

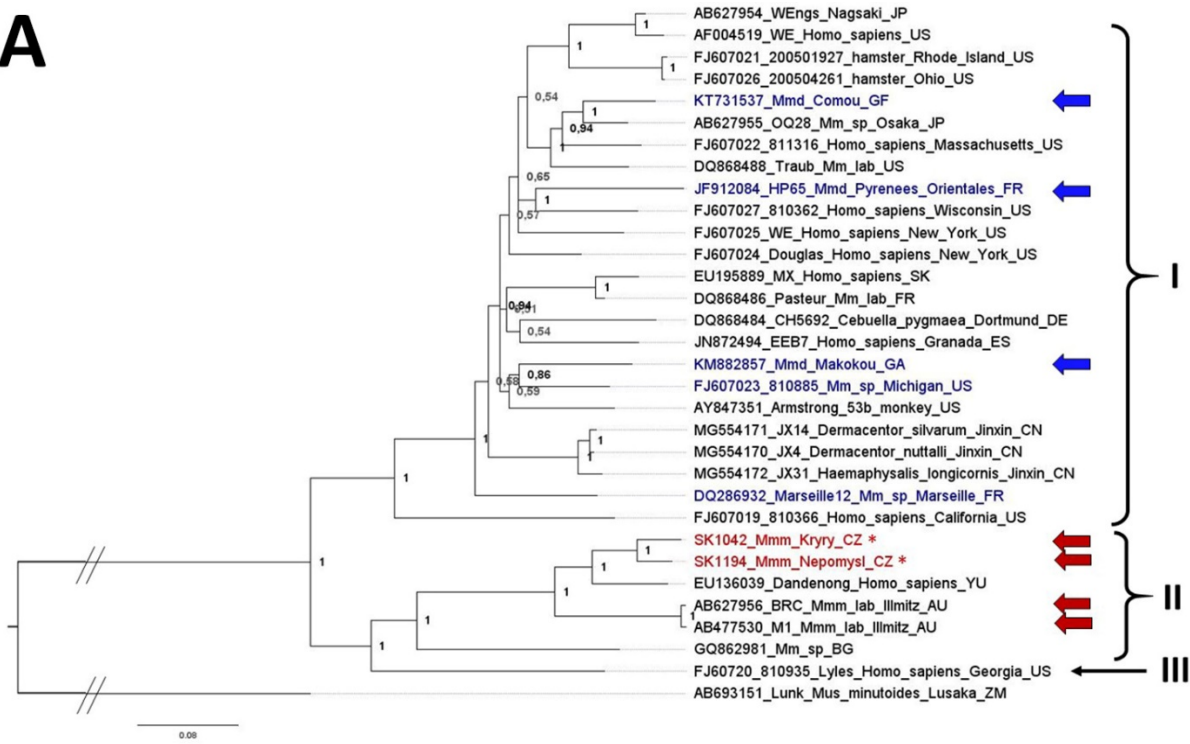
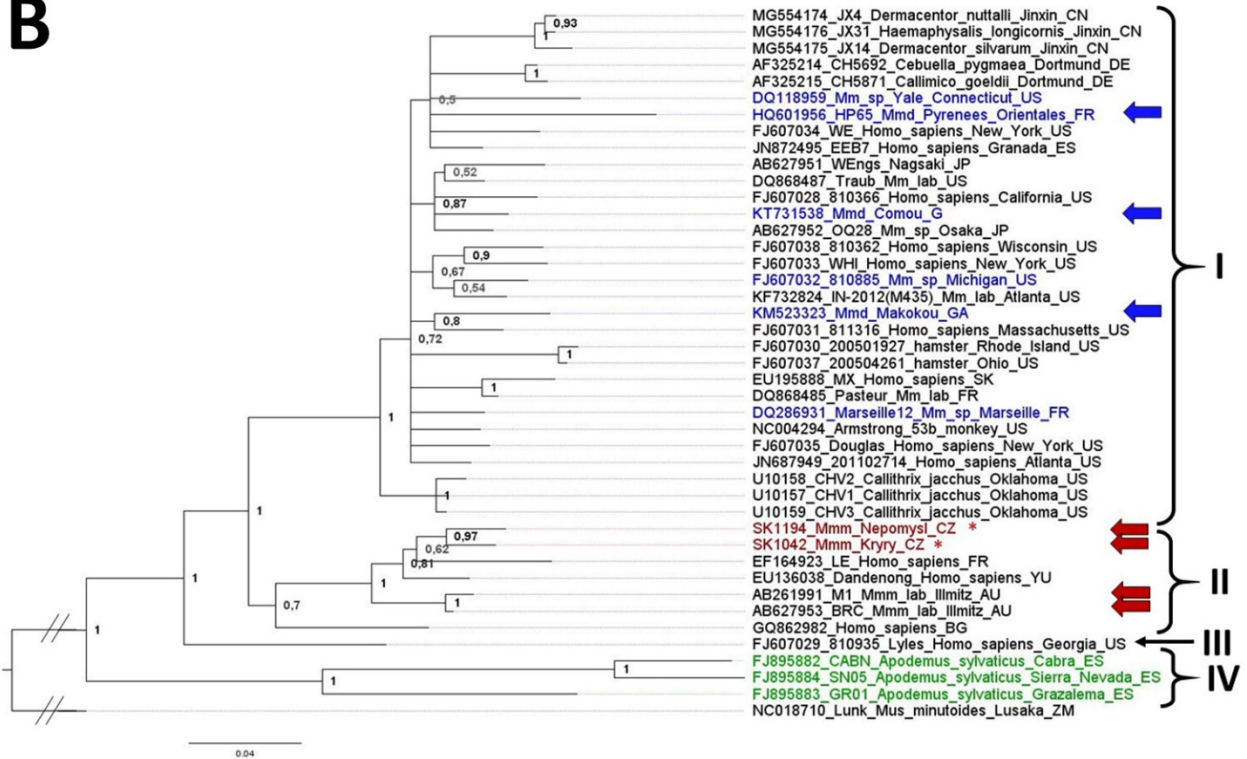
New Perspective on the Geographic Distribution and Evolution of Lymphocytic Choriomeningitis Virus, Central Europe

