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Effects of prolonged stimulation with heated tobacco products (Ploom TECH^{+}) on gingival epithelial cells

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Practitioner points:

- Long-term HTP stimulation affects epithelial differentiation and keratinization of gingival epithelial cells.
- Habitual use of Ploom TECH^{+} may be a risk factor for tobacco-related oral mucosal diseases.

Abstract

Objective and Background: Heated tobacco products have recently become commercially available. These products, as well as combustible cigarettes, produce aerosols; the risk of various diseases associated with heated tobacco products may be the same as or higher than that with combustible cigarettes. In this study, we examined the effect of Ploom TECH^{+} extract on gingival epithelial cells.

Methods: Tobacco leaves from Ploom TECH^{+} tobacco capsules and water were mixed and heated; the supernatant subsequently collected was the heated tobacco product (HTP; control: HTP not added). Normal human gingival epithelial progenitors were cultured alternately with or without HTP for a total of 1 month. Subsequently, RNA, DNA, and proteins were isolated from these samples and comprehensively analyzed using RNA sequencing (RNA-seq), reduced representation bisulfite sequencing (RRBS), and western blotting, respectively.

Results: RNA-seq revealed that 284 genes showed a two-fold increase and 145 genes showed a two-fold decrease in gene expression. A heat map showed genetic differences between the control and HTP groups. A principal component analysis plot showed a clear genetic distribution between the control and HTP. Gene Ontology (GO) analysis showed that genes related to seven GO terms, including cornification and keratinization, were induced by long-term HTP stimulation. By contrast, GO pathways with a significant decrease in component expression were not detected. RRBS revealed that CpG island methylation increased more than two-fold in 158 genes and decreased to less than two-fold in 171 genes. Methylation of these CpG islands was not correlated with changes in gene expression levels. HTP treatment increased S100A7 expression.

Conclusion: Long-term HTP stimulation affected epithelial differentiation and keratinization of gingival epithelial cells. Thus, habitual use of Ploom TECH^{+} may be a risk factor for tobacco-related oral mucosal diseases.

Introduction

Consumption of combustible cigarettes lead to systemic issues such as the development of cancer, cardiovascular disease, and respiratory illness. Cigarettes are important risk factors for oral cancer and periodontal disease, which is of concern for dental professionals.[1] Smoking cigarettes, which contain approximately 70 types of carcinogens and other harmful chemicals, often causes genetic and epigenetic alterations leading to oral cancer and induces abnormal blood circulation leading to periodontal diseases.

Recently, heated tobacco products, which do not require combustion, have become commercially available. These products can be broadly divided into two types: "high-temperature heating" type, wherein tobacco leaves are heated at 200–350°C, and "low-temperature heating" type, wherein tobacco leaves are heated at 30–40°C. IQOS is a high-temperature heating-type cigarette that generates steam by directly heating tobacco leaves in a heater. Ploom TECH$^+$ is a low-temperature heating-type cigarette that vaporizes liquid. Although many studies have reported on the risks associated with the high-temperature type, to the best of our knowledge,[2] no reliable independent data on the risks associated with the low-temperature type have been reported thus far. Heated tobacco products were initially considered less toxic than combustible cigarettes; however, an increasing number of studies have reported toxicity.[3,4] The risk of carcinogenesis owing to heated tobacco might be the same as or higher than that of combustible cigarettes.[5] Several clinical cases of fulminant pneumonia possibly attributable to use of heated tobacco have been reported.[6] An *in vitro* experiment showed that the components of this type of tobacco directly damaged bronchial epithelial cells and vascular endothelial cells.[7]

To our knowledge, the effect of heated tobacco products on the oral mucosa has not yet been shown. Heated tobacco contains many toxic substances, although to a significantly lesser degree than that in combustible cigarettes, and its use may increase the risk of oral cancer and periodontal diseases. Oral epithelium exposed to heated tobacco may experience pathological changes leading to the development of oral cancer and periodontal disease. We hypothesized that heated tobacco products induce molecular changes in the oral epithelium. Therefore, in this study, we examined the effect of Ploom TECH$^+$ extract on gingival epithelial cells. The oral mucosa of individuals who use heated tobacco products is regularly exposed to the tobacco for long time. The cells derived from oral mucosa should be stimulated for long time. The cells are usually stimulated with the chemical substances for 1 to 72 h in vitro, since

the cells have to be fed by medium every 72 h. These stimulation periods may be too short to observed the effect of the heated tobacco on the cells. We previously developed an *in vitro* model to stimulate cells for 1 month as a long-term and chronic stimulation.[8] Therefore, we subjected oral epithelial cells to prolonged stimulation using our previous model.

