



# Evaluation of the Potential Impact of Ebola Virus Genomic Drift on the Efficacy of Sequence-Based Candidate Therapeutics

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**ABSTRACT** Until recently, Ebola virus (EBOV) was a rarely encountered human pathogen that caused disease among small populations with extraordinarily high lethality. At the end of 2013, EBOV initiated an unprecedented disease outbreak in West Africa that is still ongoing and has already caused thousands of deaths. Recent studies revealed the genomic changes this particular EBOV variant undergoes over time during human-to-human transmission. Here we highlight the genomic changes that might negatively impact the efficacy of currently available EBOV sequence-based candidate therapeutics, such as small interfering RNAs (siRNAs), phosphorodiamidate morpholino oligomers (PMOs), and antibodies. Ten of the observed mutations modify the sequence of the binding sites of monoclonal antibody (MAB) 13F6, MAB 1H3, MAB 6D8, MAB 13C6, and siRNA EK-1, VP24, and VP35 targets and might influence the binding efficacy of the sequence-based therapeutics, suggesting that their efficacy should be reevaluated against the currently circulating strain.

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As the Ebola virus disease (EVD) outbreak in West Africa of 2013 continues (1), public health and emerging infectious disease officers have declared a state of emergency (2). As of 8 January 2015, the mean lethality in this outbreak, caused by Ebola virus (EBOV), reached 39.4% (<http://www.who.int/csr/don/archive/disease/ebola/en/>). Another study, utilizing different methods, calculated the real case fatality rate at 70% (3). The uncontrolled situation in the outbreak area, now spread over six West African countries, and the risk of further EBOV exportation beyond the African continent prompted the World Health Organization to adopt emergency containment measures. Among them is the testing of as-yet-unapproved medical countermeasures in the affected human population (4–7).

At the moment, there are three treatment modalities directly based on the EBOV genomic sequence that have been explored for postexposure treatment of EVD with encouraging results in nonhuman-primate models: small interfering RNAs (siRNAs) (8) and phosphorodiamidate morpholino oligomers (PMOs) (9) targeting EBOV genome *L*, *VP24*, and/or *VP35* gene transcripts and passive immunotherapy based on antibodies or antibody cocktails targeting EBOV epitopes (10–14). Briefly, they inhibit viral replication by either targeting viral transcripts for degradation (siRNA), by blocking translation (PMO), or by acutely neutralizing the virus to allow the host to mount an effective immune response against the pathogen (passive immunotherapy). The binding sites for antisense therapeutics based on siRNAs and

PMOs are described in references 8 and 15, respectively. All of them were designed specifically against sequences derived from the EBOV variant causing an EVD outbreak around Yambuku, Zaire (present-day Democratic Republic of the Congo), in 1976 (Ebola virus/*H.sapiens-tc/COD/1976/Yambuku-Mayinga*; short name, EBOV/Yam-May; RefSeq no. *nc\_002549* [16]). All monoclonal antibodies used for passive immunotherapy were generated against the glycoprotein of the EBOV variant causing an EVD outbreak in Kikwit, Zaire, in 1995 (Ebola virus/*H.sapiens-tc/COD/1995/Kikwit-9510621*; short name, EBOV/Kik-9510621; GenBank no. *ay354458* [17]). Traditional peptide-based epitope mapping allowed the differentiation of conformational and linear epitopes. Coimmunoprecipitation assays were performed against broad domains of the glycoprotein to identify binding targets of conformational antibodies (18, 19). Table 1 summarizes publicly available information (8–12, 15, 18, 19) for the three treatment types, including therapeutic targeting and efficacy in postinoculation treatment of experimental EBOV infection in animals. All postexposure studies evaluating these therapeutics were completed using EBOV/Kik-9510621 as the challenge virus.

