Positive evolution of the glycoprotein (GP) gene is related to transmission of the Ebola virus

Y.X. Jing1, L.N. Wang2, X.M. Wu2 and C.X. Song1

1Department of Computer Science, Qinghai Normal University, Qinghai, China
2The Key Laboratory of Biomedical Information Engineering of Ministry of Education, Xi’an Jiaotong University, Xi’an, China

Corresponding author: C.X. Song
E-mail: scx@qhnu.edu.cn

Genet. Mol. Res. 15 (1): gmr.15017173
Received September 14, 2015
Accepted November 5, 2015
Published March 28, 2016
DOI http://dx.doi.org/10.4238/gmr.15017173

ABSTRACT. Ebola hemorrhagic fever is a fatal disease caused by the negative-strand RNA of the Ebola virus. A high-intensity outbreak of this fever was reported in West Africa last year; however, there is currently no definitive treatment strategy available for this disease. In this study, we analyzed the molecular evolutionary history and attempted to determine the positive selection sites in the Ebola genes using multiple-genomic sequences of the various Ebola virus subtypes, in order to gain greater clarity into the evolution of the virus and its various subtypes. Only the glycoprotein (GP) gene was positively selected among the 8 Ebola genes, with the other genes remaining in the purification stage. The positive selection sites in the GP gene were identified by a random-site model; these sites were found to be located in the mucin-like region, which is associated with transmembrane protein binding. Additionally, different branches of the phylogenetic tree displayed different positive sites, which in turn was responsible for differences in the cell adhesion ability of the virus.
In conclusion, the pattern of positive sites in the \textit{GP} gene is associated with the epidemiology and prevalence of Ebola in different areas.

\textbf{Key words:} Ebola disease; Evolutionary analysis; \textit{GP} gene; Positive selection