Materials and Methods

Cell culture

Human gingival epithelial progenitors (HGEPs) were purchased from CELLnTEC Advanced Cell Systems (Basel, Switzerland) and cultured in CnT-Prime epithelial culture medium (CELLnTEC Advanced Cell Systems) at 37°C in a humidified atmosphere of 95% air and 5% CO_2. HEGPs were kept in the medium not to be differentiated.

Heated tobacco product (HTP) preparation

Ploom TECH$^+$ (Japan Tobacco Inc., Tokyo, Japan) tobacco capsules were disassembled, and the tobacco leaves in the capsules were collected in 1.5-ml tubes. Next, the leaves were weighed, and 3 ml water was added per gram of tobacco leaves. Subsequently, the mixture was heated at 60°C for 120 min.[9] Thereafter, the tobacco leaves and supernatant were separated using centrifugation at 15,000 rpm for 15 min, and the supernatant was collected and used as the extract (HTP).[9]

Cell viability assays

Cell viability was determined using the cell proliferation reagent water-soluble tetrazolium salt (WST-1; Thermo Fisher Scientific, MA, USA). The HGEPs were seeded in 96-well plates (AGC TECHNO GLASS, Shizuoka, Japan) in the culture medium and cultured overnight. The cells were treated with different concentrations of HTP (0%, 0.1%, 0.2%, 0.5%, 1%, 2%, 5%, and 10%); 0% HTP samples were used as controls. Subsequently, the plates were incubated for 24, 48, and 72 h, following which 10 µl WST-1 was added to each well and the cells were cultured for 1 h. Absorbance was measured at 450 nm using the Multiskan FC system (Thermo Fisher Scientific). The experiment was

repeated six times. Statistical analysis was performed using SPSS version 26 (SPSS, Inc., Chicago, IL, USA). Results were compared using the Kruskal–Wallis test, with a p-value of <0.05 being considered statistically significant.

Sample preparation

The HGEPs were seeded in 6-well plates (AGC TECHNO GLASS) at a density of 3.0×10^5 cells/well in culture medium and cultured overnight. The HGEPs were treated with 1% HTP. The culture medium was replaced every 3 days, while alternating with and without HTP for a total of 1 month.[8] Untreated samples were used as controls. The same amount of water as HTP was added to the controls every 3 days. Genomic DNA was extracted using the DNeasy Blood & Tissue Kit (Qiagen, Hilden, Germany), according to the manufacturer's instructions. DNA extracts were stored at −20°C until use in experiments and were utilized for bisulfite processing. Total RNA was extracted from HGEPs using the TRIzol Reagent (Thermo Fisher Scientific K.K., MA, USA) and purified using the RNeasy Mini kit (Qiagen GmbH, Hilden, Germany) according to the manufacturers' protocols. RNA extracts were stored at −80°C and used for reverse transcription. Total protein was extracted from the HGEPs using the EzRIPA lysis kit (ATTO, Tokyo, Japan) according to the manufacturer's instructions. Protein extracts were stored at −80°C until use and were utilized for western blot analysis. The experiment was repeated three times for RNA sequencing (RNA-seq) and reduced representation bisulfite sequencing (RRBS) and six times for quantitative reverse transcriptase PCR, quantitative methylation-specific PCR (qMSP), and western blotting.

RNA-seq and functional enrichment analysis

Samples were run on a BioAnalyzer to assess total RNA integrity. Only high-quality RNA samples (RNA integrity number ≥ 9.0) were used to construct the sequence library. PCR-based amplification was performed using the template prepared with the strand-specific library preparation method (dUTP method) and an index sequence-containing primer to prepare a sequence library (NEBNext Poly(A) mRNA Magnetic Isolation Module; NEBNext Ultra II Directional RNA Library Prep Kit for Illumina). RNA-seq data were obtained using the NovaSeq 6000 system (Illumina, San Diego, CA, USA). The sequence reads were trimmed using Trimmomatic (ver.0.38). Trimmed sequence reads were mapped to the reference genome (hg38) using HISAT2 (ver.2.1.0). The raw read count for each gene was calculated

using featureCounts (ver.1.6.3). The raw read count was uploaded to iDEP.95 (http://bioinformatics.sdstate.edu/idep95/) for hierarchical clustering, principal component analysis (PCA), correlation evaluation, heat map creation, and functional enrichment analysis.[10] Initial settings of iDEP were used for the analysis.