For this study, we reviewed all publicly available genomic information for the Ebola virus Makona variant (EBOV/Mak) causing the 2013–2014 West African outbreak (102 genomic sequences) (1, 20, 21) and assessed the potential of the observed EBOV/Mak genetic drift relative to EBOV/Yam-May and EBOV/Kik-9510621 to affect each therapeutic. When EBOV/Mak was

**TABLE 1** Summary of binding and postexposure efficacy data available for EBOV therapeutics<sup>a</sup>

Candidate therapeutic component	Treatment modality	Therapeutic(s)	Nucleotide position based on GenBank/RefSeq entry <sup>b</sup>	Amino acid residues of target protein	Target gene	Treatment time p.i.	Treatment success (% survival range)	Reference(s)
EK-1-mod	siRNA	Tekmira	17,396–17,418	NA	L	30 min to 6 days	66.7–100 <sup>c</sup>	8
VP24-1160-mod	siRNA	Tekmira	11,043–11,065	NA	VP24	30 min to 6 days	66.7–100 <sup>c</sup>	8
VP35-855-mod	siRNA	Tekmira	3884–3906	NA	VP35	30 min to 6 days	66.7–100 <sup>c</sup>	8
1H3 Mab	Passive immunization	ZMAB	6039–6508	1–157	GP	3–9 days	50–100 <sup>d</sup>	10, 18
2G4 Mab	Passive immunization	ZMAPP, ZMAB	7540–8039	501–676	GP	3–9 days	50–100 <sup>d,e</sup>	10, 12, 18
4G7 Mab	Passive immunization	ZMAPP, ZMAB	7414–7542	459–501	GP	3–9 days, 5 days	50–100 <sup>d,e</sup>	10, 12, 18
13C6 Mab	Passive immunization	MB-003, ZMAPP	6039–7542	1–501	GP <sup>f</sup>	1–2 days, 5 days	66.7–100 <sup>e</sup>	11, 12, 18, 19
6D8 Mab	Passive immunization	MB-003	7204–7254	389–405	GP	1–2 days	66.7	11, 19
13F6 Mab	Passive immunization	MB-003	7240–7290	401–417	GP	1–2 days	66.7	11, 19
AVI-7537	PMO	AVI-6002	10,331–10,349	NA	VP24	30–60 min	60	9, 15
AVI-7539	PMO	AVI-6002	3133–3152	NA	VP35	30–60 min	60	9, 15

<sup>a</sup> MAb, monoclonal antibody; NA, not applicable; p.i., postinoculation; PMO, phosphorodiamidate morpholino oligomers; siRNA, small interfering RNA. Recognition sequences for PMO and siRNA are listed in the supplemental methods.

<sup>b</sup> siRNA positions include both sense and antisense oligonucleotide positions. Mutations specific to each are designated in Fig. 1.

<sup>c</sup> Survival range is dependent on dosing.

