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RESEARCH PAPER

Trks are novel oncogenes involved in the induction of neovascularization, tumor progression, and nodal metastasis in oral squamous cell carcinoma

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Abstract The function of tropomyosin receptor kinase (Trk) family including *TrkA*, *TrkB*, and *TrkC* in cancer remains unknown. The role of Trks in oral squamous cell carcinoma (OSCC) was examined. Knockdown of *Trks* provided inhibition of growth or invasion and decrease of apoptosis in OSCC cells, which expressed *Trks* at high levels. *VEGF* expression was associated with *TrkA* and *TrkB* expression; a decrease of *VEGF-C* and *VEGF-D* was observed in OSCC cells with *TrkB* knockdown. *TrkC* did not affect the expression of *VEGF* family. An immunohistochemical analysis of 102 OSCCs showed that *TrkB* expression was related to microvessel density (MVD), lymph vessel density (LVD), and poor prognosis. *TrkC* expression was correlated with clinical stage, lymph node metastasis, MVD, LVD, and poor prognosis. *TrkA* expression was associated with *VEGF* expression, whereas *TrkB expression was associated with the expressions of VEGF*, *VEGF-C* and *VEGF-D*. No significant association was found between the expression of *TrkC* and genes of the *VEGF* family. Expression of *Trks* was not associated with *RUNX3* silencing by methylation in OSCC cells. *Trks* expression was inversely correlated with *RUNX3* expression in the OSCC cases. These results suggested that Trks enhances progression of OSCC through angiogenesis and lymphangiogenesis.

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Abbreviation

OSCC	Oral squamous cell carcinoma
Trk	Tropomyosin receptor kinase
NGF	Nerve growth factor
BDNF	Brain derived neurotrophic factor
NT3	Neurotrophin3
RUNX3	Runt-related transcription factor 3
VEGF	Vascular endothelial growth factor
MVD	Microvessel density
LVD	Lymph vessel density
PI3K	Phosphatidylinositol 3′-kinase
BMP	Bone morphogenetic protein
TGF	Transforming growth factor

Introduction

Head and neck cancer constitute the sixth most common malignancy worldwide [1, 2], and the incidence of oral squamous cell carcinoma (OSCC) exceeds 300,000 new cases annually worldwide [3], with a frequency of 3.7 cases per 100,000 people in Japan [4]. OSCC has a high potential for locoregional invasion and nodal metastasis that is characterized by over 50 % patient morbidity and mortality [3, 5]; overall 5-year survival rates have not improved during the past three decades [6].

Tropomyosin receptor kinases (Trks) have a high affinity for neurotrophins, and TrkA, TrkB, and TrkC are the receptors for nerve growth factor (NGF), brain-derived neurotrophic factor (BDNF), and neurotrophin 3 (NT3), respectively [7]. Details about the regulation of Trk expression are unclear, but recently it has been reported

that Trk expression is positively or negatively regulated by runt-related transcription factor 3 (RUNX3) [8, 9], a transcription factor that acts as a tumor suppressor gene. We also observed low or no expression and methylation of *RUNX3* in cases of head and neck cancer [10]. Trks regulate the survival and differentiation of developmental neurons and maintain the growth and action of neuronal synapses throughout adulthood [11]. Trks are also considered oncogenes in many tumors, and several reports have shown that *TrkB* and *TrkC* inhibit apoptosis in cancer cells [12, 13]. Overexpression of *TrkA* was observed in papillary and medullary carcinoma of the thyroid [14, 15] and in ovarian serous carcinoma [14]. Higher levels of TrkB have been found in pancreatic cancer [15], hepatoma [16], prostate cancer [17], ovarian cancer [12], and neuroblastoma [18], and are associated with more aggressive tumor behavior. Chen-Tsai et al. [19] reported that TrkC may predict neural invasion in skin cancer. However, cases with high expression of *TrkA* or *TrkC* have better prognoses in neuroblastoma [20, 21] and TrkC plays a favorable role in medulloblastoma [22]; thus, the detailed role of Trks in cancer is still controversial.

Materials and methods

Cell culture and recombinant human BDNF or NT3 treatment

Human OSCC cell lines, KON, HSC-2, HSC-3, HSC-4, Ca9-22 and SAT, cells were obtained from Health Science Research Resources Bank and maintained in Dulbbeco's modified Eagle's medium (DMEM) (Wako Pure Chemical, Osaka, Japan) supplemented with 10 % fetal bovine serum (FBS) (Sigma Chemical, St. Louis, USA) under the conditions of 5 % CO_2 in air at 37 °C. KON and HSC-3cells have high metastatic potential, HSC-4 cells have low metastatic ability, and HSC-2, Ca9-22, and SAT cells have no ability of metastasis and invasion. Each cell was treated with 10, 20, 30, and 40 μM of Recombinant human NGF (rhNGF) (R&D Systems, Temecula, USA), BDNF (rhBDNF) (R&D Systems), and NT3 (rhNT3) (R&D Systems) treatment were performed.

Quantitative reverse transcription-polymerase chain reaction

Total RNA was extracted using RNeasy Mini Kit (Qiagen, Valencia, USA) and total RNA (1 μg) was synthesized with the ReverTra Ace qRT Kit (Toyobo, Osaka, Japan). Quantitative reverse transcription-polymerase chain reaction (qRT-PCR) were performed on StepOne Plus Real-Time PCR Systems (Applied Biosystems, Foster City, USA) using TaqMan Fast Universal PCR Master Mix (Applied Biosystems) and analyze the relative standard curve quantification method. PCR condition was according to the manufacturer's instructions and ACTB mRNA level was amplified for internal control. TaqMan Gene Expression Assays of TrkA, TrkB, TrkC, VEGF, VEGF-C, VEGF-D, RUNX3, and ACTB were purchased from Applied Biosystems. All PCRs were done at triplicate.

Small interfering RNA

Stealth Select RNAi (siRNA) for TrkA, TrkB, TrkC, and RUNX3 were purchased from Invitrogen (Carlsbad, USA). AllStars Negative Control siRNA was used for control (Qiagen). Twenty-nanometer siRNA were transfected with Lipofectamine 2000 (Invitrogen) according to the provider's recommendations.

Cell growth assay

The cells were seeded at density of 2,000 cells per well of 96-well tissue culture plates and incubated for 48 h at 37 °C. Cell growth was assessed by MTT assay using the incorporation of 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (Sigma) [23]. The experiments were performed in triplicate.

