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PUTATIVE TARGET PROTEINS OF THE RIBOSOMAL PROTEIN, RPeL27 IN NASOPHARYNGEAL CARCINOMA CELLS

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Abstract

The pathogenesis of nasopharyngeal carcinoma (NPC) is multifactorial and multigenic. Despite the identification of several NPC-associated ribosomal proteins (RPs), the roles of these factors and their interacting partners in NPC tumourigenesis are poorly understood. To date, NPC-associated RP genes are either up or down-regulated in diseased/tumour situation compared to normal condition. The ribosomal protein eL27 (RPeL27) has been known to be over-expressed at both transcript and protein levels in NPC cell lines. This hypothesis was reinforced by our study herein. More importantly, using gene knockdown (RNA interference technique) followed by 2D gel electrophoresis (2D GE) and *in silico* analysis; we revealed 15 proteins that are likely to interact with RPeL27 during situation of NPC tumourigenesis. These include COTL1, MAGOHB, UBE2N, NDPKA, TMED10, PSMB6, CA2, PGAM1, RPeL14, RPeS8, TPI1, PSMA2, RPeL19, GSTP1, and TPM1. Their association with RPeL27 could attribute to gene expression alteration, cell migration disruption and invasion, promotion of cancer cell survival, immune evasion, and genomic instability. Our findings provide new theoretical insights into the mechanism and involvement of RPeL27 in NPC pathogenesis. This is pertinent in understanding the molecular pathogenesis mediated by ribosomal proteins in the malignancy of the nasopharyngeal tissues.

INTRODUCTION

Ribosome is important for protein synthesis in every cell and ribosome biogenesis is well- monitored event in the control of cell growth. Eukaryotic ribosomes, also known as 80S ribosomes, are made up of small and large subunit of ribosomal proteins (RPs). The dysregulation of RPs is often detected in cancer cells. In addition, oncogenes are known to enhance ribosome biogenesis in order to stimulate cancer cell growth [1]. To date, several RPs (*RPeL27*, *RPeL43*, *RPeL41*, *RPuS8*, *RPuS4*, *RPeS31* and *RPuL14*) have been found to be differentially expressed in nasopharyngeal carcinoma (NPC) cells lines relative to non- malignant or normal counterparts [2,3]. *RPeL27*, *RPeL43*, and *RPeL41* were found to be significantly upregulated while *RPuS8*, *RPuS4*, *RPeS31* and *RPuL14* were downregulated significantly in NPC. These findings have suggested some pivotal roles of RPs in NPC pathogenesis. However, despite a demonstration of NPC association on the basis of differential expression, very little to nothing is known with respect to the interactions between RPs and their molecular targets during NPC tumorigenesis. In the case of *RPeL27*, its markedly overexpression in NPC cells [2] was also detected in hepatocellular carcinoma, liver cancer and, gastric tubular adenoma and carcinoma [4,5,6]. To date, the biological significance of its upregulation in NPC is largely unclear. Herein, we aimed to identify and characterize the proteins that may associate with RPeL27 in the context NPC tumorigenesis. To achieve this, we first verified the overexpression of RPeL27 at transcript and protein levels in 6 NPC cell lines. Subsequently, we knocked down its expression in a representative cell line model to identified possible interacting factors. *In silico* approach was then carried out to assess logical protein-protein interaction between RPeL27 and its putative partners.

MATERIALS AND METHODS

Cell lines and Culture

Six NPC cell lines (HONE-1, SUNE-1, HK1, TW01, TW04 and C666-1) were used in this study. The non-malignant nasopharyngeal epithelial cell line (NP69) was used as a control. All these originated from the University of Hong Kong, with permission for use granted by Professor George S. W. Tsao. The NPC cell lines were cultured in RPMI-1640 (Gibco, Life Technologies, USA) with 10% (v/v) fetal bovine serum, 2mM L-