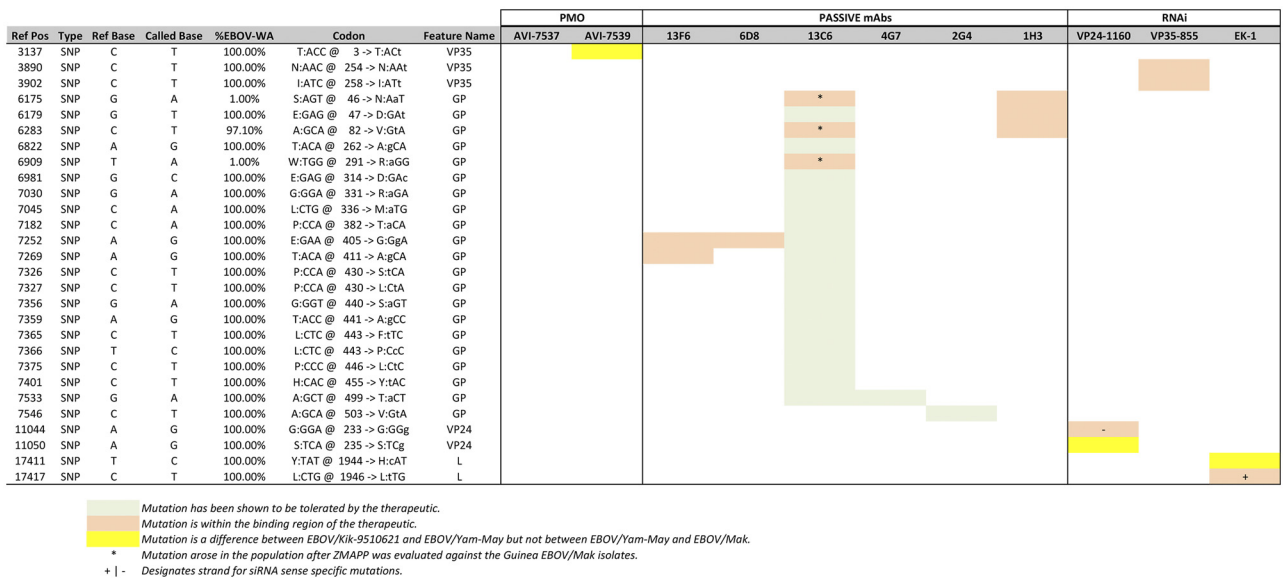
<sup>d</sup> Survival range is dependent on addition of Ad-IFN (interferon co-treatment) to treatment 1 day p.i.

<sup>e</sup> Survival range is dependent on formulation.

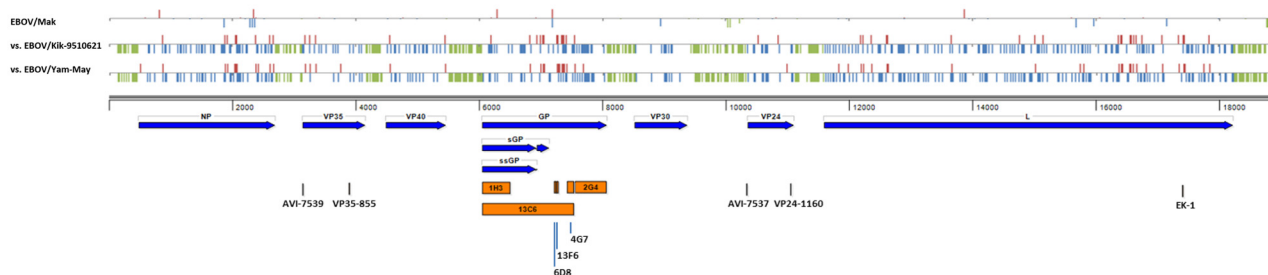
<sup>f</sup> Cross-reacts with TAFV (Tai Forest virus) and SUDV (Sudan virus) GP.

compared against EBOV/Kik-9510621, a total of 640 (3.38% of the genome) single-nucleotide polymorphisms (SNPs) were identified (327 synonymous, 76 nonsynonymous, and 237 noncoding), whereas when it was compared against EBOV/Yam-May, a total of 603 (3.18% of the genome) SNPs were identified (297 synonymous, 80 nonsynonymous and 226 noncoding). Four mutations are located in the published binding region of the siRNA- or PMO-based therapeutics, and 21 induce nonsynonymous changes to epitopes recognized by monoclonal antibodies in passive immunotherapy cocktails. Figure 1 combines an SNP table with a heat map that outlines the potential of each SNP to affect the efficacy of available therapeutics. The column designated

“%EBOV-WA” stratifies changes by the number of West African sequences that support each mutation. Changes that are present in all sequences obtained from West Africa are considered “interoutbreak”; changes that are observed in only some sequences from the West African outbreak are considered “intraoutbreak” (i.e., EBOV-WA represents <100% of the population at the specified position). Of the 28 sites observed within binding regions, 3 SNPs (21.4%) evolved during the 2013–2014 EVD outbreak (intraoutbreak), whereas 22 SNPs (78.6%) evolved prior to the outbreak (interoutbreak). None of the specific SNPs presented here have been previously associated with EBOV resistance to any therapeutic; however, there is a general lack of information surrounding



