

THE TRANSLATIONAL AND THERAPEUTIC POTENTIAL OF THE TUMOR MICROENVIRONMENT IN ORAL CANCER, 2nd Edition

EDITED BY: Keith David Hunter, Daniel Lambert and Ricardo D. Coletta
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THE TRANSLATIONAL AND THERAPEUTIC POTENTIAL OF THE TUMOR MICROENVIRONMENT IN ORAL CANCER, 2nd Edition

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Editorial: The Translational and Therapeutic Potential of the Tumor Microenvironment in Oral Cancer

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Keywords: tumor microenvironment, oral cancer, inflammation, fibroblasts, therapeutic potential

Editorial on the Research Topic

The Translational and Therapeutic Potential of the Tumor Microenvironment in Oral Cancer

It is now recognized that the tumor microenvironment (TME) can influence all the essential hallmarks of cancer, contributing to growth, progression and treatment response of tumors. The TME is composed of many cellular components including a vast repertoire of immune/inflammatory cells, blood and lymphatic vessels, peripheral nervous structures, fibroblasts and an array of non-cellular components such as extracellular matrix proteins, cytokines and growth factors. As the TME is a crucial part of the tumor, its components have become one of the key targets for tumor treatment. Although many strategies to target the TME have been developed, the results so far are disappointing, with limited impact observed on tumor burden or overall survival. This special collection encompassed 7 reviews and 2 original articles dedicated to the translational and therapeutic potential of the TME in oral cancer, highlighting opportunities and the need to concentrate efforts to overcome the barriers to develop new and efficient TME-targeted therapeutic strategies.

Several of the studies discuss emerging findings related to the tumor-infiltrating immune/inflammatory cells. It is becoming clear that a cause-effect relationship exists between inflammation and cancer, and Elebyary et al. performed an extensive review in the putative connection between oral carcinogenesis and the chronic inflammation associated with periodontitis. The authors provided evidence that the inflammatory milieu in periodontitis is ideal for cancer cell seeding, migration, proliferation and immune escape. Moreover, the authors showed evidence that dental biofilm (bacterial)-derived substances may contribute to the induction of permanent genomic alterations. Niklander extensively reviewed the literature to characterize the major TME-associated inflammatory cells and mediators that may contribute to proliferation and spread of oral cancer cells. This study also highlighted the rationale for detection of salivary inflammatory factors as biomarkers for the diagnosis of oral squamous cell carcinoma (OSCC).

Evasion of immune surveillance and induction of an immunosuppressive TME are common features of the head and neck squamous cell carcinomas (HNSCC), and one of the main immune escape mechanisms includes the overexpression of the programmed death ligand-1 (PD-L1) in the surface of the tumor cells. The article by Wondergem et al. reviewed the currently approved immune checkpoint inhibitors (drugs that block immune checkpoint proteins such as PD-L1) in HNSCC, including nivolumab and pembrolizumab (anti-PD-1 antibodies), and highlighted the potential benefits of modulating STAT3 and in PI3K/AKT/mTOR and Wnt pathways to boost the response to these inhibitors and prevent drug resistance. In this context, Dobriyan et al. reported the differences in the immune/inflammatory cells

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and cancer-associated fibroblasts (CAFs) between patients with OSCC treated with neoadjuvant pembrolizumab that displayed complete or incomplete remission. In the patients with complete remission, the tumor was replaced by a granulomatous type of inflammation, enriched with T lymphocytes, with approximately equal amounts of CD4⁺ and CD8⁺ cells, numerous CD68⁺ and CD163⁺ macrophages and absence of CAFs. The tumors with incomplete remission showed a moderate inflammatory response, with a variable CD4⁺/CD8⁺ ratio, and the presence of CAFs. These encouraging results warrant further investigation in large cohorts.

Hypoxia is an important feature of the TME, and the review by Chaudhary et al. explored its effects on the crosstalk between OSCC cells and immune cells. The authors reported that in the hypoxic microenvironment, OSCC cells and other TME components secrete immunosuppressive oncometabolites that regulate immune escape, via disturbing redox balance, mitochondrial function and ATP production through aerobic glycolysis.

The connection between inflammation and oral carcinogenesis was also reviewed in Niklander et al. by exploring the roles of interleukin 1 (IL-1) signaling, which has been shown to be activated in several types of tumors, in HNSCC. After reviewing important roles of the main IL-1 family members in the growth, differentiation and aging of normal oral keratinocytes, the authors showed that the dysregulated expression of IL-1 and IL-1R are associated with the acquisition of malignant phenotypes and reduced survival in HNSCC. The authors also provided evidence of the potential of IL-1 family members as diagnostic biomarkers and as attractive therapeutic targets for HNSCC. The participation of the IL-1/IL-1R axis in oropharyngeal squamous cell carcinomas (OPSCC) was investigated in Al-Sahaf et al.. Initially the authors demonstrated that HPV-negative OPSCC contained significantly more neutrophils than HPV-positive tumors. Applying a 3D cell culture model with HPV-negative or HPV-positive OPSCC cells in the presence of anakinra, an IL-1R inhibitor, the authors showed that both chemokine secretion and neutrophil recruitment are dependent on IL-1 β /IL-1R paracrine signaling. These features make IL-1/IL-1R axis promising biomarkers and therapeutic targets for HNSCC.

The role of CAFs in OSCC is extensively reviewed in Bienkowska et al.. Besides summarizing our current

understanding of CAF subtypes and function in controlling tumor proliferation, invasion, metabolic switch, angiogenesis, immune surveillance and therapy resistance, which all contribute to poor patient survival, the article discusses CAF-targeting therapies. The potential strategies discussed in the article include inhibiting CAF activation or function (e.g., inhibiting TGF- β or CXCL12/CXCR4 signaling pathways), “normalizing” CAF (e.g., NOX4 inhibitors) or killing CAF (e.g., FAP-based depletion). Although these strategies are promising, caution is required because those molecules are widely expressed in different conditions and tissues and their targeting may result in many side effects.

The participation of the sympathetic nervous system in the development and progression of HNSCC was explored in Vincent-Chong and Seshadri, by investigating the neurovascular interactions mediated via the adrenergic signaling. This study also brought a basis to support the therapeutic potential for HNSCC of directly targeting adrenergic signaling in tumor cells or indirectly targeting neurovascular interactions.

This Research Topic is a useful reference of the current understanding about the vital role of TME in oral cancer development and progression, highlighting its potential to development of new strategies for oral cancer treatment.

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Hypoxic Transformation of Immune Cell Metabolism Within the Microenvironment of Oral Cancers

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Oral squamous cell carcinoma (OSCC) includes tumors of the lips, tongue, gingivobuccal complex, and floor of the mouth. Prognosis for OSCC is highly heterogeneous, with overall 5-year survival of ~50%, but median survival of just 8–10 months for patients with locoregional recurrence or metastatic disease. A key feature of OSCC is microenvironmental oxygen depletion due to rapid growth of constituent tumor cells, which triggers hypoxia-associated signaling events and metabolic adaptations that influence subsequent tumor progression. Better understanding of leukocyte responses to tissue hypoxia and onco-metabolite expression under low-oxygen conditions will therefore be essential to develop more effective methods of diagnosing and treating patients with OSCC. This review assesses recent literature on metabolic reprogramming, redox homeostasis, and associated signaling pathways that mediate crosstalk of OSCC with immune cells in the hypoxic tumor microenvironment. The likely functional consequences of this metabolic interface between oxygen-starved OSCC and infiltrating leukocytes are also discussed. The hypoxic microenvironment of OSCC modifies redox signaling and alters the metabolic profile of tumor-infiltrating immune cells. Improved understanding of heterotypic interactions between host leukocytes, tumor cells, and hypoxia-induced onco-metabolites will inform the development of novel theranostic strategies for OSCC.

Keywords: hypoxia, immune cells, metabolism, microenvironment, oral cancer

INTRODUCTION

Squamous cell carcinoma (SCC) accounts for more than 95% of all cancers affecting the head and neck region, with high rates of associated mortality and morbidity that represent a major public health burden worldwide [1, 2]. In oral squamous cell carcinoma (OSCC), the predominant sites involved include the tongue and the gingivobuccal complex, and mortality rates can be substantially reduced by early detection and prevention strategies [3]. However, despite the development of several high-throughput multimodal diagnostic tools, early stage detection is still problematic; hence, 5-year survival rates in recurrent and metastatic disease remain extremely poor [4]. It remains unclear to what extent radiotherapy or chemotherapy exerts stimulatory or suppressive effects on host leukocyte responses [5]. The immune cell composition, function, and metabolic status are strongly influenced by the tumor microenvironment (TME) [6–8]. The complex dynamics of the OSCC microenvironment alter spatiotemporal distribution and effector

functions of infiltrating leukocytes to modify/diminish host defense mechanisms in favor of tumor cell survival [9, 10]. In particular, local oxygen depletion leads to the induction of reactive oxygen species (ROS) that promote cancer cell proliferation and drive autophagic/lysosomal loss of stromal caveolin-1 [an inhibitor of transforming growth factor- β (TGF- β) signaling] in cancer-associated fibroblasts (CAFs), resulting in tumor recurrence and metastasis and affecting patient survival [11–14]. Furthermore, the elevated levels of ROS result in detrimental stabilization of hypoxia-inducible factor (HIF)-1 α , which activates pro-angiogenic genes including vascular endothelial growth factor (VEGF) [15–17]. HIF-1 α acts as a master regulator of oxygen concentration to stimulate hypoxia-adaptive responses in cells. Immune signaling can be altered through the production of onco-metabolites that may further influence the clinical course of OSCC [18]. Consequently, a better understanding of how hypoxic stress, ROS generation, and onco-metabolites alter immune function in the TME is now a priority issue for the OSCC research community. The present article therefore reviews current knowledge of how redox factors alter leukocyte metabolism to promote the immune suppressive microenvironment of hypoxic OSCC.

HYPOXIA AND REDOX BALANCE IN THE ORAL SQUAMOUS CELL CARCINOMA MICROENVIRONMENT

Hypoxic TME alters local ROS generation and metabolic profile of both constituent tumor cells and infiltrating leukocytes [19–21]. Glycolysis is a metabolic process carried out in cell cytoplasm to generate two ATPs and pyruvates; this pyruvates serves as a fuel for tricarboxylic acid (TCA) cycle and oxidative phosphorylation (OXPHOS) under aerobic conditions [22, 23]. However, under anaerobic conditions, pyruvate is reduced to lactate, and this lactate is secreted into extracellular matrices [24]. The metabolic features of cancer cells are very heterogeneous where OXPHOS and aerobic glycolytic activities are impaired [25].

Intriguingly, cancer cells specifically express pyruvate kinase M (PKM)-2 that oxidizes and generates reduced nicotinamide adenine dinucleotide phosphate (NADPH) to maintain redox buffering; besides, this PKM-2 gene trans-activates HIF-1 α target genes, leading to a significant shift in metabolic activity and cancer cell signaling [26, 27]. In solid tumors like OSCC, increased production of ROS, cytokines, and CAFs stimulates the production of pro-angiogenic factors in an attempt to promote neovascularization and enhance survival (Figure 1) [28, 29]. In addition, the cancer cells undergo a metabolic shift from OXPHOS to glycolysis, which produces lactate and increases serum levels of lactate dehydrogenase (LDH), which has been linked with poor survival in patients with OSCC [30]. Tumor cells therefore have the capacity to utilize both OXPHOS and aerobic glycolysis for baseline metabolic activity and rapid energy production *via* the lactate pathway (Figure 1). In this regard, Otto Warburg proposed that due to mitochondrial defects, the predominant metabolism in cancer cells is aerobic

glycolysis rather than OXPHOS. Warburg's historic findings were called Warburg effect [31]. However, the metabolic coupling between OSCC cells and associated stromal cells is mainly determined by growth requirements; these effects are called dual/reverse Warburg effect [32, 33]. A previous NMR-based study suggested that OSCC can contravene the Warburg effect and implicated malonate (a competitive inhibitor of succinate) to induce drastic alterations in the TCA cycle that produce more fatty acid for membrane biogenesis in OSCC [34–36]. Among various glycolytic enzymes, alpha-enolase is crucial to produce phosphoenolpyruvate. As the mortality of OSCC is known to be due to metastasis, enolase in particular seems to play a major role in the malignant transformation of dysplastic epithelium in oral pre-cancer through promoting cell surface receptor enolase [37–40]. In addition to altered glucose metabolism, modified amino acid metabolism also occurs in OSCC. The amplified glutamine catabolism creates glutamine scarcity in hypoxic tumor core and leads to a dramatic histone hypermethylation [41]. In order to better understand the effects of hypoxia on OSCC, we will require new immunological paradigms that consider how dysregulation of crucial metabolic pathways can impact on both tumor growth and host leukocyte responses.

