DUSP1 Phosphatase Regulates the Proinflammatory Milieu in Head and Neck Squamous Cell Carcinoma

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Abstract

DUSP1 is a dual-specificity phosphatase that regulates mitogen-activated protein (MAP) kinase activity. Studies have associated loss of DUSP1 expression with certain cancers, but there has been no report of a mechanism by which this supports tumor progression. In this study, we found DUSP1 mRNA and protein decreased in human head and neck squamous cell carcinoma tissues compared with adjacent nontumor controls. To evaluate the impact of this difference, we compared the susceptibility of Dusp1-deficient mice with oral squamous carcinogenesis induced by 4-nitroquinoline 1-oxide. Dusp1-deficient mice displayed enhanced disease progression, characterized by advanced onset, histologic stage, and tumor burden. In a syngeneic model of tumor progression, subcutaneous injection of EO771 cells formed faster-growing tumors in Dusp1-deficient mice, an effect abrogated by inhibition of p38 MAP kinase with SB203580. Histologic and quantitative assessments demonstrated increased inflammation and deregulated chemokine and cytokine expression in Dusp1-deficient tumor tissues. Specifically, proinflammatory cytokine IL1β was elevated. IL1β production was recapitulated ex vivo in primary bone marrow–derived macrophages from Dusp1-deficient mice. Together, our results clearly establish the role of Dusp1 as a tumor suppressor gene that regulates cancer-associated inflammation. Cancer Res; 74(24): 1–7. ©2014 AACR.

Introduction

Inflammatory cells and their secreted products influence cancer cell growth, angiogenesis, tissue remodeling, and more (1). Chronic inflammation is known to enhance neoplastic processes, as in gastrointestinal and hepatocellular carcinomas (2). However, in other tumor types including head and neck squamous cell carcinoma (HNSCC), studies have identified immunosuppressive states characterized by infiltrating regulatory T and myeloid-derived suppressor cells (3). This dichotomy between enhanced proinflammatory inflammation and suppressed antitumor immunity highlights the need to understand complex functions of inflammatory cells in the tumor microenvironment and identify therapeutic targets in these distinctive pathways.

DUSP1 is a dual-specificity Thr/Tyr phosphatase that regulates mitogen-activated protein kinase (MAPK) signaling pathways by dephosphorylating p38 and JNK MAPKs (4). Dusp1-deficient mice are highly susceptible to immune challenge, such as lipopolysaccharide (LPS) in sepsis and inflammatory bone loss models, due to prolonged MAPK activity and exuberant cytokine production (5, 6). In bladder, prostate, and colon cancers, Dusp1 expression is elevated in early stages of disease, but lost in a majority of poorly differentiated and metastatic tissues (7). In the present study, we assess the impact of Dusp1 deficiency in a murine model of carcinogen-induced oral cancer. Tumor progression was also enhanced in a syngeneic subcutaneous injection of breast cancer cells, rescued by p38 inhibition. Increased susceptibility and disease burden of Dusp1-deficient mice, in addition to development of a highly inflammatory microenvironment, suggest DUSP1 plays a key role in negatively regulating tumor-associated inflammation, in part through expression of the inflammatory cytokine IL1β. To our knowledge, this is the first study to demonstrate a tumor suppressive role of DUSP1.

Materials and Methods

Animal models

Protocls were approved by Medical University of South Carolina (MUSC) Institutional Animal Care and Use Committee. Male and female Dusp1−/− and Dusp1+/+ mice of C57/129 mixed genetic background, ages 6- to 8-week-old, and weighing 18 to 22 g were treated with 4-nitroquinoline 1-oxide (4NQO), as previously described (8). Animals were euthanized at week 32 or when greater than 20% weight loss.
was documented. Dusp1−/− and Dusp1+/+ mice backcrossed to C57BL/6 background for 10 generations were used for subcutaneous syngeneic tumor cell injections. Mice ages 6 to 8 weeks received 5 × 10⁷ EO771 cells in 100 μL PBS in a subcutaneous injection over the right flank. Tumor volume (l × w²/2) was measured with digital calipers every two days, and animals were euthanized if tumor size exceeded 1,500 mm³. After tumors reached >50 mm³ (day 7), animals received daily intraperitoneal injections of 5 mg/kg SB203580 or dimethylsulfoxide vehicle.

