Simultaneous Expression of Furin and Vascular Endothelial Growth Factor in Human Oral Tongue Squamous Cell Carcinoma Progression

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ABSTRACT

Purpose: Squamous cell carcinoma (SCC) of the tongue is a common malignancy of the oral cavity. Furin convertase activates several precursor matrix metalloproteinases involved in the degradation of the extracellular matrix. The pattern of expression of furin and vascular endothelial growth factor-C (VEGF-C), two key molecules in neoplasm development, was examined during the progression from normal epithelium to invasive SCC.

Experimental Design: We evaluated furin and VEGF-C expression and microvessel density (MVD) by immunohistochemistry in human tongue sections harboring normal epithelium, dysplastic epithelium, and/or SCC. Sections from 46 glossectomy specimens were assessed for furin expression. A selected group of 15 cases, each containing normal epithelium, precursor lesions, and invasive SCC, were further studied for furin and VEGF-C expression and MVD quantification. We also evaluated the pattern of furin expression and VEGF-C processing by Western blot analysis in three SCC cell lines with different degrees of aggressiveness.

Results: Furin and VEGF-C expression was notably higher in most precursor lesions and SCCs than in normal epithelia. Approximately 60% (n = 26) and 100% (n = 15) of the normal epithelia showed low-intensity staining for furin and VEGF-C, respectively. Intense staining for furin and VEGF-C was detected in ~80% (n = 34) and 100% (n = 15) of the SCCs, respectively. A significant correlation was seen between the expression of these two markers (Spearman’s test, P < 0.00002). We found a statistically significant increase in MVD when either dysplasia (432 ± 19.06; P < 0.05) or SCC (546 ± 17.24) was compared with normal epithelium (315 ± 17.27; P < 0.0001). SCC71, the most aggressive cell line analyzed, was the one with the highest furin expression. This cell line totally processed the VEGF-C proform, whereas the less aggressive line SCC9, exhibiting the least furin expression, did not. SCC15, of intermediate aggressiveness and furin expression, showed intermediate pro-VEGF-C processing.

Conclusions: These findings suggest that furin is a useful marker of tumor progression and is responsible for VEGF-C processing. This in turn would enhance angiogenesis, leading to increased MVD associated with preinvasive and invasive neoplasia.

INTRODUCTION

Squamous cell carcinoma (SCC) accounts for >90% of the head and neck cancers worldwide. It constitutes ~4% of all cancers in the United States and 5% in the United Kingdom. SCC of the tongue is a common malignancy of the oral cavity, with an annual rate of 1.51 among males and 0.99 among females per 100,000 persons in the United States (1).

The sequential changes that take place in malignant neoplasms, gradually giving rise to more aggressive malignant phenotypes, is usually known as tumor progression (2). In the case of SCC, tumor progression is frequently associated with partial or total loss of squamous differentiation and the eventual appearance of a more anaplastic or spindle cell morphology accompanied by a more invasive and metastatic behavior (3–5). The most common molecular changes associated with SCC progression are mutation of the p53 tumor-suppressor gene, inactivation of the cyclin-dependent kinase inhibitor p16, and overexpression of epidermal growth factor receptor. Some of these molecular changes appear in precursor lesions (6–8).

Proprotein convertases (PCs) of the subtilisin family are Ca2+-dependent serine endoproteases that recognize and cleave precursor inactive proteins at the COOH terminus of basic paired amino acids within the consensus motif RXR/KR (9). The proteolytic activation of protein precursors renders mature bioactive molecules with many functions, such as matrix metalloproteinases, growth factors, growth factor receptors, neurotrophins, enzymes, and adhesion molecules (10–15). Many of these molecules have been implicated in the acquisition of the tumorigenic phenotype, invasion, and metastasis.

To date, eight members have been identified in mammals, including furin, PC1/PC3, PC2, PC4, PACAP43, PC5/PC6, PC7/LPC/PC8, and SKI-1/S1P (16–19). Furin, one of the best known members of this kexin-like PC family, has a transmembrane domain, cycles between the trans-Golgi network and the cell surface, and is involved in the processing of proteins secreted via the constitutive pathway (20–22).