MITOCHONDRIAL HOMEOSTASIS AND IMMUNE DYSFUNCTION IN ORAL SQUAMOUS CELL CARCINOMA

In the hypoxic/acidic TME, reduced OXPHOS and electron transport chain (ETC) activity in local immune cells lead to altered mitochondrial membrane potential and impaired generation of ATP [42, 43]. The immune system not only kills cancerous cells but also modifies the TME in three phases—elimination, equilibrium, and escape [44]. The growing and transformed cells can be eradicated by immune response in the elimination phase; however, immune selection and reorganization create an immune resistant environment, namely, the equilibrium phase [45]. Consequently, immune surveillance escapes to kill tumor cells, and tumor cells grow in an uncontrolled manner [46]. In the last phase of cancer immunoeediting (i.e., “escape” phase), cancer cells produce large amounts of “pro-tolerogenic” kynurenine catalyzed by indoleamine 2,3-dioxygenase (IDO) processing of tryptophan [47]. Tryptophan catabolites have affinity to bind aryl hydrocarbon receptors (AhRs) of mitochondria, which persuade mitochondrial dysfunction in T cells and natural killer (NK) cells [48, 49]. Thus, under conditions of acute tryptophan depletion, central mitochondrial metabolic processes and synthesis of NADPH are disrupted such that infiltrating immune cells will undergo apoptosis rather than eradicating the tumor [50].

HETEROTYPIC IMMUNE MODULATION IN HYPOXIC ORAL SQUAMOUS CELL CARCINOMA

Hypoxic OSCC reprograms cellular metabolism in order to modify the repertoire of infiltrating immune cells toward a

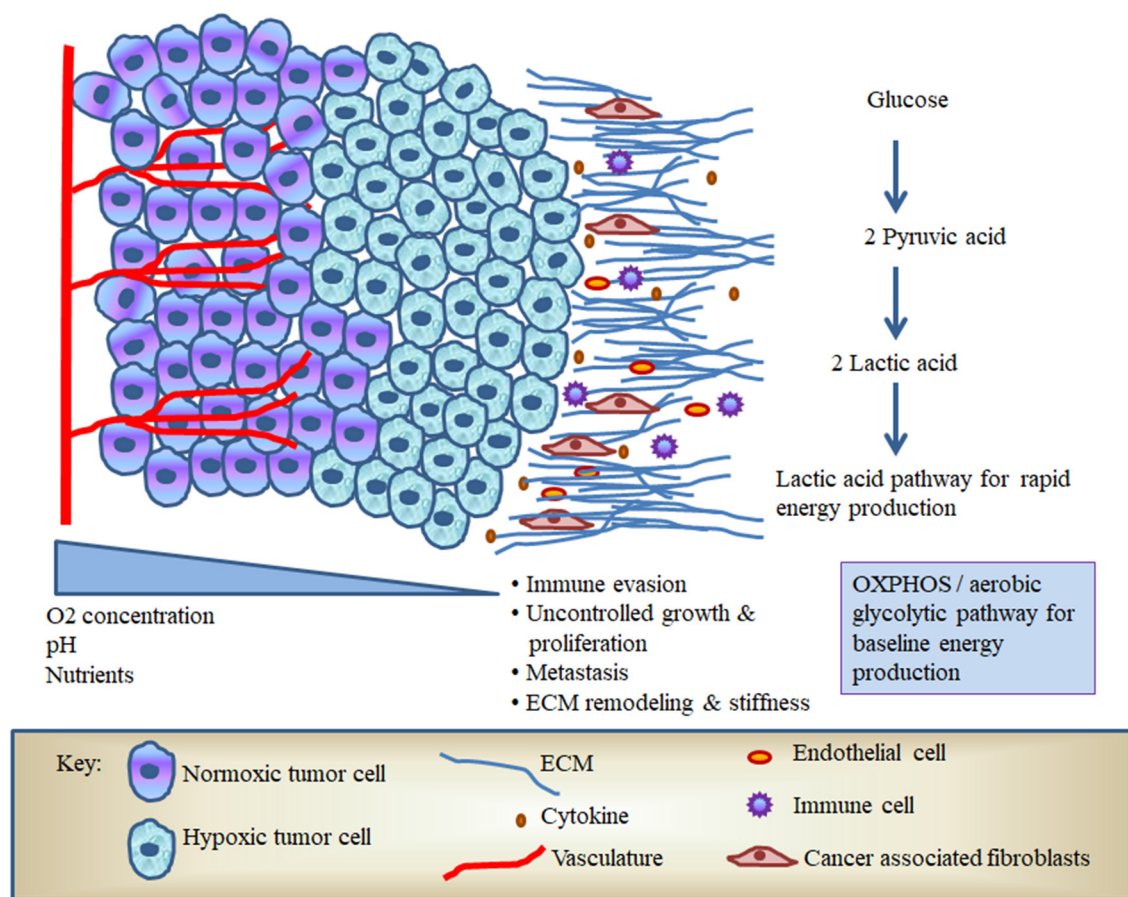


FIGURE 1 | The hypoxic microenvironment of oral squamous cell carcinoma (OSCC).

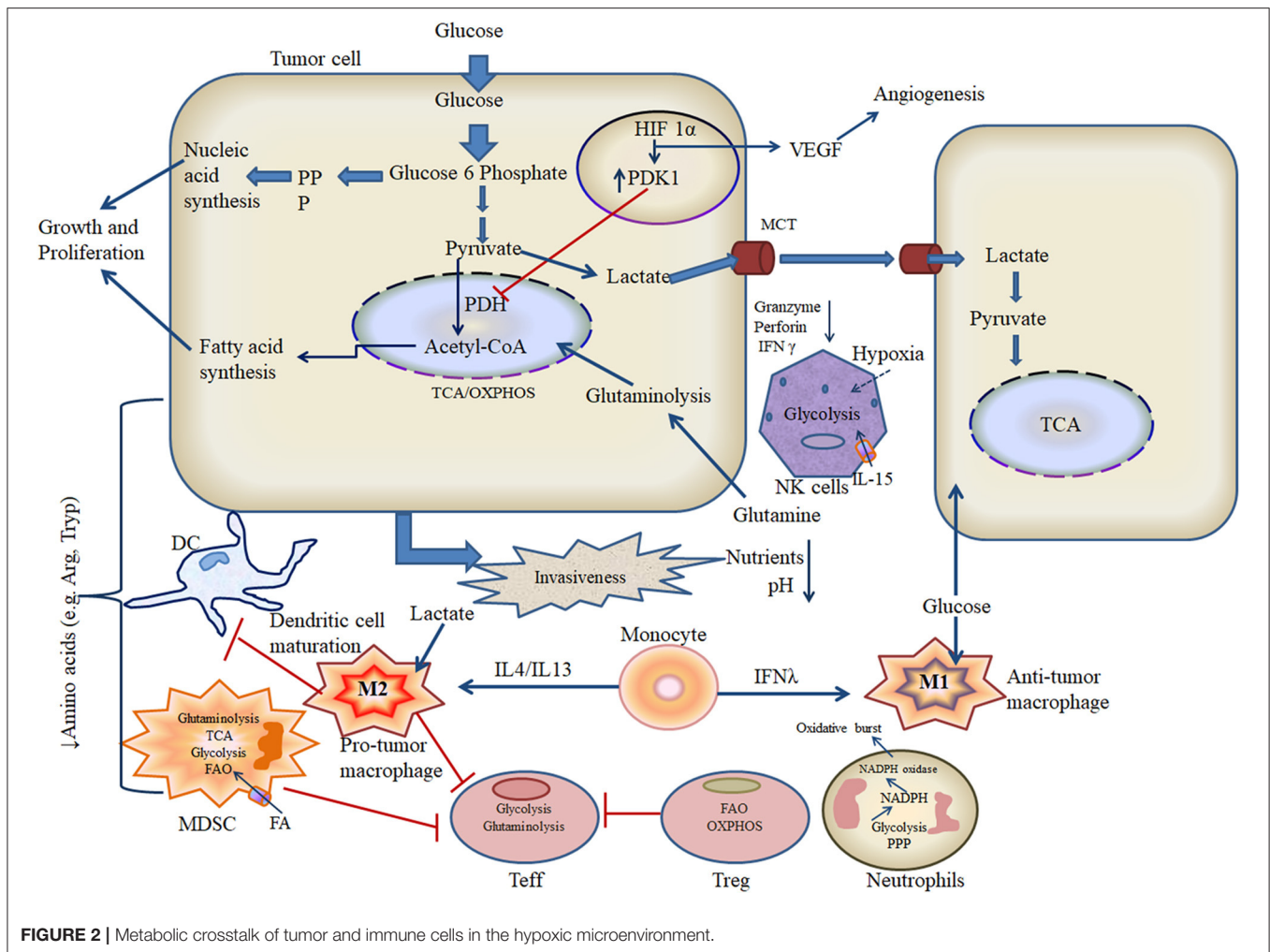
more tumor-permissive profile [51]. For example, macrophages located within hypoxic tumors tend to polarize toward an “anti-inflammatory” M2 phenotype, whereas cytotoxic T lymphocytes shift from glycolysis to OXPHOS-based metabolism (Figure 2) [52, 53]. Since essentially all OSCC tumors are subject to hypoxia upon reaching a certain mass, it is important to study how innate and adaptive immune cells alter their metabolism under these conditions in order to fully understand their influence on disease progression.

Hypoxia “Edits” Immune Signaling

The OSCC microenvironment has two forms of immune responses: innate and adaptive. Innate immune responses are non-specific and instant against pathogens, allergens, and non-self proteins. Phagocytes [myeloid-derived suppressor cells (MDSCs), neutrophils, monocytes, and macrophages] and NK cells are the main cells of innate immunity. Phagocytes engulf the foreign particles and digest through lysosomal enzymes, whereas NK cells kill the foreign bodies using altered major histocompatibility complex I (MHC class I) proteins, perforin, and granzyme-mediated apoptosis [54]. Dendritic cells (DCs) serve as a crucial link between innate and adaptive immune responses under physiological conditions. DCs process antigens and present them to T lymphocytes via MHC class I or II [55].

Adaptive immunity is composed of mainly T and B lymphocytes; B cells are professional antigen-presenting cells (APCs) that can activate T cells in tertiary lymphoid structures, allowing coordination of B and T cell responses in OSCC [56, 57]. In head and neck squamous cell carcinoma (HNSCC), regulatory T cells (T_{reg}) situated in the center of the tumor mass have been reported to be more strongly immunosuppressive than circulating T_{reg} [58]). T_{reg} can impede T effector (T_{eff}) cell function to reduce antitumor activity and contribute to poor prognosis in multiple types of cancer. Activated CD8+ T_{eff} are dominant antitumor cells that secrete granzymes, perforin, and pro-inflammatory cytokines, such as tumor necrosis factor (TNF) and interferon (IFN)- γ , whereas CD4+ T cells can either inhibit or promote tumor cell activity *via* the specific activities listed here [59, 60].

The macrophage subtypes M_1 and M_2 are activated in response to microbial and cancer-derived stimuli, respectively [61]. M_1 polarization of macrophages is induced by T helper type 1 (T_H1) cytokines such as IFN- γ and signaling through signal transducer and activator of transcription 1 (STAT1), whereas M_2 polarization is promoted by T helper type 2 (T_H2) cytokines such as IL-4 and IL-13 that trigger the STAT6 pathway [62]. Functionally, M_1 macrophages produce pro-inflammatory cytokines, ROS and reactive nitrogen species (RNS), while



mediating antigen presentation *via* MHC class II molecules. M₁ macrophages also actively phagocytose pathogens and are considered to suppress tumor development [63]. In contrast, M₂ macrophages are activated by cytokines including IL-4/IL-13, IL-10, TGF- β , and glucocorticoids that promote secretion of anti-inflammatory mediators. Further, M₂ macrophages inhibit the lytic activity of CD8⁺ cytotoxic T cells [55]. Despite their opposing roles, both M₁ and M₂ macrophages can coexist within the same tumor.