Quantitative reverse transcriptase PCR

The extracted RNA (2 μg) was reverse-transcribed to cDNA using the ReverTra Ace® qPCR RT Master Mix (TOYOBO, Osaka, Japan). mRNA expression levels were measured using a LightCycler®96 system (Roche Diagnostics, Basel, Switzerland). Table 1 lists the primer sequences used in this study. Real-time PCR was performed using the obtained cDNA, KAPA SYBR FAST qPCR Mix (Kapa Biosystems, MA, USA), and a pair of primers, according to the manufacturers' protocols. The PCR program was as follows: pre-incubation at 95°C for 3 min; denaturation at 95°C; and 40 cycles each of denaturation at 95°C for 10 s, annealing at 60°C for 20 s, and elongation at 72°C for 1 s. The relative mRNA expression levels were calculated in terms of the Cq value (value obtained by subtracting the Cq value of GAPDH mRNA from the Cq value of the target mRNA) using the ΔΔCq method.[11] Specifically, the amount of target mRNA relative to GAPDH mRNA was expressed as $2^{-(\Delta Cq)}$. Data have been expressed in terms of the ratio of the target mRNA to GAPDH mRNA. Results were compared using the Mann–Whitney U test, with a p-value of <0.05 being considered statistically significant.

Western blot analysis

Thirty micrograms of protein was used for western blot analysis. Pre-cast gels (5–20% gradient polyacrylamide gels; e-PAGEL, ATTO, Tokyo, Japan) were used for sodium dodecyl sulfate–polyacrylamide gel electrophoresis. The separated protein bands were transferred onto a polyvinylidene fluoride transfer membrane (ATTO). Blocking was performed using Tris-buffered saline (TBS) containing 5% skimmed milk for 1 h at 20°C. The primary antibodies used were polyclonal rabbit anti-cytokeratin 13 (1:1000; Proteintech Group, IL, USA), polyclonal rabbit anti-kallikrein 12 (1:1000; Thermo Fisher Scientific), polyclonal rabbit anti-S100A7 (1:1000; Proteintech Group, IL, USA), and monoclonal mouse anti-GAPDH (1:10,000; Proteintech Group) antibodies. The membranes were

incubated with each primary antibody overnight at 4°C, washed three times with TBS containing 0.05% Tween-20, and further incubated with secondary antibodies for 1 h at 20°C. The secondary antibodies used were horseradish peroxidase (HRP)-conjugated goat anti-rabbit IgG (1:10,000, Proteintech Group) and HRP-conjugated goat anti-mouse IgG (1:10,000, Proteintech Group) antibodies. Cytokeratin 13 (KRT13), kallikrein 12 (KLK12), S100A7, and GAPDH bands were visualized using an enhanced chemiluminescence system (Clarity Western ECL substrate; Bio-Rad, CA, USA) and WSE-6100 LuminoGraph I (ATTO). Intensities of KRT13, S100A7, and GAPDH were recorded using the ImageSaver6 software (ATTO), and the bands were quantified using the image analysis software CS Analyzer 4 (ATTO). The ratios of intensity of KRT13, S100A7, and GAPDH in HTP-treated (HTP) or untreated (control) HGEPs from two independent experiments were calculated. Results were compared using the Mann–Whitney U test, with a p-value of <0.05 being considered statistically significant.

