Foot-and-mouth disease virus (FMDV) is responsible for one of the most economically important infectious diseases of livestock. The virus spreads very easily and continues to affect many countries (mainly in Africa and Asia). The risks associated with the introduction of FMDV result in major barriers to trade in animals and their products. Seven antigenically distinct forms of the virus are known, called serotypes, but serotype C has not been detected anywhere for many years and may now be extinct. The serotypes have been further divided into topotypes (except for serotype Asia-1 viruses, which comprise a single topotype), genotypes, lineages and sub-lineages, which are usually restricted to specific geographical regions. However, sometimes, trans-regional spread of some strains occurs. Due to the error-prone replication of the RNA genome, the virus continuously evolves and new strains frequently arise (e.g. with modified antigenicity). Using nucleotide sequencing technologies, this rapid evolution of the viral genome can be followed. This allows the tracing of virus transmission pathways within an outbreak of disease if (near) full-length genome sequences can be generated. Furthermore, the movement of distinct virus lineages, from one country to another can be analyzed. Some important examples of the spread of new strains of FMD virus are described.