

Lassa virus circulation in small mammal populations in Bo district, Sierra Leone

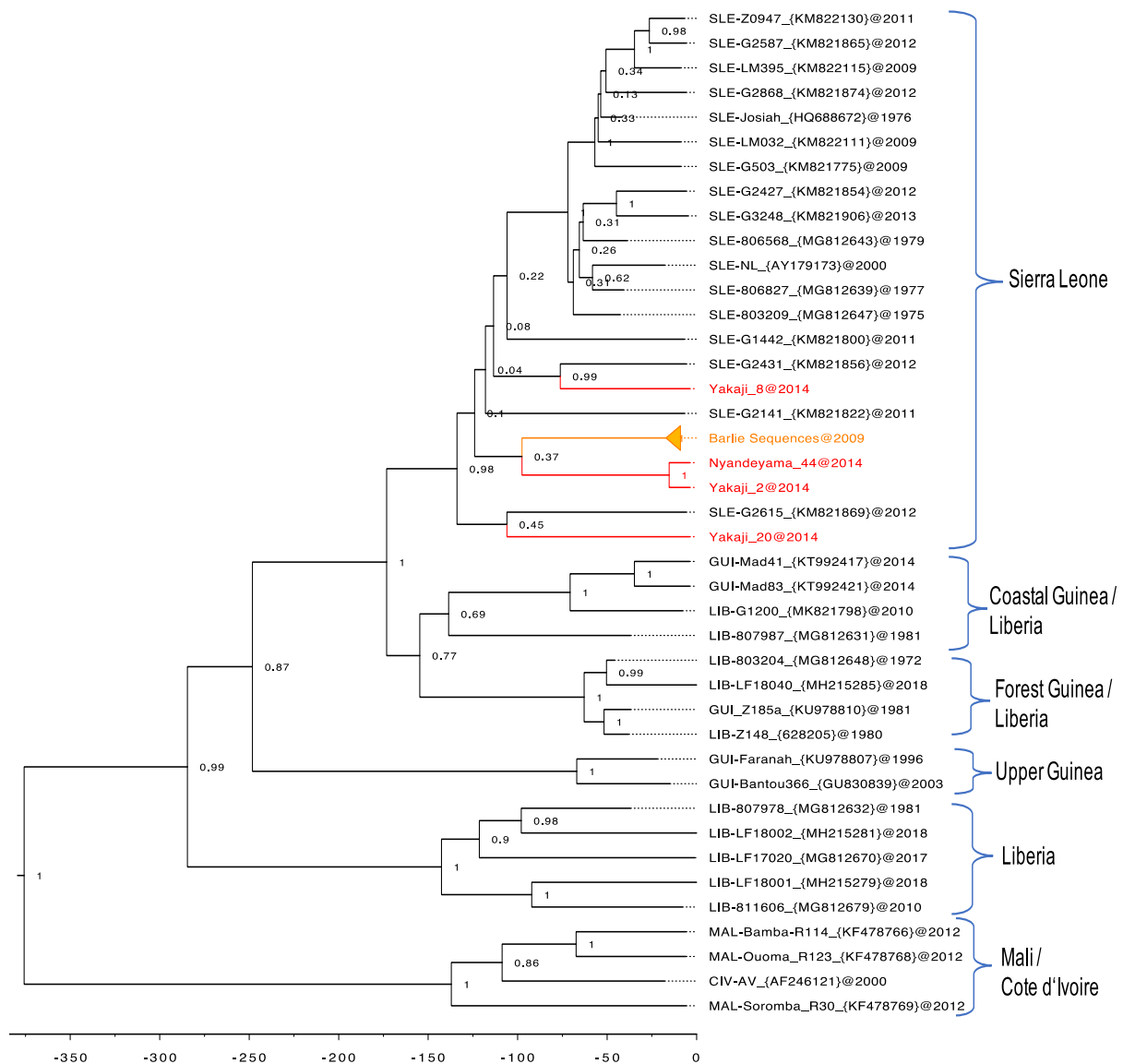
Supplementary information

Table 1. Oligosequence primers used in this study to perform the different PCR assays.