qMSP

Samples were run on a BioAnalyzer to assess total DNA integrity. Only high-quality DNA samples (DNA integrity number ≥ 9.0) were used to construct the sequence library. The extracted DNA was treated with sodium bisulfite using the EpiTect Plus Bisulfite Kit (Qiagen). DNA methylation of *KRT13*, *KLK12*, and *S100A7* was analyzed using SYBR Green–based qMSP. Two sets of PCR primers were designed using the MethPrimer program (http://www.urogene.org/methprimer/). Methylated and unmethylated primers were designed targeting the promoters (Table 1). The PCR mixture (20 µl) comprised 1.0 µl bisulfite-treated DNA template, 10 µl KAPA SYBR FAST qPCR Mix, and a pair of primers. DNA methylation was analyzed using the LightCycler®96 system. The PCR program was as follows: pre-incubation at 95°C for 3 min; denaturation at 95°C; and 50 cycles each of denaturation at 95°C for 10 s, annealing at 60°C for 20 s, and elongation at 72°C for 1 s. The DNA methylation percentage in the samples was estimated using the following formula: DNA methylation (%) = $M/(M + U) \times 100 = 1/(1 + U/M) \times 100 = 1 / (1 + 2^{(-\Delta Cq)}) \times 100$, where M is the copy number of the methylated gene, U is the copy number of the unmethylated gene, and $\Delta Cq = Cq_U - Cq_M$.[12] Results were compared using the Mann–Whitney U test, with a p-value of <0.05 being considered statistically significant.

RRBS

The samples were run on a BioAnalyzer to assess genomic DNA integrity. Only high-quality DNA samples (DNA integrity number ≥ 9.0) were used to construct the sequence library. To perform methylation analysis of the CpG region, the CpG-rich region was enriched by cutting genomic DNA with the restriction enzyme Mspl, adding a TruSeq adapter, performing bisulfite treatment, and adding an index sequence. The RRBS library was prepared using the Zymo Research Zymo-Seq RRBS Library Kit (Zymo Research, Irvine, CA, USA). RRBS data were obtained using the NovaSeq 6000 system (Illumina). Sequence reads were trimmed using Trim Galore (ver.0.5.0). Trimmed sequence reads were mapped to the reference genome using Bismark (ver.0.20.0). The methylation rate was calculated, and comparison analysis was performed using methylKit (ver.1.16.0). A heat map was drawn using the differentially methylated cytosine/differentially methylated region methylation rate using stats (ver.3.6.1) and gplots (ver.3.0.1.1). We examined this correlation further by plotting expression logFC versus methylation (CpG island) logFC for all genes using the method described by Chen et al.[13]

Results

Cell viability

To determine appropriate experimental conditions for analyzing cell viability maintenance in HTP-stimulated cells, we analyzed cell viability while using different HTP concentrations. Using the WST-1 assay, cell viability was estimated at 24, 48, and 72 h with different HTP concentrations. At 24, 48, and 72 h, cell viability did not significantly differ at the same time point between any HTP concentration and the control. Cell viability with ≥10% HTP was significantly lower than that in the control ($p < 0.05$, Fig. 1). Based on these data, culture was repeated under the following conditions: 3 days with 1% HTP alternating with 3 days without HTP, for a total of 1 month.

Gene expression profiles

For comprehensive RNA-seq analysis, HGEPs alternately cultured with or without 1% HTP for a total of 1 month were used for RNA extraction. The heat map shows differences between the control and HTP for all genes identified using RNA-seq (Fig. 2A). The PCA plot revealed clear differences between the control and HTP (Fig. 2B). Among

differentially expressed genes (DEGs), 284 showed a greater than two-fold increase ($p < 0.05$, Fig. 2A–C, Table 2) and 145 showed a more than two-fold decrease ($p < 0.05$, Fig. 2A–C, Table 2). Gene Ontology (GO) analyses included the biological process, cellular component, and molecular function categories. According to the functional enrichment results, only seven biological process terms were significantly enriched in DEGs. GO analysis revealed that long-term HTP stimulation increased the expression of components belonging to the GO pathways cornification (70 upregulated genes, such as *KRT13*, *KLK12*, and *PI3* in descending order; $p < 0.05$), keratinization (84 upregulated genes, such as *KRT13, KLK12,* and *PI3*.; $p < 0.05$), epidermal development (279 upregulated genes, such as *KRT13*, *KLK12*, and *S100A7*; $p < 0.05$), epidermal cell differentiation (196 upregulated genes, such as *KRT13, KLK12*, and *S100A7*; $p < 0.05$), skin development (248 upregulated genes, such as *KRT13, KLK12*, and *S100A7*; $p < 0.05$), keratinocyte differentiation (155 upregulated genes, such as *KRT13, KLK12*, and *S100A7*; $p < 0.05$), and epithelial cell differentiation (498 upregulated genes, such as *KRT13, KLK12*, and S100A7; $p < 0.05$) (Fig. 2D, E). Reproducibility was confirmed for *KRT13* (seven pathways), *KLK12* (seven pathways), and *S100A7* (five pathways), which are related to upregulated GO pathways in the iDEP analysis and are the upregulated DEGs.

