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Jeff J. Johnson, University of Notre Dame
Daniel L. Miller, University of Missouri
Rong Jiang, Emory University
Yueying Liu, University of Notre Dame
Zonggao Shi, University of Notre Dame
Laura Tarwater, University of Notre Dame
Russell Williams, Indiana University
Rashna Balsara, W. M. Keck Center for Transgene Research
Edward R. Sauter, University of Texas
M. Sharon Stack, University of Notre Dame

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Jeff J. Johnson†§, Daniel L. Miller‡, Rong Jiang§, Yueying Liu†§, Zonggao Shi‡§, Laura Tarwater*, Russell Williams**, Rashna Balsara‡, Edward R. Sauter‡§, and M. Sharon Stack‡§1

From the †Harper Cancer Research Institute and §Department of Chemistry and Biochemistry, University of Notre Dame, South Bend, Indiana 46617, the §Department of Pathology and Anatomical Sciences, University of Missouri School of Medicine, Columbia, Missouri 65212, the ‡Department of Human Genetics, Emory University, Atlanta, Georgia 30342; the **Department of Biology, Indiana University South Bend, South Bend, Indiana 46634, the ***W. M. Keck Center for Transgene Research, South Bend, Indiana 46617, and the ¶Department of Surgery, University of Texas Health Science Center, Tyler, Texas 75799

Oral cancer is the sixth most common cause of death from cancer with an estimated 400,000 deaths worldwide and a low (50%) 5-year survival rate. The most common form of oral cancer is oral squamous cell carcinoma (OSCC). OSCC is highly inflammatory and invasive, and the degree of inflammation correlates with tumor aggressiveness. The G protein-coupled receptor protease-activated receptor-2 (PAR-2) plays a key role in inflammation. PAR-2 is activated via proteolytic cleavage by trypsin-like serine proteases, including kallikrein-5 (KLK5), or in inflammation. PAR-2 activation induces pro-inflammatory mRNAs. Little is known, however, about PAR-2 regulation of inflammation-related microRNAs. Here, we assess PAR-2 expression and function in OSCC cell lines and tissues. Stimulation of PAR-2 activates Nf-κB signaling, resulting in RelA nuclear translocation and enhanced expression of pro-inflammatory mRNAs. Concomitantly, suppression of the anti-inflammatory tumor suppressor microRNAs let-7d, miR-23b, and miR-200c was observed following PAR-2 stimulation. Analysis of orthotopic oral tumors generated by cells with reduced KLK5 expression showed smaller, less aggressive lesions with reduced inflammatory infiltrate relative to tumors generated by KLK5-expressing control cells. Together, these data support a model wherein KLK5-mediated PAR-2 activation regulates the expression of inflammation-associated mRNAs and microRNAs, thereby modulating progression of oral tumors.

Squamous cell carcinoma of the oral cavity (OSCC)2 is a highly inflammatory disease that ranks as the 6th most frequently diagnosed cancer worldwide, with a poor 5-year survival rate of about 50% (1). Early diagnosis of OSCC is challenging, predominantly because early oral cancers and premalignant lesions are often subtle and asymptomatic. Although many patients present for diagnosis with stage III or IV disease, premalignant lesions in the oral mucosa often precede invasive OSCC (2). Furthermore, unlike most solid tumors that are monoclonal in origin, multiple distinct foci of dysplastic cells may be present in the oral mucosa. These epithelial dysplasias are categorized as mild, moderate, severe, or carcinoma in situ based on the histologic abnormalities present in the oral epithelium (3). Studies show that ~12–36% of epithelial dysplasia progress to carcinoma (4, 5); however, current approaches do not enable accurate identification of premalignant lesions likely to undergo malignant transformation.

The link between inflammation and cancer is now well established, and inflammatory mediators are present in the microenvironment of virtually all solid tumors (6–10). Many studies have associated proteinase-activated receptor-2 (PAR-2) with both inflammation and tumor progression (11–15); however, the expression of PAR-2 in OSCC has not been evaluated. PAR-2 is a G protein-coupled receptor that is activated by trypsin-like serine proteinases. Proteolytic cleavage of the extracellular amino terminus generates a “tethered ligand” that binds to the receptor, initiating G protein signaling. PAR-2 can also be activated by PAR2-activating peptides that mimic the tethered ligand amino acid sequence and generate all of the hallmarks of an inflammatory response (11, 12).

