

7. The expression of leukemia-specific markers is currently being studied in the EVs isolated from the paired AML blood samples.


http://dx.doi.org/10.1016/j.pbj.2017.07.120

PS229

Circulating EVs for AML minimal residual disease biomarkers detection

P.C. Nunes 1,*, H.R. Caires 2, M.A. Sobrinho-Simões 3, M.H. Vasconcelos 4

1 Cancer Drug Resistance Group, IPATIMUP – Institute of Molecular Pathology and Immunology of the University of Porto, Portugal; i3S – Instituto de Investigação e Inovação em Saúde, University of Porto, Portugal; ICRAS-UP – Institute of Biomedical Sciences Abel Salazar of the University of Porto, Portugal

2 Cancer Drug Resistance Group, IPATIMUP – Institute of Molecular Pathology and Immunology of the University of Porto, Portugal; i3S – Instituto de Investigação e Inovação em Saúde, University of Porto, Portugal

3 Cancer Drug Resistance Group, IPATIMUP – Institute of Molecular Pathology and Immunology of the University of Porto, Portugal; i3S – Instituto de Investigação e Inovação em Saúde, University of Porto, Portugal; FMUP – Faculty of Medicine of the University of Porto, Portugal; HSJ – Hospital de São João, Porto, Portugal

4 Cancer Drug Resistance Group, IPATIMUP – Institute of Molecular Pathology and Immunology of the University of Porto, Portugal; i3S – Instituto de Investigação e Inovação em Saúde, University of Porto, Portugal; FFUP – Faculty of Pharmacy of the University of Porto, Portugal

E-mail address: pnunes@ipatimup.pt (P.C. Nunes).

Aim: We propose to evaluate the feasibility of a peripheral blood EV-based liquid biopsy method for AML disease monitoring in real time with molecular precision.

Introduction: Acute myeloid leukemia (AML) is a hematopoietic stem cell disorder with high mortality rate mainly due to the high frequency of post-treatment relapse. Minimal residual disease (MRD) determination in AML patients receiving treatment is useful to assess chemotherapy response and predict relapse. One approach to upgrade the current invasive MRD monitoring (traditionally based on bone marrow aspirates/biopsies) is to use methods that identify cancer-associated biomarkers in patients’ blood. Recently, extracellular vesicles (EVs) have been increasingly recognized as a potential source of biomarkers, since the levels of EVs are markedly increased in cancer patients’ blood and those EVs potentially carry molecular signatures associated with specific cancer phenotypes.

Methods: The profile of EVs isolated from AML patients’ blood plasma collected from paired AML diagnostic and complete remission samples is being compared and correlated with clinical data. A size-exclusion chromatography (SEC) method was optimized to isolate the plasmatic EVs. The EVs profile is then characterized according to their size, plasmatic concentration, morphology and protein content.

Results: EVs with decreasing size were successfully isolated between SEC fractions 3 to 6, with a size ranging from 300 nm to 30 nm, respectively. Fraction 7 presented the smaller EVs, although mixed with some plasmatic protein contaminants. The expression of EV markers such as CD63, HSP70 or Syntenin-1 was confirmed and allow to distinguish EV subpopulations between fractions 3 to 7. The expression of leukemia-specific markers is currently being studied in the EVs isolated from the paired AML blood samples.

Conclusion: The presented EV-based liquid biopsy proposed method for AML monitoring could unravel biomarkers for diagnostic and prognostic purposes in AML patients.

http://dx.doi.org/10.1016/j.pbj.2017.07.121

PS232

The association of Generalized Epilepsy with Febrile Seizures plus (GEFS+) with FEB1 gene: A new insight to the etiology of GEFS+

Ali Rafati 1,*, Shahram Teimourian 2

1 Student Research Committee, School of Medicine, Iran University of Medical Sciences, Tehran, Iran

2 Department of Medical Genetics, Iran University of Medical Sciences Tehran Iran

E-mail address: rafatiali1995@gmail.com (A. Rafati).

PS037

Genetical variability of VP1 gene of BK virus in HIV-infected patients

O. Lijeskić, S. Leštarević, D. Karalić

1 School of Medicine, University of Belgrade, Portugal
2 Institute of Microbiology and Immunology, School of Medicine, University of Belgrade, Portugal

E-mail address: oljalol2@gmail.com

Abstract: The aims of this study were: to determine the prevalence of BK viruria in HIV-infected patients, to determine the distribution of BKV subtypes and the presence of nucleotide substitutions and mutations in the VP1 gene of BKV isolates.

Introduction: A broad range of diseases associated with BKV such as nephritis, haemorrhagic cystitis, encephalitis, retinitis and pneumonia have been reported in HIV-infected patients over the last few years. However, these diseases do not occur in all HIV-infected patients, suggesting that other factors, such as genetic variability of BKV, can contribute to their occurrence. Mutations in the BC loop of the VP1 gene may lead to selection of more aggressive variants of BKV.