To confirm the reliability of the expression profiles generated using the RNA-seq and DEG analyses, qRT-PCR was applied to examine the expression of the upregulated candidate genes (*KRT13, KLK12,* and *S100A7*). *KRT13* and *KLK12* were GO-related genes. *S100A7* is associated with epidermal development, epidermal cell differentiation, skin development, keratinocyte differentiation, and epithelial cell differentiation. As expected, the qRT-PCR results basically matched the RNA-seq results, confirming the relationship of *KRT13, KLK12*, and *S100A7* with elevated component expression in GO pathways; increased expression was confirmed for all three genes ($p < 0.05$; Fig. 3A–C).

Protein expression

HTP treatment increased S100A7 expression levels, but did not change the KRT13 and GAPDH expression levels (Fig. 3D). KLK12 expression was not detected. The ratios of intensity of KRT13/GAPDH in HGEPs treated with or without 1% HTP were 1.00 ± 0.11 and 0.94 ± 0.06, respectively. No significant difference was observed in the ratio of intensities of KRT13/GAPDH between control and HTP. The ratios of intensity of S100A7/GAPDH in HGEPs

treated with or without 1% HTP were 1.00 ± 0.91 and 13.43 ± 6.83, respectively. The p-value for the ratio of intensities of S100A7/GAPDH between HTP-treated and untreated HGEPs was <0.05 (Fig. 3E, F).

DNA methylation

For comprehensive RRBS analysis, HGEPs were alternately cultured with or without 1% HTP for a total of 1 month, followed by DNA extraction. Read counts were normalized using methylKit, and differentially methylated cytosines (DMCs) and differentially methylated regions (DMRs) were extracted through logistic regression. A heatmap was drawn using the methylation rate of DMC/DMR. Heatmap analysis showed that the CpG methylation differed between the control and HTP groups (Fig. 4A). CpG regions were classified and annotated as follows. CpG island: A genomic region of 200 bases or more, with a total guanine and cytosine content of 50% or more, and a ratio of the actual frequency of occurrence of CG sequences to the predicted value of ≥0.6. CpG islands accumulate in gene promoter regions and are involved in the promotion or suppression of gene expression.[14] CpG shore: Peripheral part of CGI (approximately 2 kb). The methylation status of CpG island shores is tissue specific. CpG shelf: A region between 2 and 4 kb around CGI. interCpG (interCGI): Regions not classified above. When overlapping with multiple divisions, priority was assigned in the order of CGI, shore, shelf, and inter CpG. A total of 158 genes showed greater than two-fold hypermethylation (Table 3) and 171 genes showed greater than two-fold hypomethylation (Table 4) in CpG islands. Changes in DNA methylation were not correlated with gene expression levels (Fig. 4B). Furthermore, DNA methylation levels did not significantly differ between the control and HTP groups for *S100A7*, *KLK12*, and *KRT13* (Fig. 4C–E).

Discussion

In the current study, we comprehensively analyzed the effects of long-term HTP stimulation on gingival epithelial cells using RNA-seq and RRBS. To the best of our knowledge, our study is the first to report genome-wide analysis of the effects of HTP on gingival epithelial cells. We found that HTP significantly increased *KRT13*, *KLK12*, and *S100A7* expression, which was accompanied by keratinocyte differentiation. GO analysis confirmed that HTP increased the expression of components of the pathways related to keratinocyte differentiation, such as those involved

in cornification, keratinization, keratinocyte differentiation, and epithelial differentiation. These results indicate that heated tobacco use may stimulate keratinocyte differentiation in the gingiva. Pathological keratinization, called dyskeratosis, can be observed in tobacco-related oral mucosal diseases, such as leukoplakia, lichen planus, nicotine stomatitis, and squamous cell carcinoma.[15] HTP-stimulated keratinocyte differentiation may thus lead to tobacco-related oral mucosal diseases. Thus, habitual use of Ploom TECH$^+$ may be a risk factor for tobacco-related oral mucosal diseases. Further studies are required to confirm this hypothesis.