Kallikrein 5 (KLK5) is a secreted serine protease that is involved in regulated skin desquamation during epidermal differentiation (16). We have previously reported that KLK5 is up-regulated at the mRNA and protein levels in oral cancer cell lines and human OSCC tissues (17) and catalyzes cleavage of the cell-cell adhesion molecule desmoglein-1, promoting loss of junctional integrity and enhanced invasive activity in vitro (18). Activity of KLK5 is tightly controlled via expression of the proteinase inhibitor lympho-epithelial Kazal-type inhibitor (LEKTI, encoded by SPINK5). In Netherton syndrome, loss-of-function mutations in LEKTI enable unopposed KLK5 activity, leading to stratum corneum detachment and defective skin barrier function (19, 20). Expression of LEKTI is also lost in OSCC,
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indicative of unregulated KLK5 activity (21, 22). An additional substrate of KLK5 is PAR-2. KLK5 cleavage of the receptor triggers a PAR-2 signaling cascade and activation of Nf-κB target genes, including the pro-inflammatory mediators TNF-α, IL8, ICAM1, and TSLP (16).

PAR-2 regulation of pro-inflammatory mediators in both tumor cells and immune cells is effected principally through the Nf-κB signaling pathway (16, 23–25). Downstream of PAR-2 signaling, phosphorylation of RelA by IKKβ and nuclear translocation of RelA-containing Nf-κB dimers activate transcription of an array of pro-inflammatory cytokines and chemokines such as IL8 (CXC-8). IL8 is consistently up-regulated in OSCC, is produced by tumor cells as well as cells in the tumor microenvironment, is a reliable biomarker for the disease, and is associated with angiogenesis, invasion, metastasis, and poor survival in OSCC and other cancers (26–31). Although PAR-2-mediated regulation of pro-inflammatory mRNAs is well established, regulation of microRNA expression by PAR-2 activation has not been evaluated. In this study, we examined KLK5 or peptide-mediated activation of PAR-2 in oral cells and tissues and the resulting effect on mRNA/microRNA expression and tumor progression.

Materials and Methods

Reagents and Antibodies—TNF-α was obtained from Shenandoah Biotechnology (Warwick, PA.); sc-514 was purchased from Dr. J. Rheinwald (Brigham & Women’s Hospital, Harvard Institutes of Medicine). OKF6/T cells are derived from normal oral keratinocytes immortalized with the telomerase catalytic subunit human TERT (32). These cells retain keratinocyte growth controls and differentiate normally in culture. SCC1 and SCC25 cell lines were established from normal oral keratinocytes immortalized with the telomerase catalytic subunit human TERT (32). These cells do not stratify in organotypic culture, display growth factor-independent growth, and are tumorigenic in nude mice. In our studies, the SCC1-initiated tumors produce pulmonary metastases in nude mice (34). SCC25-initiated tumors invade tongue muscle, nerve bundles, and blood and lymphatic vessels (35, 36); however, distant metastasis is not observed prior to sacrifice for ethical considerations due to difficulty with feeding. Generation of an SCC25 cell line with reduced KLK5 expression (KLK5 knockdown, designated SCC25-KLK5-KD) and empty vector control cells (SCC25-Vcc) was previously described (18). KLK5 mRNA expression in KLK5-KD cells is reduced by 90% relative to corresponding vector controls, as determined by qPCR, and loss of KLK5 protein was shown by immunocytochemistry (18). SCC25-derived cell lines were routinely maintained in DMEM/F-12 1:1 media (Corning) containing 10% fetal calf serum and supplemented with 100 units/ml penicillin, 100 μg/ml streptomycin, and 0.2 μg/ml puromycin. Immortalized normal oral keratinocytes (OKF6/T cell line) were maintained in keratinocyte-SFM (Life Technologies, Inc.) supplemented with 100 units/ml penicillin, 100 μg/ml streptomycin, 0.2 ng/ml epidermal growth factor (EGF), 25 μg/ml bovine pituitary extract, and 0.4 mM CaCl2. The SCC1 cell line was maintained in Eagle’s minimal essential medium with Earle’s salts and l-glutamine (Corning) containing 10% fetal calf serum supplemented with 100 units/ml penicillin and 100 μg/ml streptomycin. For studies requiring serum-free media, cells were washed three times with PBS, and OSCC cells were transferred to media without fetal calf serum, whereas OKF6/T cells were transferred to media without bovine pituitary extract or EGF. Cell lines were routinely passaged at 70% confluence and did not experience extremes of pH. For passage, cells were washed with PBS and trypsinized with 0.25% trypsin, 2.2 mM EDTA (2.5 ml/10-cm plate) for 4 min at 37 °C. Trypsinization was stopped by the addition of 5 ml of medium containing FBS or appropriate media.

