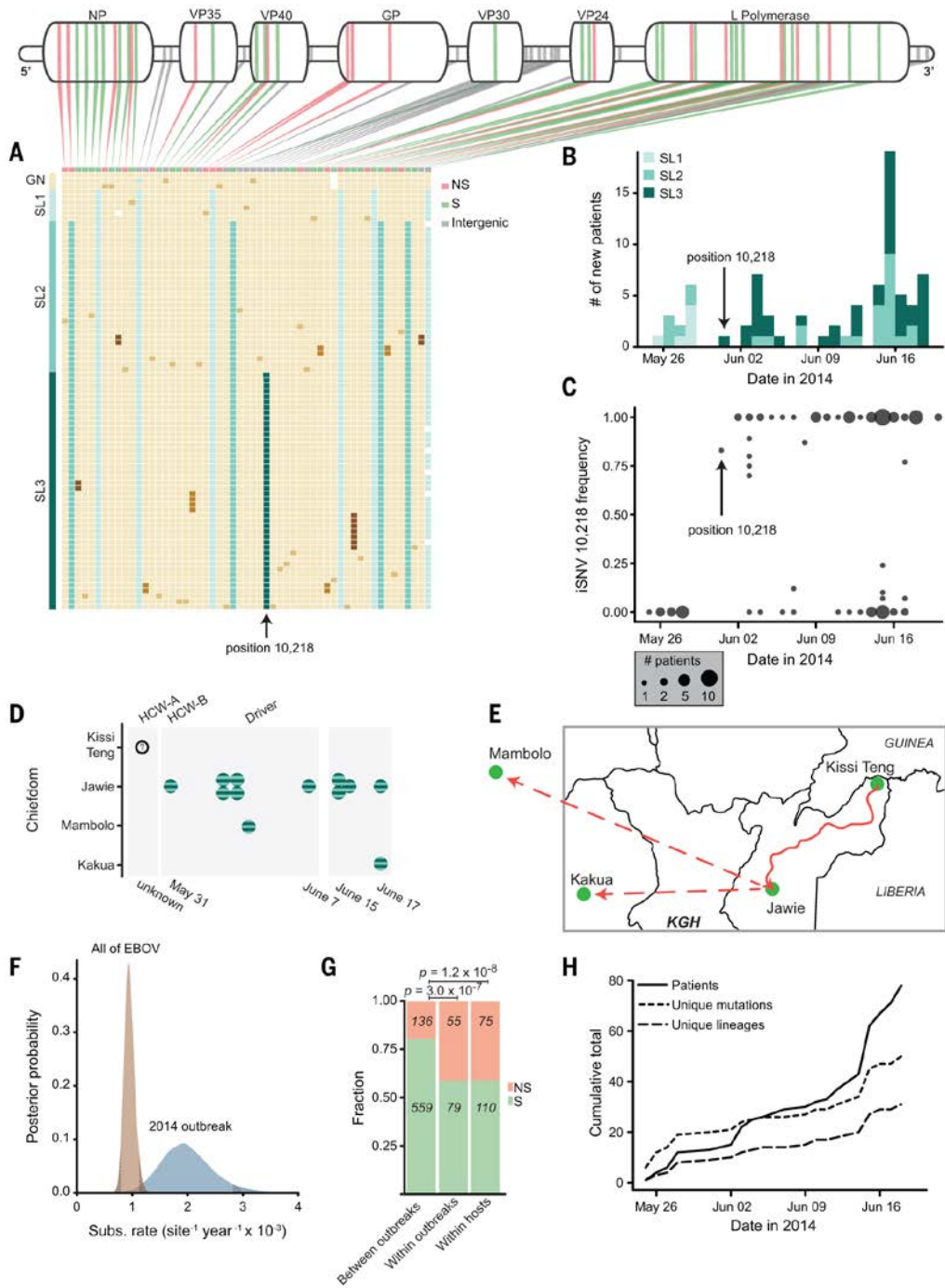


Fig. 4. Viral dynamics during the 2014 outbreak. (A) Mutations, one patient sample per row; beige = identical to Kissidougou Guinean sequence (accession KJ660346). The top row shows the type of mutation (green: synonymous, pink: nonsynonymous, intergenic: gray), with genomic locations indicated above. Clusters assignments are shown on left. (B) Number of EVD-confirmed patients per day, colored by cluster (arrow: first appearance of the derived allele at position 10,218, distinguishing clusters 2 and 3). (C) Intrahost frequency of SNP 10,218 in all 78 patients (absent in 28 patients, polymorphic in 12, fixed in 38). (D and E) 12 patients carrying iSNV 10,218 cluster geographically and temporally (HCW-A = unsequenced health care worker, Driver drove HCW-A from Kissi Teng to Jawie, then continued alone to Mambolo, HCW-B treated HCW-A). (F) Substitution rates within the 2014 outbreak and between all EVD outbreaks. (G) Proportion of nonsynonymous changes observed on different time scales (green = synonymous; pink = nonsynonymous). (H) Acquisition of genetic variation over time. 50 mutational events (short dashes) and 29 new viral lineages (long dashes) were observed (intra-host variants not included).