Molecular diagnosis of nasopharyngeal carcinoma using detection of Epstein-Barr virus latent membrane protein-1 gene in archival tissues

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Introduction and Objectives: The association of nasopharyngeal carcinoma (NPC) with the Epstein-Barr virus (EBV) was firmly established as early as 1973. A clear understanding of its etiology is still lacking, but nasopharyngeal carcinoma is widely suspected to be the result of both a genetic susceptibility and exposure to environmental factors or Epstein-Barr virus infection. Because of high prevalence of NPC in the young age from one hand and young age of our country in the other hand we set forth to study the level of infection with EBV.
Material and Methods: This study was performed to determine the association of EBV in NPC by means of PCR compared to control group. Thus, a 25-person group of NPC patient as the case group and a 25-person group of patients considered to be at risk of developing NPC as the control group was studied. In the course of the study, the methodology of obtaining DNA from archival tissue sections and using it as template in PCR was established.
Results: In case group 23 patients were positive for EBV-DNA and 2 were negative for EBV-DNA. When in control group 12 patients were positive for EBV-DNA and 13 were negative for EBV-DNA. The LMP-1 gene was detected with a sensitivity of 92%, specificity of 48%, positive predictive value of 60.53%, and negative predictive value of 1%.
Conclusion: Our data demonstrate that EBV is present at the site of tumor development in the low-risk population. This survey supports the concept of NPC pathogenesis as a multifactorial process.

Developing methods for isolation and identification of densonucleosis viruse as a paratransgenic tool from Culicidae mosquitoes with emphasis on main malaria vector, Anopheles stephensi

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Introduction and objective: Paratransgenesis as a new method has a great potential to control vector-borne diseases such as malaria. With application of this technology genetically modified symbiotic organisms that express specific molecules (such as toxins or inhibitor molecules) can prevent pathogen development or its transmission by the vector. Symbiotic densoviruses are attractive and suitable agents for genetic manipulation. In current study, it was aimed to develop methods for identification and isolation of densovirus as a paratransgenic tool from *Culicidae* mosquitoes with emphasis on *An. stephensi* collected in Baluchistan of Iran. Further, the susceptibility of different insectary-reared larval stage of *An. stephensi* to AalDNV was examined.
Material and methods: Detection of densovirus in *Culicidae* species collected from Chabahar, Bahookalat, Pishin and Sarbaz was performed by Nested PCR detection with specific primers ID and NS1. 1217 specimens in 26 pools (30 to 60) from 3 genera of *Anophels, Culiseta* and *Culex spp* were examined. Contaminated C6/36 *Aedes albopictus* cell line to densovirus was cultured in laboratory and exposed by various methods to first and third instar larvae of *An. Stephensi,* which reared in insectary.
Result: Until now, no densovirus has been identified in *An. stephensi* mosquitoes that collected from different districts of Baluchistan of Iran. However, *An. stephensi* reared in insectary proved to be susceptible and could be infected by *Aedes albopictus* densovirus.
Conclusion: The important finding of this study was to confirm the absence of densovirus within the examined field collected *Culicidae* including *An. stephensi*, *Culex* and *Culiseta spp* in Iran, which could act as the baseline and essential data for further advanced experiments. On the other hand, the protocols developed for infecting the insectary reared mosquito vectors provided the infrastructure for follow up studies of paratransgenic by using DNVs.

A natural component of the scorpion Hemiscorpius lepturus venom inhibits the in vitro replication of HIV.

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Introduction and Objectives: During the recent years, significant progress has been achieved on development of novel antiviral drugs. It has been believed that the natural products are the potential sources for novel antiviral drugs. There are some previous studies reporting the antiviral agents in venoms. Here we studied the venom of Hemiscorpius lepturus, Mesobuthus eupeus, Buthus schach and Apis mellifera for inhibition of HIV-1 and HSV replication.
Material and Methods: The authenticity of scorpions was identified using anatomical and morphological techniques. The antiviral activity was measured by using single cycle HIV (NL4-3) replication and HSV (KOS) plaque reduction assays. The cellular toxicity was examined using proliferation assay.
Results: Total venoms from M. eupeus and B. schach significantly induced the replication of HIV virions. The M. eupeus venom (200µg/ml) increases the HIV replication by 2.3 fold however the venom from H. lepturus inhibited this virus by 73% at the same concentration. H. lepturus also inhibited the cell free viral particles in virucidal assay. Purified 30kda protein from H. lepturus venom inhibited HIV virions with IC_{50} of 20µg/ml. Venoms from H. lepturus, M. eupeus and B. schach did not show cytotoxicity however A. mellifera venom was highly toxic. The tested venoms showed no inhibitory activity for HSV replication.
Conclusion: These results suggest that H. lepturus venom contains components with considerable anti-HIV activity. This venom has virucidal activity that offers a novel therapeutic approach to HIV infection. Our result suggests a promising lead for HIV drug discovery in natural products.