Histology and Immunohistochemistry—Tissue microarrays were constructed containing de-identified cores of premalignant oral lesions from Temple University (collected by ER Sauter). The premalignant TMA contained 203 cases, including mild (110 cores), moderate (70 cores), and severe dysplasia (23 cores) as well as carcinoma in situ (24 cores). Human TMDs, OR481and T273, purchased from United States Biomax Ltd., Rockville, MD, contained 24 cores of grade I-II tongue OSCC. In microarrayed tissue sections, not every core was usable in every section. Prior to immunohistochemical staining, endogenous peroxidase activity was quenched with 3.3% hydrogen peroxide in methanol for 30 min. Antigen retrieval was enhanced by microwaving in 10 mM sodium citrate, pH 6.0. Nonspecific binding was blocked with 3% normal horse serum in PBS for 30 min. Sections were incubated with primary antibody (1:25 to 1:200 dilution, as indicated) at 4 °C overnight in 1% BSA in PBS. Staining was detected using an avidin-biotin horseradish peroxidase system (Vectastain Universal Elite ABC kit, Cat. PK-6200, Vector Laboratories, Burlingame, CA), with positive cells stained brown using diaminobenzidine chromogen and hydrogen peroxide substrate (twp-component DAB kit HK542-XAK, BioGenex, San Ramon, CA). Slides were counterstained with Gill’s III hematoxylin and then saturated lithium carbonate. Tissue sections were dehydrated through graded ethanol and mixed xylene and mounted onto coverslips with mounting medium (Surgipath Micromount, Leica Biosystems, Richmond, IL). Staining was designated as absent, weak, moderate, or strong by a pathologist (Z. S.). Immunohistochemical positivity was recorded as a percentage of cells stain-
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ing with moderate-strong immunoreactivity per ×40 field, with enumeration at 200 cells/sample.

Murine tongue tumor sections (described below) were cut into thin sections (4 μm), incubated at 65 °C, de-paraffinized with xylene, rehydrated in a series of ethanol washes, and stained using hematoxylin and eosin (H&E) using standard procedures. Sections cut from the approximate middle of each tumor were H&E-stained, scanned with an Aperio Slidescanner, and area quantified using Aperio ImageScope software. Lymphocytes were enumerated (by Z. S. and J. J. J.) from H&E-stained sections for each high power field containing or immediately adjacent to tumor nests to provide a correlate to systemic inflammation. Results were presented as counts per high power field. Immunostaining for host (murine) mast cell tryptase with a mouse monoclonal anti-tryptase antibody was performed using the Vector M.O.M. (mouse-on-mouse) kit (Vector Laboratories catalog no. BMK-2202) according to the manufacturer’s specifications. Tryptase-positive mast cells were quantified using the hot spot method, starting with the high power field with the most positivity and comparing only fields with similar tumor burden. Results were presented as counts per high power field.

Flow Cytometry Analysis—Cells were collected at 70% confluence and trypsinized briefly with 0.25% trypsin, 2.21 mM EDTA (2.5 ml per 10-cm plate) for 4 min at 37 °C. Trypsinization was stopped by the addition of 5 ml of the appropriate media. After centrifugation, primary antibody (or vehicle) was applied in serum-free media for 30 min at room temperature with occasional gentle mixing. Cells were washed three times in PBS and then incubated with the corresponding fluorescein isothiocyanate-conjugated secondary antibody (Molecular Probes, catalog. no. GM488, Eugene, OR; 1:500 dilution) for 30 min in the dark at room temperature. Cells were washed three times in PBS and resuspended in media for the assay. Fluorescence analysis was done on a Beckman FC5500 flow cytometer (Beckman Coulter, Hialeah, FL). Control experiments contained only the appropriate secondary antibody.

