Characterization of the immune response against Testudinid herpesvirus 3.

M. Tecilla\textsuperscript{a*}, P. Roccabianca\textsuperscript{a}, P. Pilo\textsuperscript{b}, F. Origgi\textsuperscript{c}

\textsuperscript{a} Department of Veterinary Science and Public Health (DIVET), School of Veterinary Medicine, University of Milan, 20010, Milan, Italy.
\textsuperscript{b} Institute of Veterinary Bacteriology, Vetsuisse Faculty, University of Bern, Laenggassstrasse 122, 3012, Bern, Switzerland.
\textsuperscript{c} Centre for Fish and Wildlife Health (FIWI), Vetsuisse Faculty, University of Bern, Laenggassstrasse 122, 3012, Bern, Switzerland.

Abstract

Numerous infectious diseases have been documented in reptiles, however minimal information is available concerning their immunological response. One of the most diffuse and lethal reptile pathogen is Testudinid herpesvirus 3 (TeHV3), a Alphaherpesvirinae. All species of tortoises (Testudinidae) are considered susceptible to TeHV3, however the virus is over represented in the genus Testudo, which includes, among others, T. graeca, T. hermanni, T. marginata, and T. horsfieldii, that are popular pets in Europe. Incidence of TeHV3-associated disease is highest right after hibernation (Origgi, 2012).

The aim of this work is to partially characterize the immunological response of T. graeca against TeHV3. A bacteriophage library composed of about 5,000 clones containing genomic DNA fragments of TeHV3 was produced. Bacteriophages were amplified in a specific strain of E. coli and were screened with TeHV3-seropositive sera from T. graeca. Phagemids were excised from the positive bacteriophages, sequenced, and compare with the TeHV3 genome to identify the encoding genes. Six different structural and non-structural proteins have identified as immune relevant. Vero cells where transfected with phagemids of the positive clones, to confirm previous results. TeHV3's proteins expression was assessed by F.A.C.S using T. graeca seropositive sera. Of all the six selected clones, only that expressing the partial sequence of the glycoprotein B (gB) showed a positive signal in the F.A.C.S. analysis. This result is consistent with the well-known immunogenicity of gB of other herpesviruses including those infecting humans and with the highly conserved role that gB plays in host-pathogen interaction across species and evolution (Beals et al., 2016).

References