In vitro invasion assay

A modified Boyden chamber assay was performed using the BD BioCoat Cell Culture Inserts glued to type IV collagen (Becton–Dickinson, Bedford, USA) as described previously [23]. Cells were suspended in 500 μl of DMEM and placed 4 in the insert. After 48 h incubation at 37 °C, the filters were stained with hematoxylin. The stained cells were counted in whole inserts at 100× magnification. Each experiment was repeated at least three times.

Apoptosis assay

Apoptotic cells were detected by the terminal deoxynucleotidyl transferase (TdT)-mediated dUTP-biotin nick and labeling (TUNEL) assay using the In Situ Cell Death Detection Kit, POD (Roche, Indianapolis, USA). We also confirmed the activation of caspase-3 was detected using CaspACE Assay system, Colorimetric (Promega, Madison, Wisconsin, USA) according to the manufacturer's protocol. The experiments were performed in triplicate.

Immunoblotting

Whole-cell lysate were obtained using M-PER Mammalian Protein Extraction Reagent (Thermo Fisher Scientific Inc.,

Rockford, IL, USA) according to the manufacturer's protocol. Fifty-microgram lysates were subjected to immunoblotting in 12.5 % SDS-PAGE followed by electrotransfer to nitrocellulose filters. The filters were incubated with primary antibody then with peroxidase-conjugated IgG antibody (MBL, Nagoya, Japan). The immune complex was visualized by ECL Western Blotting Detection System (GE Healthcare Ltd., Amersham place, UK). The primary antibodies used were anti-TrkA (Santa Cruz Biotechnology, Santa Cruz, USA, clone C-14), anti-TrkB (Santa Cruz Biotechnology, clone 794), anti-TrkC (Santa Cruz Biotechnology, clone WW6), anti-VEGF-A (Santa Cruz Biotechnology, clone 147), anti-VEGF-C (Santa Cruz Biotechnology, clone F-10), and anti-VEGF-D (Santa Cruz Biotechnology, clone C-18). Anti-GAPDH antibody (Santa Cruz Biotechnology, clone V-18) was used for internal control.

Enzyme-linked immunosorbent assay in culture medium

Cultured medium was filtered with 0.2 μm push filter (Millipore, Bedfold, MA, USA) and enzyme-linked immunosorbent assay (ELISA) system for VEGF (Calbiochem, Darmstadt, Germany), VEGF-C (Bender MedSystems GmbH, San Bruno, CA, USA), VEGF-D (R&D Systems), matrix metalloproteinase (MMP)-2 (R&D Systems), and MMP-9 (R&D Systems) was used. The assay was performed according to the provider's instruction in at least triplicate.

Methylation-specific polymerase chain reaction (MSP)

Genomic DNA was extracted using QIAamp DNA Mini Kit (Qiagen). For the bisulfate modification of DNA, 2 μg of genomic DNA was treated with Epitect Bisulfite Kit (Qiagen) according to the manufacturer's instructions. For analysis of DNA methylation of RUNX3, we carried out MSP using an Epitect MSP Kit (Qiagen). PCR products were separated on 6 % non-denaturing polyacrylamide gels, stained with ethidium bromide (Sigma) and visualized under UV light.

Methylated or unmethylated RUNX3 primer set is as follows [10, 24]: 5′-TTA TGA GGG GTG GTT GTA TGT GGG-3′ and 5′-AAA ACA ACC AAC ACA AAC ACC TCC-3′ for unmethylated RUNX3; 5′-TTA CGA GGG GCG GTC GTA CGC GGG-3′ and 5′-AAA ACG ACC GAC GCG AAC GCC TCC-3′ for methylated RUNX3. All primers were synthesised by Sigma Genosys (Ishikari, Japan).

5-Aza-2′-deoxycytidine treatment

Each cell was seeded at a density of 1×10^6 cells/ml. After 24 h, cells were treated with 1 μM 5-Aza-2′-deoxycytidine (5-Aza-dc) (Sigma) for 4 days. Treat with 300 nm trichostatin A (TSA) (Sigma) was also performed for 24 h. Cells then were harvested for DNA and RNA extractions.

Tissue samples

For immunohistochemical analysis, total of 102 (68 men and 34 woman, Age range, 48–79 years; means, 68.7 years) cases of primary OSCCs containing the deepest lesion and underwent without preoperative therapy were used. Tumor staging was carried out according to TNM classification [25] and the histology of OSCCs are classified according to WHO classification [26]. Medical records and prognostic follow-up data were obtained from the patient database administered by the hospital. For qRT-PCR, 20 OSCCs (13 men and 7 woman, age range, 52–74 years; mean, 63.2 years) and 5 non-tumorous oral mucosa (all samples were gingival mucosa which was excised at the time of the extraction of mandibular third molar, 4 men and 1 woman, age range, 22–40 years; mean, 28.4 years) were used. Samples were frozen immediately in liquid nitrogen and stored at −80 °C until use. All specimens were randomly selected at Nara Medical University Hospital, Kashihara, Japan. Because written informed consent was not obtained, identifying information for all samples was removed before analysis for strict privacy protection; the procedure was in accordance with the Ethical Guidelines for Human Genome/Gene Research enacted by the Japanese Government.

Immunohistochemistry

Consecutive 4 μm sections were cut from each block, and immunohistochemistry was performed as we described previously [27]. Briefly, an immunoperoxidase technique was done following antigen retrieval with microwaving in citrate buffer at 95 °C or pepsin (DAKO, Carpinteria, USA) treatment. After endogenous peroxidase block by 3 % H_2O_2-methanol, anti-TrkA (Santa Cruz Biotechnology, clone C-14), TrkB (Santa Cruz Biotechnology, clone 794), and TrkC (Santa Cruz Biotechnology, clone WW6) antibody, anti-NGF antibody (Santa Cruz Biotechnology, clone H-20), anti-BDNF antibody (R&D Systems, clone UY02), anti-NT3 antibody (CHEMICON, Minneapollis, USA, clone AB1779SP), anti-CD34 antibody (DAKO, clone QBEnd 10), and anti-LYVE-1 antibody (Abcam, Tokyo, Japan, clone ab33682) diluted at 0.5 μg/ml were used for primary antibody and peroxidase-conjugated anti-mouse, anti-rabbit, and anti-goat antibody (MBL) diluted at 0.5 % were used for secondary antibody. According to the attached reference of company, anti-TrkA and TrkC antibody are detection of only each Trks and anti-TrkB antibody is no cross-reaction of TrkB-T1 or TrkBT-Shc and recognizes

only TrkB. The specimens were color-developed with diaminobenzidine (DAB) solution (DAKO) and specimens were counterstained with Meyer's-hematoxylin (Sigma).

