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The transcriptional landscape of nasopharyngeal carcinoma defined by RNA-seq

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Next-generation sequencing technology is a powerful and cost-efficient tool for ultra-high-throughput transcriptome analysis. We applied paired-end RNA-seq to generate a deep unbiased transcriptome map of a EBV positive nasopharyngeal carcinoma (NPC) cell C666 and normal cell NPEC2. Using effective bioinformatics pipelines, we unambiguously detected many differentially expressed genes, novel transcripts, a variety of transcript isoforms and chimeric transcripts. Most importantly, we have identified a novel fusion gene which might play a oncogenic function in pathogenesis of NPC. Finally, we found that 78% EBV genes are transcribed, which indicate that the expression pattern of EBV in NPC is more complex than previously expected.

Biography

Dr. Zeng received his PhD degrees from Sun Yat-sen University of Medical Sciences and then worked as a postdoctoral fellow at the Department of Radiation Oncology in Tufts University-New England Medical Center in Boston. Currently, Dr. Zeng is a principal investigator in the State Key Laboratory in South China, China. He has published more than 30 papers in reputed journals.

Dr. Zeng's research on EBV variation led to the analysis of the whole genomic sequence from a Cantonese NPC derived EBV. The studies on cellular oncogenes led to identification of the potential role of the polycomb protein Bmi-1 in NPC as well as establishment of Bmi-1 immortalized nasopharyngeal epithelial cell lines. His current research focuses on the molecular events required for early transformation of nasopharyngeal epithelial cells as well as early diagnosis of NPC.