Primers	Oligosequence, 5'→3'	Target gene	Reference
L7 H15915 F-49 R-505 F-607 R-813	ACC AAT GAC ATG AAA AAT CAT CGT T TCT CCA TTT CTG GTT TAC AAG AC CAT TCA TTG ACC TAC CTG CT AGA ATC CCC CTC AAA TTC AC 5'-CGG GCT CTA ATA ACC CAA CG TTC TGG TTT GAT ATG GGG AGG T	Cytochrome b	[1] [1] [2] [2] [2] [2]
LVS36 LVS-339-d LVS 612+ LVS 1474- OWS 1000- OWS 700+ OWS 1430- LVSsl 1430- LVSsl 1682+ LVSsl 1687+	ACC GGG GAT CCT AGG CAT TT GTT CTT TGT GCA GGA (AC)AG GGG CAT (GT)GT CAT ACCTTCATGAGRATGGCTTGGGG atgCCCATGTGrTTsAGyCTrTG AGCATGTCACAGAAYTCYTCATCATG TGATTATTCAGAAAYACAWCCTGGGA CCTWYTATGTGYCTATGTGTTGG CCCACAATRTGCCTATGRGTTGG CTGCTGCGTCAAACATGATG GCGTCAAACATGATGCAGTC	GPC	[3] [3] [4] [4] [5] [5] [5] This study This study This study
LVS 1607+ LVS 1629+ LVS 2429- LVS 2535- LVSsl2535- OWS 2165A+ OWS 2165B+ OWS 2170+ OWS 2840A- OWS2840B- OWS 2805+ OWS 2810+ OWS 3400- OWS 3400A-	GGTGTGATGTTCTAAASACC TGTCTCTGGGCAGCACTGCTC TGTTTGTCTCAGACACTCCYGGTG GCCTGCATGTTGGATGGTGGC GCYTGCATGYTGGATGGTGGTAAC TCT TCA GGT CTC CCT TCW ATG TCN ATC CAN GT TCT TCA GGT CTC CCT TCW ATG TCN ATC CA CTC CCT TCW ATG TCN ATC CAN GT AAY AAY CAG TTT GGG ACN ATG CCA AG AAY AAY CAG TTT GGG ACN ATG CC GTC AGG CTT GGC ATT GTC CCA AAC TGR TTR TT CTT GGC ATT GTC CCA AAC TGR TTR TT GCG CAC AGT GGA TCC TAG GC CGC AGA GTG GAT CCT AGG CTA TTK GAT TGC GC	NP	[6] [6] [6] [6] This study [5] [5] [5] [5] [5] [5] [5] [5]
LVL 3359D_Y+ LVL_3359G_Y+ LVL 3754A_R- LVL 3754D_R-	AGAATCAGTGAAAGGGAAAGCAAYTC AGAATTAGTGAAAGGGAGAGTAAYTC CACATCATTTGGTCCCCATTACTATGRTC CACATCATTTGGTCCCCATTACTGTGRTC	L	[7] [7] [7] [7]

Table 2: Accession numbers of the murine and Lassa virus sequences by village and by date of collection.

Label	Village	Date	Organism				
			<i>Mastomys natalensis</i>		Lassa virus		
			Cytochrome b	Accession No.	GP	NP	Accession No.
NYA 44	Nyandeyama	28 April 2014	+	MW030681	+	+	MW039388
YAK 02	Yakaji	10 April 2014	+	MW030682	+	+	MW039388
YAK 08	Yakaji	10 April 2014	+	MW030683	+	+	MW039388
YAK 20	Yakaji	11 April 2014	+	MW030684	+	+	MW039388



Supplementary figure 1: Maximum clade credibility tree of partial nucleoprotein gene (620 nt) of LASV. The analysis includes sequences generated in this study (coloured red), those from Barlie in Bo district [8](coloured orange) and others from Sierra Leone (SLE), Guinea (GUI), Liberia (LIB), Mali (MAL) and Cote d'Ivoire (CIV). Statistical support of grouping from Bayesian posterior probabilities is indicated at the nodes. Country names, strains, GenBank accession numbers and year of collection are shown on the tips label.

In this figure, we cannot clearly distinguish the Bo sub - clade from that of Kenema due to low posterior values (nodes < 0.5). However, the Sierra Leonean clade is clearly separated from Guinea with high posterior value (node = 1). It might therefore, be certain that all our sequences are also belonging to sub - clade B within the Sierra Leonean clade.

References

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