Evaluation of immunohistochemistry

Immunoreactivity of Trk, BDNF, and NT3 were classified according to Allred's score (AS) [28] and we divided the immunoreactivity into four grades by AS; Grade 0, AS is 0; Grade 1, AS is 2–4; Grade, AS is 5, 6; Grade 3, AS is 7, 8. Cases with Grade 2 and 3 were regarded as immunopositive [29]. The microvessel density (MVD) and lymphovessel density (LVD) were measured on anti-CD34 and anti-LYVE-1 positive vessels, respectively. Five areas of tissue with the greatest number of distinctly highlighted vessels (the "hot spot") and counted under a 200-fold magnification by microscope and averaged [29–31]. To determine the MVD and LVD, we divided into low or high groups according to density those with values higher the mean value for the entire group and those with than the group mean value [31].

Statistical analysis

Statistical analysis was carried out with JMP8 (SAS Institute, Cary, USA). Statistical differentiation was calculated with unpaired Mann–Whitney *U* test, Student-*t* test, Fischer's exact probability test, and χ^2 test. Disease-free survival was analyzed by the Kaplan–Meier method, and differences between groups were calculated by means of a logrank test. *P* values less than 0.05 were regarded as statistically significant.

Results

Expression and functional analysis of Trks in OSCC cells

At first, six OSCC cells were evaluated for Trk expression by qRT-PCR and immunoblotting. Although TrkA was expressed to a similar extent in each cell, highly metastatic KON and HSC-3 cells exhibited higher expression of TrkB and TrkC than other cells (Fig. 1a).

It was previously reported that Trks regulate angiogenesis [32–34]. Next, we examined the change in VEGF, VEGF-C, and VEGF-D expression levels following Trk siRNA treatment in KON and HSC-3 cells. Gene expression levels of *VEGF*, *VEGF-C*, and *VEGF-D* in KON and HSC-3 cells were higher than in other cells (data not shown). Expression of VEGF was decreased following TrkA or TrkB siRNA treatment, whereas decreases in VEGF-C and VEGF-D expression were observed only with TrkB knockdown in both cell types. No change in the expression of VEGF family was observed following TrkC siRNA treatment. We also observed reduction of secretion levels of VEGF family in TrkA or TrkB siRNA treated OSCC cell culture medium, however, TrkC siRNA did not affect the concentration of VEGF family in culture medium compared to control siRNA treated culture medium (Fig. 1b).

Next, we analyzed the effect of *Trk* on cell growth, invasion, and apoptosis of KON and HSC-3 cells by *Trk* siRNA treatment. Number of the cells, growth ability, and invasive capacity were decreased by *TrkB* and *TrkC* siRNA treatment, respectively (Fig. 1c). Concentration of MMP-2 and MMP-9 in cell culture medium was only decreased by TrkB siRNA treatment (Fig. 1d). Apoptotic cells and caspase-3 activation were increased following *TrkA*, *TrkB*, or *TrkC* siRNA treatment (Fig. 1e).

Recombinant human BDNF and NT3 treatment in KON and HSC-3 cells

We also performed treatments with various concentrations of rhBDNF (a TrkB ligand) and rhNT3 (a TrkC ligand) and examined the effects on cell growth, invasion, and expression of angiogenic/lymphangiogenic factors in KON and HSC-3 cells (Fig. 2a–d). Cells were treated with rhBDNF or rhNT3 and pretreated with 20 nm TrkB or TrkC siRNA, respectively. Both cells showed restoration of growth ability and *VEGF*, *VEGF-C*, and *VEGF-D* expression following treatment with rhBDNF (Fig. 2a, b). Treatment with rhNT3 increased invading cells but did not change the expression levels of the VEGF family in KON and HSC-3 cells (Fig. 2c, d). We also confirmed that rhNGF (ligand of TrkA) treatment and pretreatment with *TrkA* siRNA restored *VEGF* expression dose dependently (Fig. 2e).

Effect of RUNX3 on the expression of Trks in KON and HSC-3 cells

Trk expression is regulated by *RUNX3* in neurons [8, 9]. To confirm whether *RUNX3* regulated *Trk* expression in OSCC, we compared *Trk* expression with the expression and methylation of *RUNX3*. The methylation-specific PCR (MSP) position was located in the *RUNX3* exon1 region [10, 24]. *RUNX3* mRNA was not detected (data not shown) and methylation of *RUNX3* was observed in KON and HSC-3 cells (Fig. 3a). To confirm whether *RUNX3* regulated *Trk* expression in OSCC, we observed the *Trk* expression corresponding to the demethylation of *RUNX3*. Treatment with 5-Aza-dc induced expression of *RUNX3* and significantly decreased *TrkA*, *TrkB*, and *TrkC* expression, whereas treatment with 20 nm *RUNX3* siRNA on day

