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SELECTIVE DIFFERENTIAL EXPRESSION OF THE RIBOSOMAL PROTEIN GENES *eL14* AND *uS19* IN A WELL-DIFFERENTIATED EPITHELIAL CELL LINE OF NASOPHARYNGEAL CARCINOMA

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ABSTRACT

Besides ribosome biogenesis and protein synthesis, ribosomal proteins (RP) are associated with congenital diseases and cancers. A small subset of ribosomal protein genes has shown expression pattern indicative of their association with nasopharyngeal carcinoma (NPC). Nevertheless, the list of RP genes that are NPC-associated factors is largely incomplete. Herein we report the expression patterns of *eL14* and *uS19* in NPC normal nasopharyngeal epithelium cell lines. Expression levels of *eL14* and *uS19* in the NPC-HK1 cell line was comparatively analysed with a normal nasopharyngeal cell line (NP69) using Reverse Transcription – Polymerase Chain Reaction (RT-PCR). We revealed that the transcript level of *eL14* was significantly down-regulated in HK1 when compared to NP69. The expression behaviour of *eL14* is demonstrated for the first time in the NPC context. In contrast, the transcript level of *uS19* was up-regulated in NPC/HK1 compared to NP69, but not to a statistically significant extent. This study provides new evidence of differential expression of the ribosomal protein gene, *eL14* in an NPC cell line derived from well-differentiated squamous cell carcinoma of human nasopharynx. It adds to the list of NPC-associated ribosomal protein genes amenable for development of biomarkers for improved molecular diagnosis of nasopharyngeal cancer.

Key words: Ribosomal protein genes, *eL14*, *uS19*, nasopharyngeal carcinoma, gene expression analysis

INTRODUCTION

The basic function of RP genes constitutes ribosome-mediated protein biosynthesis. Eukaryotic RP genes are divided into two broad types. In human, these comprise genes for the small (40S) ribosomal subunits (*e/uS1 – S15*, *e/uS17*, *e/uS19*, e*S21*, *eS24 – S28*, *eS30*, *eS31*, and *RACK1*), and those of the large (60S) ribosomal subunit (*e/uL1 – L8*, *uL10*, *uL11*, *e/uL13 – L16*, *e/uL18 – L24*, *e/uL27 – L34*, *eL36 – L43*, and *PI/P2*) (Ban *et al*., 2014). Despite a unified mechanism for control of transcription and translation, each is distinguishable by its expression level and tissue-specificity (Ishii *et al*., 2006). Their functions often extend beyond ribosome biogenesis and protein synthesis to include extra-ribosomal roles such as interactions with oncogenic factors and/or tumour suppressors in the tumorigenesis of a variety of cancer types (deLas-Heras-Rubio *et al*., 2014). The association of some RP genes with nasopharyngeal carcinoma (NPC) cells has been reported (Fang *et al*., 2008; Sim *et al*., 2008, 2010, 2016, 2017).

The *uS19* gene is up-regulated in non to poorly differentiated squamous cell carcinoma of the nasopharynx (Fang *et al*., 2008). Its activity in well-differentiated type of NPC cells is unknown. Located at 19p13.3, it functions in the maturation and assembly of the 40S ribosome subunit (Robledo *et al*., 2008), and is presumably involved in the initiation and elongation steps of translation (Kitagawa *et al*., 1991; Rouquette *et al*., 2005). Its nuclear respiratory factor (NRF) acts as a transcriptional activator, and its activator protein (AP-1) is associated with cellular proliferation, apoptosis and differentiation (Ishii *et al*., 2006). Expression of *uS19* is high in tumour cells of insulinomas, and oesophageal and colon cancers

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