



Figure 23.5. **Alphavirus phylogenetic tree produced using the E2, 6K, and E1 structural protein genes and Bayesian methods with midpoint rooting.** The tree includes representatives from all alphavirus species, and the *dashed line* indicates the recombination between ancestors of Sindbis and eastern equine encephalitis viruses that led to the western equine encephalitis virus (WEEV) group. Roman numerals indicate major subtypes of some species, and scale indicates 50% nucleotide sequence divergence. All posterior probabilities