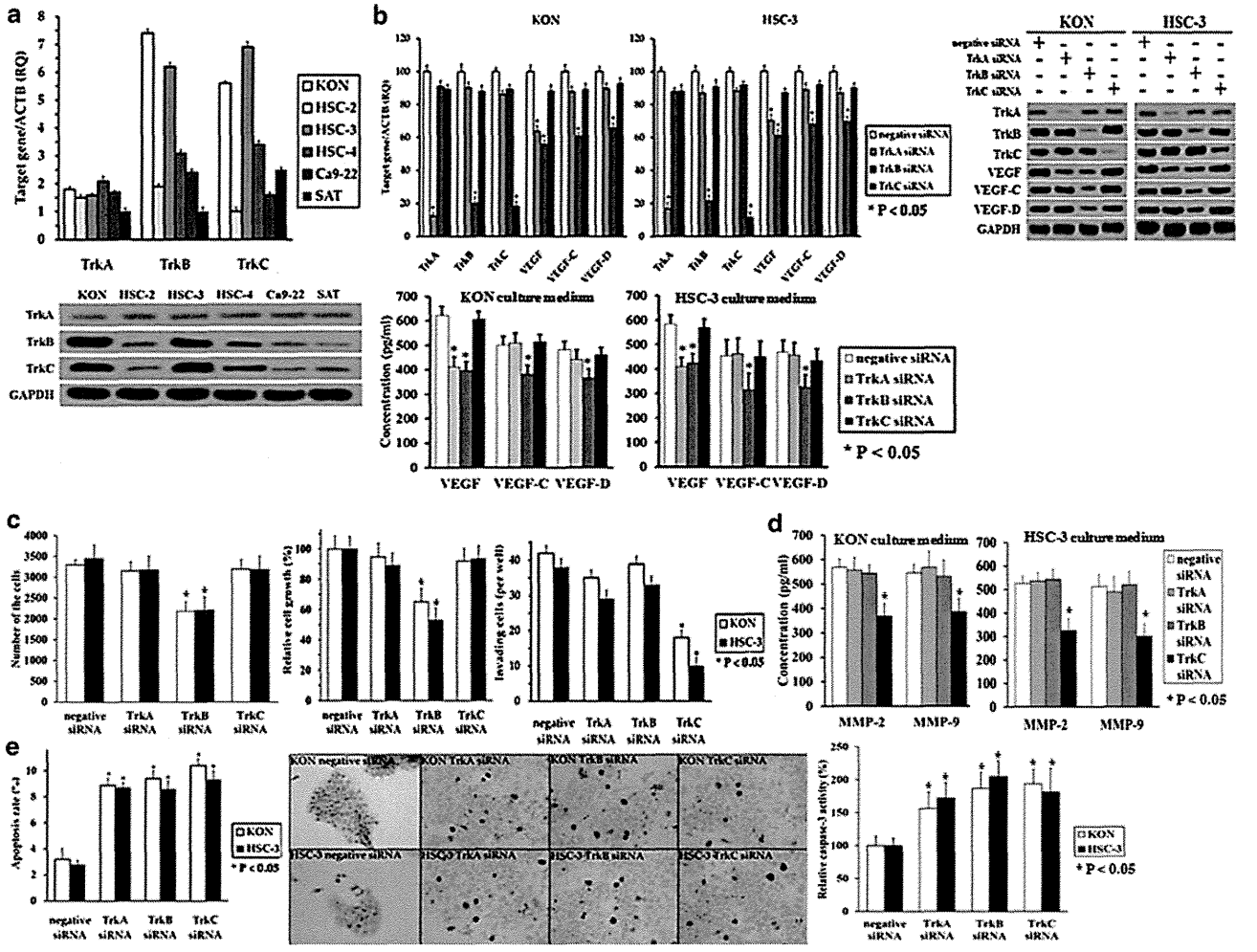

Fig. 1 Effect of Trks in OSCC cell lines. **a** Expression of Trks in six OSCC cells measured using realtime RT-PCR and immunoblotting. Highly metastatic KON and HSC-3 cells showed higher expression of TrkB and TrkC. Expression levels of TrkA was similar extent in each cells. **b–e** Effects of *Trk* siRNA treatment in KON and HSC-3 cells on expression of the *Trk* and VEGF families and secretion of VEGF, VEGF-C, and VEGF-D (**b**), direct cell counting, cell growth, and invasive ability (**c**), secretion of MMP-2 and MMP-9 (**d**), and apoptosis (**e**). Expression of each gene was evaluated by realtime RT-PCR and each protein expression levels was investigated by immunoblotting. Secretion levels of VEGF, VEGF-C, VEGF-D, MMP-2, and MMP-9 were measured by ELISA system. Growth and invasive ability were examined by the MTT assay and an in vitro invasion assay. Apoptotic cells were detected by the TUNEL assay. We also measured caspase-3 activity. Expression and secretion levels of VEGF was decreased by TrkA or TrkB siRNA treatment and decreases in VEGF-C and VEGF-D expression and secretion were observed in TrkB siRNA treated OSCC cells (**b**). Growth ability and invasive capacity were decreased in TrkB and TrkC siRNA treated OSCC cells, respectively (**c**). Decrease of secretion levels of MMP was found in TrkB siRNA treated cells (**d**). Induction of apoptosis and activity of caspase-3 were found in TrkA, TrkB, or TrkC siRNA treated OSCC cells (**e**)

3 after 5-Aza-dc treatment decreased expression levels of *RUNX3*, and restored expression levels of *TrkA*, *TrkB*, and *TrkC* to some extent (Fig. 3b). Treatment with TSA did not change *RUNX3* and *Trk* expression levels (data not shown). These results suggested that *RUNX3* regulated *Trk* expression.

Immunohistochemistry of Trks in cases with OSCC

On the basis of the in vitro results, we examined *Trk* expression in 102 cases with OSCC by using immunohistochemistry. *TrkA*, *TrkB*, and *TrkC* expression levels were negative or very weak in non-tumoral oral mucosa, whereas the immunoreactivity of *TrkA* (Fig. 4a), *TrkB* (Fig. 4b), and *TrkC* (Fig. 4c) was observed in the cell membranes of some OSCC cells. Immunoreactivity of *TrkA*, *TrkB*, and *TrkC* was observed in 90 % (92/102), 31 % (32/102), and 47 % (48/102) of OSCC cases, respectively. Percentages of patients exhibiting co-expression of *TrkA* and *NGF* (Fig. 4d) or *TrkB* and *BDNF* (Fig. 4e) or *TrkC* and *NT3* (Fig. 4f) were 95.7 % (88/92), 88 % (28/32), and 83 % (40/48), respectively. Mean ± SD

