

Expression Trend of Selected Ribosomal Protein Genes in Nasopharyngeal Carcinoma

Sim EDMUND¹, Ling TECK-YEE¹, Tiong THUNG-SING¹,
Subramaniam SELVA¹, Khoo ALAN²

Submitted: 30 Aug 2012

Accepted: 17 Sep 2012

¹ Universiti Malaysia Sarawak, Department of Molecular Biology,
Faculty of Resource Science and Technology, Universiti Malaysia Sarawak
Kota Samarahan Sarawak 94300, Malaysia

² Institute for Medical Research, Molecular Pathology Unit, Cancer Research
Centre Kuala Lumpur, Malaysia

Abstract

Background: Ribosomal proteins are traditionally associated with protein biosynthesis until recent studies that implicated their extraribosomal functions in human diseases and cancers. Our previous studies using GeneFishing™ DEG method and microarray revealed underexpression of three ribosomal protein genes, *RPS26*, *RPS27*, and *RPL32* in cancer of the nasopharynx. Herein, we investigated the expression pattern and nucleotide sequence integrity of these genes in nasopharyngeal carcinoma to further delineate their involvement in tumourigenesis. The relationship of expression level with clinicopathologic factors was also statistically studied.

Methods: Quantitative Polymerase Chain Reaction was performed on nasopharyngeal carcinoma and their paired normal tissues. Expression and sequence of these three genes were analysed.

Results: All three ribosomal protein genes showed no significant difference in transcript expressions and no association could be established with clinicopathologic factors studied. No nucleotide aberrancy was detected in the coding regions of these genes.

Conclusion: There is no early evidence to substantiate possible involvement of *RPS26*, *RPS27*, and *RPL32* genes in NPC tumourigenesis.

Keywords: NPC, RP, *RPS27*, *RPS26*, *RPL32*, transcript expression

Introduction

Nasopharyngeal carcinoma (NPC) is a distinct type of head and neck cancer that refers to the malignancy of the nasopharynx tissue. NPC has its highest incidence in Southern China and South East Asia, and is more prevalent in the population of Cantonese-Chinese heritage (1). Interestingly, in the East Malaysian state of Sarawak, the native Bidayuh population was found to exhibit highest age-standardized rates of NPC occurrence in the world (2). Although many molecular studies have been carried out, NPC remains one of the most commonly misdiagnosed diseases due to the nature of the disease itself (3). Thus, the development of a suitable biomarker is important and essential in the early diagnosis of the disease to better control the prognosis of the cancer.

Traditionally, ribosomal proteins (RP) are thought to play an important role mainly in catalysing protein translation. However, in 1996 extraribosomal functions of RPs was discovered

(4). In a more recent review (5) a list of RPs associated with many extraribosomal functions that are independent of their own involvement in the protein biosynthesis was summarized. Ribosomal proteins have been implicated in many human diseases and disorders. Gazda's group (6) reported association of *RPS19* with Diamond-Blackfan Anemia, in which mutations of *RPS19* together with downregulation of other RP genes, alter transcription, translation, apoptosis and promote oncogenic pathways in the disease. In colorectal carcinoma, the differential expression of RP genes has been found (7,8). Studies by Amesterdam's group (9) using Zebrafish as model suggested RP genes to be candidate cancer causing genes. Developmental defects were also reported in RP knockdown Zebrafish (10). A recent study by MacInnes et al. (11) reported loss of *p53* synthesis in Zebrafish carrying heterozygous mutations for 17 different RP genes hence possibly predisposing Zebrafish to malignant peripheral nerve sheath tumours.

In our previous studies, *RPS26* and *RPS27*