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Furin up-regulation occurs in tumors and cell lines (23–26). Elevated expression of PCs has been reported in many cancers. The fact that VEGF-C is processed by furin at the RXXR motif in tumor metastases (31) has been identified as having a significant role in the lymphatic vascular cell carcinogenesis and progression. To minimize site-related variations, we selected SCCs of the oral tongue for this analysis.

Among the several vascular cell growth factors, VEGF-C has been identified as having a significant role in the lymphatic propagation of head and neck SCCs (44, 45). VEGF-C is mainly a ligand for the lymphatic endothelial receptor VEGF receptor-3 (Flt4), but it also binds to VEGF receptor-2, which is the major mitogenic signal transducer for VEGF in blood vessel endothelial cells (46, 47). Human VEGF-C cDNA encodes a protein of 419 residues with a predicted molecular mass of 59 kDa (46–49). The fact that VEGF-C is processed by furin at the RXXR motif (50) prompted us to examine the patterns of expression of furin and VEGF-C during the progression from normal epithelium to invasive SCC, and to determine whether the expression of these two tumor molecular markers, as well as the MVD, change simultaneously during the process of squamous cell carcinogenesis and progression. To minimize site-related variations, we selected SCCs of the oral tongue for this analysis.

### Table 1

<table>
<thead>
<tr>
<th>Diagnosis</th>
<th>Percentage of samples (n) expressing furin (immunostaining intensity)</th>
<th>Average MVD&lt;sup&gt;a&lt;/sup&gt; Mean (±SE)</th>
<th>Percentage of samples (n) expressing VEGF-C (immunostaining intensity)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal tongue epithelium (lateral)</td>
<td>41% (19) 56.8% (26), except for the basal cells</td>
<td>315 ± 17.27</td>
<td>0% (0) 100% (15) 0% (0)</td>
</tr>
<tr>
<td>Dysplastic lesions SCC&lt;sup&gt;a&lt;/sup&gt;</td>
<td>19% (4) 57% (12) 24% (5)</td>
<td>432 ± 19.06</td>
<td>0% (0) 60% (9) 40% (6)</td>
</tr>
<tr>
<td>SCC&lt;sup&gt;a&lt;/sup&gt;</td>
<td>0% (0) 23.81% (10) 76.19% (34)</td>
<td>546 ± 17.24</td>
<td>0% (0) 0% (0) 100% (15)</td>
</tr>
</tbody>
</table>

<sup>a</sup> Vessels/mm<sup>2</sup>, quantitated at ×200 magnification.

<sup>b</sup> SCC, squamous cell carcinoma.

### MATERIALS AND METHODS

#### Cell Lines

Three SCC cell lines, SCC9, SCC15 and SCC71, were used in these experiments. The cell lines were obtained from the laboratory of Dr. J. G. Rheinwald (Harvard Skin Disease Center, Boston, MA). All cells were grown in Eagle’s MEM, spinner modification (S-MEM), with the addition of 2 mM l-glutamine, 100 units/ml penicillin, 100 µg/ml streptomycin, and 10% fetal bovine serum. SCC9 and SCC15 are derived from well-differentiated SCC of the tongue, and SCC71 is derived from a moderately differentiated SCC of the soft palate. In vivo invasion assays and s.c. tumorigenesis assays showed that SCC9 and SCC15 have a low to moderate in vivo growth pattern, whereas SCC71 has a markedly invasive in vivo growth pattern (51).

#### Human Tongue Specimens

Oral tongue specimens from 46 subjects who underwent surgical excision at the Fox Chase Cancer Center (Philadelphia, PA) were evaluated. Cases were selected based on containing both the pathological lesion—either dysplasia (n = 21) or invasive carcinoma (n = 44)—and normal adjacent lateral tongue epithelium (n = 46). Of the 21 dysplasias, 13 were mild dysplasias, 7 were moderate dysplasias, and 1 was a severe dysplasia. All tissues were accrued by the Fox Chase Cancer Center Tumor Bank Facility after completing the process of informed consent and under the supervision of the Institutional Review Board.

