

of HBV vaccination. These were more likely to be vaccinated compared to those who had not been sensitized ($p < 0.001$).

Conclusion: There is a high rate of accidental exposure to blood and a very low HBV vaccination uptake among medical students in Cameroon, leading to a high occupational risk of HBV infection. HBV vaccination should be strongly recommended for medical students and the vaccine made available free of charge at the beginning of their training

<http://dx.doi.org/10.1016/j.ijid.2014.03.1345>

Type: Poster Presentation

Final Abstract Number: 64.016

Session: Virology and Viral Infections (Non-HIV) II

Date: Saturday, April 5, 2014

Time: 12:45-14:15

Room: Ballroom

Exploring the evolution of filoviruses in vitro

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Background: Filoviruses are negative sense RNA viruses that are highly pathogenic in both humans and non-human primates. They have a mortality rate of up to 90% and study of infectious virus requires BSL-4 containment. We have performed experiments to show that filoviruses are highly mutable and have mutation rates similar to other negative sense RNA viruses. Consequently, at the sequence level, filoviruses appear to exist as populations of highly related but not identical variant populations.

Methods & Materials: To ask if the mutability resulted in genotypic and phenotypic changes following growth in cell culture, we serially passaged Ebola virus, Sudan virus, and Marburg virus from passage 2 through 18 in Vero E6 cells. At each passage viruses were subjected to deep sequencing to determine consensus sequence changes in addition to changes in minor populations.

Results: Interestingly, the pattern of the observed changes was different for each of the viruses. In parallel, experiments were performed to investigate the effects of passages on growth kinetics and plaque morphology. Overall, we have observed changes in genome sequences during passages and it is likely that these changes can be correlated to phenotype and function.

Conclusion: Our data suggest that filoviruses can rapidly adapt to new selection pressures. This could have major implications for future filovirus research on emergence, virulence, drug-resistance, and vaccine development.

<http://dx.doi.org/10.1016/j.ijid.2014.03.1346>

Type: Poster Presentation

Final Abstract Number: 64.017

Session: Virology and Viral Infections (Non-HIV) II

Date: Saturday, April 5, 2014

Time: 12:45-14:15

Room: Ballroom

Human papillomavirus 16 variants and their association with cervical lesion in multiple infections



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Background: Human papillomavirus (HPV) infection is the primary cause of cervical cancer and HPV 16 and 18 estimate 70% of it.

E6 and E7 genes are used to describe variants and the expression of these genes from high risk HPV induces cellular immortalisation and transformation.

The aim of our study was to characterize the genomic variability of E6, E7 and L1 genes in HPV 16 multiple infection patient samples and analyze the relationship between intratypic variants and lesion grade.

Methods & Materials: Samples were analyzed by Clinical Microbiology and Infection Control Department from 2007 to 2013.

Three region type-specific primers were used to amplify HPV 16 multiple infection samples and the fragments were sequenced using the "Big Dye Terminator Cycle Sequencing kit".

HPV sequences were aligned and compared to prototype using Chromas Lite and Clustal W: European (E), African (AF) and Asian-american (AA).

Phylogenetic trees were built using Maximum likelihood method implemented in MEGA software.

Lesions were categorized into three categories: negative (no lesion was found), low- or high-grade lesion.

Results: HPV 16 was detected in 151 samples and 86.7% of them were European, 7.9% Asian-american and 5.3% African. Among women, European variants mean age was 29.3 years, whereas in non-European variants average age was 40.5 (AF) and 36.6 (AA).

Genome variations such as A104del, T109C, A131G, G132C, G145T, T286A, A289G, C335T, T350G, A532G, G6690A, T6693C, G6719A, A6803T, C6852T, C6863T, 6902insAT, 6902insATC and GAT6949del had as a result missense mutations whereas T732C, T789C, T795G, G849A and T921C changes lead to silent mutations.

Phylogenetical analysis showed European and Non-European separated branches.

High grade lesions were more related to African and Asian-American variants.

Conclusion: European variants are more usual in our country. Non-European variants are found in older women.

Nucleotide substitutions in E6, E7 and L1 genes discriminate among E, AA and AF variants which have as a result distinct branches in phylogenetic tree.

Nucleotide variations may influence viral persistence and progression to cancer and consequently non-European variants and coinfections should be considered.

Funding: S-PC11BF002 project (Saiotek, Department of Industry, Basque Government) and EHU13/04 (University of Basque Country, UPV/EHU).