Appendix 2

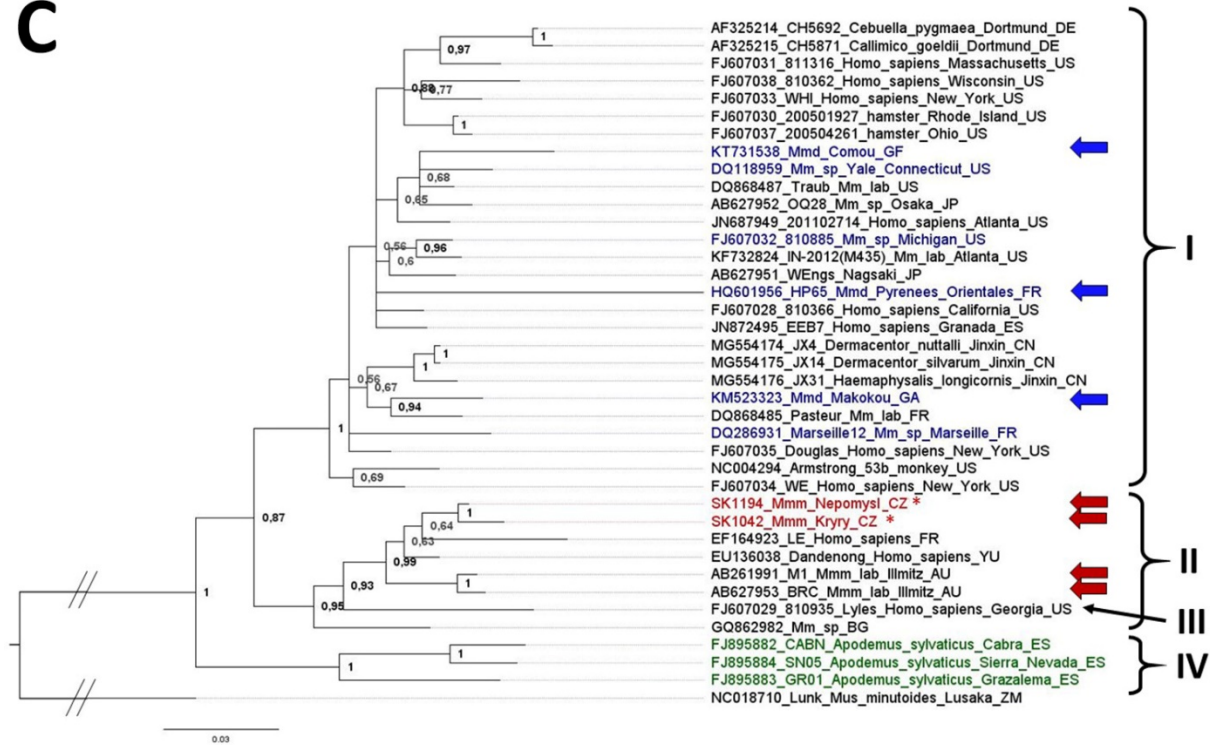
Appendix 2 Table. Primers used in study of geographic distribution and evolution of lymphocytic choriomeningitis virus, central Europe