#### Protein Analysis

We seeded 1 × 10<sup>6</sup> cells for each cell line in 100-mm plates and incubated them overnight in serum-free S-MEM for VEGF-C analysis. Conditioned medium was collected and concentrated 120 times down to 25 µl by filtration (Centriprep Microcon YM-10; Millipore). The whole concentrated conditioned medium harvested from each cell line was fractionated by 10% SDS-PAGE under reductive conditions and transferred to a nitrocellulose membrane. The membrane was immunoblotted with rabbit antihuman VEGF-C IgG (Santa Cruz Biotechnology, Santa Cruz, CA) and, after washing, with horseradish peroxidase-labeled antirabbit IgG.

After harvesting of the conditioned medium, cells were washed three times with cold PBS buffer. We added 0.4 ml of RIPA lysis buffer (1 × PBS, 0.1% SDS, 0.5% sodium deoxycholate, 1% NP40) with the protease inhibitors aprotonin (1 µM), phenylmethylsulfonyl fluoride (100 µM), and N<sub>a</sub>V<sub>0</sub> (100 µM) to the cultures and incubated them at 4°C for 15 min. Cells were scraped, passed through a 21-gauge needle, and incubated at 4°C for 30 min. Cell lysates were centrifuged at 10,000 × g.
for 5 min, and the supernatants were separated. Fifty μl of the cell lysates were fractionated by 8% SDS-PAGE. The proteins were electroblotted onto a nitrocellulose membrane and probed with the antifurin monoclonal antibody MON-152 (Alexis, San Diego, CA) and, after washing, with horseradish peroxidase-conjugated antimouse IgG.

An enhanced chemiluminescence detection system (Amer- sham Biosciences, Piscataway, NJ) was used for band detection.

**Immunohistochemistry.** Furin and VEGF immunohis- tochemistry was performed on histological sections from paraf- fin-embedded cases. After rehydration, sections were subjected to antigen retrieval by microwave boiling at a low setting in distilled water for 10 min. Mon-152 was used as primary anti- body at a 1:50 dilution to reveal furin convertase in 46 glossec- tomy specimens. In addition, 15 selected samples that contained normal epithelium, dysplastic lesions, and SCC were chosen to assess VEGF-C staining and determine MVD. A rabbit poly- clonal antibody directed to human VEGF-C (Santa Cruz Bio- technology) at 1:100 dilution was used. To determine MVD, slides were incubated with a mouse monoclonal antibody to factor VIII-related antigen (Dako Corp., Carpinteria, CA). In the latter, enzyme predigestion was performed by incubating depar- affinized sections for 15 min in Pronase. In all of the cases, an avidin-biotin-peroxidase kit (Bio Genex, San Ramon, CA) was

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**Fig. 1** Immunohistochemical detection of furin. A, when present (56.8% of the cases), the normal tongue epithelium showed mild furin expression. Note the cytoplasmic staining in the upper spinous layer. B, 40% of normal epithelia showed membrane-bound furin-associated immunostaining localized within the spinous layer. Note the absence of stain in the basal and parabasal cells. This micrograph corresponds to the only sample of normal oral mucosa that exhibits intense furin immunostaining (grade II). C, moderate dysplastic lesion shows intense immunostaining in the spinous layer with milder expression in the basal and parabasal keratinocytes. D, moderate to severe dysplasia shows mild immunostaining in all layers. E, furin is expressed intensely in all squamous cell carcinoma (SCC) cells. No SCC was negative when stained for furin. F, furin staining is present in the invading front of a SCC. Furin immunohistochemistry with hematoxylin counterstain (magnification, ×100).
then used, followed by the chromogen 3′,3′-diaminobenzidine to develop the immunostain. Negative controls, not incubated with primary antibody, were used. As positive controls, sections from known specimens containing salivary glands (positive for furin) and SCC of the head and neck (positive for VEGF-C and factor VIII) were used (26, 43). All sections were counterstained with hematoxylin, mounted, and analyzed.