<http://dx.doi.org/10.1016/j.ijid.2014.03.1347>

Type: Poster Presentation

Final Abstract Number: 64.018

Session: *Virology and Viral Infections (Non-HIV) II*

Date: Saturday, April 5, 2014

Time: 12:45–14:15

Room: Ballroom

Performance and cost-effectiveness of immunochromatography based rapid diagnostic test (RDT) kits in diagnosis of dengue infection in resource limited set up



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Background: Dengue infection occurs among more than 50 million annually. In India, the case fatality rate is up to 3–5%. Early diagnosis is crucial to the clinical care. However the currently recommended diagnostic tests by WHO is costly, time consuming, labor and technologically demanding which may not be available in the resource limited set up where the large burden of dengue related illness occur.

This study evaluated the role of immunochromatographic method based rapid diagnostic test kits (RDT) and cost-effectiveness for the diagnosis of acute dengue infection.

Methods & Materials: 281 adult patients presenting to Christian Medical College, Vellore, India with community acquired acute febrile illness between September 2012 to February 2013 were recruited for the study. The patients with other proven etiology were used as negative control. 132 cases of dengue and 149 cases of non-dengue infection were enrolled. The RDTs tested from 4 manufacturers were Panbio, SD, J.Mitra and Reckon. SPSS version 16.0.1 was used for statistical analysis.

Results: Performance of the RDTs based on IgM: The sensitivity, specificity, PPV and NPV of Panbio, SD, Reckon and J.Mitra. The inter-rater kappa agreement between Panbio with SD duo of 0.54 was found to be moderate.

Performance of the RDTs based on NS1 detection: The sensitivity, specificity, PPV and NPV of the SD, Reckon, and J.Mitra. The inter-rater kappa agreement between SD with Reckon of 0.79 was found to be best and substantial.

Combination of RDTs: the best sensitivity of 99.2% was achieved by testing Panbio and SD in parallel. The best specificity of 99.9% and 100% respectively was obtained when Reckon with Panbio or SD was performed in series.

None of the RDTs could not adequately differentiate between acute primary and secondary dengue.

Conclusion: In the region of high dengue endemicity, Panbio RDT alone is highly sensitive, cost effective (~13.6 USD), easier to perform and shorter turnover time makes it a test of choice in resource limited set up during an outbreak season.

<http://dx.doi.org/10.1016/j.ijid.2014.03.1348>

Type: Poster Presentation

Final Abstract Number: 64.019

Session: *Virology and Viral Infections (Non-HIV) II*

Date: Saturday, April 5, 2014

Time: 12:45–14:15

Room: Ballroom

Hepatitis C viral infection in our region



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Background: To present the basic characteristics of Hepatitis C viral infection (HCVi) in the region of Bitola, Republic of Macedonia, in the period from October 2010 to October 2013.

Methods & Materials: Past medical history, epidemiological data, standard biochemical analyses, Elisa antibodies, PCR, and liver biopsy, were used in order to set the diagnoses. 74 patients had been analyzed: 49 male (66.22%) and 25 female (33.78%). According to age, the patients were between 18 and 65 years old. All of them were from the urban area. 52 patients (70%) were intravenous drug abusers.

Results: Hepatitis C virus (HCV) genotype 1 was diagnosed in 23 patients (31%), and HCV genotype 3 in 51 patients (69%). The patients were treated with Peg-interferon alfa 2-a/Ribavirin under current standards (180 mcg once weekly/1200 mg daily), during 24 or 48 weeks. Therapy was completed in 49 patients (66%). In 6 patients (8%) therapy was not completed due to the side effects (generalized urticaria, pancitopaenia, colon neoplasm), and 19 patients (26%) are still receiving therapy. SVR were documented in all of the patients.

Conclusion: According to sex, most of the patients were male: 49 (66.22%). Most of the patients were intravenous drug abusers: 52 (70%). According to age, most of the patients were between 18 and 30 years old: 58 (78%). HCVi became a great problem in our region in the recent years, especially among the young population and intravenous drug abusers.

<http://dx.doi.org/10.1016/j.ijid.2014.03.1349>

Type: Poster Presentation

Final Abstract Number: 64.020

Session: *Virology and Viral Infections (Non-HIV) II*

Date: Saturday, April 5, 2014

Time: 12:45–14:15

Room: Ballroom

Human cytomegalovirus gB genotype distribution among HIV infected patients from Pretoria



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Background: Human cytomegalovirus (HCMV) is a double stranded DNA virus in the Herpesviridae family latently infecting 60–100% of world population. A severe HCMV disease is associated with congenital infection and immunosuppression. The HCMV major envelope glycoprotein gB is involved in the host cell entry,