**Histologic and FACS analyses**
Formalin-fixed paraffin-embedded tissues were used for histology and immunohistochemistry. Two pathologists, blinded to experimental group, evaluated sections for pathology and inflammation. Inflammation was scored on a 0 to 4 scale [0, normal mucosa; 1, minimal inflammation (occasional scattered granulocytes and leukocytes); 2, mild inflammation (scattered granulocytes with occasional infiltrates); 3, moderate inflammation (scattered granulocytes with patchy infiltrates); and 4, severe inflammation (multiple extensive areas with abundant granulocytes and marked infiltrates)], as previously described (9).

Immunohistochemistry was performed in EDTA antigen retrieval buffer, as previously described (6), using antibodies against CD11b (Abcam), F4/80 (Abcam), and Ly6G (Novus Biologicals). DAB-positive cells in tumor-positive fields of view were acquired at ×10 magnification and quantified using Viziopharm acquisition and analysis software, and expressed as the number of positive cells in each histologically defined area. Single-cell suspensions were generated from spleen and cervical lymph nodes from tumor-bearing mice for flow cytometry. Cells were stained according to manufacturer’s protocol against CD11b-APC, Ly6G-FITC, Ly6G-Pacific Blue, and F4/80-PE with at least 10,000 events analyzed by Miltenyi MACSQuant cytometer and software.

**Primary bone marrow–derived macrophage isolation**
Bone marrow cells were obtained from 8- to 12-week-old mice, as previously described (6). Macrophages were primed with LPS from Aggregatibacter actinomycetemcomitans (strain Y4, serotype B) followed by treatment with ATP or nigericin (Sigma-Aldrich), as previously described (10).

**Human tissue samples**
Snap-frozen tissues from patients with HNSCC were acquired from MUSC Hollings Cancer Center Tissue Biorepository, according to protocols approved by MUSC Institutional Review Board. Tissue pathology and tumor percentage within representative frozen sections were verified by Biorepository research pathology.

**Western blotting**
Tissue and cell lysates were processed as previously described (11). Primary antibodies were directed against DUSP1 (Millipore), caspase 1 p20 (Millipore) and p10 (Santa Cruz Biotechnology), IL1β (Abcam), GAPDH, and α-tubulin (Cell Signaling Technology). Secondary antibodies were hors eradish peroxidase–conjugated anti-rabbit antibodies (Cell Signaling Technology).

**Gene expression**
Gene expression was determined using probe-primer TaqMan sets for delta-delta Ct calculations: Ptprc, IL1b, Gapdh, 16s rRNA, DUSP1, and ACTB. The nCounter analysis system (NanoString Technologies) was used to quantify gene expression in a custom panel. Each sample profile was normalized to geometric mean of four reference genes, Eif4a2, Oaz1, Ncln, and Gfra2, chosen for lowest variance across experimental samples.

**Statistical analyses**
For matched human tissues, a paired t test was performed. When comparing effect of genotype, a two-sample t test was performed using the Satterthwaite method for unequal variances, Mann–Whitney U test in absence of normal distribution, or pooled method for all other comparisons. For distributions of categorical scores, a Fischer exact test was used. A repeated measures mixed model, with random intercept and time effect, was used to test effect of genotype on weight gain and inhibitor treatment by genotype interaction. Survival analyses (event = tumor volume ≥ 1,500 mm³) with Kaplan–Meier estimates were performed using a log-rank test. Adjusted P values using Tukey–Kramer multiple comparisons method are provided when comparing least square mean estimates. All analyses were performed using SAS 9.4.