**MVD Determination.** The subepithelial vascular plexus localized within 100 μm of the epithelial basement membrane of normal epithelium and preinvasive lesions were evaluated. Subepithelial vascular plexus within 100 μm of the peripheral edge of invasive lesions were counted. An image analysis system (Fairfield Imaging, United Kingdom) was used to assist in the quantitation (0.104 mm²/field) of any brown-staining endothelial cells or endothelial cell clusters that were differentiable from adjacent vasculature, tumor cells, and other connective-tissue elements, and they were considered a single, countable microvessel based on the criteria of Weidner et al. (41). Vessel lumens were not necessary for a structure to be defined as a microvessel, and red cells were not used to define a vessel lumen. Three noncontiguous ×200 fields associated with the area of interest (normal epithelium, dysplastic epithelium, or tumor) were randomly selected without bias toward areas of “highest neovascularization.” Recognizing that tumors are often heterogeneous in their MVD, we determined average MVD after the lowest and highest manual counts were discarded; this allowed the counts to be more representative of the histology as a whole. MVD was expressed as number of microvessels/mm².

**Quantification of Furin and VEGF Immunostaining.** Grading of furin and VEGF-C immunostaining was based on semiquantitative evaluation of stain intensity from 0 to II. No or marginal staining of <5% of cells was called negative (0), mild to moderate stain of 5–50% of cells was graded as I, and moderate to intense staining comprising >50% of the cells was classified as II. Section grading was based on stain intensity per field (for tumors) or epithelial layer (for epithelia). Staining evaluation of the slides was performed in a blind fashion.

**RESULTS**

**Furin Expression Patterns Associated with Different Lesions.** Furin immunohistochemistry was performed on 46 specimens to assess its expression during the process of tumor development. As shown in Table 1, 56.8% of the normal epithelia showed mild furin immunostaining (grade I; Fig. 1A). Only one case showed moderate immunostaining (grade II; Fig. 1B). Except for the cells in the basal layer, which did not stain at all, all other layers of the normal epithelia showed a mild expression of this PC. The pattern of furin staining in the normal epithelium was not uniform in all cases. Sixty percent of the specimens had cytoplasmic immunostaining (Fig. 1A), whereas another 40% showed membrane-bound furin-associated immunostaining (Fig. 1B).

Approximately 24% of dysplastic lesions expressed moderate to high levels of furin immunostaining (grade II; Fig. 1C), whereas 19% were negative for furin immunostaining. The remaining lesions had mild immunostaining (grade I; Fig. 1D). Approximately 50% of furin-positive dysplastic lesions exhibited a cytoplasmic staining pattern. Similarly, the basal layer stained positively for furin in nearly 50% of the lesions.

Previous investigators have proposed that furin expression is up-regulated in more aggressive tumors and cell lines (26). In the present study, 100% of the tumors tested were positive for furin staining (Fig. 1E). It is important to note that the intensity of furin staining was higher in the tumors than in the normal epithelium. Most invasive SCCs analyzed (76.19%) showed strong immunostaining (grade II). The outermost or basaloid cells of the tumors facing the connective tissue were positive when stained for furin (Fig. 1F).

**MVD Associated with Different Lesions.** MVD was measured in normal and abnormal human tongue tissues by immunohistochemical staining for factor VIII-related antigen (Fig. 2). Immunohistochemistry was performed on 15 specimens, each containing normal, dysplastic, and neoplastic epi-
thelial tissues. Normal tongue epithelium contained few capillaries distributed within the lamina propria contiguous to the epithelium basal cell layer (Fig. 2A). The number and distribution of vessels in the dermis was altered in the dysplastic lesions (Fig. 2B) and carcinomas (Fig. 2C). The vessels were more densely packed and closer to the basal layer of the lesions than in the normal epithelium. Quantification of vascularization in tongue sections at each stage of neoplastic progression revealed a statistically significant increase in MVD when normal epithelium (315 ± 17.27) was compared with dysplasia (432 ± 19.06; P < 0.05) or carcinoma (546 ± 17.24; P < 0.0001; Table 1). Table 2 shows the MVD data and grading of immunostaining for furin and VEGF-C in 15 of the 46 cases depicted in Table 1, each containing normal epithelium, precursor lesions, and invasive SCC.