Real Time Calcium Imaging—To evaluate cellular response to PAR-2 agonists (50 μM SLIGRL-NH₂ or 3.23 mM KLK5), real time calcium imaging was used. The PAR-2-activating peptide SLIGRL-NH₂ has been shown to be specific for activation of PAR-2 agonists (50 μM) prior to addition of KLK5 (3.23 μM) and monitoring the calcium response as described above.

Western Blotting Analysis—To examine PAR-2 protein levels in cell lines, cells were grown to 70% confluence and harvested in lysis buffer (modified RIPA buffer, with an added protease inhibitor mixture tablet), and protein concentration of samples was determined using a detergent-compatible protein assay kit (Bio-Rad). Proteins were separated by SDS-PAGE and then transferred onto a polyvinylidene di-fluoride (PVDF) microporous membranes (Millipore). After blocking nonspecific binding to membranes in 3% BSA in TBST for 1 h at room temperature, membranes were incubated with primary anti-PAR-2 antibodies for 3 h at room temperature or overnight at 4 °C and then with HRP-conjugated secondary antibodies. Immunoreactivity was determined by SuperSignal West Dura Extended Duration Substrate kit (Thermo Scientific). Blots were stripped with 0.4 nM glycine, pH 2.8, for 30 min, washed three times in TBST, then blocked again, and probed with antibodies against GAPDH to ascertain equal protein loading. Images were acquired with Fuji Film LAS-4000 luminescent image analyzer. Western blots were performed in triplicate.

Immunofluorescence—Cells were plated on 22-mm² glass coverslips in 6-well plates to 50% confluence to ensure areas of separated cell clusters, washed three times in PBS, and serum-starved overnight. Cells were treated with 100 ng/ml TNFα (1.9 mM, positive control for NF-κB activation and RelA nuclear translocation), with 20 μM SLIGRL-NH₂ or with 3.23 μM KLK5 for 30–120 min. Cells were washed once with PBS, and then fixed in 4% paraformaldehyde in PBS containing 0.12 M sucrose for 20 min at room temperature and permeabilized for 5 min in 0.3% Triton in PBS. Cells were rinsed twice in PBS and blocked with 10% BSA in PBS for 1 h. Primary antibody in 1% BSA was applied for 1 h at room temperature (1:100 dilution). Cells were washed three times in PBS followed by application of the secondary antibody (Alexa-Fluor 488) for 30 min (1:500 dilution). Cells were washed three times in PBS and rinsed one time with water, and coverslips were allowed to air-dry protected from light. Coverslips were inverted onto 10 μl of Vectashield containing DAPI on glass slides. Fluorescence was examined on an inverted AMG EVOS All-In-One digital microscope.

Real Time Quantitative PCR for mRNA and miRNA—The following primer sets were employed for comparative quantitation of mRNA: IL8 forward, 5'-GAGGGTTGTGGAGGAAGACCTTTTTTATGTC-3', and reverse, 5'-CTGGGATCTTTACGGTATGATGGTATGGT-3'; IL1A forward, 5'-GCTCTCTGAACTGCTTCTACTTTCTC-3', and reverse, 5'-CATCTGAACTTTATCCTG-3'; IL1B forward, 5'-GCTCTGTGCTTATGCTGATTGATGGTATGGT-3', and reverse, 5'-GGTCTGCAATCAGGCTGCTGATTGATGGTATGGT-3'. Oligo-
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Efficient, rapid, and reverse transcription was performed with 5 μg of total RNA from each cell population using the RT2 First Strand kit or 1 μg of total RNA using the miScript II RT kit (Qiagen) with Hi-Flex buffer. Real time PCR was performed with SYBR Green Master Mix (Applied Biosystems, Foster City, CA). PCR cycling conditions were 95 °C for 10 min followed by 40 cycles of 95 °C for 15 s and 55 °C for 1 min. Melt curve cycling consisted of 81 30-s cycles beginning at 55 °C and increasing by 0.5 °C to 95 °C. Each sample was analyzed in triplicate for each PCR measurement. Melt curves were checked to ensure specificity. Relative quantification of mRNA expression was calculated using the standard curve method with the endogenous housekeeping gene PGK level as normalizer and control sample as calibrator, or using the ΔΔCT method where the efficiency of amplification of the target gene was similar (within 10%) to the efficiency of the endogenous control gene (PGK1). The % inhibition of expression was calculated based on the up-regulation of IL8 by SLIGRL-NH2 alone as a control.