Tumor cells can secrete IL-10, colony-stimulating factor (CSF)-1, and various chemokines [C-C motif chemokine ligand (CCL)-2, CCL-18, CCL-17, and C-X-C motif chemokine ligand (CXCL)-4] that appear to favor M₂ polarization [64]. In addition to cytokine expression, hypoxic tumors can further direct macrophage phenotypes and responses via release of exosomes loaded with soluble factors and suppressive micro RNA [65]. In human HNSCC, the acidic TME has been reported to promote HIF-1 α activation and tumor-associated macrophage (TAM) expression of M₂-specific markers CSF1R and CD163, as well as driving concomitant production of arginase and VEGF [66, 67]. NK cells have the capacity to kill tumor cells and activate

antitumor T cell responses by secreting IFN- λ and cytotoxic molecules such as granzyme and perforin, but these activities can be severely restricted by the concomitant presence of MDSCs [68, 69]. MDSCs are known for their immune suppressive activity for both innate and adaptive immunity. The two subtypes of MDSCs are monocytic (M-MDSCs) and polymorphonuclear (PMN-MDSCs), which have variable capacities to inhibit the function of activated CD8⁺ T cells [70, 71]. MDSCs are thought to suppress T cell responses by expressing a range of inhibitory factors including arginase, inducible nitric oxide synthase (iNOS), TGF- β , IL-10, cyclooxygenase (COX)-2, and IDO [72]. HIF-1 α appears to play a key role in this immunosuppressive process by driving the expression of cytokines that promote MDSC infiltration of the tumor mass [73]. In addition, granulocyte MDSCs (G-MDSCs) are classified as T cell-suppressive neutrophils because of similar morphology and cell surface markers as mature neutrophils [74, 75]. Neutrophils migrate toward and infiltrate tumors under the influence of potent chemokines such as IL-8, after which these cells appear to enhance tumor proliferation and are correlated with poor survival in solid cancers [76, 77]. Several clinical observations indicate that

neutrophil activity is further modulated under the influence of the TME to assist cancer development [78]. However, tumor-associated neutrophils (TANs) may exert a dual role, since these cells appear capable of promoting either CD8⁺ T cell activity or tumor progression, depending on the prevailing level of TGF- β within the TME [79].

Likewise, with the polarization of TAMs, TANs exhibit two polarization phenotypes, i.e., N1 (antitumor neutrophils) and N2 (pro-tumor neutrophils), where TGF- β signaling plays a vital role [80]. Obstruction of TGF- β signaling or type I IFNs activates N1 phenotype with accretion of TNF- α and type 1 IFN, whereas augmentation in TGF- β signaling leads to N2 phenotype with high levels of neutrophil elastase (NE) and arginase in oral cancers [81]. Immature DCs are activated by pathogen-associated molecular patterns such as toll-like receptor (TLR) ligands, thereafter migrating to lymphoid organs and presenting antigen to T cells in the context of MHC [82]. In this process, phosphoinositide 3-kinase (PI3K)/Akt signaling pathway regulates the metabolic switch through inhibiting AMP-activated protein kinase and promotes glycolysis [83]. While adenosine signaling limits DC activation, ATP detection by P2YR and P2XR promotes DC migration and IL-1 secretion, respectively [84]. Hypoxic TME not only alters the innate immune signaling but also modifies adaptive immune signaling. Likewise, under hypoxic conditions, B cell caspase signaling is activated and kinase complex mammalian target of rapamycin complex 1 (mTORC1) pathway is reduced, leading to cell death via apoptosis [85]. B cells also secrete IL-10 under hypoxic stress; however, in-depth molecular pathway is not well-characterized [86]. The role of HIF-1 α transcription factor in tumor-infiltrating T cells remains unclear [87]. However, in cancer cells, HIF-1 α interaction with hypoxia response element (HRE) in the programmed cell death ligand 1 (PD-L1) promoter can trigger rapid expression of this immune checkpoint molecule, which is also capable of signaling more effectively in the lactate-rich TME [59, 88]. PD-L1 ligation of programmed cell death protein 1 (PD-1) on T_{eff} can inhibit T cell receptor (TCR) signaling and attenuates the PI3K/Akt and Ras/mitogen activated protein kinase (MEK)/extracellular signal-regulated kinase (ERK) pathways to restrict antitumor responses [89, 90]. Accordingly, antibodies targeting the PD-1: PD-L1 axis and other immune checkpoints have the ability to restore glucose levels in the hypoxic TME and have proven highly effective in the treatment of OSCC [91–93]. In particular, abnormal metabolic processes within cancer cells can generate neo-antigens that are presented by MHC class I molecules on the cell surface of antigen-presenting cells for recognition by CD8⁺ cytotoxic T cells [94].

Hypoxia Modifies the Resting Metabolic Status of Immune Cells

The resting metabolic status and associated effector functions of local immune cells play vital roles in determining the nature of host antitumor responses. In particular, glucose transport regulates pyruvate flow into the TCA cycle and is essentially

“rate-limiting” for host immunity, since leukocytes typically require rapid energy generation in order to achieve full activation. The hypoxic TME is a key driver of M₂ polarization in infiltrating macrophages likely via the expression of specific cytokine signals that activate nuclear factor (NF)- κ B, although the underlying mechanism has yet to be precisely defined in OSCC [95, 96]. Like other myeloid lineage cells, macrophage mitochondria can generate both superoxide and NO, which react to form the powerful oxidant peroxynitrite, which is highly toxic to cancer cells [97, 98]. While some investigators have reported that mitochondrial ROS (mROS) stimulate macrophage expression of pro-inflammatory cytokines, other researchers have instead observed the induction of an anti-inflammatory phenotype; hence, further study is required to fully understand these events [99–102]. The glycolytic reprogramming of TAM is regulated by oxygen sensors including prolyl-hydroxylases (PHDs) and is accompanied by proton pumping and acidification of M2 macrophages that subsequently impair antitumor responses [103]. Similarly, while resting NK cells typically utilize OXPHOS, exposure to high doses of tissue damage-associated cytokine IL-15 stimulates conversion to glycolytic activity [104]. For tumor-infiltrating neutrophils, the principal metabolic pathways employed are aerobic glycolysis and the pentose phosphate pathway (PPP), which support chemotaxis and microbicidal activities, respectively (Figure 2) [105]. Metabolic shift toward PPP is also required for formation of neutrophil extracellular traps, which envelope and attach to the circulating cancer cells and expedite metastasis to distant sites [106]. Tumor-associated MDSCs predominantly utilize fatty acid (FA)- β oxidation (FAO) and thus display high rates of oxygen consumption (Figure 2) [107]. In the hypoxic TME, MDSCs display potent immunosuppressive activity, which depends on the endoplasmic reticulum (ER) stress response transcription factor CCAAT-enhancer-binding protein homologous protein (CHOP) [108]. DCs are the critical components of the immune system against cancer as they have robust antigen-presenting ability to educate T cells [109, 110]. Upon microbial stimulation, DCs typically shift from OXPHOS to glycolysis; however, in TME, DCs promote immune suppression through galectin-1 [111]. In this regard, how metabolic profiles influence DC function and tumor progression *in vivo* is not yet well-defined [56, 112]. Activated B cells can secrete antibodies that can bind and induce tumor cell killing, but these processes can be strongly influenced by mitochondrial generation of ROS and heme synthesis. While the presence of CD20⁺ B cells within the TME indicates a good prognosis in lung cancer, gastric cancer, and melanoma, the role played by B cells in HNSCC has yet to be fully investigated. Variable hypoxia across the developing OSCC tumor is thought to alter tissue distribution of local B cells, which generate immune complexes and produce cytokines that then modify myeloid cell function to assist tumor progression [113]. B cells utilize glycolytic metabolism during early development in the bone marrow. Later survival, maturation, and functional activity of B cells are instead regulated by HIF-1 α and depend on glucose transporters and phosphofructokinase. The oncogenic Myc expression in B cells hindered the oxidation of acetyl-CoA in TCA cycle as it persuades lactate dehydrogenase for conversion

of pyruvate (glycolysis intermediate) to lactate [114]. Naive T cells employ OXPHOS and fatty acid metabolism before shifting glycolysis in order to support T_{eff} functions [112]. Memory T cells also depend on OXPHOS for energy generation in the resting state, whereas T_{reg} favor fatty acid oxidation. It is noteworthy that while glycolytic metabolism predominates among T_{eff} and T_{reg} , both populations have been observed to maintain OXPHOS within the TME (Figure 2), which may contribute to detrimental cancer-associated inflammation, further mutation, and eventual metastasis [115, 116]. Metabolic alterations in the T cell pool may also impede the differentiation of T_{eff} while increasing the generation of T_{reg} and “exhausted” populations, thus further supporting cancer evasion of host immunity [50].

Hypoxic Oral Squamous Cell Carcinoma Produces Immunosuppressive Onco-Metabolites

The metabolic products of cancer cells (onco-metabolites) are intimately linked with the control of the immune cell function [117]. For example, the microenvironment of OSCC is characterized by hypoxia, low pH, and elevated lactate levels, which disturb ETC operation and leads to deposition of citrate and succinate [21]. Citrate is converted into acetyl-CoA and utilized in several biosynthetic pathways. Oxidation of succinate produces ROS and promotes HIF-1 α activation. Hypoxia-generated lactate also drives macrophage differentiation toward an M2 phenotype [118]. TAMs are unable to utilize extracellular arginine due to rapid enzymatic breakdown by arginase and must instead use extracellular glutamine to produce this “semi-essential” amino acid [119]. TANs also produce high levels of arginase to disrupt TCR signaling. Increased lactate concentration in the hypoxic TME favors decreased NK cell expression of granzyme/perforin and Nkp46, leading to reduced anticancer cytolytic activity (Figure 2) [120]. The nuclear factor of activated T cells (NFAT) has also been implicated in downregulation of NK cell activity *via* an increase in cancer-associated lactate dehydrogenase expression [121]. Other hypoxia-induced onco-metabolites such as adenosine and lactic acid have previously been reported to impair DC activation (Figure 2) [122]. The tumor-associated dendritic cells (TADCs) stimulate arginase, which then depletes arginine in the extracellular matrix (ECM) and arginine scarcity impairs CD8+ T cell responses [123]. Some stable onco-metabolites (like kynurenine and quinolinate) along with specific cytokine milieu promote AhR signaling in non-functional T_{reg} , Foxp3+-induced T_{reg} (iT_{reg}), and T_H17 cells. These signaling pathways further de-differentiate T_{reg} , iT_{reg} , and T_H17 cells into functional iT_{reg} and endorse immune tolerance [124, 125]. IDO contributes to the tolerogenic ability of DCs to inhibit T_{eff} functions and promotes T_{reg} activity [126, 127]. The by-products (highly reactive aldehyde) of anomalous lipid peroxidation (triggered by ROS) create ER stress on TADCs and lower antitumor responses [128]. In addition, acylcarnitine and 2-hydroxyglutarate (2-HG) have been identified as a prominent onco-metabolite in HNSCC [129]. This 2-HG skews T_H17 polarization and alters T_{reg} metabolism by promoting the OXPHOS and destabilizing HIF-1 α [130, 131].

IMMUNE-TUMOR METABOLIC SWITCH UNDER HYPOXIA

Tumor hypoxia is characterized by local tissue acidification and nutrient depletion, thereby creating metabolic competition and generating active biomolecules that influence cancer cell interactions with host leukocytes. Competition for key metabolites along with cholesterol esterification, release of adenosine, and expression of prostaglandin E2 inhibits effector T cells [132]. Hypoxic OSCC modifies pro- and antitumoral $\gamma\delta$ T cell populations *via* exosomes [11]. OSCC can also express a range of different TLRs, with high levels of TLR-2 and TLR-4 correlating with tumor progression and chemoresistance, respectively. HIF-1 can deregulate *TLR3* and *TLR4* in OSCC cell lines under hypoxia stress, leading to potent effects on tumor cell survival, proliferation, and metastatic potential [133].

CONCLUDING REMARKS AND FUTURE DIRECTIONS

Hypoxia-related metabolic stress inhibits the activity of host immune cells to support oncogenic transformation and inflammation in OSCC. The hypoxia signaling in immune cells not only alters the glycolysis but also modifies other metabolic pathways like amino acid, FAO, PPP, and TCA, resulting in onco-metabolite production. Further, these onco-metabolites disturb the redox balance, mitochondrial function, and ATP production through aerobic glycolysis in OSCC.

In future studies, it will be important to elucidate the correlation between spatial distributions of immune cells in hypoxic/non-hypoxic OSCC. Novel and advanced therapeutic approaches like interfering with HIF-1 α signaling in immune cells through antisense or small interfering RNA, modulating the metabolic status of immune cells through gene editing technology [clusters of regularly interspaced short palindromic repeats-caspase 9 (CRISPR-Cas9)], and designing new smart oxygen-sensitive chimeric antigen receptor (CAR) T cell may provide new insight to overcome the challenges associated with hypoxic OSCC in the future.

AUTHOR CONTRIBUTIONS

AC conceptualized, conceived, and wrote the manuscript. SB conceptualized and organized the review. NA guided and revised the manuscript. VR revised and approved the manuscript. DM guided, revised and approved the manuscript. GM guided to write, organized and revised the manuscript. All authors contributed to the article and approved the submitted version.

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The Crossroads of Periodontitis and Oral Squamous Cell Carcinoma: Immune Implications and Tumor Promoting Capacities

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Periodontitis (PD) is increasingly considered to interact with and promote a number of inflammatory diseases, including cancer. In the case of oral squamous cell carcinoma (OSCC) the local inflammatory response associated with PD is capable of triggering altered cellular events that can promote cancer cell invasion and proliferation of existing primary oral carcinomas as well as supporting the seeding of metastatic tumor cells into the gingival tissue giving rise to secondary tumors. Both the immune and stromal components of the periodontium exhibit phenotypic alterations and functional differences during PD that result in a microenvironment that favors cancer progression. The inflammatory milieu in PD is ideal for cancer cell seeding, migration, proliferation and immune escape. Understanding the interactions governing this attenuated anti-tumor immune response is vital to unveil unexplored preventive or therapeutic possibilities. Here we review the many commonalities between the oral-inflammatory microenvironment in PD and oral-inflammatory responses that are associated with OSCC progression, and how these conditions can act to promote and sustain the hallmarks of cancer.