**Results and Discussion**
**DUSP1 expression is decreased in HNSCC samples**
DUSP1 mRNA and protein expression were lost in human oral squamous cell carcinomas compared with adjacent non-tumor control tissues (Fig. 1A and B). These findings were consistent with reports of DUSP1 downregulation or loss in other cancers (7). Expression of the proform of IL1b, an mRNA previously identified in salivary exosomes from patients with oral cancer (12), was also elevated in eight of the eleven pairs of HNSCC tissues (Fig. 1B).

**Dusp1 deficiency enhances susceptibility to carcinogen-induced oral cancer**
The development of cancer results from the interplay between genomic alterations, such as those induced by carcinogen exposure, and a supportive tumor microenvironment. To understand how DUSP1 deficiency alters oral cancer development and progression, wild-type and Dusp1-deficient mice were subjected to a carcinogen-induced oral cancer model, previously optimized to generate heterogeneous oral lesions that evolve into squamous cell carcinomas (8). This model has been described as generating little inflammation with low levels of COX-2 expression and stromal infiltrate in C57BL/6 mice at the time of invasive SCC development (8, 13). However, these studies propose an
inflammatory microenvironment develops in response to carcinogen-induced oral tumorigenesis, enhanced by Dusp1 downregulation, to promote disease progression. Although Dusp1-deficient mice are more susceptible to innate immune activation in sepsis and other models of acute inflammation (5, 6), its phenotype in tumorigenesis is not well defined.

Animals were exposed to 4NQO, a surrogate for chronic tobacco exposure, in drinking water for 16 weeks, and monitored for development of oral lesions (Fig. 2A).

Change in weight, as an estimate of disease burden, was reduced in Dusp1-deficient mice over time (Fig. 2B). Wild-type mice continued to gain weight, from 10 to 15 weeks, whereas weight gain in Dusp1-deficient mice stopped by 10 weeks, likely due to increasing tumor burden. Disease onset was accelerated in Dusp1-deficient mice by 2 to 3 weeks (Supplementary Fig. S1). No difference in weight gain was noted in Dusp1-deficient mice in vehicle treatment group compared with wild-type controls (Supplementary Fig. S2). At 32 weeks, significant elevation of
total tumor burden and enhanced histologic disease progression were found in Dusp1-deficient mice (Fig. 2C). Wild-type mice lesions were distributed across the spectrum of hyperplasia, dysplasia, and in situ and invasive squamous cell carcinomas, whereas the majority of Dusp1-deficient lesions were invasive squamous cell carcinomas (Fig. 2D).

**Dusp1 deficiency enhances tumor-associated inflammation**

Enhanced leukocyte abundance was observed, both histologically and by Ptprc gene expression in Dusp1-deficient mice (Fig. 3A). Nanostring analysis of tumor tissues did not reveal significant perturbations in markers of cellular infiltrate but suggested increased M2 macrophage polarization.
progression in this model highlights the utility in identifying squamous cell carcinoma. In this model, Dusp1-decreased chemokines was identified a link between loss of DUSP1 expression and advanced disease in vitro as previously suggested in patient and sera, IL1b (14, 15). The broad impact of Dusp1 deficiency increases IL1b expression

A pair of tumor tissues from Dusp1-deficient and wild-type mice, matched for histologic stage and inflammation score, were analyzed by targeted qPCR array to assess expression levels of 89 cytokines, chemokines, and receptors. The initial screen showed IL1b elevated 70-fold in the Dusp1-deficient sample (data not shown), then validated by qPCR in a larger set of tissues (Fig. 4A). Western blot analyses of caspase-1 and IL1B demonstrate high levels of both protein proforms, likely secondary to increased inflammatory infiltrate and IL1b transcript abundance in Dusp1-deficient mice (Fig. 4B). A strength of 4NQO exposure is its mirroring of human cancer progression from hyperplasia to invasive squamous cell carcinoma. In this model, Dusp1-deficient mice demonstrate accelerated tumorigenesis with increased inflammation and provide first evidence for a mechanistic link between loss of DUSP1 expression and advanced disease progression. Although a panel of increased cytokines and chemokines was identified by qPCR and Nanostring analyses, IL1B may be a major contributor, particularly in HNSCC as previously suggested in patient and in vitro studies (14, 15). The broad impact of Dusp1 deficiency on tumor progression in this model highlights the utility in identifying an upstream regulator of protumorigenic inflammatory response for therapeutic targeting with greater impact than biologics against a single cytokine.

