Crimean-Congo Hemorrhagic Fever Virus (CCHFV) is a zoonotic virus that infect life stock then transfer to human via direct contact with animal or by ticks that live on animals as a parasite through their bites.The minimum evolution phylogenetic tree was also analyzed for the main eight strains collected from different countries including South Africa, Uganda, Nigeria, China, Pakistan, Russia, Congo and Senegal.Methods: It has been depending on database available on NCBI website for searching on accession number of recorded viruses gene sequences, and used the minimum evolution phylogenetic tree algorithm for drawing phylogenetic trees.Objectives: Determining the origin of infection geographically, drawing phylogenetic tree among viruses strains, and give the chance to detect and identify the viruses and attempt to making vaccines.The infected people appear some symptoms such as, malaise, vomiting, mucosal and gastrointestinal (GI) bleeding, hypotension, and edema.In Iraq, the infection of CCHFV appeared and was recorded in 1979, then in 1992, 1996 and 2012.Genomic of the virus was detected at the molecular level and sequenced.The phylogenetic tree showed that South Africa and Uganda were located in one clade, and Nigeria shared the same ancestor.Results: The first record of the virus was in the Crimean Peninsula in Russia in 1944, then recorded in the Congo basin in the middle of Africa in 1956.Strain 1 was the same clade as strain 1 of Oman, whereas strain 2 was located with the same clade as of strain 2 of Turkey.Strain 3 of the virus in Iraq, Oman and China were in one clade.Whereas Russia, Congo and Senegal were out groups.The virus was also recorded in some countries in Asia, Africa and Europe.The local molecular studies showed three strains of the virus.China and Pakistan were the same clade.

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