Keywords: periodontitis, oral pathogens, inflammation, oral squamous cell carcinoma, innate immunity, tumor microenvironment

PERIODONTAL PATHOGENS AND THE HOST RESPONSES: WAR AND TRUCE

A strong correlative link exists between inflammation and the development and progression of many cancers. Approximately 20% of all human cancers have been related to chronic inflammatory conditions, raising speculation regarding the specific roles of inflammatory processes in driving carcinogenesis [1]. These highly-regulated multicellular responses involve a large network of both immune and stromal cells and result in major alterations in the abundance of reactive oxygen and nitrogen species, prostaglandins, cytokines, and chemokines within the microenvironment encompassing the cellular milieu in various tissues [2]. It can be inferred that initiation of tumorigenesis and tumor progression might be derived by these environmental modifications which can alter the cellular behavior and change the composition of the surrounding extracellular matrix.

In relation to the above, the putative role played by inflammation in tumorigenesis can be observed in the oral cavity [3]. The healthy oral cavity harbors an abundant commensal microbial community with varied microbial floral diversity. It represents one of the most ecologically complex niches within the human body where the oral microbiota–host equilibrium remains balanced in health conditions (truce) and shifts to disease state when immunoresponses are altered in retaliation to dysbiosis (war). Indeed, dysbiosis of the commensal oral microbiota and their subsequent invasion of the tooth supporting structures (e.g., the gingiva, periodontal ligament and bone) leads to the initiation and propagation of an inflammatory condition termed periodontitis or periodontal disease (PD) [4, 5].

PD is considered to be, by far, the most common inflammatory condition affecting the oral cavity and it has been designated as an enabling characteristic of cancer development [6–8]. The presence of PD has been correlated to the presence of several types of malignancies including but not limited to breast, pancreatic and colorectal cancers [9–13] (**Figure 1**). However, whether this is a correlative or a causative association is not clear, and further investigation of the potential role of PD in cancer pathogenesis and potential systemic mechanistic effects is required. One group pointed out that although the link between PD with oral and other cancers has been well-documented in systematic reviews, these are often of limited power, and further research is necessary to fully confirm this association [8].

An association between PD and OSCC, two conditions that co-exist within the oral microenvironment, has been confirmed in many studies, suggesting that the immunologically distinct oral setting in PD could support tumor progression [14, 15]. Based on this observation one might reasonably predict that the most common site of primary squamous cell carcinomas in the oral cavity will be the gingival tissue, from which periodontal disease arises, however this was found not to be the case. Other sites in the oral cavity such as the lateral border of the tongue and the floor of the mouth have been recognized as common sites for OSCC and account for the majority of primary lesions [16]. This does not rule out the involvement of PD in supporting pathogenesis of OSCC at these sites. The specific sites where OSCC is commonly manifested in the mouth are known to have a greater permeability to carcinogenic factors compared to other oral tissues, and therefore are more susceptible to pathogenesis upon exposure to carcinogens [17]. The gingiva is covered by a thick protective layer of keratinized mucosa, which renders it less permeable to external carcinogenic insults, thus making it less affected [18]. Since the lateral border of the tongue and the floor of the mouth are common locations for premalignant oral conditions, the development of malignancies at these same areas may be a reflection of this pattern [19, 20]. Potential mechanisms through which the environmental conditions in the oral cavity associated with the presence of PD could support the progression of these lesions to develop carcinomas are the primary focus of this review.

Periodontal pathogens can contribute to carcinogenesis at locations other than the gingiva especially at the most common site, the lateral border of the tongue. Based on its anatomical location, this area comes in direct contact with the lingual

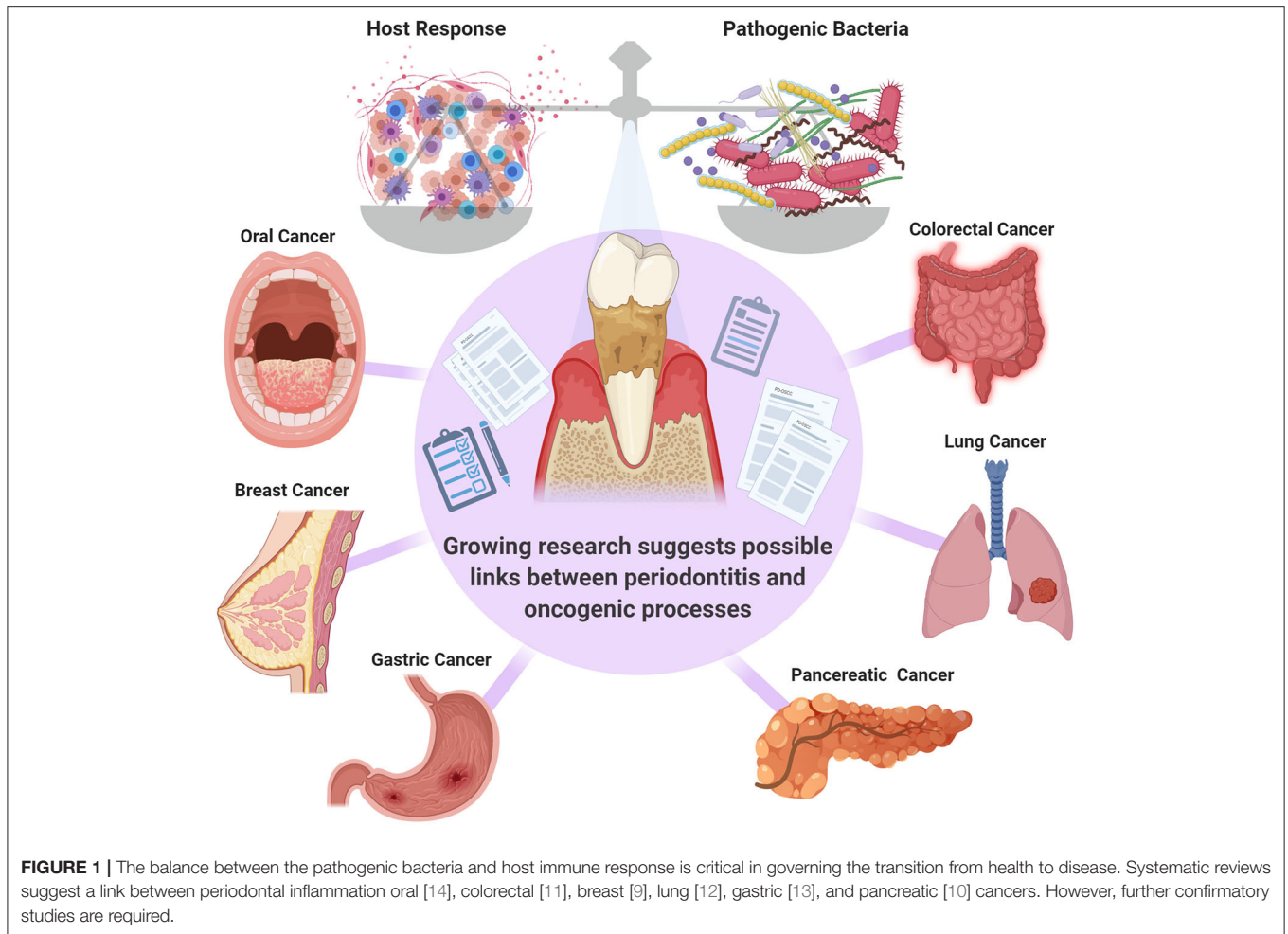
aspect of mandibular molars, sites that have been reported to have the highest index of plaque accumulation and gingivitis [21]. Therefore, it can be inferred that the mucosa of the lateral border of the tongue is constantly exposed to the damaging effects of pathogenic periodontal bacteria and their toxins. Certain bacterial species, such as the putative periodontal pathogen *Porphyromonas. gingivalis* and *Tannerella Forsythia*, where detected in higher amounts in both the subgingival regions and the tongue of periodontally affected patients [22]. This supports the model that PD is a potential contributing factor or an accelerator to the development of primary oral cancer. Further studies are required to determine whether or not periodontitis can directly promote initiation of OSCC.

The gingiva has been identified as the most common site for metastatic carcinomas when compared to all the other soft tissues of the oral cavity [23]. These tumors have been reported as metastatic lesions of other primary cancers from distant sites including lung cancers, renal cell carcinomas, hepatocellular carcinomas and breast cancers [24]. Furthermore, metastatic gingival carcinomas have been strongly linked to the presence of teeth, which highlights the importance of the dentoalveolar structure in this pathogenic process [23]. Thus, the deregulated environment of gingival tissue in PD may form an attractive milieu for the seeding and growth of these metastatic cells.

A recent study suggested that periodontal pathogens can be regarded as a risk factor for PD independent of other well-known risk factors such as smoking, alcohol and human papilloma virus (HPV) infections [25]. Moreover, it has been suggested that periodontal therapy may result in a dramatic decrease in the risk of developing future OSCC [3]. This type of reversibility argues strongly in favor of the presence of a mechanistic link between PD and the development of both primary and secondary OSCCs. Given the high mortality and poor survival rate of OSCC (~50%), more investigations are being undertaken to determine what could be the underlying mechanisms that link PD with an increased risk of OSCC development [26]. In this review, we will explore the possible role played by the inflammatory environment created by PD in relation to carcinogenesis.

Interaction of Malignant Cells and the Extracellular Matrix: Possible Links to the Development of Cellular Mutagenesis

When epithelial cells accumulate oncogenic mutations, complex interactions of these cells with their surrounding stroma contribute to initiation, progression and metastasis of OSCC [27]. It has been suggested that the deregulated microenvironment that exists in PD could contribute to various steps in carcinogenesis [28]. It has been well-established that chronic inflammatory conditions, including periodontitis, generate a mutagen-enriched environment [29]. Elevated levels of carcinogens such as reactive oxygen species (ROS) and bacterial-derived carcinogenic substances including volatile sulfur compounds, acetaldehyde, lactic acid, acetic acid, butyric acid, and isocaproic acid are associated with PD [30]. These compounds directly predispose the oral environment to promote host-cell DNA damage and the development of cellular



abnormalities that may give rise to malignant transformation. The genotoxic effect of PD on buccal mucosa was assessed in an attempt to estimate whether or not PD can be used as a marker for genomic instability in oral tissues [31]. In accordance with the severity of PD, more DNA damage was observed in the form of nuclear bud formation, and chromosomal instability in cells of the buccal mucosa [31]. One of the most recognized genomic alterations in PD is that of the *TP53* gene encoding the p53 tumor suppressor protein, regarded as the *guardian of the genome*. When p53 is upregulated it has destructive effects that compromise periodontal integrity, suggesting its contribution to tumorigenesis [32]. Interestingly, the frequency of *TP53* gene expression in neoplastic conditions is similar to that seen in PD. Overexpression of *TP53* was linked to the pathogenesis of oral malignancies including squamous cell carcinoma and Kaposi's sarcoma, and was suggested to be a poor prognostic marker [33, 34]. Furthermore, the role of PD in cancer initiation has been demonstrated in a murine model where the size and number of OSCC lesions induced by the carcinogen, 4-nitroquinoline-1-oxide (4-NQO), were increased when putative periodontal pathogenic bacteria were co-introduced (orally) as compared to germ-free mice that received the carcinogen only [35].

In terms of the contribution of PD to cancer progression, it has been reported that a key periodontal pathobiont *P. gingivalis* is capable of disrupting immune surveillance by activating STAT3 signaling [36]. This in turn induces the generation of immunosuppressive myeloid-derived dendritic suppressor cells (MDSCs) from monocytes, which help to sustain oncogenic cell-proliferation and sponsor immune escape [36]. Periodontal-associated pathogens can also interfere with the expression of the Notch signaling pathway, the latter playing a major role in the development of chemoresistance in mutated cells [37].

Bidirectional Relationship Between OSCC and PD

Recent findings suggest that the link between PD and OSCC could be reciprocal or bidirectional, with OSCC contributing to the development and/or the exacerbation of PD and *vice versa*. When the carcinogen 4-NQO was administered to rats in order to induce the development of OSCC, the group of rats that developed OSCCs upon 4-NQO exposure had significant spontaneous alveolar bone resorption compared to both the control group that did not receive 4-NQO and the treated-group that did not develop OSCC. Thus, this enhanced alveolar bone loss could be correlated to the development of squamous

cell carcinoma lesions in the oral cavity [38]. Interestingly, Pushalkar et al. had found significant variations in the microbiota diversity between tumor and non-tumor sites in individuals affected with OSCC [39]. In that study, tumor sites tended to have more distinct pathogenic microbial populations than those found at non-tumor sites in the same subjects. This microbial shift was suggested to induce a chronic inflammatory state at tumor sites, which can support the progression of adjacent tumors. This highlights the interconnectivity of both diseases, and how changes in the oral environment could induce conditions that are permissive to the development of either PD, OSCC or both.