Treatment of primary bone marrow–derived macrophages from Dusp1-deficient mice with LPS (100 ng/mL) resulted in significantly increased levels of IL1b mRNA (Fig. 4C). Despite the striking level of procaspase-1 detected in Dusp1-deficient tumor tissues, no significant elevation of caspase-1 expression or cleavage product was detected in primary cultures (Fig. 4D). This discrepancy may be due to differences in cellular constituents of tumor tissues between wild-type and Dusp1-deficient mice, as suggested by the increased numbers of inflammatory cells by histologic scoring and immunohistochemistry (Fig. 3), which can be normalized in ex vivo culture systems of primary macrophages.

Conclusions

Loss of DUSP1 expression has implications on biologic activities of many tumor cellular constituents, which are not fully dissected in these experiments. A recent survey of over 400 human HNSCC tissues revealed highly elevated p38 MAPK activity in nearly 80% of cases, with significant impact on cancer cell growth, lymphangiogenesis, and angiogenesis in xenograft studies (16). Immunohistochemistry of 4NQO-induced tumors in both wild-type and Dusp1-deficient mice shows the same trend of elevated expression of phospho-p38 but not ERK1/2 nor SAPK/JNK MAPKs in tumor epithelial tissues (Supplementary Fig. S5). No differences in phospho-p38 staining were seen in wild type of Dusp1-deficient tumor despite altered MAPK activity and expression in immunoblots of whole tissue lysates (Supplementary Fig. S6), suggesting a more critical role of MAPK signaling in infiltrating immune cells versus supporting stromal cells, such as fibroblasts and endothelial cells, must be addressed in future studies.

Although numerous reports have identified downregulation of DUSP1 across diverse tumor tissues, this is the first study to demonstrate a tumor suppressive role. Results from these in vivo and ex vivo studies also highlight a mechanism for upregulation of proinflammatory cytokine IL1B in oral cancer, previously shown to be elevated as mRNA in salivary exosomes (12) and secreted protein (14). Using a model mimicking genetic heterogeneity of human HNSCC following long-term carcinogen exposure, these findings support IL1B’s role as potential biomarker. Additional work must be done to address its impact on disease progression.

In light of cytokine and chemokine findings discussed above, implications of these studies may extend well beyond HNSCC, as DUSP1 expression has been shown to be dysregulated in other cancers, such as breast, and may be predictive of response to targeted therapies, such as cetuximab (7, 17). Genomic studies have not identified a...
common mutation or deletion, but a recent DNA methyl-
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hypermethylation in over 80% of oral cancer tissues (18).
Pharmaceutical intervention to induce DUSP1 expression,
with rosiglitazone and mapracorat, is currently being
explored in vitro with promising results (19, 20). In sum-
mary, results presented here demonstrate for the first time
that DUSP1 plays an important role within the tumor
microenvironment, regulating key cytokines such as IL1β.
Downregulation of DUSP1 leads to enhanced disease pro-
gression. Thus, restoring DUSP1 expression represents a
promising target of pharmacologic intervention and merits
further investigation as a suppressor of tumor-promoting
inflammation.

Figure 4. Dusp1 deficiency enhances IL1β expression in tumor tissues and primary macrophages. A, expression levels of IL1β mRNA by qPCR. n = 7–8 per group; **, P = 0.003. B, immunoblots of pro-caspase-1 and pro IL1β in tissue lysates. C, expression of IL1β mRNA after LPS stimulation (n = 4; P = 0.003). D, expression of IL1β and caspase-1 and cleavage products in macrophage lysates and supernatant.
Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

Authors' Contributions

Conception and design: X. Zhang, K.L. Kirkwood
Development of methodology: X. Zhang, H. Yu
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): X. Zhang, H. Yu
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): X. Zhang, J.M. Hyer, H. Yu, N.J. D'Silva, K.L. Kirkwood
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