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Supplementary appendix

This appendix formed part of the original submission. We post it as supplied by the authors.

Supplement to: Pfaff F, Hoffmann D, Beer M. Monkeypox genomic surveillance will challenge lessons learned from SARS-CoV-2. *Lancet* 2022; **399:** 22–3.

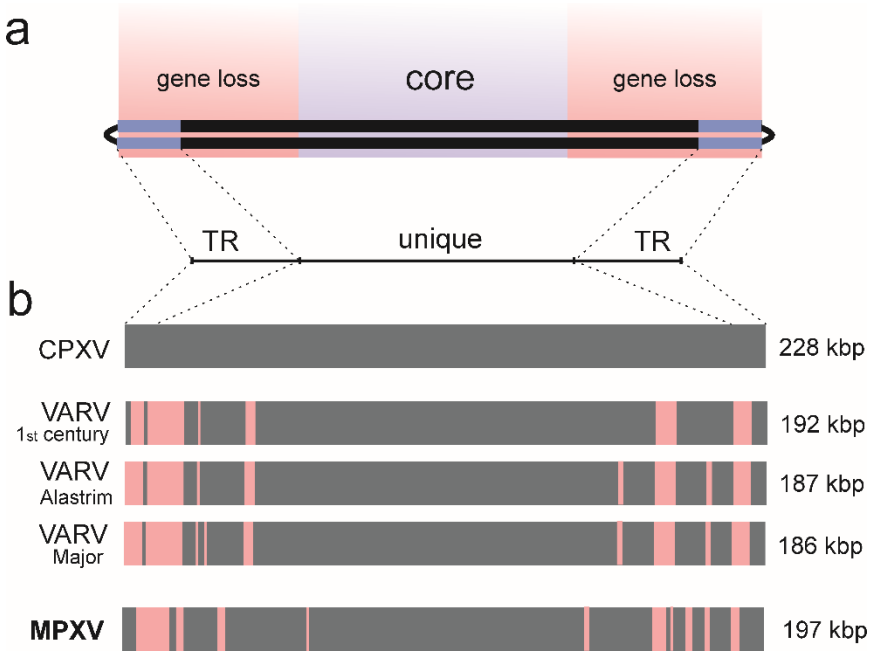

Figure 1: Orthopoxvirus (OPV) genome organization (a) and gene loss during host adaption (b). a: The genome of OPVs consists of a unique region that is flanked by two inverted terminal repeats (TR). Within the unique region is an evolutionary stable and conserved core sequence, that is shared by most OPV species. Some OPV species, that are highly adapted to a single host species tend to lose genes within the terminal regions of the genome during adaptation. **b**: The species *Cowpox virus* (CPXV) has the most complex genome of all OPV (grey area) and therefor reflects the complete spectrum of genes within this genus. It is also the species with the broadest host spectrum. Variola virus (VARV) was highly adapted to humans and lost many genes during adaptation in comparison to CPXV (red areas). Also, ancient VARV sequences from the 1st century had more genes then recent VARVs. The milder VARV strain "Alastrim" had some more genes then its highly pathogenic counterpart "Major". Monkeypox virus (MPXV) shows a similar but distinct pattern of gene loss when compared to VARV.