Identification of primers	Region of screening and length of fragment	Primer sequence	Reference
LVL_3359D_Y+ LVL_3359G_Y+ LVL_3754A_R- LVL_3754D_R-	Large segment, 395 bp	5'- AGA ATC AGT GAA AGG GAA AGC AAY TC-3' 5'- AGA ATT AGT GAA AGG GAG AGT AAY TC-3' 5'- CAC ATC ATT GGT CCC CAT TTA CTA TGR TC-3' 5'- CAC ATC ATT GGT CCC CAT TTA CTG TGR TC-3'	(1)
OWS2805+ OWS2810+ OWS3400- OWS3400A-	Nucleoprotein, 648 bp	5'- GTC AGG CTT GGC ATT GTC CCA AAC TGR TTR TT-3' 5'- CTT GGC ATT GTC CCA AAC TGR TTR TT-3' 5'- GCG CAC AGT GGA TCC TAG GC-3' 5'- CGC AGA GTG GAT CCT AGG CTA TTK GAT TGC GC-3'	(2)
LCMV_L_F1 LCMV-L_R1 LCMV-L_F2 LCMV-L_R2	Large segment, 442 bp	5'- TGR TCA TCA CTW GAH GTR TA-3' (first round) 5'- TRA GRA CHA ARA TGT TYA C-3' (first round) 5'- ATY CCY TGH CCC ATR TCA AT-3' (second round) 5'- TRG ARG AYT AYT TTG ARTC-3' (second round)	Nested assay, present study
OWS0001+ OWS1000-	Glycoprotein, 993 bp	5'-GCG CAC CGG GGA TCC TAG GC-3' 5'-AGC ATG TCA CAA AAY TCY TCA TCA TG-3'	(3)
LCMV_IGR_L_F1 LCMV_IGR_L_R1	Intergenic region, 408 bp	5'-GTC ATG CTG GCA GAG GTT TG-3' 5'-CTG TGA TGA CTG GCT GAG G-3'	Present study

*Sequencing primers are indicated in bold. bp, base pair; +, forward primers; -, reverse primers.

A**B**

C



Appendix 2 Figure. Phylogenetic analyses performed on the amino acid sequences of lymphocytic choriomeningitis virus (LCMV) strains using Bayesian inference. Bayesian posterior probabilities were used to assess node support. Lunk virus from *Mus minutoides* (Africa) was used as outgroup. Names of LCMV strains are composed of GenBank number, strain name, host species, place and country of origin (if known), or isolation. Country code is defined as ISO code (<https://countrycode.org>). Colors indicate LCMV strains isolated from wild rodents where there is a match between expected mouse subspecies on the basis of geographic region and sampling area; blue indicates *Mus musculus domesticus*, red indicates *M. musculus musculus*. Arrow indicates known origin of mice subspecies on the basis of genetic data, asterix indicates LCMV strains from this study, and lineages are indicated by roman numerals. LCMV strains isolated from *Apodemus sylvaticus* are indicated in green (lineage IV). Scale bars indicate nucleotide substitutions per site. Mmd, *M. musculus domesticus*; Mmm, *M. musculus musculus*; Mmm_lab, laboratory mouse strain derived from *M. musculus musculus*; Mm_lab, laboratory mouse strain; Mm_sp, *Mus musculus* spp. A) Phylogenetic tree based on amino acid sequences of large gene, B) phylogenetic tree based on amino acid sequences of glycoprotein gene, C) phylogenetic tree based on amino acid sequences of nucleoprotein gene.

References

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