Recently, an *in vitro* study reported the effects of IQOS heated tobacco on oral keratinocytes and fibroblasts after 24 h. In these experiments, use of IQOS extracts increased the number of cells in the S and G2/M phase and increased and decreased Bcl2 and p53 expression, respectively. The study suggested that the extract increased oral keratinocyte proliferation.[16] In our study, at 24, 48, and 72 h, HTP treatments did not show higher cell counts than the control (without HTP) at any concentration. Ploom TECH$^+$ stimulation did not induce cell proliferation. Because the oral mucosa of individuals who use heated tobacco is regularly exposed to the tobacco, we repeatedly stimulated the gingival epithelial cells for 1 month, in accordance with the findings in our previous research.[9] Our experimental design may better reflect habitual cigarette use than the abovementioned study conducted by Pagano et al in 2021.[16]

High levels of KRT13 and KRT4 are expressed in the suprabasal layer of the normal human buccal mucosa, suggesting early differentiation of non-keratinized squamous mucosa.[17] Aberrant KRT13 expression is involved in several pathological conditions. Decreased KRT13 expression has been observed in oral squamous cell carcinoma and dysplasia.[18] KRT13 deficiency was found to cause white sponge nevus.[19] Elevated KRT13 expression might promote tumor metastases.[20,21] In the current study, the upregulated KRT13 expression noted may reflect keratinocyte differentiation or may be related to pathological conditions in gingival epithelial cells. KRT13 upregulation was confirmed at the mRNA level, but no obvious increase was observed at the protein level. Therefore, KRT13 upregulation may not greatly affect gingival epithelial cells.

KLK12 is a type of tissue kallikrein, a subgroup of serine proteases encoding a family of 15 closely related serine proteases.[22] These enzymes are involved in shedding during squamous epithelial desquamation.[21] Many types of kallikreins, including KLK1, KLK4, KLK5, KLK6, KLK7, KLK8, and KLK13, have been detected in skin and keratinocytes,[23] but KLK12 has not been found in keratinocytes. High KLK12 expression might be involved in breast,

gastric, and colorectal cancers.[24-27] HTP-induced upregulation of KLK12 expression may be involved in the malignant potential of epithelial cells. However, we detected *KLK12* mRNA, but not protein, indicating that upregulated KLK12 expression did not considerably affect gingival epithelial cells.

S100A7, also known as psoriasin, is highly expressed in patients with psoriasis and other inflammatory diseases. It induces keratinocyte differentiation, resulting in skin and oral epithelial stratification.[28] The involvement of S100A7 in gingivitis and oral squamous cell carcinoma has been reported. Increased S100A7 expression was found in experimentally induced gingivitis.[29] This increased expression may be due to the inflammatory stimulation, since IL-1α stimulates the upregulated expression of S100A7 in gingival keratinocytes.[30] In the current study, we observed increased S100A7 expression at both mRNA and protein levels. Therefore, HTP stimulation may increase S100A7 expression resulting from inflammatory changes and keratinocyte differentiation. The involvement of S100A7 in gingivitis and oral squamous cell carcinoma has been reported, and has been suggested for use as a diagnostic biomarker.[31,32]

Transcriptional alterations are often caused by genetic methylation in individuals who smoke tobacco.[33] CpG island methylation often affects transcription, and hyper- and hypomethylation directly lead to the down- and upregulation of mRNA expression, respectively. Therefore, we examined whether alterations in CpG island methylation were involved in the differential expression of *KRT13*, *KLK12*, and *S100A7*. However, the methylation levels of these genes did not show significant alterations. We performed global analysis of CpG island methylation with the same experimental models. Although many genes showed hyper- or hypomethylation in HTP-treated samples, a scatter plot of methylation levels versus gene expression levels showed that transcriptional levels were not correlated with methylation levels. Therefore, the overall altered mRNA expression may be unaffected by methylation alterations in HTP-treated samples.