**Table 2** Microvessel density data and results of immunostaining for furin and vascular endothelial growth factor-C (VEGF-C) in 15 of the 46 cases depicted in Table 1, each containing normal epithelium, precursor lesions, and invasive squamous cell carcinoma (SCC).

<table>
<thead>
<tr>
<th>Tissue type</th>
<th>Patient</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal</td>
<td>Furin expression (grade)</td>
<td>I</td>
<td>0</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>VEGF-C expression (grade)</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>I</td>
</tr>
<tr>
<td></td>
<td>MVD a</td>
<td>357.16 ± 27.96</td>
<td>335.47 ± 88.6</td>
<td>444.57 ± 104.5</td>
<td>392.30 ± 62.81</td>
<td>369.80 ± 25.82</td>
<td>313.03 ± 96.57</td>
<td>355.13 ± 63.92</td>
</tr>
<tr>
<td>Dysplastic</td>
<td>Furin expression (grade)</td>
<td>II</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>II</td>
</tr>
<tr>
<td></td>
<td>VEGF-C expression (grade)</td>
<td>II</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>II</td>
</tr>
<tr>
<td></td>
<td>MVD a</td>
<td>406.13 ± 21.21</td>
<td>421.63 ± 28.77</td>
<td>393.33 ± 79.79</td>
<td>374.43 ± 24.28</td>
<td>392.40 ± 25.36</td>
<td>688.30 ± 75.34</td>
<td>430.77 ± 53.94</td>
</tr>
<tr>
<td>SCC</td>
<td>Furin expression (grade)</td>
<td>II</td>
<td>II</td>
<td>II</td>
<td>I</td>
<td>I</td>
<td>II</td>
<td>II</td>
</tr>
<tr>
<td></td>
<td>VEGF-C expression (grade)</td>
<td>II</td>
<td>II</td>
<td>II</td>
<td>I</td>
<td>I</td>
<td>II</td>
<td>II</td>
</tr>
<tr>
<td></td>
<td>MVD a</td>
<td>659.07 ± 31.63</td>
<td>565.80 ± 29.4</td>
<td>621.70 ± 77.95</td>
<td>424.07 ± 72.66</td>
<td>669.17 ± 28.62</td>
<td>538.83 ± 24.76</td>
<td>614.57 ± 4.3</td>
</tr>
</tbody>
</table>

a MVD, microvessel density (vessels/mm²) quantitated at ×200 magnification. Mean ± SE of three values.

**VEGF-C Expression Patterns Associated with Different Lesions.** Immunohistochemical staining for VEGF-C was performed on 15 specimens, each containing three distinct tissues, *i.e.*, normal epithelium, dysplastic epithelium, and invasive SCC (Fig. 3). The results are summarized in Tables 1 and 2. Low or mild expression (grade I) of VEGF-C was found in all normal epithelia (Fig. 3A). Strong (grade II) staining was detected in 40% of dysplastic epithelia (Fig. 3C). The remaining 60% of specimens showed a low or mild staining intensity for VEGF-C (grade I; Fig. 3B). All of the SCC showed strong staining (grade II; Fig. 3D). No tumors showed low expression of VEGF-C.

![Fig. 3](image_url) Assessment of vascular endothelial growth factor-C (VEGF-C) immunostaining. A, normal epithelium showing mild VEGF-C staining. B, mild dysplasia showing moderate VEGF-C staining. C, moderate dysplasia exhibiting intense immunostaining. D, intense VEGF immunostaining in an invasive squamous cell carcinoma. VEGF-C immunohistochemistry with hematoxylin counterstain (magnification, ×100).
Correlation between Furin and VEGF-C Expression. We compared furin expression with VEGF-C expression in normal and dysplastic epithelia and SCCs; the results are summarized in Table 1. VEGF-C showed increased expression in association with a simultaneous increase in furin immunostaining. A strong relationship was seen between the expression of these two markers (Spearman’s test, P < 0.00002). The normal epithelium showed mild or absent furin and VEGF expression. On the other hand, almost 80% of the invasive carcinomas showed strong staining for both markers.