Extracted RNA was also evaluated for candidate microRNAs. Primer assays were purchased for candidate microRNAs and several putative normalizer genes from Qiagen (Gaithersburg, MD). A PCR array, the human inflammatory response and autoimmunity miScript miRNA PCR array, was also obtained from Qiagen. Reverse transcription was performed with 5 μg of RNA isolated above using the miScript II RT kit using the Hi-Spec buffer. Real time PCR was performed with the miScript SYBR Green PCR kit (Qiagen). PCR cycling conditions were 95 °C for 15 min followed by 40 cycles of 94 °C for 15 s, 55 °C for 30 s, and 70 °C for 30 s. Melt curve cycling was identical to the mRNA procedure listed above. Relative quantification was calculated as above with RNU6 and RNU44 as normalizers. For inhibitor studies, the % inhibition was calculated based on the effect of treatment with SLIGRL-NH2 alone. The mRNA and microRNA panel experiments were performed in triplicate. The results with the array and the panel were internally consistent. The microRNA qPCR experiments with inhibitors were conducted in duplicate. The results with the SLIGRL-NH2 positive controls (without inhibitors) were also consistent with previous results.

Murine Orthotopic OSCC Model—To evaluate the effect of reduced KLK5 expression on tumor progression, an orthotopic murine model of OSCC of the tongue, which produces tumors that closely resemble human OSCC, was utilized (17, 35, 36). Briefly, 6-week-old male athymic nu/nu mice (n = 10 per cohort) were anesthetized using 2.5% isoflurane, and a 1-ml syringe with a 25-gauge needle was used to inject 30 μl of SCC25-KLK5-KD cells (18) or SCC25-Vec cells (0.8 × 10⁶ cells) into the lateral border of the tongue just anterior to the junction of the anterior ½ and posterior ½ of the tongue. After 9 weeks, mice were sacrificed, and tissues were fixed in paraformaldehyde, embedded in paraffin, and evaluated as described above.

Tumor surface area was quantified by analysis of scanned H&E sections using Aperio ImageScope software. Data were exported to Excel for further analysis. The experiment was repeated in duplicate. All procedures were conducted with approval of the IACUC, University of Notre Dame.

Results

Expression of PAR-2 and KLK5 in Pre-malignant and Malignant Oral Lesions—To examine PAR-2 expression in pre-malignant and malignant human oral tissues, TMAs were evaluated by immunohistochemistry. PAR-2 expression was heterogeneous, with examples of weak and strong staining shown in Fig. 1, A and B, for premalignant and Fig. 1, C and D, for malignant oral tissues. As PAR-2 is also expressed by inflammatory cells, a contribution from these cells cannot be ruled out; however, extensive visible inflammatory influx in the TMA core sections was not evident by H&E staining (data not shown). As quantified in Table 1, PAR-2 staining is moderately enhanced in malignant oral tissues relative to pre-malignant lesions. KLK5 was also expressed in premalignant and malignant oral lesions (Fig. 1, E–G; Table 1). Similar to our previous results (17, 18), KLK5 expression is also enhanced in OSCC (Table 1).

PAR-2 Activation and Nf-κB Signaling in OSCC Cell Lines—To complement human tissue staining, PAR-2 expression was examined in OSCC cell lines and compared with tert-immortalized oral keratinocytes (OKF6/T). Examination of OSCC and immortalized oral mucosal cell lines by both Western blotting and flow cytometry showed enhanced expression and surface localization of PAR-2 in OSCC cell lines (Fig. 2, A–E). To determine whether surface PAR-2 was active, cells were treated with the PAR-2-activating peptide SLIGRL-NH2. Robust PAR-2
activation was triggered by the activating peptide SLIGRL-NH$_2$ in OSCC cell lines relative to immortalized oral keratinocytes as demonstrated by enhanced calcium mobilization (Fig. 2, F and G). Similarly, incubation of OSCC cells with KLK5 also enhanced calcium mobilization (Fig. 2H). Desensitization experiments (Fig. 2I), in which cells were treated with SLIGRL-NH$_2$ prior to addition of KLK5, demonstrated that the KLK5-induced calcium response was due to PAR-2 activation. As PAR-2 regulation of pro-inflammatory mediators is effected principally through the NF-$\kappa$B signaling pathway, nuclear localization of RelA was examined following PAR-2 activation. Incubation