Although the inflammatory oral microenvironment has been recognized to orchestrate a predominantly pro-tumor immune response, there are also paradoxical effects that can be anticarcinogenic one of which is that of the CXCL14 chemokine [40]. CXCL14 is normally expressed in healthy oral tissues yet it is decreased or absent in malignant oral epithelium [41]. CXCL14 was found to completely block OSCC establishment in SCID mouse xenografts [42]. A more recent study, explained that the anti-tumor functions exerted by CXCL14 are carried out by means of suppressing PD-L1 expression and NF- κ B mediated EMT [43]. Periodontal pathogen *P. gingivalis* is able to stimulate the expression of the CXCL14 from oral epithelial cells both directly and by antagonizing epidermal growth factor (EGF)-induced activation of the MEK-ERK1/2 pathway known to repress CXCL14 transcription [44]. This CXCL14 involvement in PD may be considered as one of the methods by which anti-tumor responses are supported. However, further research will be necessary to understand the complex interactions between PD and OSCC.

OSCC IMMUNE PERMISSIVE ENVIRONMENT INDUCED BY PERIODONTAL DISEASE

Intense focal influx of immune cells into sites affected by pathogenic bacteria leads to a cumulative build-up of their numbers within the oral environment [45]. Changes in the behavior of immune cells under the critical influence of pathogenic bacteria, or interactions between these cells and other immune-regulatory networks e.g., cytokines, chemokines, and growth factors can disrupt productive immune surveillance in PD [46]. Any “corruption” of the immune response could hypothetically permit the homing of metastatic tumor cells into these sites or possibly induce the development of primary malignant lesions. Interestingly, in PD many immune cells adopt behaviors or characteristics similar to those observed in immune cells recruited by tumors that favor their progression. Hence, the “re-education” of dysfunctional oral immune cells by means of periodontal therapy could conceivably lead to beneficial results insofar as the development and/or treatment of OSCC are concerned. Herein, we discuss how cells of both the myeloid and lymphoid lineages are affected by PD, and how they contribute to the etiopathology of OSCC (Figure 2).

Myeloid Derived Cells PMNs

Neutrophils, also called polymorphonuclear leukocytes (PMNs), are the most abundant primary innate immune responders in the gingival crevice and periodontal pocket. They play an indispensable role in maintaining periodontal health and their greatly upregulated recruitment is observed in response to oral microbial dysbiosis [47–50]. PMNs have been implicated in prolonging the extent and severity of inflammatory PD leading to substantial damage to bone and soft connective tissues surrounding the teeth [51, 52]. In cancer, different PMN subsets with either anti-tumor or pro-tumor characteristics have been identified. This has led to the emergence of a new classification of PMNs, based on anti-tumor (N1) and pro-tumor (N2) cancer-associated PMNs [53]. In OSCC, it was noted that an increase in the oral PMN infiltrate is correlated with a reduced survival rate and an increased recurrence rate [54]. Furthermore, co-cultures of peripheral blood PMNs and OSCC cells were found to increase the invasiveness of the cancer cells, independently of direct cell contact [55]. Hence, the presence of abundant pro-inflammatory PMNs in PD could contribute to the pathogenesis of oral cancers.

In PD, changes in oral PMN phenotype were observed. This was characterized by PMNs that survived longer in the oral cavity due to upregulation of anti-apoptotic genes of the Bcl-2 family, and downregulation of pro-apoptotic transcripts [56]. Moreover, direct interaction between PMNs and regulatory T-cells (Tregs) that had been stimulated with lipopolysaccharides (LPS) promoted an abnormal production of the immunosuppressive cytokine IL-10 by the PMNs, and these IL-10-producing PMNs were observed in the oral cavity of patients with PD [57]. Interestingly, similar, longer lived, IL-10+ PMN phenotypes were identified in the tumor microenvironment (TME) of OSCC [58, 59]. These PMNs displayed a clear upregulation of the anti-apoptotic genes of both the Bcl-2 and NF- κ B families upon entering the TME and transitioning into N2 tumor associated neutrophils (TAN).

Another common feature between PMNs associated with both OSCC and PD is the downregulated expression of PMN gelatinase-associated lipocalin (NGAL) [60, 61]. The downregulation of NGAL observed in OSCC has been implicated in improving the survival of cancer cells while upregulating their ability to migrate and invade tissues. This is related to the activation of mTOR signaling and the suppression of autophagy as a result of reduced expression of LC3B [61]. The resemblance between PMN behavior in the microenvironment of both PD and OSCC, suggests that PMNs in PD can augment and potentiate the development of OSCC by exerting the same pro-tumor functions as TANs in the oral microenvironment.

PD deregulates the expression of many PMN-secreted products, which can impair certain PMN functions and provide a favorable environment for cancer cells to thrive. For instance, the defensins, human neutrophil peptides 1, 2 and 3 (HNPI-3), are known to induce cytolytic effects on their target cells, particularly cancer cells. It has been suggested that higher levels of defensins might promote preferential oncolysis and provide a better host response to tumor invasion (i.e., prevention). Suppression

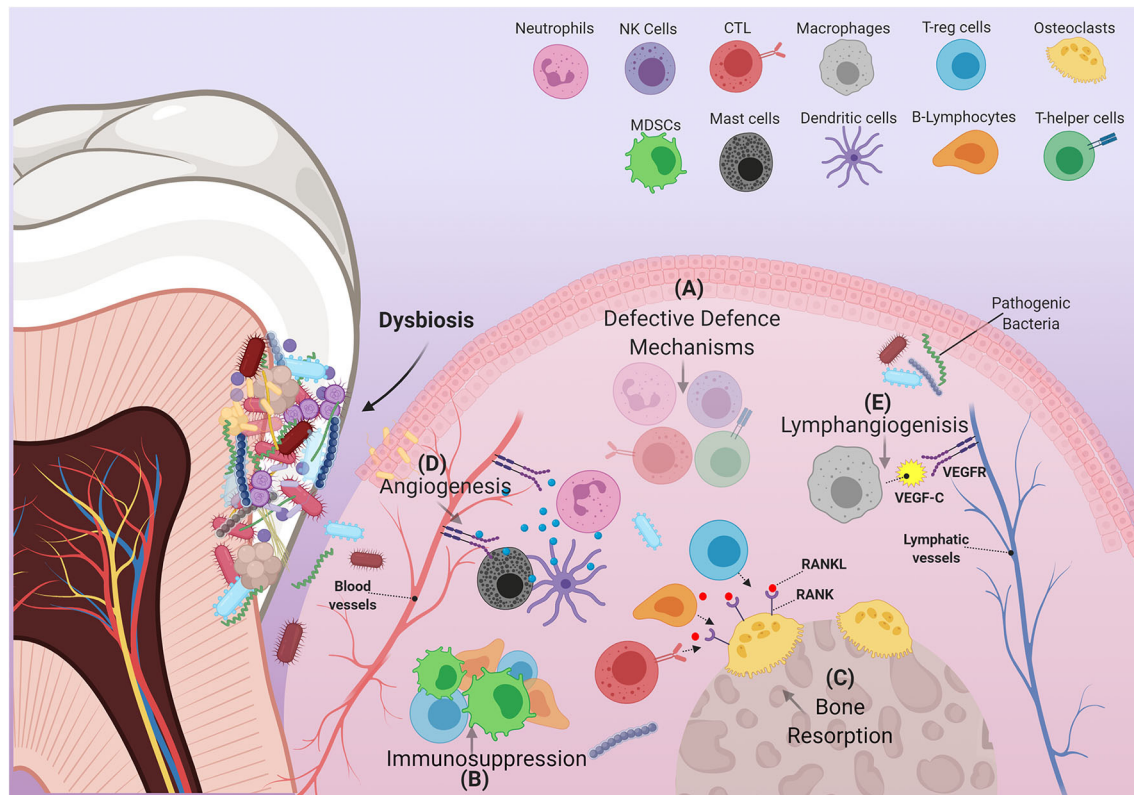


FIGURE 2 | Schematic illustration of immune cells in inflamed periodontium. The figure shows how the immune cell infiltrate in PD can exert several alterations within the gingival tissue environment that are able to support the pathogenicity of OSCC. **(A)** In PD, many immune cells fail to carry out some of their characteristic defensive functions. These cells include, but are not limited to, (1) Neutrophils: decreased defensins and defective NETs formation, (2) cytotoxic T-lymphocytes: decreased IFN- γ production, (3) T-helper cells: suppressed effector Th1 response, and (4) natural killer cells: reduced granzyme and IFN- γ production. **(B)** Immune suppressive cells: MDSCs, T-regs, B-regs (a subtype of B-lymphocytes) are recruited to the site of inflammation, disrupting immune surveillance. **(C)** Increased RANKL expression by several immune components including T-regs, B-lymphocytes and Cytotoxic T-lymphocytes, induces resorption of alveolar bone. **(D)** Expansion of the vascular compartment of the periodontium is mediated by several factors produced by certain immune cells. These include MMP-9, which is mainly produced by neutrophils and dendritic cells, as well as many angiogenic products released by mast cells (VEGF, tryptase, heparin, histamine, IL-8, basic fibroblast growth factor). **(E)** Macrophages contribute to the expansion of lymphatic vessels by producing VEGF-C.

of antimicrobial peptides HNP1-3 was observed in patients with PD [62]. This suppression could therefore be anticipated to cause a loss of PMN mediated oncolysis. Additionally, in PD, PMN-mediated expression of pro-angiogenic matrix metalloproteinase-9 (MMP-9) is accompanied by a substantial decrease in the expression of their inhibitors, tissue inhibitors of matrix metalloproteinases (TIMPs) [63, 64]. In combination, this unopposed upregulated MMP-9 expression can lead to conditions that are permissive for angiogenesis required for tumor growth and intravasation and therefore, progression of tumors such as OSCC.

In chronically inflamed gingival tissue, increased PMN-expression of a proliferation-inducing ligand, known as APRIL, was shown to increase the proliferation, survival, and invasion capacity of tumor cells in oral cancer [65]. An increased rate of tumor growth and aggressiveness was associated with APRIL-rich breast cancers compared to those with reduced expression of APRIL [66]. Other PMN products such as neutrophil elastase (NE), which have the capacity to degrade most extracellular

proteins, has been implicated as a biomarker in both PD as well as head and neck squamous cell carcinoma (HNSCC). A direct link between increased levels of NE in PD and its potential role as a co-factor in the initiation and advancement of OSCC has recently been established. A considerable increase in salivary levels of NE in patients with combined PD and OSCC, as compared to those affected by either PD or OSCC, highlights the important role of NE in contribution to oral cancer [67].

One of the strategies that PMNs use to counteract infectious agents is formation of web-like neutrophil extracellular traps (NETs) [68]. These extruded structures, generated by a process referred to as NETosis, are composed of chromatin and are able to trap pathogenic moieties and destroy them by delivering high concentrations of anti-microbial agents such as histones, proteases and PMN granule proteins [69]. Excessive NETosis, evident in exacerbated inflammatory conditions, has been linked to unfavorable consequences such as autoimmune diseases, thrombus formation and cancer metastasis [70]. In HNSCC, it has been proposed that monitoring NET levels can be a

successful approach to predict if patients are at a high risk of developing metastatic tumors [71]. PMN NETs are highly prevalent in PD, and may therefore stimulate the metastatic potential of oral cancer cells [49, 72]. Furthermore, NETs formed under the influence of PD were found to have defective functions. *P. gingivalis*, which can cleave the protease-activated receptor-2 (PAR2) on the surface of PMNs, was found to trigger excessive formation of NETs that lacked their characteristic bactericidal activities [73]. These NETs were unable to restrain and kill *P. gingivalis* and other pathogenic bacterial species, allowing them to thrive. Although it hasn't been extensively explored, it can be suggested that this defective function of NETs can also be beneficial to cancer cells, allowing them to escape PMN-mediated destruction.

Collectively, these findings indicate that PD is associated with functional alterations in the oral PMN population, which suppress PMN immune surveillance by modifying the production of many PMN-secreted products. These changes are not dissimilar to characteristics of the N2 pro-tumor PMN. Accordingly, in the presence of PD, the PMNs that are recruited to the OSCC TME could augment the progression of cancer instead of limiting its progression.