The limitation of this study is that the heated tobacco extracts were crude; therefore, the individual chemicals involved in their effects on gingival epithelial cells are not known. Ploom TECH^{+} contains many chemical substances such as formaldehyde, acrolein, benzaldehyde, propylene glycol, and glycerol[5]; further research is required to identify the chemicals that exerted the greatest effect on our samples. The crude components may lead to the inhibition of cell growth. Glycerol and propylene glycol are involved in carcinogenesis and may be involved in the dysmorphic and

hyper keratinization of gingival epithelial cells.[34] Moreover, we focused on *KRT13, KLK12,* and *S100A7* as upregulated candidate genes in this study. However, it is possible that some other genes may be more effective for oral mucosa.

In conclusion, because long-term HTP stimulation affects epithelial differentiation and keratinization of gingival epithelial cells, habitual Ploom TECH$^+$ use may be a risk factor for tobacco-related oral mucosal diseases. However, the mechanism underlying induction of epithelial differentiation and keratinization by HTP remains unclear. Our data may aid in further clarifying the disadvantages of heated tobacco use; however, further research is required to confirm this hypothesis.

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Conflicts of interest

The authors declare no conflict of interest.

Data availability statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Authors' contributions

OU, NN, DH, and YA designed the study. OU, NN, DH, DP, NS, TM, KY, and YK collected and analyzed the data. OU, NN, DH, YK, TS, YF, HM, and YA interpreted the data. OU, NN, DH, DP, YK, and YA drafted and revised the manuscript. All authors have approved this manuscript for submission.

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Table legends

Table 1 Primer sequences used for quantitative reverse transcriptase PCR and quantitative methylation-specific PCR

Table 2 Up- and downregulated differentially expressed genes (DEGs) due to the heated tobacco products (top 10)

Table 3 Gene Ontology (GO) biological processes

Table 4 Hyper- and hypomethylation of genes (CpG island) due to the heated tobacco products (top 10)

Figure legends

Figure 1. Cell viability assays. Cell counts and viability were estimated by performing water-soluble tetrazolium salt (WST-1) assays at 24, 48, and 72 h with different heated tobacco product (HTP) concentrations. Cell viability showed time-dependent increase with use of up to 5% HTP. At 24, 48, and 72 h, cell viability did not significantly differ at the same time point between any HTP and the control. Cell viability was significantly lower with ≥10% HTP than in the control. Data are presented as mean ± standard deviation (SD), with a p-value of <0.05 indicating significance.

Figure 2. Gene expression profiles. (A) Heat map constructed using the most variable genes shows separate hierarchical clustering between the control and heated tobacco product (1% HTP) group samples. (B) Principal component analysis plot shows clear clustering between the control and HTP samples. (C) Volcano plot shows the differentially expressed genes. Compared to the control, the HTP showed higher expression for 284 genes and lower expression for 145 genes (>2-fold change). (D) Gene Ontology analysis (GO) shows that long-term HTP stimulation induced genes related to cornification, keratinization, epidermis development, epidermal cell differentiation, skin development, keratinocyte differentiation, and epithelial cell differentiation. (E) Network of GO terms and number of related genes in each biological process. This interactive plot also shows the relationship between enriched pathways. Two pathways (nodes) are connected if they share 30% (default, adjustable) or more genes. Green represents downregulated pathways. Darker nodes represent more significantly enriched gene sets. Bigger nodes represent larger gene sets. Thicker edges represent more overlapped genes.

Figure 3. Confirmation and reproducibility of data for differentially expressed genes and Gene Ontology biological processes. RNA sequencing (RNA-seq) analysis shows that *KRT13*, *KLK12*, and *S100A7* were upregulated in the heated tobacco product (1% HTP) group and were related to the elevated Gene Ontology terms involving biological processes. (A–C) Quantitative reverse transcriptase PCR confirmed that the *KRT13*, *KLK12*, and *S100A7* mRNA levels with HTP treatment were also significantly higher than those in the control. (D) Western blot results of the

S100A7 protein are in accordance with its mRNA expression levels (E, F). Data are presented as the mean ± standard deviation (SD), with a p-value of <0.05 indicating significance.

Figure 4. Correlation between methylation and gene expression levels. (A) Heat map shows that the methylation levels in the gene promoter region differed between the heated tobacco product (1% HTP) and control. (B) Scatter plot of methylation levels versus gene expression levels shows that these changes in DNA methylation levels were not correlated with the gene expression levels. (C–E) *KRT13*, *KLK12*, and *S100A7* methylation levels did not show significant alterations. Data are presented as the mean ± standard deviation (SD).