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<th>TABLE 1</th>
<th>PAR-2 and KLK5 expression in human oral tissues</th>
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<td>Microarrayed human oral tissues were immunostained for PAR-2 or KLK5 as described under “Materials and Methods,” and staining was scored as absent, weak, moderate, or strong. The average percentage of cells scored as moderate/strong is shown. Mild, moderate, and severe refer to levels of dysplasia; CIS means carcinoma in situ; stage I–II indicates oral squamous cell carcinoma stage I–II.</td>
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<td>Pre-malignant</td>
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<td>PAR-2</td>
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<td>KLK5</td>
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FIGURE 2. PAR-2 expression and activation in OSCC cell lines. A, Western blot showing elevated PAR-2 protein in SCC1 and SCC25 cell lines relative to immortalized oral keratinocyte line OKF6/T. Cell lysates were electrophoresed on 9% SDS-polyacrylamide gels and electroblotted to Immobilon. Upper panel, blots were probed with murine anti-PAR-2 antibody (1:100 dilution) followed by an HRP-conjugated secondary antibody (1:4000 dilution). Loading controls (lower panel) were probed with mouse anti-GAPDH (1:500) and an HRP-conjugated secondary antibody (1:10,000). The experiment was repeated in triplicate, and a representative blot is shown. B–E, flow cytometry analysis of cell surface PAR-2. B and C, OKF6/T; C and E, SCC1 cell lines were incubated on ice with vehicle (B and C) or anti-PAR-2 antibody (1:100) (D and E) followed by FITC-conjugated secondary antibody (1:500) and evaluated using a Beckman/Coulter FC500 cell sorter. F–I, analysis of PAR-2 activation-induced calcium signaling. Cell lines were loaded with Fura2AM and incubated with the PAR-2 agonist peptide SLIGRL-NH$_2$ (50 $\mu$M) or KLK5 (3.23 $\mu$M), as indicated. Shown in each trace is a representative single cell Ca$^{2+}$ response measured as 340/380 fluorescence intensity (F.I.) ratio. The calcium response is the difference in the peak value and baseline value. F, peptide (SLIGRL-NH$_2$, 50 $\mu$M) activation of PAR-2 in SCC1 cell line. G, peptide (SLIGRL-NH$_2$, 50 $\mu$M) activation of PAR-2 in OKF6/T cell line. H, KLK5 (3.23 $\mu$M) activation of PAR-2 in SCC1 cell line. I, de-sensitization experiment showing lack of additional calcium response in SCC1 cells treated with SLIGRL-NH$_2$ (50 $\mu$M) followed by KLK5 (3.23 $\mu$M).
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of OSCC cell lines with either SLIGRL-NH$_2$ or KLK5 induced RelA nuclear translocation (Fig. 3, A–F). Positive controls included incubation of cells with TNFα (1.9 nm), which induced robust RelA nuclear translocation (Fig. 3B).

**PAR-2 Activation Regulates Both mRNA and MicroRNA Expression**—Numerous studies have shown that PAR-2 activation induces Go-mediated signaling, mobilizing intracellular calcium and Nf-κB signaling, and leading to increased expression of pro-inflammatory mRNAs (11–15). To determine whether PAR-2 activation in OSCC cell lines induces expression of candidate mRNAs known to be associated with inflammation in OSCC, expression of three pro-inflammatory genes known to be regulated downstream of PAR-2 activation was evaluated (27, 39, 40). Interleukin 8 (CXCL8 gene, IL8 protein) is a member of the pro-inflammatory CXC chemokine gene family. Expression levels are elevated in the saliva of oral cancer patients, and high serum IL8 levels correlate with a poor clinical outcome in OSCC (41, 42). The interleukin encoded by the IL1A gene is a potent mediator of inflammation and is involved in epithelial barrier function (43). Expression of IL1A can trigger inflammation leading to tumor formation in differentiated epidermal cells (44). Matrix metalloproteinase 9 (MMP9) is an inflammation-associated marker that may be used to differentiate OSCC from leukoplakia (45). Up-regulation of MMP9 correlates with enhanced inflammation and advanced metastatic OSCC (46). As shown in Fig. 4A, activation of PAR-2 in OSCC cells increased expression of control pro-inflammatory mRNAs encoding IL8, IL1A, and MMP9.