Methods: The study included 50 HIV-infected patients. Semi-nested PCR was used for amplification of 290-nt fragment within the VP1 gene and all the positive PCR products were then directly sequenced. The sequence analysis was performed by using appropriate bioinformatics tools.

Results: The frequency of BK viruria in HIV-infected patients was 56%. The predominant BKV subtype was I, followed by subtype IV. The majority of mutations were located within BC loop of VP1. The most frequent mutation was E82D.

Conclusion: The increased levels of BKV replication are associated with a higher incidence of mutations in the BC loop of VP1, and mutations in this domain may lead to changed tropism and the selection of more aggressive variants of BKV. Further studies are needed in order to select the patients with a higher risk of developing BKV-associated-diseases.

http://dx.doi.org/10.1016/j.pbj.2017.07.122

PS182

Cellular interaction in central and peripheral immune organs due to chronic light stress

Bocharova Tetiana

Kharkiv National Medical University, Ukraine
E-mail address: bochata@ukr.net.

Abstract: Study cellular interaction in central and peripheral immune organs at prolonged all-day illumination in an experiment on rabbits.

Introduction: Prolonged all-day illumination is considered nowadays as one of the stress-factors for the living organism and causes malfunctions of the neuroendocrine system and may initial immune dysfunction.

Methods: Experimental rabbits (n = 10) were in artificial lighting in the day and electric lighting at night during 12 months. Control animals (n = 5) were kept in natural day and night lighting conditions. Cell density in immune organs (thymus, bone marrow, spleen) were measured in surface area which was determined by a rectangle 100 × 100 μm. The results were processed with standard statistical methods and reported as mean ± standard deviation (SD).

Results: The cell density in the thymus and the bone marrow was decreased: in the cortex of the thymus was 359.6 ± 2.9, in the medullar part – 250.8 ± 2.9, in the bone marrow – 176.4 ± 2.9 (cells in 100 × 100 μm). An intensified formation of the connective tissue, an increasing of involutive processes and degenerative changes of lymphocytes were microscopically found in the spleen and the thymus. The cell density in the spleen was decreased too: in T zone – 235.8 ± 3.7, in B-zone – 159.5 ± 1.9 (cells in 100 μm × 100 μm). The causes of these changes, probably, may be decrease of the differentiation and migration of lymphocytes as result negative influence of the prolonged light on central immune organs.

Conclusion: These changes in organs of the immune system indicate both a premature aging of the spleen and the thymus and probably of all the immune system. Significant reduction in cell density in the immune organs associate with negative effects of the chronic light stress and leads to expressed immune dysfunction.

http://dx.doi.org/10.1016/j.pbj.2017.07.123

PS217

Intermittent low-level lead exposure causes anxiety and cardiorespiratory impairment

L. Shvachiy, V. Geraldes, Â. Amaro-Leal, I. Rocha

1 Centro Cardiovascular da Universidade de Lisboa; Faculdade de Medicina, Universidade de Lisboa, Portugal
2 Instituto de Fisiologia, Faculdade de Medicina, Universidade de Lisboa, Avenida Professor Egas Moniz, 1649-028 Lisboa, Portugal
E-mail address: shvachiy.liiana@gmail.com

Abstract: The aims of this study were: to determine the prevalence of lead contamination in children, to determine the distribution of lead subtypes and the presence of nucleotide substitutions and mutations in the VP1 gene of BKV isolates.

Introduction: A broad range of diseases associated with BKV such as nephritis, haemorrhagic cystitis, encephalitis, retinitis and pneumonia have been reported in HIV-infected patients over the last few years. However, these diseases do not occur in all HIV-infected patients, suggesting that other factors, such as genetic variability of BKV, can contribute to their occurrence. Mutations in the BC loop of the VP1 gene may lead to selection of more aggressive variants of BKV.

Methods: The study included 50 HIV-infected patients. Semi-nested PCR was used for amplification of 290-nt fragment within the VP1 gene and all the positive PCR products were then directly sequenced. The sequence analysis was performed by using appropriate bioinformatics tools.

Results: The frequency of BK viruria in HIV-infected patients was 56%. The predominant BKV subtype was I, followed by subtype IV. The majority of mutations were located within BC loop of VP1. The most frequent mutation was E82D.

Conclusion: The increased levels of BKV replication are associated with a higher incidence of mutations in the BC loop of VP1, and mutations in this domain may lead to changed tropism and the selection of more aggressive variants of BKV. Further studies are needed in order to select the patients with a higher risk of developing BKV-associated-diseases.

http://dx.doi.org/10.1016/j.pbj.2017.07.122