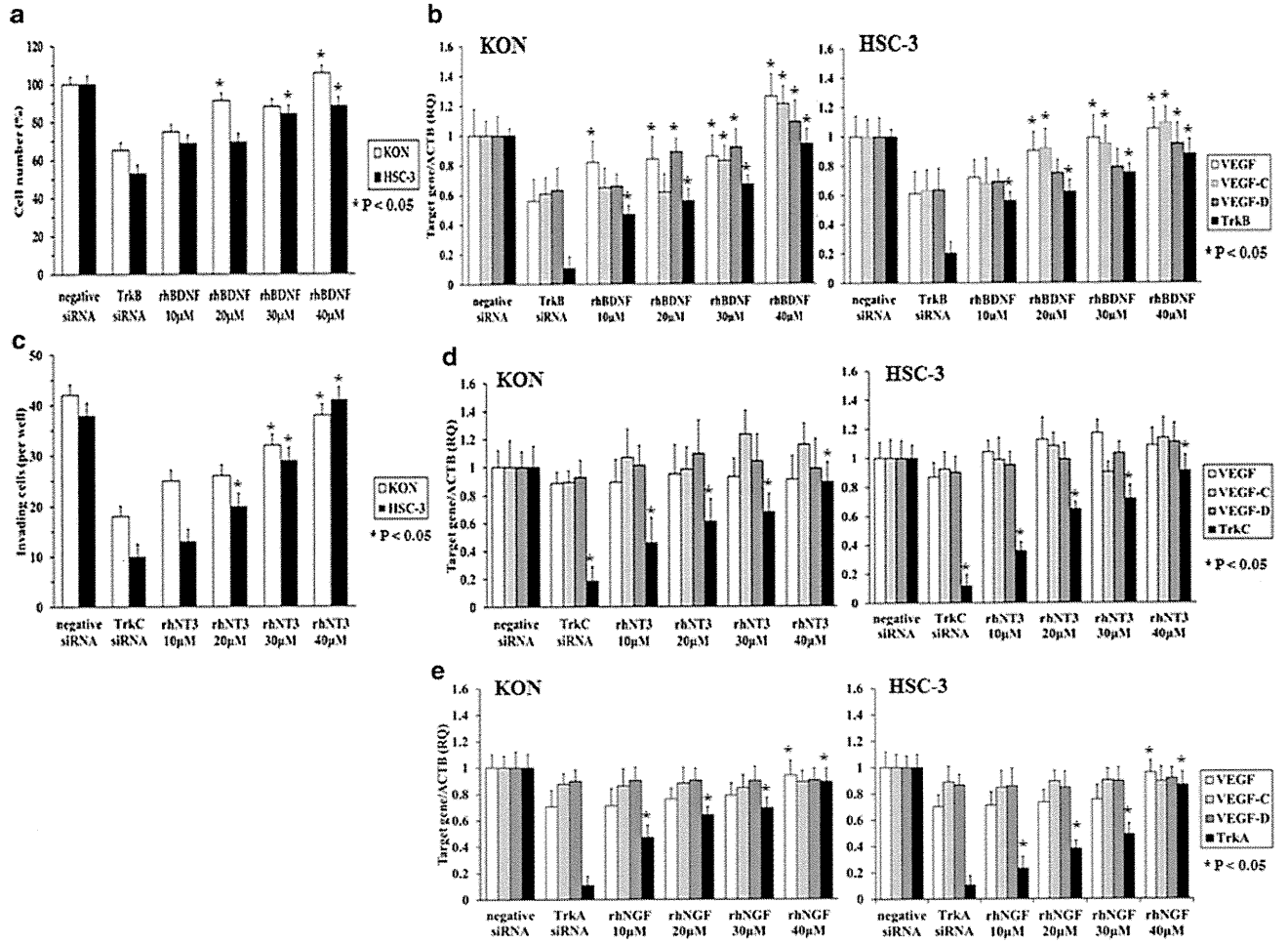

Fig. 2 Effect of BDNF on OSCC cells. Influence of rhBDNF treatment on growth ability (**a**) and *VEGF* family gene expression (**b**), and of rhNT3 treatment on invasive ability (**c**) and expression of genes of the *VEGF* family (**d**). KON and HSC-3 human OSCC cells were used for all experiments. Restoration of growth ability and *VEGF*, *VEGF-C*, and *VEGF-D* expression were found in rhBDNF treated OSCC cells (**a**, **b**). Increase of invading cells was observed but did not change the expression levels of the VEGF family in rhNT3 treated OSCC cells (**c**, **d**)

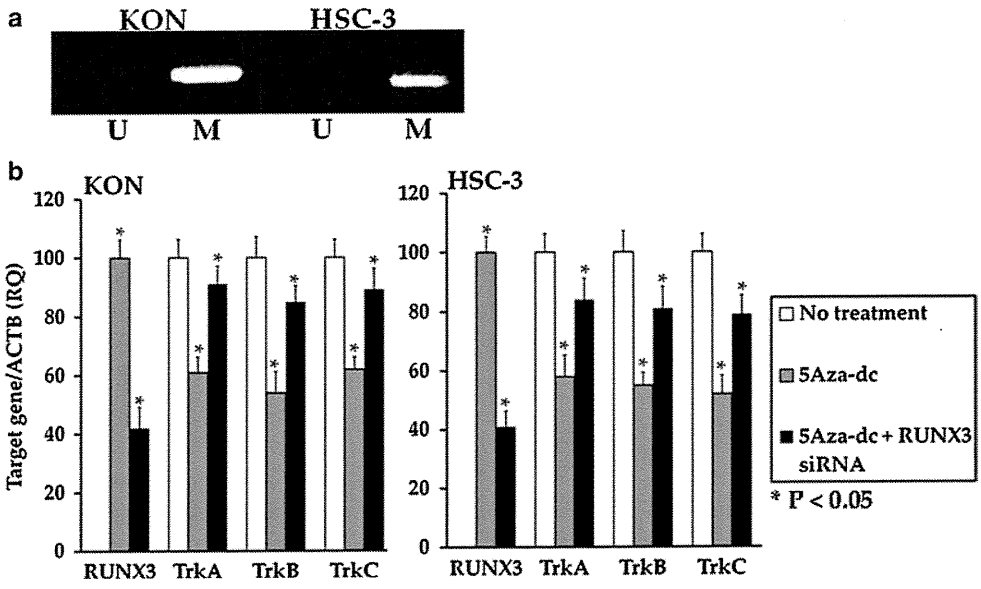

Fig. 3 Methylation status of *RUNX3 gene*. **a** Methylation status of *RUNX3*, evaluated by methylation-specific PCR (MSP) in KON and HSC-3 cells. *U* and *M* means unmethylated and methylated RUNX3, respectively. Methylation of *RUNX3* was observed in KON and HSC-3 cells. **b** Impact of treatment with 5-Aza-dc or 5-Aza-dc + *RUNX3* siRNA on expression of *RUNX3* and Trks in KON and HSC-3 cells. Cells with 5-Aza-dc treatment decreased expression levels of *RUNX3*, and restored expression levels of *TrkA*, *TrkB*, and *TrkC*

(standard deviation) of MVD and LVD in OSCC were 42.41 ± 18.13 and 56.23 ± 23.69, respectively. Cases were divided into a high (Fig. 4g, i) and low group (Fig. 4h, j) based on both parameters. No significant association was found between *TrkA* expression and clinicopathological characteristics; however, a significant relationship was observed between high expression of *TrkB* and MVD ($P = 0.0034$) and LVD ($P = 0.0388$). Immunoreactivity of TrkC was also strongly correlated with gender ($P = 0.0098$), age ($P = 0.0094$), clinical stage ($P = 0.0005$), nodal metastasis ($P = 0.0004$), MVD ($P = 0.0048$), and LVD ($P = 0.0327$) (Table 1).

Disease-free survival analysis

Disease-free survival rates in OSCC patients showed that the prognosis of TrkB-positive cases was significantly worse than that of cases without *TrkB* expression ($P = 0.0166$) (Fig. 5a). High *TrkC* expression cases were also markedly related to a poor prognosis ($P = 0.0036$) (Fig. 5b); however, *TrkA* expression level did not influence survival (data not shown).