MicroRNAs are also involved in inflammation; however, regulation of inflammation-related microRNAs by PAR-2 has not been investigated. We therefore investigated a panel of inflammation-related microRNAs and a commercially available qPCR array of inflammation- and immunity-related microRNAs. Our results showed that the anti-inflammatory microRNAs (miRNAs) let-7d, miR-23b, and miR-200c are consistently suppressed in OSCC cell lines after treatment with SLIGRL-NH$_2$ (Fig. 4B). Pre-treatment with pertussis toxin, an inhibitor of Go signaling, reversed PAR-2-mediated down-regulation of let-7d, miR-23b, and miR-200c (Fig. 4C, white bars). Similarly, inhibitors of NF-κB signaling, includ-
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ing sc-514 (which inhibits IKKβ phosphorylation of RelA at Ser-536) and SB 747651A (which prevents MSK1-mediated RelA phosphorylation at Ser-276), also reversed PAR-2-me-
diated suppression of all three microRNAs (Fig. 4C, dark gray and light gray bars, respectively).

Down-regulation of KLK5 Expression Reduces Tumor Progression and Inflammation—To evaluate the effect of KLK5 expression on tumor progression, an orthotopic murine tongue xenograft model was utilized (17, 35, 36). Cells with diminished KLK5 expression (designated SCC25-KLK5-KD) (18) or vector controls (SCC25-Vec) were injected into the lateral border of the base of the tongue and allowed to grow for 9 weeks. Examination of the resulting tumors by H&E staining showed that SCC25-Vec cells formed moderately differentiated SCC. Some tumors were poorly circumscribed with invasive cords (Fig. 5, A–C) with evident vascular and perineural invasion (data not shown). By contrast, SCC25-KLK5-KD cells formed smaller, well circumscribed, and well differentiated tumors with numerous keratin pearls and with fewer examples of vascular or perineural invasion (Fig. 5, D–F). Tumors formed from SCC25-KLK5-KD cells were significantly smaller than tumors formed from SCC25-Vec cells (Fig. 5G). As our data showed that PAR-2 activation enhanced pro-inflammatory mRNAs and reduced expression of anti-inflammatory miRNAs, inflammatory cell recruitment to the oral tumor microenvironment was assessed. Tumors initiated with SCC25-KLK5-KD cells had significantly less lymphatic infiltrate relative to tumors initiated with SCC25-Vec cells (Fig. 6, A–C). Tryptase-positive mast cells were also significantly reduced in tumors from SCC25-KLK5-KD cells relative to SCC25-Vec cells (Fig. 6, D–F).

Discussion
Chronic inflammation is an established risk factor for cancer development, and inflammatory cells are a component of the tumor microenvironment in virtually all solid tumors. Increased presence of inflammatory cells and inflammatory mediators contributes to the complex cross-talk between the
tumor and its microenvironment, regulating proliferation, angiogenesis, and metastasis. Many pro-inflammatory mRNAs, including those encoding cytokines and chemokines, are regulated downstream of PAR-2 through activation of the transcription factor NF-κB (16, 22–25). We have shown previously that the secreted serine protease KLK5 is overexpressed in OSCC (17). In this study, we show that KLK5 and PAR-2 expression are elevated in pre-malignant and malignant oral tissues. Interestingly, expression of the KLK5 inhibitor LEKTI (encoded by SPINK5) is lost in human OSCC (21, 22), indicative of unregulated KLK5 activity. KLK5-catalyzed activation of PAR-2 results in calcium mobilization and activation of NF-κB signaling. The downstream effects on expression of pro-inflammatory mRNAs and suppression of anti-inflammatory microRNAs may modify the tumor microenvironment and alter tumor progression. This is supported by data showing that tumors initiated by cells with reduced KLK5 expression were less aggressive and exhibited reduced inflammatory cell influx relative to KLK5-expressing controls. Our data support a model wherein KLK5-mediated PAR-2 activation regulates the expression of inflammation-associated mRNAs and microRNAs, thereby modulating progression of oral tongue tumors.

