BMC Cancer

Meeting abstract

Differential expression of HacaT cells transfected with E6 oncogen from the HPV18 Asian-Amerindian and European variants

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from 24th Annual Meeting of the National Cancer Institute of Mexico
Mexico City, Mexico. 14–17 February 2007

Published: 5 February 2007

BMC Cancer 2007, **7**(Suppl 1):A20 doi:10.1186/1471-2407-7-S1-A20

This article is available from: http://www.biomedcentral.com/1471-2407/7/S1/A20

Background

In Mexico cervical cancer is the first cause of death in women. The causal of high risk human papillomavirus in all cancers of uterine cervix has been firmly established biological and epidemiologically. HPV 16 and 18 account for about 70% of all cervical cancers. In both HPV types intra type variants with differences in their pathogenic potentials have been found. HPV 18 variants have shown differences in viral transcription, as well as differences in relation to E6 oncogen expression and their interaction with important cellular proteins such as p53, hDlg, Bax, etc. European (E) and Asian-Amerindian (AsAi) HPV 18 variants have been associated with a worse prognosis because they are predominantly found in cervical cancers and infrequently in premalignant lesions. However, most of the HPV18 positive cancers contain the European variant. These facts suggest that HPV18 European variant could have a biological advantage over the AsAi isolate. The aim of this study was to determine if human immortalized keratinocytes cells (HaCaT) transfected with HPV18 E6 variants (E and AsAi) have different genomic expression patterns.

Materials and methods

RNA from HaCaT cells transfected with E6 oncogen from the HPV18 European and AsAi isolates were tested twice through hybridization on 10 KB Human microarrays. Statistical analysis was done with GenArise software. Microsoft Acces data base was used to match genes with a differential expression ratio. Biological process was studied by FatiGO data base.

Results

Our results show that within cells transfected with the different E6 variants, 165 genes were differentially expressed; 95 were up-regulated and 70 down-regulated. Even global expression differences seem to be minor, particular differential expression in genes involved in cell proliferation and differentiation was found (IFI-16, NRPI, HOXA6, and HOXD9, etc).

Conclusion

Although this analysis shows minor cellular differences due to E6 HPV18 variants, the analysis of particular genes with a differential expression could help to explain in part, different pathogenic potentials already attributed to HPV18 variants.

Acknowledgements

This work was supported by CONACYT Ref: Salud-2004-01-067 and UNAM.