Macrophages

In addition to PMNs, macrophages play a central role in the immune response observed in PD and contribute to both the onset and resolution of inflammation [74]. Functionally, macrophages can be classified into two main phenotypes, M1 and M2, based on the type of activation they acquire upon interacting with the microenvironment at diseased sites. M1, or classically activated macrophages, differentiate in the presence of IFN- γ , LPS, or TNF- α ; and are the primary producers of pro-inflammatory cytokines, such as IL-1, IL-12, and TNF- α [75]. Additionally, these cells have potent anti-tumor capabilities and treatments that can induce tumor-associated macrophages to adopt an M1 phenotype hold potential therapeutic promise [76]. M2, or alternatively activated macrophages, are induced in the presence of IL-4, IL-10, or IL-13 [74]. They are involved in immunoregulation, tissue repair, and angiogenesis, and are linked to carcinogenesis and tumor progression [77].

Although PD is more often associated with elevated numbers of M1 anti-tumor macrophages [75, 78], this does not necessarily rule out the presence of M2 pro-tumor macrophages. In a recent study, the effect of periodontal inflammation on macrophages demonstrated the presence of increased numbers of M1 macrophages as well as elevated numbers of M2 macrophages [79]. Furthermore, when screening for changes in cytokine expression in gingival tissue derived from participants with PD, the M1 cytokines, TNF- α and IL-1 β , and the M2 cytokine, IL-10, were all significantly increased [79]. These findings have challenged the prevalent concept of macrophages being solely pro-inflammatory within the context of PD, and have proposed the presence of a more heterogeneous macrophage population in PD. Based on this, it cannot be assumed that changes in macrophages in the presence of PD will only favor the pro-tumor response.

Secreted factors produced by macrophages can play a role in the pathogenesis of OSCC. For instance, elevated levels of TGF- β 1 in the PD environment can induce vascular endothelial growth factor-C (VEGF-C) production by macrophages, which stimulates the proliferation of new lymphatic vessels through stimulation of VEGF receptor-3 (VEGFR-3) on lymphatic endothelial cells [80]. In the same context, inflammatory macrophages had been recognized previously to be able to transdifferentiate into lymphatic endothelial cells that express endothelial markers such as LYVE-1 and Prox-1, thereby integrating into lymphatic vessels promoting their expansion [81]. In cancer, this can have a negative impact on the overall prognosis for patients with OSCC, as increases in microvascular density might support metastasis of malignant cells to nearby and distant lymph nodes. This was shown when OSCC of the tongue was studied. In this regard, higher levels of VEGF-C were considered to predict poor cancer-specific survival [82].

Macrophage migration inhibitory factor (MIF) has been noted to play a role in both periodontitis and cancer. MIF is a well-known pro-inflammatory effector cytokine expressed by a variety of immune and non-immune cells including macrophages. In inflammation, it promotes the migration and recruitment of leukocytes to the infected sites in response to pathogenic stimuli. Investigations have recognized MIF as a central participant in the cancer-associated immune response, having the capacity to support the development of HNSCC by its pleiotropic roles in mediating hypoxia response, angiogenesis, and epithelial-mesenchymal transition (EMT) [83]. Moreover, gene inactivation of MIF receptor (CD74) or the use of MIF agonist ISO-1 resulted in a significant reduction in the proliferation of gastric cancer cells [84]. Therefore, the higher concentrations of serum and salivary MIF observed in PD might stimulate the proliferation, metastasis and invasion, of oral cancer cells into other tissues [85].

Myeloid-Derived Suppressor Cells

The expansion of immune suppressive cells, including myeloid-derived suppressor cells (MDSCs), and their accumulation at the sites of malignant lesions is one of the main mediators of cancer progression [86]. Not only do these cells contribute significantly to the immune response regulation, but they also provide an environment that is capable of sustaining angiogenesis, stemness, and metastasis [86]. Although these recently discovered cells have not been extensively studied in the context of PD, emerging evidence suggests that they are more involved in PD and in PD induced OSCC than previously suggested. Strains of *P. gingivalis* that express Mfa1-fimbriae were found to mediate immune escape by invading monocytes and inducing their differentiation into myeloid-derived dendritic suppressor cells (MDDSCs), which were characterized by being highly resistant to apoptosis [36]. Additionally, these cells appeared to be compatible with the immune suppressive environment created by the indoleamine 2, 3 dioxygenase (IDO) enzyme found at chronically inflamed sites including PD.

Furthermore, the expansion in the MDSC population has been linked directly to promoting the development of either primary or metastatic cancers in the oral cavity as follows. A

recent study revealed that *P. gingivalis* can induce differentiation of MDSCs from monocytes, and also invade oral pre-malignant lesions thereby inducing a substantial influx of MDSCs [87]. This is achieved by upregulating the expression levels of certain chemokines (CCL2 and CXCL2) and cytokines (IL-6 and IL-8) in dysplastic oral keratinocytes. Accordingly, this “biases” the immune system toward supporting oncogenesis. Hence, this suggests that patients with PD could be more susceptible to developing primary oral cancers from pre-existing oral dysplastic lesions.

It has been suggested that periodontal inflammation can shape the pre-metastatic immune microenvironment in the gingiva. In a very recent study, gingival fibroblasts showed increased production of IL-1 β upon sustained exposure to LPS, which resulted in increased expression of CCL5, CXCL12, CCL2, and CXCL5, potent chemotactic factors for MDSCs [88]. This generates a pre-metastatic niche at sites of inflammation, which promotes metastatic events, for example, progression of breast cancer to head and neck tissues [88].

Dendritic Cells

Dendritic cells (DCs) are specialized antigen presenting cells (APCs) that can be activated by different stimuli including bacteria, viruses, and damaged tissues, thereby potentiating their phagocytic activities [89]. These cells have been linked strongly to the induction of T cell responses and therefore it has been suggested that they play a key role in mediating anti-tumor immunity [90]. However, compelling evidence indicates that the function of DC is impaired in cancer. Decreased function of DC is thought to be related to the presence of immunosuppressive conditions that induce a network of factors capable of suppressing these cells [91]. A greater understanding of how DCs respond to PD is necessary in order to determine how this can contribute to tumor immune responses.

Periodontal pathogens can, in many ways, alter the response of DCs to suppress the local immune surveillance mechanism, allowing them to invade periodontal tissues. For example, LPS derived from *P. gingivalis* has been shown to induce alterations in the MMP-9/TIMP-1 ratio in DCs similar to those described previously for PMNs. MMP-9 is expressed in significant amounts in concert with reduced production of TIMP-1 resulting in a higher MMP-9/TIMP-1 ratio that favors local tissue destruction. In laryngeal cancer, higher levels of MMP-9 were correlated with increased counts of tolerogenic DCs [92]. These tolerogenic DCs have altered functionality and produce immune-regulatory molecules, including retinoic acid and TGF- β , so that they appear to induce the development of laryngeal cancer specific T-regs that suppress the production of the cytotoxic T-lymphocyte effector molecule granzyme B [93]. Moreover, it was found that *P. gingivalis* strains having minor fimbria can bind to the DC-SIGN receptor expressed by DCs [94]. This binding is followed by internalization of these bacterial strains which was shown to alter DC function, retarding their maturation and minimizing their production of inflammatory cytokines. This also results in a Th2-biased weak immune response that promotes immune escape [94].

Plasmacytoid dendritic cells (pDCs) are a unique subset of DCs that can detect the nucleic acids of pathogenic microorganisms and respond rapidly by releasing an enormous amount of type 1 interferon (INF) [95]. The negative regulation of these cells by TAM signaling was found to be repressed in PD, which explains their increased influx in the gingiva of patients with PD [96]. Later studies have indicated that the number of tumor-infiltrating pDCs is linked with lymph node metastasis and poorer prognostic outcomes in patients with OSCC as these cells were dysfunctional with relatively low production of IFN- α , IL-6, and TNF- α as compared to circulating pDCs [97]. This functional impairment came as a result of many inhibitory factors present in the TME including VEGF, TGF- β , and IL-10 which inhibit the activation of pDCs and prevent antigen presentation. Therefore, although PD appears to induce higher pDC recruitment in oral cancer, these cells are functionally repressed by the TME, and therefore fail to contribute to anti-tumor immunity. Therefore, current results support the model that PD suppresses anti-tumor functions of DCs, indicating that reduction in periodontal inflammation could restore anti-tumor functions of DCs.

Mast Cells

Mast cells (MCs) are immune cells linked principally to allergic reactions, but they are also functionally associated with many other pathological conditions including cancer and PD [98, 99]. Morphological features include their distinct cytoplasmic granularity related to the presence of unique basophilic granules that are rich in inflammatory mediators including histamine and heparin [100]. These cells reside in all the connective tissue components of the oral cavity, including the periodontal ligament and gingiva, and are distributed mainly along the available vasculature [101]. Their unique location, in close proximity to other immune responders, allows them to rapidly take action whenever they sense changes within their immediate microenvironment. In PD, constant irritation from the plaque biofilm stimulates MCs to proliferate, which denatures the composition of the normal gingival tissue [102]. This increase in number results in differential expression of MC mediators within the oral connective tissues, and the subsequent functional consequences of this have the potential to contribute directly to the pathologic processes of OSCC.

Other than the basophilic granular content of MCs, they have the ability to synthesize and express many mediators that induce several characteristic functions; such as the chymase and tryptase proteolytic enzymes. In PD, the production of MC chymase has the ability to activate many factors including collagenase, MMP-3, and MMP-9 which are known to induce disruption of the basement membrane [102, 103]. As such, the increase in MC chymase levels can reflect one potential means by which MCs promote the progression of oral malignant and premalignant lesions. Although it has not been studied in OSCC, the increase in levels of chymase has been shown to influence prostate cancer progression via downregulation of expression of signals for the androgen receptor expressed in prostate cancer cells thereby increasing the invasive ability of these cells [104]. As for tryptase, the severity of periodontal inflammation was found to be

correlated positively with its expression levels [105]. This elevated expression can impact the role MCs play in cancer as MC-derived tryptase is considered a key fibroblast activator prompting them to adopt a tumor-favoring phenotype [103]. MC-activated cancer-associated fibroblasts (CAF) stimulate the migration, proliferation, and malignant transformation of keratinocytes and have the ability to alter the tumor immune response by their sustained TGF- β production, which regulates the activity of natural killer (NK) cells [106].

Another function of MCs, which might be linked to their role in evolving malignant lesions, is their ability to prompt MC-directed vascular expansion. Given their strategic location in close proximity to the oral vasculature, they are able to drive neovascularization aided by angiogenic factors, including VEGF, or substances that can have angiogenic properties, such as tryptase, IL-8, TNF, basic fibroblast growth factor (bFGF), heparin, and histamine [101]. Angiogenesis facilitates the invasion and metastasis of cancer cells by remodeling the TME, and provides increased oxygen and nutrients for tumor growth. In the context of OSCC, a positive correlation between the MC and vascular densities in OSCC has been recently established, suggesting the ability of these cells to regulate angiogenesis [107]. This may explain the aggressive behavior and metastatic tendencies of these oral tumors. Although the angiogenic effects of MCs are only one of many pathways that induce vascular expansion within the TME, which responds to angiogenic factors from a variety of different sources, it is clear that MCs are effective inducers of this process and their role should be further investigated.

Lymphoid Derived Cells

Regulatory T-Lymphocytes

In PD, when dysbiotic bacteria attack the gingival tissue, an exaggerated host immune response is triggered in an attempt to avoid the dissemination of these micro-organisms, which results in tissue damage [108]. Consequently, Immunosuppressive T-regulatory cells (T-regs) are recruited into these sites to attenuate this aberrant inflammatory response and promote immune homeostasis. The main purpose of these cells is to minimize collateral tissue damage, which in turn promotes the survival of periodontal pathogens [109]. These cells limit the immune response by modulating the activities of other immune cells by a number of mechanisms, including: (1) binding of the T-reg expressed CTLA-4 to CD80/86 on DCs which inhibits co-stimulatory signals; (2) limiting the availability of IL-2 needed for effector T-cell activation; (3) producing immunosuppressive factors (ex. TGF- β , IL-10, IL-35); and (4) IDO-mediated T-cell dysfunction [110]. As one of the central players in PD, the recruitment of these immunosuppressive cells into the oral milieu will impact the development of further diseases including malignancies. Indeed, infiltration of Foxp3+ T-regs into the oral environment was shown to promote malignant transformation of oral premalignant lesions giving rise to OSCC [77].

