Infectious Agents and Cancer

Oral presentation

Profiling of cellular and viral microRNAs in Kaposi sarcoma and viral-associated lymphoma

DP Dittmer*[1], AJ O'Hara[1], L Wang[1], BJ Dezube[2], W Harrington Jr[3] and B Damania[1]

Address: [1]Department of Microbiology and Immunology, Lineberger Comprehensive Cancer Center, and Curriculum in Genetics and Molecular Biology, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA, [2]Beth Israel Deaconess Medical Center, Cambridge, Massachusetts, USA and [3]Sylvester Comprehensive Cancer Center, University of Miami, Miami, Florida, USA

* Corresponding author

from 11th International Conference on Malignancies in AIDS and Other Acquired Immunodeficiencies (ICMAOI): Basic, Epidemiologic, and Clinical Research
Bethesda, MD, USA. 6–7 October 2008

Published: 17 June 2009

Infectious Agents and Cancer 2009, **4**(Suppl 2):O19 doi:10.1186/1750-9378-4-S2-O19

This abstract is available from: http://www.infectagentscancer.com/content/4/S2/O19

MicroRNAs are regulated by gene alteration at the DNA level, transcriptional regulation, and mature miRNA processing via Dicer. Thus far, few studies have simultaneously assessed all three levels of regulation. Using real-time quantitative polymerase chain reaction (QPCR)-based arrays, changes in gene copy number, pre-miRNA and mature miRNA levels for a large set of primary effusion lymphomas (PELs) and primary Kaposi Sarcoma biopsies (KS) has been determined; this includes miRNA gene alterations and concordant changes in pre-miRNA and mature miRNA expression levels. The real-time QPCR based approach confirmed many of the KSHV viral and cellular miRNAs previously cloned from PEL. However, array-based profiling also uncovered many novel PEL-specific miRNAs, since cloning-based approaches are not always saturating. The miRNA expression pattern for neither viral nor cellular miRNAs has hitherto been determined for KS. Furthermore, comprehensive SNP analysis of the viral miRNAs has been profiled to further examine the effects of sequence and processing. This defines the miRNA signature of PEL, KS, KSHV-infected cancers and experimental models. It shows that the transcriptional regulation of pre-miRNA as well as mature miRNA levels contribute non-redundant information that can be used in the classification of human tumors.