**FIG 1** Mutation analysis of candidate therapeutic binding sites. An SNP table is combined with a heat map based on three categories: (i) mutation shown to be tolerated by the therapeutic (10), (ii) mutations that are within the binding region of the therapeutic but have not been tested (8–12, 15, 18, 19), and (iii) tolerated diversity between development strains. %EBOV-WA, percentage of genomes containing a change in the West African (WA) sequences of 2014 from EBOV/Kik-9510621.



**FIG 2** EBOV therapeutic map. Each of the therapeutics was mapped onto the genome of EBOV/Kik-9510621 according to published binding information. Blue arrows represent the nine open reading frames conserved among all Ebola viruses. A graphic representation of the SNPs is above the genomic position scale. Red vertical bars denote nonsynonymous mutations, blue vertical bars represent synonymous mutations, and green vertical bars represent noncoding mutations.

the appearance of viral resistance to EBOV therapeutics compared to viral systems like influenza virus and HIV due to the limitations of gain-of-function experiments. Eighteen of the changes have been demonstrated to be tolerated by the ZMAPP cocktail (13C6, 4G7, and 2G4), which demonstrated an increased binding affinity to the EBOV/Mak glycoprotein sequence (12), thus minimizing the potential impact of the mutations. Nevertheless, some of the intraoutbreak changes observed in this region still need to be evaluated. The changes observed in the West African sequences that are already represented in EBOV/Yam-May are also listed as tolerated (yellow), as the therapeutics discussed here have had testing completed with both viruses or mouse/guinea pig-adapted version of the virus and are not different between EBOV/Yam-May and EBOV/Mak (19, 22–24). The other ten mutations, affecting the binding sites of MAb 13F6, MAb 6D8 (part of MB-003), MAb 13C6 (part of MB-003 and ZMAPP), MAb 1H3 (part of ZMAB), and siRNA EK-1, VP24, and VP35 targets, might influence the binding efficacy of the sequence-based therapeutics; their efficacy should be tested against the currently circulating strain (Fig. 2).

Closing this gap might be critical to ongoing efforts to control the outbreak. A robust genomics screening, pre- and post-treatment, would allow clinicians to make informed choices in treatment regimen as well as clarify what signs of viral resistant development should be tracked.

Our risk assessment is not without caveats. (i) This analysis is limited to the binding regions of candidate therapeutics, yet deleterious changes may not be limited to these regions. (ii) Changes in the binding regions may be well tolerated and not influence therapeutic efficacy. (iii) As EBOV/Mak genomes from humans treated with these therapeutics have not yet been determined, conclusions about intrahost selection pressure cannot be made at this stage. It is also important to note that some of the therapeutics have been deliberately designed to be tolerant to possible target mutation: for instance, siRNAs and PMOs were targeted to areas of higher conservation where mutation was thought to be unlikely (based mainly on conservation on all available EBOV sequences at the time of design), and monoclonal antibody cocktails were designed to include several antibodies that bind to distinct regions of the EBOV glycoprotein (18, 19). This multitarget development may ensure that multiple genetic bottlenecks are present to minimize the impact of individual mutations of an evolving EBOV variant.

In summary, the information presented here offers a concise evaluation of the potential impact of the evolutionary drift of Ebola virus Makona in the development of sequence-based ther-

apeutics based on sequence information available in September 2014. Given the ongoing continued person-to-person transmission, it is imperative that more current isolates be sequenced and evaluated in a similar manner.

### SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at <http://mbio.asm.org/lookup/suppl/doi:10.1128/mBio.02227-14/-/DCSupplemental>.

Text S1, DOCX file, 0.01 MB.

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