Chapter 7

MOLECULAR EVOLUTION OF ORTHOPOXVIRUSES

7.1 Phylogenetic Interrelations of Orthopoxviruses

With accumulation of sequencing data on complete genomes, clarification of evolutionary interrelations of orthopoxviruses was attempted. At the first stage, it was determined that VARV and VACV evolved from a common ancestor independently from one another (Shchelkunov, 1995). Then, it was discovered that CPXV DNA contained the most complete set of genes found in the viral genomes of this genus (Shchelkunov et al., 1998; Appendices 1 and 2). The rest orthopoxvirus species have lost certain part of the genes with reference to CPXV. Note that VARV contains the least set of actual genes. This observation suggests that CPXV is most close to the ancestor of orthopoxviruses, while the rest species emerged later due to deletions, recombinations, and mutations. Assuming that more virulent virus variants are less effectively preserved in the biosphere, it is logical to infer that variola minor was the first to appear and then evolved in places with a high enough population density into the variola major variant. In addition, the species Variola virus is an example of the evolutionary cul-de-sac, as its host range narrowed to one species (humans) and it lost the capability of persisting, which presumably was characteristic of the ancestor virus. Comparison of VARV and MPXV genomes suggested that neither virus is the direct ancestor to the other (Shchelkunov et al., 2001). Of the orthopoxviruses studied, camelpox virus (CMLV; Gubser & Smith, 2002) appeared most closely related to VARV according to phylogenetic analysis of the genomes. However, it was inferred that evolution of one species from the other is unlikely and VARV and CMLV evolved from closely related ancestor, possibly a rodent virus.
Orthopoxviruses Pathogenic for Humans

Figure 7-1. Phylogenetic tree based on the coding part of vCCI gene constructed by minimal evolution method. Each branch corresponds to one unique sequence variant. Figures at the branch roots show the results of permutation analysis of statistical significance involving 1000 trees. Only the values exceeding 50% are indicated. The scale shows units of genetic distance. Designations of orthopoxviruses: V, vaccinia virus; C, cowpox virus; S, variola (smallpox) virus; CP, camelpox virus; E, ectromelia virus; and M, monkeypox virus.