It has been noted that CCL20, a chemokine linked with recruiting CCR6-expressing cells (including CCR6+ T-regs), is upregulated in both gingival fibroblasts and in periodontal

ligament cells during periodontal inflammation [111, 112]. Co-stimulation of gingival fibroblasts by IL-1 β and IL-22, present in the inflammatory milieu of PD, enhanced the activation of the C-Jun N-terminal kinase and the NF- κ B pathway resulting in the upregulation of CCL20 [111]. In a similar manner, IL-6/sIL-6R stimulation enhanced CCL20 production in IL-1 β -stimulated periodontal ligament cells by activating the STAT3 signaling pathway [112]. Although CCL20 has been mainly linked to recruiting Th17 cell, a correlation between the expression of CCL20 and FOXP3 mRNA in OSCC was noted. This led to a further study demonstrating that oral cancers with high CCL20 expression favor the selective recruitment of CCR6+ T-regs [113]. These CCR6+ cells are phenotypically and functionally distinct from CCR6- T-regs and possess enhanced suppressive activity, IL-10 production and FOXP3 expression [113]. Further studies are necessary to determine if the intensified recruitment of CCR6+ T-regs by CCL20/CCR6 signaling in PD can promote the progression OSCC.

In PD, the triad of molecules that regulate bone homeostasis/pathology, receptor activator of nuclear factor- κ B ligand (RANKL), its receptor RANK and its decoy receptor osteoprotegerin (OPG) are imbalanced resulting in bone loss. RANKL, which is upregulated in PD, promotes T-reg induction, while RANKL inhibition interferes with the migration of T-regs, and induces lower expression levels of the T-reg-related cytokines IL-10 and TGF- β [114]. This RANKL-mediated T-reg activation is further sustained in PD by the downregulation of osteoprotegerin that can block RANKL in the saliva and GCF of patients with PD [115, 116]. This RANKL-RANK signaling in OSCC has been shown to stimulate cancer metastasis in concert with the presence of active tumor-infiltrating T-regs [117]. Therefore, the imbalance of the RANKL/RANK/OPG signaling in PD may contribute to developing a T-reg mediated downregulated immune response which allows oral cancer cells to evade immune destruction.

Natural Killer Cells

Natural killer cells (NKs) are innate lymphoid cells that are actively involved in the destruction of foreign, infected and cancerous cells that are deemed to be of danger to the host [118]. Their cytotoxic activity is mediated by trafficking their granular content into the cytosol of their targets resulting in their lysis in a granzyme B and perforin-dependent fashion. Additionally, these cells produce an array of pro-inflammatory cytokines and chemokines (IFN- γ , TNF, IL-6, GM-CSF, and CCL5) that shape both the innate and adaptive immune response [119]. In PD however, the NK population has been linked to unresolved immune responses leading to the progression of PD [120]. This is due to immunosuppressive molecules in the periodontal inflammatory microenvironment that are capable of suppressing these NK cells.

Immune suppressive molecules including (IL-10, TGF- β , and IL-35) were found to be expressed locally as well as systemically under the impact of PD [121, 122]. In OSCC patients, IL-10 and TGF- β have been found to reduce the ability of peripheral NK cells to lyse their targets, and reduced their expression of IFN- γ , their key effector molecule [123]. TGF- β specifically has

been found to severely compromise an important stimulator of the effector function of cytotoxic lymphocytes and NKs. NKG2D, a receptor found on the surface of these cytotoxic cells, upon engaging with their NKG2D ligand expressed on tumor cells a stimulatory signal is transmitted into these cells allowing immunosurveillance of cancer cells [124]. TGF- β was found to interfere with this process by reducing the NKG2DL expression by tumor cells and downregulating NKG2D on NK cells [125]. On the other hand, IL-35 has the ability to reduce granzyme B production in NK cells impeding this cytolytic defense mechanism [126]. Another cytokine readily available in PD, that may contribute to impairing NK function, is IL-17 which plays a role in accelerating the phosphorylation of GSK-3 β [127]. This increased GSK-3 β phosphorylation was found to be involved in weakening the cytotoxic response of NK cells. These findings highlight several NK suppressive mechanisms adopted in PD that can compromise the effectiveness of the NK mediated anti-tumor immune response.

Pathogenic microorganisms might also contribute to modulating the activities of NKs. This was observed recently when *Fusobacterium nucleatum*, a pathogen strongly associated with PD, was discovered to bind to CEACAM1 (an inhibitory receptor on various immune cell subsets) [128]. The activation of CEACAM1 impairs degranulation of NK cells preventing the release of their lytic content and also diminishes their production of the immune-activating cytokine IFN- γ . Therefore, due to the suppressive influence of cytokines and microorganisms in PD, it is most likely that these cells will not function efficiently to kill tumor cells in OSCC.

Cytotoxic T-Lymphocytes

Cytotoxic T-lymphocytes (CTL) are the key effector arm of the adaptive immune response. They adopt one of three mechanism to mediate the clearance of foreign, infective or malignant cells: (1) releasing cytokines that stimulate killing of their targets, predominantly TNF- α and IFN- γ ; (2) binding of their Fas ligand of to the Fas receptor expressed on their targets, triggering apoptosis; and (3) trafficking pre-synthesized destructive granzymes and perforin into the intercellular space of the opposed cells [129]. Increased levels of CTL were observed in PD, yet, these cells were in fact linked to the etiopathogenesis of PD, leading to a more rapid onset of severe tissue destruction [129].

Recent studies postulate that the different cellular and molecular elements found within the inflammatory setting of PD may modify the function of CTLs. For example, the increased frequency of MDSCs, as described earlier in PD, has been confirmed to impede the function of CTLs in OSCC [130]. These MDSCs hamper expression of the CD3- ζ chain on CTLs, modifying the cytoplasmic signaling that leads to their activation [130]. MDSCs have also been implicated in decreasing IFN- γ production from these cytotoxic cells, impairing one of their most prominent destructive mechanisms [130]. Finally, MDSCs suppress the proliferative ability of CTLs, through inhibiting the TCR-driven cycling [130]. Together, this supports the establishment of an inflammatory state that supports the advancement of tumors.

Another mean by which PD can limit functionality of CTLs is through the production of programmed death-ligand 1 (PD-L1), a ligand that signals for T cell apoptosis. The binding of PD-L1, a transmembrane protein belonging to the B7 family, to its receptor (PD-1) is considered an important factor for suppression of the adaptive immune response. It can result in stunting the activities of immune cells leading to their apoptosis. The upregulated expression of both PD-1 and PD-L1 on CTLs, with the concomitant increase of PD-L1 mRNA in saliva of PD patients will, without doubt, affect the immune response in OSCC [131, 132]. The effect of these CD8+PD-1+ cells was observed in OSCC, where they were found to be less responsive than those CD8+ cells lacking PD-1 expression [133]. This is consistent with the observation that higher grades of oral premalignant and malignant lesions were positively linked to higher expression of PD-1/PD-L1 [134].

B-Lymphocytes

B cells are regarded for their role in mediating the humoral part of the adaptive immune response given their chief role in antibody production [135]. They have been subdivided into many different subsets depending on various contacts and cytokine stimuli present within the local issue in which they respond. One of these functional B cell subsets, which is significantly increased in PD is the IL-10 producing regulatory B cells (B-regs) [136]. The conversion of human B cells into B-regs was found to be induced by the immunosuppressive cytokine IL-35, which is, as previously mentioned, upregulated in patients with PD [122, 137]. These recruited cells halt the progressive bone loss associated with PD by modifying the expression of pro-inflammatory cytokines and local proliferation of Th17 cells [136]. The immunosuppressive properties of these cells are likely to impact oral malignancies, for example, in tongue squamous cell carcinoma, the frequency of B-regs within the microenvironment was positively correlated to IL-10 mediated conversion of CD4+T cells to T-regs and thus was an indicator of poor prognosis [138].

One of the most notable features of B cells that were observed in both OSCC and PD was their distribution. In these diseases B cells were mainly arranged on the periphery and peri-lesion areas mostly toward its advancing edge [139, 140]. Furthermore, in PD all B cell subsets had elevated expression of RANKL, promoting osteoclast formation and bone recession [141]. In a parallel phenomenon, B cells promoted invasion and metastasis of oral cancer cells, and increased B cell infiltration in OSCC was significantly correlated with lymph node metastasis [140].

From another perspective, growing evidence supports the involvement of Epstein-Barr virus (EBV) in the pathogenesis of PD. This is linked directly to the function of B cells present in the PD inflammatory microenvironment, as EBV infects B cells promoting their expansion and differentiation before remaining latent in the circulating memory B cells [142]. Through this, PD supports the amplification and viral spreading of EBV in a B cell dependent manner. This may favor the development of OSCC, as the vast majority of OSCC cases are located in B cell rich areas,

with EBV+ tumors having a more rapid onset and more invasive potential [143].

Although the role of B cells in both PD and OSCC has been understudied, the findings summarized here are promising, and suggest an important role of these cells.

T-Helper Cells

T-helper (Th) cells are pivotal moderators of the inflammatory immune response. They assist the other leukocytes in delivering an effective immune response by several means such as: the induction of B-cell maturation; CTL and macrophage activation; and recruitment of PMNs [144]. Several subsets of these CD4+ T-lymphocytes have been characterized including Th1, Th2, Th3, Th17, and T follicular helper (Tfh) cells, with each harboring unique features and functions [145]. Originally, Th1 and Th2 were shown to play a role in the pathogenesis of PD. However, with the emergence of new Th subsets and a deeper understanding of their plasticity under the influence of environmental conditions, this Th1/Th2 model has been altered considerably [146]. Herein, we discuss how the effects of each of the three dominant Th subsets in PD (Th1, Th2, & Th17) might also contribute to OSCC pathogenesis.

Th1 cells function by enhancing phagocytosis, complement fixation, and opsonization, strengthening the immune response against pathogens. Th1 cells differentiate from naïve T cells under the influence of the inductive signals IL-12 and IFN- α . In PD, an upregulation of GATA-3 signaling was noted [147]. GATA-3 was previously reported to suppress STAT4 signaling and thereby limit the differentiation capacity of Th1 cells and in the meantime enhance that of Th2 cells [148]. Likewise, overexpression of GATA-3 was identified in OSCC samples, consistent with another study reporting that Th1 cytokines (IL2, IFN γ) had lower expression in the sera of OSCC patients [149, 150]. The prior upregulation of GATA-3 in PD patients may augment the GATA-3 suppressive effect on Th1 in OSCC impairing the Th1 mediated immune response.

On the contrary, the Th2 subsets are involved in weaker innate responses and are more prevalent in OSCC facilitating the progression of cancer cells [151]. A very recent study highlighted that, in tongue squamous cell carcinoma, the immune response was biased toward Th2, with their cytokines (IL-4, IL-10) suppressing the cytotoxicity of CTL [152]. The involvement of these Th2 cells has been established in PD; however, in this context it has been suggested that Th2 cells promote a generalized state of immunosuppression through additional means. The elevated levels of the Th2-secreted cytokine, IL-4, within the inflammatory milieu induces CCR4-dependent recruitment of immunosuppressive T-regs into the periodontium [153]. Together, this Th2-mediated suppression of the adaptive immune response in PD is likely to exhibit similar defective mechanisms toward any forthcoming OSCC lesions.

It has only recently been suggested that the Th17 subset might play a role in periodontal diseases. As the principal producers of IL-17, Th17 cells play a central role in recruiting PMNs by upregulating the CXCL8 expression [154]. Th17 cells are now accepted as one of the critical upregulated cellular elements present in periodontally inflamed sites. Indeed, their presence

was shown to be directly proportional to probing depths in patients with PD [155], and higher IL-17 levels were detected in the saliva, serum and GCF of diseased patients [155, 156]. Generally, Th17 cells have been linked to unfavorable prognostic outcomes in patients with cancer in the head and neck region [157]. This may come as a result of the tumor promoting activities of IL-17, which regulates the levels of VEGF-A and IL-6 promoting the proliferation of oral cancer cell [157].