Gene expression of Trks, RUNX3, and angiogenic/lymphangiogenic factors in cases with OSCC

Finally, experiments were conducted to confirm the correlation between *Trk* expression and expression of *RUNX3*, *VEGF*, *VEGF-C*, or *VEGF-D*, in 20 cases with OSCC. For controls, five non-tumoral oral epithelium samples were used. In OSCCs, *TrkA*, *TrkB*, and *TrkC* expression was significantly higher than in non-tumorous oral mucosa (Fig. 6). Decreased or absent expression of *RUNX3* was significantly inversely correlated with the overexpression of *TrkA* (Fig. 6a), *TrkB* (Fig. 6b), and *TrkC* (Fig. 6c). We also confirmed that the RUNX3 protein was detected in non-cancerous oral mucosa, whereas it was not detected in OSCC specimens, by immunohistochemistry (data not

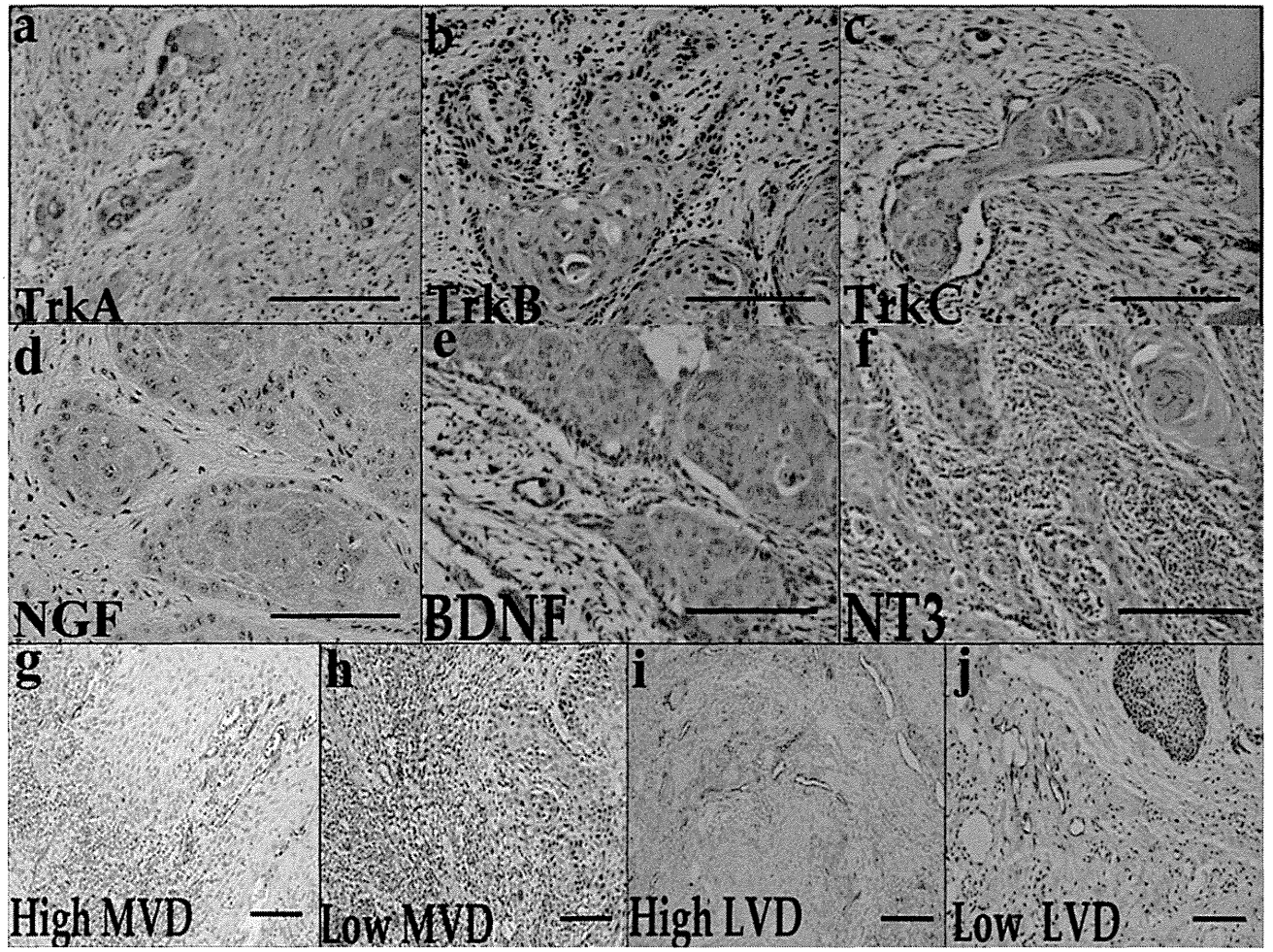

Fig. 4 Expression of Trks in OSCC cases. Immunohistochemical analysis of *TrkA* (**a**), *TrkB* (**b**), *TrkC* (**c**), *NGF* (**d**), *BDNF* (**e**), *NT3* (**f**) expression, MVD (**g**, **h**), and LVD (**i**, **j**). Immunoreactivity of Trks and their ligand were observed in cytoplasm of cancer cells. Original magnification, 400-fold (**a**–**e**) and 200-fold (**g**–**i**). *Bar*, 100 μm

Table 1 Relationship between Trk expression and clinicopathological parameters

Parameters	TrkA		TrkB		TrkC	
	(−)	(+)	(−)	(+)	(−)	(+)
Location						
Tongue	6	41	35	12	25	22
Gingiva	3	31	19	15	17	17
Other	1	20	16	5	12	9
P value	NS		NS		NS	
Gender						
Male	7	61	47	21	30	38
Female	3	31	23	11	24	10
P value	NS		NS		0.0098	
Age						
≤60	1	29	18	12	10	20
>60	9	63	52	20	44	28
P value	NS		NS		0.0094	
Histological differentiation						
Well	9	55	43	21	31	33
Mod, Por	1	37	27	11	23	15
P value	NS		NS		NS	
T classification						
1, 2	7	44	38	13	28	23
3, 4	3	48	32	19	26	25
P value	NS		NS		NS	
Clinical stage						
I, II	5	32	28	9	28	9
III, IV	5	60	42	23	26	39
P value	NS		NS		0.0005	
Nodal metastasis						
Negative	5	50	40	15	38	17
Positive	5	42	30	17	16	31
P value	NS		NS		0.0004	
Microvessel density (MVD)[a]						
Low	4	36	34	6	28	12
High	6	56	36	26	26	36
P value	NS		0.0034		0.0048	
Lymph vessel density (LVD)[a]						
Low	3	44	37	10	30	17
High	7	48	33	22	24	31
P value	NS		0.0338		0.0327	