One of the pro-inflammatory mediators regulated by PAR-2 activation is the chemokine interleukin 8 (IL-8). Previous studies have shown that IL-8 is significantly up-regulated in OSCC and is a biomarker associated with proliferation, angiogenesis, migration, invasion, metastasis, and poor prognosis (26–31). IL-8 contributes to cross-talk between the tumor and its microenvironment via induced differentiation of CD163-positive M2 macrophages from monocytes, which produce IL-10. Although it is clear that PAR-2 activation culminates in the transcription of pro-inflammatory mRNAs in OSCC, including IL-8, IL1A, and MMP9, PAR-2 regulation of inflammation-related microRNAs in OSCC is a novel finding of this study. Here, we demonstrate that PAR-2 activation suppresses three anti-inflammatory microRNAs: let-7d, miR-23b, and miR-200c.

let-7d has been shown to target pro-inflammatory mRNAs encoding IL6, IL13, and TLR4 (47–49). miR-23b limits tissue inflammation via suppression of NF-κB activation and inflammatory cytokine expression by targeting TAB2, TAB3, and IKKα (50). miR-200c directly targets many pro-inflammatory genes, including IL-8, VEGFA, and VEGFR2. Additionally, miR-200c also targets IKKβ (IKBKE), thereby decreasing NF-κB signaling and inhibiting scores of pro-inflammatory NF-κB-target genes (51–53). Furthermore, as let-7d, miR-23b, and miR-200c are established tumor suppressor genes that are significantly down-regulated in OSCC, our data provide a potential mechanism whereby PAR-2 activation contributes to tumor progression (54–61).

In addition to targeting DICER1, which suppresses proliferation in numerous cell types, knockdown of let-7d promotes epithelial-mesenchymal transition (EMT), leads to expression of TWIST and SNAIL, and promotes invasion in OSCC cells (56). Down-regulation of let-7d is associated with poor survival, disease recurrence, and distant metastasis in oral cancer (62). Similarly, down-regulation of miR-200c correlates with EMT and loss of E-cadherin (66). miR-23b is a known suppressor of cancer metastasis. Putative target genes that are up-regulated in oral cancer include the proliferation and motility gene MARCKS, the RAS oncogene RAP1B, and the growth factor HDGFRP3 (58, 63). miR-23b also suppresses EMT by reduction of vimentin and Snail and up-regulation of E-cadherin (64–66). Thus, down-regulation of miR-23b mediates multiple steps in progression and metastasis, including EMT, tumor growth and survival, cell migration, invasion, and angiogenesis.

PAR-2-mediated up-regulation of IL-8 and suppression of let-7d, miR-23b, and miR-200c were reversed by pretreatment with inhibitors of Goα (pertussis toxin) and NF-κB (sc-514 and SB747651A) signaling. We have previously shown that SB747651A and sc-514 are potent inhibitors of OSCC invasion (67). The restoration of anti-inflammatory/tumor suppressor microRNAs, inhibition of pro-inflammatory mediators, and the resulting effects on tumor cell behavior suggest the utility of PAR-2 antagonists or NF-κB inhibitors in the treatment of inflammatory diseases and cancer. Although the inhibition of NF-κB leads to undesirable effects due to the influence of NF-κB target genes on numerous other pathways in health and disease, inhibition of PAR-2 may have clinical potential because murine PAR-2 knock-out mice are viable and exhibit very mild phenotypic changes (14). Although complete inhibition of the PAR-2 pathway has yet to be achieved, the most promising antagonist thus far has been the small molecule PAR-2 specific antagonist GB88. GB88 can reversibly inhibit activation of PAR-2 by proteolytic and non-proteolytic agonists at low concentrations, blocking intracellular Ca2+ release, cAMP stimulation, receptor internalization, and pro-inflammatory cytokine release (68). GB88 is also serum-stable and orally active and has already been utilized in a number of animal models of human inflammatory diseases and cancer. The results of this study suggest that evaluation of PAR-2 antagonists such as GB88 for efficacy in OSCC is warranted.

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References
PAR-2-mediated Nf-κB Activation Suppresses MicroRNA