VEGF-C Processing in SCC Cell Lines. To confirm that furin-expressing SCC-derived cells are able to process VEGF-C, we analyzed whole conditioned medium from three SCC cell lines by Western blotting. We also assessed furin expression in these cell lines. As shown in Fig. 4A, SCC9, SCC15, and SCC71 cells, expressing low, intermediate, and high amounts of furin (Ref. 26; Fig. 4B), respectively, were capable of processing the VEGF-C precursor. The band corresponding to the mature form of the growth factor (~30 kDa) was markedly more prominent in SCC71. SCC9, the least aggressive of the three cell lines and the one that expressed the least amount of furin (Fig. 4B; Ref. 26), showed a predominance of the band corresponding to the proform (~59 kDa), and no processing of the precursor could be detected. On the other hand, SCC15 showed intermediate processing of the growth factor, in accordance to its intermediate aggressiveness and furin expression level (Fig. 4B) compared with the other two cell lines.

**DISCUSSION**

Tumor progression is driven by complex mechanisms that produce an enhanced malignant phenotype. Among the processes involved in the acquisition of the invasive/metastatic phenotype, angiogenesis plays a major role by increasing tumor cell oxygenation by providing a conduit for delivery of nutrition and by providing increased blood and lymphatic vessel surface areas for tumor cells to penetrate into the newly formed vessels, reach the general circulation, and metastasize (32, 33, 52). In previous studies we have shown that furin is able to enhance tumor progression by processing several metalloproteinases and growth factors (53–55). In addition, Siegfried et al. (50) have recently demonstrated that furin is able to process VEGF-C in a colon cancer cell line. To date, of the five members of the VEGF family, VEGF-C is the only demonstrated furin substrate. VEGF-C plays a significant role by enhancing the neoformation of lymphatic and blood vessels in several human malignancies, including cancer of the head and neck (45, 56, 57). Regional lymph node metastasis is a significant factor in the therapy and prognosis of oral cavity SCC (58). Among the VEGF family, VEGF-C has a role in inducing both angiogenesis and lymphangiogenesis via VEGF receptor-2 and, more importantly, via VEGF receptor-3 (47, 59). Expression of VEGF receptor-3 is highly restricted to the lymphatic endothelial cells and is stimulated mainly by VEGF-C and to some extent by VEGF-D (60). Kishimoto et al. (44) reported that VEGF-C expression in oral SCC biopsies strongly correlated with lymph node metastasis. Two recent studies showed that an up-regulation of VEGF-C

Fig. 4  A, Western blot analysis of vascular endothelial growth factor-C (VEGF-C). Concentrated total conditioned medium from SCC9, SCC15, and SCC71 human head and neck cell lines was fractioned by 10% SDS-PAGE. Note the higher proportion of processed form in SCC71 (arrow) and the higher proportion of the proform in SCC9 (arrowhead). SCC15 showed intermediate processing of the VEGF-C proform. B, Western blot analysis of furin expression. Fifty µl of cell lysates were submitted to 8% SDS-PAGE. Immunoblotting was performed with the antifurin monoclonal antibody MON-152. Note the high furin expression in the most invasive cell line (SCC71) than in the less aggressive cell line (SCC9). The least invasive cell line (SCC9) showed the lowest furin expression.
Expression of Furin and VEGF in SCC of the Tongue

(56) and a high intratumoral lymphatic MVD (61) positively correlated with lymph node metastasis in oral cancers. Sedivy et al. (62) demonstrated a significant correlation of VEGF-C expression with an elevated lymphatic MVD and with lymph node metastasis in patients with oral SCC. Mandriota et al. (60) reported that VEGF-C-induced lymphangiogenesis mediates tumor cell dissemination and the formation of lymph node metastases in studies in vivo. Thus, in oral SCC progression, VEGF-C is a very significant factor that influences regional lymph node metastasis and survival.