Relationship between expression of Trk and clinicopathological parameters were calculated by χ^2 test or Fischer's exact t test, respectively. T classification and clinical stage were classified according to the TNM classification

NS not significant; Histological differentiation: *Well* well-differentiated squamous cell carcinoma, *mod* moderately differentiated squamous cell carcinoma, *por* poorly differentiated squamous cell carcinoma

[a] To determine the MVD and LVD, we divided into low or high groups according to density those with values higher the mean value for the entire group and those with than the group mean value

shown). Next, for the gene expression analysis of the Trk and VEGF families, we divided samples into two groups according to expression levels: those with values higher than the mean value for the entire group and those with values lower than the group mean value. The mean ± SD values for each gene were as follows: *TrkA*, 2.71 ± 1.35; *TrkB*, 3.18 ± 2.54; *TrkC*, 3.35 ± 2.65; *VEGF*, 2.59 ± 1.68; *VEGF-C*, 3.94 ± 2.07; and *VEGF-D*, 4.14 ± 2.33. A significant relationship was found between expression levels of *VEGF* and *TrkA* ($P = 0.0349$) or *TrkB* ($P = 0.0124$); *VEGF-C* and *VEGF-D* expression were only correlated with *TrkB* expression ($P = 0.0399$ and $P = 0.0092$, respectively) in cases with OSCC (Table 2). No significant association was found between expression of *TrkC* and *VEGF*, *VEGF-C*, or *VEGF-D*. All the above-mentioned results suggested that Trk participates in angiogenesis and lymphangiogenesis and that Trk expression is regulated by the expression and methylation of *RUNX3*.

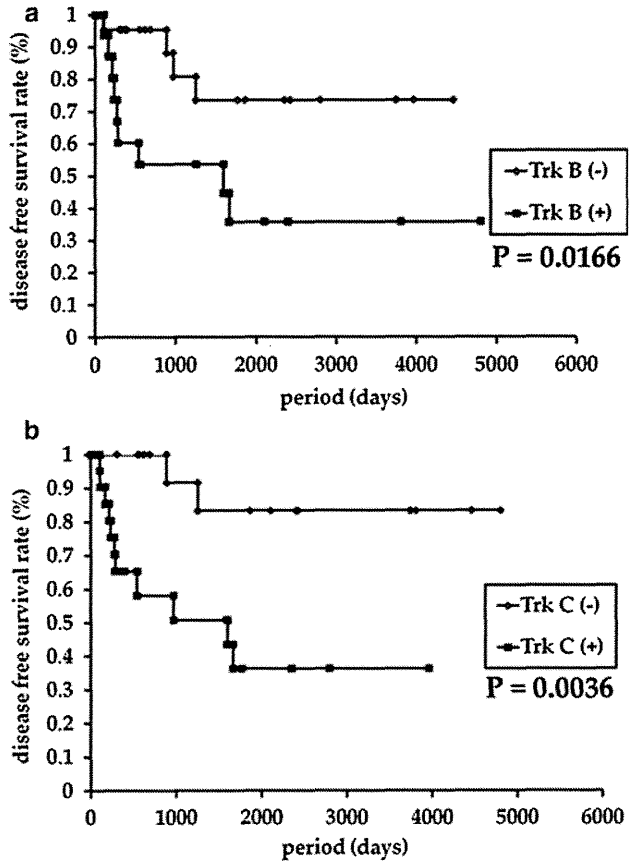

Fig. 5 Relation of expression of Trk B and TrkC and survivals of OSCC cases. Disease-free survival curves for OSCC, using the Kaplan–Meier method. Patients with *TrkB* (**a**) or *TrkC* (**b**) expression had significantly worse outcomes than did patients not showing *TrkB* or *TrkC* expression

Discussion

Trks are considered oncogenes; however, the function of Trks in cancer is still controversial [12–22, 32, 33, 35, 36]. We previously reported that angiogenesis and lymphangiogenesis are significantly associated with tumor progression, nodal metastasis, and poor prognosis in OSCC [31]. We also found that activation of *VEGF* and *VEGF-C* or *VEGF*, *VEGF-C*, and *VEGF-D* promotes angiogenesis or lymphangiogenesis, respectively [31]. Trks are known to accelerate angiogenesis [32–34], whereas the lymphangiogenic roles of Trks are still unknown. In the present study, we examined the expression and function of Trks and compared these to the clinicopathological parameters, including angiogenesis and lymphangiogenesis; expression levels of Trks in OSCC were higher than non-cancerous oral mucosa.

Although *TrkA* expression was correlated with expression and secretion of *VEGF* and the immunopositivity rate of *TrkA* cases with OSCC was very high, no relationship was found between TrkA expression and clinicopathological characteristics by immunohistochemistry. However, induction of apoptosis were observed following TrkA siRNA treatment. It was previously reported that a negative relationship was found between *VEGF* expression and the number of apoptotic cells in cancer [37], and it was also shown that expression levels of *VEGF* were in this step of carcinogenesis [38]. *TrkA* may be involved in oral carcinogenesis by the activation of *VEGF* and reduction of apoptosis.

Several reports indicated that *TrkB* brings about drug resistance by suppression of apoptosis through activation of phosphatidylinositol 3′-kinase (PI3K)-Akt signaling [12, 39] and that tumors expressing high levels of *TrkB* have a bad prognosis [18]. *TrkB* also induces angiogenesis [32]. In OSCC, *TrkB* expression promoted cell growth, inhibited apoptosis, activated *VEGF* expression and secretion, and was significantly associated with angiogenesis and poor prognosis. These findings were mainly in accordance with previous descriptions; no reports are available on the relationship between TrkB expression and lymphangiogenesis via expression of *VEGF*, *VEGF-C*, and *VEGF-D*. Further studies are needed to clarify whether *TrkB* regulates lymphangiogenesis.

