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LETTER TO THE EDITOR

TERT Promoter Mutation and Telomere Length in Salivary Gland Tumors

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To editor

Telomeres are well known structure that protects the ends of chromosomes from end-to-end fusion and contribute the stability of the chromosomes. Telomerase reverse transcriptase (TERT), which is subunit of telomerase, maintains the length of telomeres. Recently, the somatic mutation in the promoter region of αTERT were reported in various tumors including melanoma [1, 2], gastric cancer [3, 4], thyroid carcinoma [5], and urothelial cancer [6]. In the salivary gland, however, it has been barely investigated telomere related tumorigenesis mechanism including shortening length of telomere and the mutation in the promoter region of TERT.

In Korean population, the incidence of the salivary malignancy was 0.9 cases per 100,000 population in 2013, which is only 0.2% of all malignancies and about 15% of cancers of the head and neck [7]. Because of its rarity, little is known about the molecular profiles of the salivary tumor. In this study, thus, we analyzed the promoter region of TERT and the length of telomere in the salivary gland tumor. We gathered clinical data and tumor samples from 36 cases after curative resection. Histology type of the collected tumor sample was identified by pathologist. Most abundant type was pleomorphic adenoma (n = 19), followed by Warthin tumor (n = 8), basal cell adenoma (n = 1), chronic sclerosing sialadenitis (n = 1) and epidermal inclusion cyst (n = 1). One case of benign tumor was unremarkable. Five cases of malignant salivary tumors were adenosquamous carcinoma, poorly differentiated adenocarcinoma, epithelial-myoepithelial carcinoma, adenoid cystic carcinoma and salivary duct carcinoma. For convenience of statistical analysis comparing between different histology type, we clustered the cases in 4 main group consist of pleomorphic adenoma, Warthin tumor, malignancy and another benign type.

Based on our previous finding [4], we sequenced the promoter region of TERT including well-known hot spot region and other potential mutational regions. Unfortunately, however, we found no hTERT promoter region mutation in all of the samples. To investigate the involvement of the telomere length shortening in tumorigenesis of the salivary gland, we analyzed the length of telomere and compared between the histologic groups (Fig. 1). The telomere length of pleomorphic adenoma, Warthin tumor, carcinoma and another benign type was 12.3 ± 25.5, 6.2 ± 8.4, 3.1 ± 4.5, 10.3 ± 9.7, respectively. Although the telomere length

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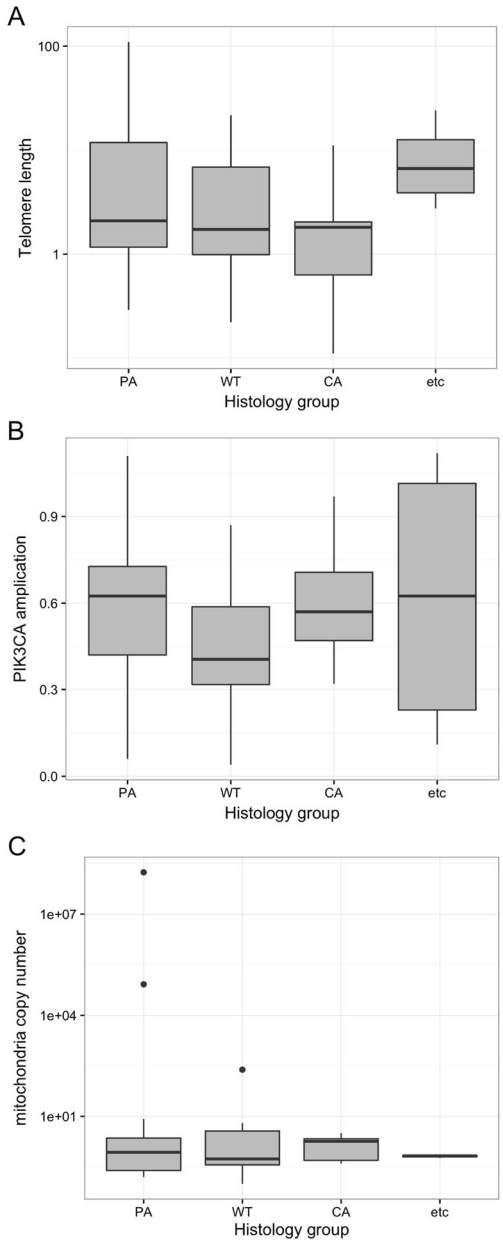

Fig. 1 Box plot of the telomere length for each histology group. The vertical line extends from the smallest non-outlier to the largest non-outlier. The box was drawn from 25 to 75 percentiles. The thick horizontal line in the box means the median of the data. PA, pleomorphic adenoma; WT, Warthin tumor; CA, carcinoma; etc., another benign tumor

of carcinoma was shorter than other group, there was no significant difference between the histology groups (p = 0.781, ANOVA test).

To the best of our knowledge, this is the first paper that reports the results of sequencing the TERT promoter region in various type of salivary gland tumor. Considering the discrepancies of the TERT promoter mutation prevalence according to the origin of tumor [1, 2], it is not surprise that no mutation was detected in 36 cases of the salivary gland tumor. Nevertheless, the number of collected data was too small to confirm that the tumorigenesis effects of TERT promoter mutation would be less likely in the salivary glands. Recent study reported that the presence of TERT promoter methylation was associated with the carcinoma ex pleomorphic adenoma which is believed as malignant form resulting from transformation of the pleomorphic salivary adenoma [8]. Thus, it is needed to gather more cases of the salivary tumor to examine the mechanism of regulating telomere length in the malignancy as well as the benign tumor.

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