The fact that furin-expressing head and neck cell lines and primary tumors showed increased aggressiveness in vivo (26, 54) may be explained in part by enhancement of VEGF processing, resulting in increased tumor-associated angiogenesis. This hypothesis is supported by results obtained by Siegfried et al. (50), who found that CHO cells stably expressing VEGF-C, when s.c. injected into nude mice, enhanced angiogenesis and lymphangiogenesis compared with nontransfected cells.

In the present report we show that expression of furin and VEGF-C increases simultaneously along with MVD in a series of preinvasive lesions and SCCs of the tongue. Although angiogenesis in head and neck SCC is a complex phenomenon driven by many stimulatory factors (63), it is reasonable to hypothesize that increased furin expression promotes the processing of several members of the PDGF/VEGF family, including VEGF-C, that are known substrates of this convertase (50, 64). This increase in the available mature form could thus induce the increase in neovascularization seen in dysplastic epithelia and SCCs. This is further supported by the finding that three head and neck SCC cell lines known to express furin process VEGF-C.

Sauter et al. (43) found, in a limited series of cases from several head and neck sites, that VEGF expression correlated with MVD of preinvasive and invasive lesions of the head and neck. Similarly, in a small series of head and neck lesions from the oral cavity, larynx, and pharynx, Ninck et al. (63) described that the expression of the furin substrates VEGF and platelet-derived growth factor-AB correlated with poor survival in SCC patients. In addition, they observed that the tumors expressed angiogenic growth factors, whereas the normal adjacent epithelium did not.

To avoid site heterogeneity in vascularization within the head and neck, we focused on lesions of the oral tongue. For the purpose of this study, we evaluated glossectomy specimens that showed stages of tumorigenesis from normal epithelium to invasive SCC, including dysplasia. Our data confirmed that angiogenesis, as measured by MVD, occurs in association with preneoplastic changes in human tongue epithelium before invasion. No significant differences in furin or VEGF-C expression and MVD were seen among the lesions of different degrees of dysplasia. The increment in MVD was associated with an increase of VEGF-C.

In this study we found that there is a positive correlation between furin and VEGF-C up-regulation during tumor progression. We also analyzed the staining intensity ratio between the basaloid (or peripheral) cells of the tumors and the basal cells of normal epithelium. The results obtained showed that in 81% of the specimens studied, the ratio of intensity (ratio of intensity of basaloid cells of the tumor to intensity of basal cells of normal epithelium) was >1. This result suggests that furin expression is increased at the invasive front of the tumors, where processing of tumor progression-related substrates, such as metalloproteinases and VEGF-C, takes place. We confirmed with in vitro studies that the ability to process VEGF-C (Fig. 4A) is in direct relationship with the degree of malignancy and furin expression (Fig. 4B) of the cell lines analyzed. SCC9, the least malignant cell line, did not process all of the available proform of the growth factor, whereas SCC71 did. SCC15 showed an intermediate processing of the growth factor, in accordance with its intermediate aggressiveness and furin expression. It is important to note that furin expression was highest in SCC71 and lowest in SCC9 (Fig. 4B).

The hypothesis that neoplastic cells stimulate angiogenesis early during their progression to an invasive cancer has been suggested by recent studies combining in vitro angiogenesis assays and specimens taken from transgenic mice. These studies suggest that angiogenesis begins before the emergence of invasive cancer (65–67). Furthermore, increased MVD has been reported in other models of preinvasive progression, such as human colon and precursor lesions of the mouse skin (68, 69).

The present study shows that there is a close association between progressive squamous carcinogenesis in the human tongue, epithelial furin expression, VEGF-C expression, and neovascularization. This suggests that furin may promote tumor-associated angiogenesis through enhanced VEGF-C processing.

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