It has been shown that *TrkC* is overexpressed in favorable neuroblastoma and medulloblastoma [21, 22], while other reports have shown that *TrkC* act as oncogene in skin cancer [19] and in the inhibition of bone morphogenetic protein (BMP) in breast cancer [35] and of transforming growth factor (TGF)-β signaling in colon cancer [40]. In the present study, we showed that cases with nodal metastasis and worse prognosis exhibited a high expression of *TrkC* as well as a reduction of invasive ability and restoration of apoptotic ability following TrkC siRNA treatment in OSCC. It was surprising that *TrkC* directly promoted angiogenesis and lymphangiogenesis because VEGF family expression and secretion levels were not changed, as shown using the gene knockdown technique for *TrkC*. *TrkC* might be a novel candidate gene, responsible for accelerated angiogenesis and lymphangiogenesis in cancer. We must accurately elucidate the detailed mechanism by which *TrkC* induces angiogenesis/lymphangiogenesis and investigate the possibility that it activates other angiogenic/lymphangiogenic factors in OSCC.

Trks are the receptors for neurotrophins [7] and we observed co-expression of *TrkB* with *BDNF* and *TrkC* with *NT3* in OSCC. We also confirmed the co-expression of *TrkA* with *NGF*. In in vitro analysis, rhBDNF treatment restored cell growth and *VEGF*, *VEGF-C*, and *VEGF-D* expression and rhNT3 treatment increased invasive ability but did not change expression levels of the VEGF family in OSCC cells. We also found that rhNGF treatment restored *VEGF* expression. Although induction of apoptosis and activation of caspase-3 were observed in all Trks

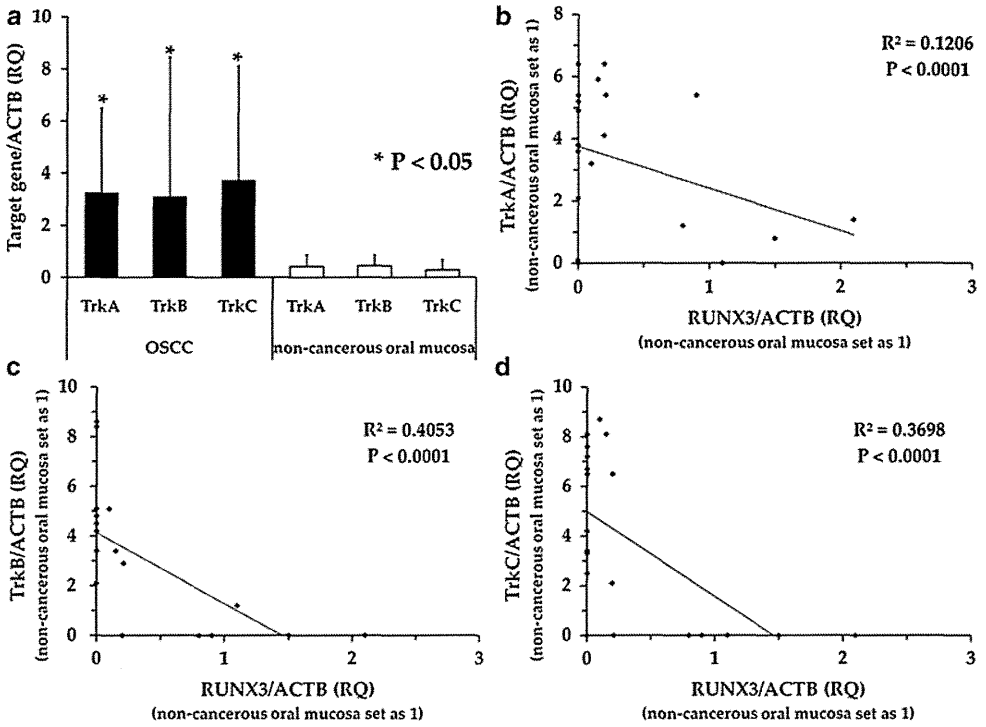

Fig. 6 Expression of *RUNX3* and Trks in OSCC cases. **a** Expression of Trks in non-cancerous oral mucosa and OSCC. Expression levels of Trks in OSCCs were higher than non-cancerous oral mucosa. **b–d** Relationship between expression of *RUNX3* and *TrkA* (**b**), *TrkB* (**c**), or *TrkC* (**d**) in 20 samples of OSCC. Trks expression were reversely associated with expression levels of RUNX3

Table 2 Relationship between gene expression of *Trks* and *VEGF* family

	TrkA		TrkB		TrkC	
	Low	High	Low	High	Low	High
VEGF						
Low	7	2	7	2	6	3
High	3	8	2	9	4	7
P value	0.0349		0.0124		NS	
VEGF-C						
Low	5	3	6	2	7	5
High	5	7	3	9	3	5
P value	NS		0.0399		NS	
VEGF-D						
Low	4	4	8	3	4	4
High	6	6	1	8	6	6
P value	NS		0.0092		NS	

NS not significant

siRNA treated cells, cell growth was only inhibited in *TrkB* siRNA treated cells. Further, inhibition of invasive ability was only found in *TrkC* siRNA treated cells. MMP-2 and MMP-9 makes a basal membrane disintegrate and one of the key factors in the invasion of the cancer cells [29]. In the present study, TrkC displayed regulated MMP-2 and MMP-9 secretion from OSCC cells. These results indicated that *TrkB* or *TrkC* was associated with not only resistance of apoptosis but also cell growth or invasion in cancer cells, respectively. Further studies are in progress to clarify the functional role of Trks in OSCCs.

RUNX3, a transcription factor belonging to the TGF-β superfamily [41], induces apoptosis [42] and is a novel tumor suppressor gene whose expression is decreased or abolished by CpG island hypermethylation of its promoter region in several tumors, including salivary gland cancers [10, 43]. Although it has been reported that *RUNX3* expression was attenuated by *TrkB* expression and that RUNX3 positively regulated expression of *TrkA* and *TrkC* in neuroblastoma and dorsal root ganglion neurons [8, 9], in this study, methylation of *RUNX3* in OSCC revealed a negative association between expression of *RUNX3* and expression of Trks. In this study, we used gingival mucosa, which was removed at the time of the extraction of mandibular wisdom teeth, for the non-cancerous oral mucosa; however, Tsunematsu et al. [44] reported that inflammatory oral epithelium expressed high levels of *RUNX3* compared to the non-inflammatory epithelium. The reason for the discrepancy between our present results and other previous reports may be accounted for by our use of inflammatory oral mucosa for the control.

In conclusion, We clarified TrkB and TrkC are strongly associated with angiogenesis, lymphangiogenesis, tumor progression, nodal metastasis, and poor prognosis and also found that Trks expression are regulated by methylation of *RUNX3* in OSCC. Tumoral vessels are irregular, making it difficult to deliver anti-cancer drugs [31, 45]. Recently, it has been proposed that normalization of tumoral vessels could improve the effectiveness of anti-cancer therapy