Introduction: Long interspersed nuclear element-1 (L1) is a family of non-LTR retrotransposons in the human genome and comprises about the 17% of it. It consist of two open reading frames (ORF1p and ORF2p) required for retrotransposition. L1-ORF1 and ORF2 are upregulated in a variety of malignancies. The present study aimed to analyze the epigenetic profile of L1 among prostate circulating tumor cells (CTCs), prostate cancer stem cells (CSCs), differentiated prostate cancer cells and healthy individuals.

Results: The DNA analysis revealed the presence of both L1-ORF1 and L1-ORF2 in all samples. The qPCR experiments demonstrated that only ORF2 was expressed in the above samples. The difference in ORF2 expression was statistical significant among CTCs and the rest cell types, with higher expression levels for CTCs (p<0.001). Among the other types there was no significant different (Normal-CSCs p=0.809 and CSCs-Differentiated cells (p=0.713).

Materials & Methods: Blood samples were collected from 3 healthy donors and 3 prostate cancer patients. Panctytokeratin positive selection was performed for cancer samples, while CD45 negative selection was followed for healthy individuals. Commercial prostate CSCs (Celprogen) and the DU145 (ATCC) cell line were also used. DNA and RNA was extracted from the above samples and qPCR was performed for L1-ORF1 and L1-ORF2. The relative quantification was performed according to Livak method, by using 18SrRNA as housekeeping gene. All the reactions were performed in triplicates. Finally, statistical analysis was performed by setting p<0.05.

Conclusion: Among prostate cancer, the ORF2 RNA expression is higher in CTCs than in CSCs or differentiated prostate cancer cells. There is no significant difference among healthy individual and differentiated cells indicating that L1 might be essential for tumor initiation. Further experiments, including more samples, should be performed to confirm the above so to be used at clinical level.

Introduction of L1 in prostate cancer
Pantopikou K1, Apostolou P1, Papasotiriou I1
1 Research Genetic Cancer Centre Ltd. (R.G.C.C. Ltd.). Industrial Area of Florina GR53100, Florina, Greece

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