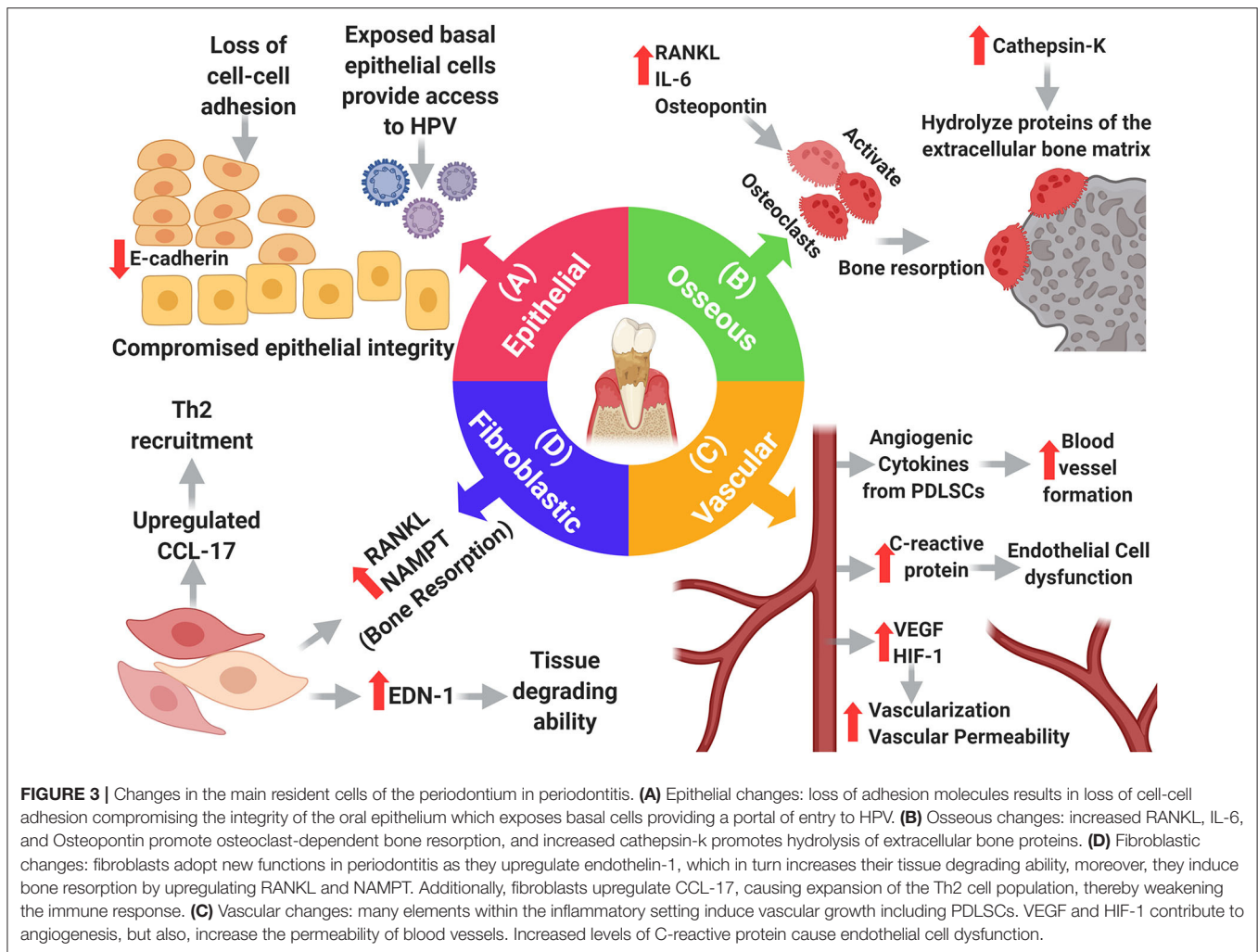
CHANGES IN THE PERIODONTAL MICROENVIRONMENT THAT CONTRIBUTE TO THE PATHOGENESIS OF OSCC

The interactions that cancer cells make with their surrounding environment are critical for tumor initiation and progression. Changes in the oral microenvironment in periodontitis can profoundly impact the development of oral cancer. Periodontal inflammation and associated bacterial pathogens cause damage to, and otherwise alter, the specialized tissue that surrounds the teeth (epithelium, connective tissue, vasculature, and bone). These changes can increase the potential for metastatic seeding, survival and growth of cancer cells, explaining why the gingiva, out of all the oral soft tissues, is the most common site for developing metastatic oral carcinomas [23]. Therefore, it is important to discuss some of these PD-induced changes and how they can potentially affect carcinogenesis. Here, we focus on specific changes that may directly influence OSCC [3] (**Figure 3**).

Epithelial Changes

The oral epithelial barrier has a critical function of protecting its underlying structures from pathogenic invaders, exogenous substances and mechanical stresses excreted by masticatory forces [158]. Once pathogenic microorganisms breach this protective barrier, gaining access to the tooth supporting structures, they elicit a chronic, persistent inflammatory state with subsequent connective tissue and bone destruction as the severity of inflammation increases [159]. Therefore, disruption of the epithelial barrier and ingress of pathogenic bacteria can cause further epithelial injury in a feed-forward manner. Downregulated expression of E-cadherin, an adhesion molecule that is fundamental for the cell-cell adhesion in the epithelial monolayer, contributes to the compromised integrity of the epithelium. Reduced E-cadherin expression is partly a consequence of increased macrophage production of TNF- α , a well-known E-cadherin down-regulator [160]. Loss of E-cadherin marks the advancement of premalignant, benign lesions into aggressive, metastatic prone carcinomas and is considered a hallmark of EMT in OSCC [161]. Upon exposure to periodontal pathogens, primary oral keratinocytes show increased nuclear activity of Snail-1 [162], which results in down-regulated E-cadherin, and increased expression of vimentin, another EMT biomarker.

The transcription factor, Twist, also an EMT mediator, increases the motility of epithelial cells allowing them to detach and adopt invasive characteristics of mesenchymal-like cells



[161]. Higher Twist expression is coupled with higher grades of dysplasia in oral premalignant lesions, making it a useful indicator of malignant transformation in oral epithelium [161]. When periodontal pathogens were co-cultured with OSCC cell lines, Twist expression was upregulated in the malignant cells, and these cells had increased migration [163]. This suggests that PD promotes upregulation of Twist expression, and facilitates cell migration and EMT. The inflamed periodontal tissues also show differential expression of several members of the laminin family including (laminin gamma 2 and laminin beta 3) [164, 165]. These glycoproteins contribute to cancer-related cellular processes, and interact with receptors expressed by cancer cells to stimulate production of collagenase IV, which facilitates cancer cell migration [166]. The same laminin members that were upregulated in PD were also found to be upregulated in OSCC [167].

The loss of cellular adhesion, in addition to the continuous deepening of the periodontal pocket, results in successive exposure of basal epithelial cell layers. As basal cells are the exclusive cellular targets for human papillomavirus (HPV) in the oral cavity, these exposed basal cells provide access points to HPV

infections [168]. Further proliferation of these cells favors the persistence of the HPV infection by sustaining viral replication, thus making the infected periodontal pockets reservoirs of this virus [168]. As a central risk factor for cancer development, around 70% of oropharyngeal cancers have been linked to HPV infections [169]. Although only a few studies have explored this association, strong evidence supports the involvement PD mediates HPV-induced carcinogenesis in the oral cavity. Additional longitudinal studies to confirm this interaction will help to reinforce the insight that maintaining periodontal health may prevent the deleterious effects of HPV, specifically in relation to cancer.

Osseous Changes

When untreated, the breakdown of the periodontal tissue and the subsequent bone destruction in PD ultimately results in tooth loss. This devastating consequence comes as a result of not only microbial invasion, but most importantly, the elicited host inflammatory response, which is central to this local osteolytic process. Hints for an association between osseous changes that occur in PD and the pathogenesis of OSCC have been suggested.

The bony changes that occur in PD are involved in the underlying molecular and cellular etiopathological mechanisms governing OSCC, and can also be considered significant risk predictors of OSCC. A study reported that there is a 5.2-fold increase in the risk of developing squamous cell carcinoma of the tongue with every millimeter alveolar bone loss observed in patients with PD [170].

Osteoclast regulators, RANKL, its receptor RANK, and decoy receptor OPG are the core elements orchestrating the osteo-immune bone destruction in PD. Elevated RANKL expression by many inflammatory cell types including, but not limited to, B and T lymphocytes and stromal cells, has been shown at sites with destructive periodontal activity [171]. RANKL induces maturation of osteoclasts, which are directly responsible for resorption of the dento-alveolar bone complex. Treating periodontal conditions was found to result in a significant reduction of RANKL levels in the gingival crevicular fluid, confirming the significance of RANKL in the inflammatory periodontal process [172]. In oral cancer, this amplified osteoclastic activity in PD supports the invasion of cancer cells into bone, which promotes their metastatic spread [173].

Many other osteoclastogenic cytokines are predominant in PD, disrupting the balance between bone resorption and bone formation. IL-6, a cytokine that has been identified as being upregulated in both the saliva and serum in PD, was shown to induce the activation of local osteoclasts and as a result potentiate bone resorption in periodontally inflamed sites [174, 175]. As for its role in oral malignancies, cases of OSCC that harbored greater osteoclast-derived IL-6 mRNA expression were associated, to a larger extent, with mandibular invasion, demonstrating its pro-invasive capacity in OSCC [176]. Osteopontin (OPN), a major non-collagenous bone protein, is key for many biological activities and is well-known for its involvement in bone diseases including PD. OPN enhances the proliferative and differentiation abilities of osteoclasts, and also suppresses osteoblasts [177]. Recently, an important role of OPN was revealed when it was found to induce nuclear translocation and phosphorylation NF- κ B, which upregulates the transcription of genes that encode the production of bone damaging products in osteoclasts [177]. This OPN rich environment in PD is likely to also boost osteoclast-mediated bone resorption in the context of OSCC. Furthermore, OPN was shown to have direct effects on cancer cells. When OSCC cells were cultivated in the presence of OPN, they developed greater adhesive, proliferative, and invasive capacities and expressed greater levels of IL-6 and IL-8 [178].

The cysteine protease Cathepsin K, known to hydrolyze proteins of the extracellular bone matrix, was increased in the GCF of PD patients, with its concentration reflecting disease severity [179]. Mice with experimentally induced PD that were treated with odanacatib, a small molecular inhibitor of Cathepsin K, significantly suppressed the activity of osteoclasts, essentially weakening the bone resorptive process [180]. The involvement of Cathepsin K in PD may contribute to more destructive forms of OSCC, since upregulation of Cathepsin K was shown to be linked with lymph node metastasis and unfavorable prognosis in OSCC [181].

Fibroblast Changes

Gingival fibroblasts are the most abundant cellular component of the periodontal connective tissue [182]. They function to shape the structural framework of the tissue by continuously regulating the turnover of the extra cellular matrix. However, they also have functions beyond their structural role, and make important contributions to pathological processes. Fibroblasts are one of the first cells that encounter pathogenic threats, and they are able to produce inflammatory mediators, and induce the expression of RANKL and OPG in PD. Invading periodontal micro-organisms were found to upregulate the expression of RANKL and reduce OPG expression in gingival fibroblasts [183]. Pathogen exposed fibroblast exhibit a similar phenotype to those found in the OSCC TME. Cancer associated fibroblasts (CAF) have also been observed to modulate RANKL expression, contributing to bone invasion by promoting osteoclastogenesis [184].

Several other key GF products have been shown to have altered expression upon encountering pathogenic bacteria, and these changes mirror the CAF phenotype present in the TME of OSCC. *P. gingivalis* prompts the expression of Galectin-1 (Gal-1), a beta-galactoside-binding protein, in gingival fibroblasts [185]. This deregulates the cytokine network in PD, limiting the migration of leukocytes and thereby allowing further colonization by pathogenic bacteria. In OSCC, Gal-1 was found to activate CAF and their expression of alpha-smooth muscle actin (α -SMA) inducing their transdifferentiation into myofibroblasts [186]. This results in upregulated expression of fibroblast monocyte chemotactic protein-1 (MCP-1), which then binds to CCL2 on cancer cells, promoting the metastatic ability of these malignant cells. Knockdown of Gal-1 in CAF results in quiescence of these fibroblasts and reverses their ability to promote migration of cancer cells [186].

Other molecules that govern the expression of different GF products show comparable contributions in both PD and OSCC [187, 188]. For instance, the pleiotropic peptide endothelin-1 (EDN-1) is elevated in both diseases. EDN-1 induces fibroblast tissue degrading capacity and breakdown of the oral stroma, which can promote the invasion by OSCC cells [188]. Nicotinamide phosphoribosyltransferase (NAMPT) regulates GFs in both diseases [189, 190]. In PD, NAMPT is critical for inducing GF expression of bone destructive mediators, including COX2, MMP1, and MMP3, supporting progressive bone loss [189]. In OSCC, upregulation of NAMPT was observed, suggesting it may play a role in oral dysplastic pathologies [190].

Vascular Changes

Aberrant vascularization is one of the most prominent features of inflamed periodontium. Many cells contribute to the vascularization process, which is intensified by the dense inflammatory infiltrate. Periodontal ligament stem cells (PDLSCs) are one of the most prominent cell types involved in this process. In the inflammatory milieu, PDLSCs promote angiogenesis by activating autophagy, which in turn enhanced the production of angiogenic cytokines including basic fibroblast growth factor (bFGF) and angiogenin [191]. Although vascular density was found to be increased in PD, endothelial and microvascular dysfunction has been reported in cases of severe

PD [192]. Moreover, elevated levels of IL-6 and C-reactive protein (CRP) in the peripheral blood of periodontal patients was found to predispose to an increased risk of developing peripheral arterial diseases which are regarded as an independent risk factors for developing cancer [193, 194].

CRP, a plasma protein mainly produced by the liver, is a valuable inflammatory biomarker and has been shown to promote endothelial dysfunction. In PD, levels of this protein were found to be elevated both in the local inflammatory site as well as systemically [193]. It has been recognized that this local increase comes as a result of stimulation of endothelial cells by IL-6 and IL-1 β produced by other inflammatory cells. This local increase was augmented by extra-hepatic production of CRP to induce the systemic elevation manifested in PD. High CRP levels are associated with OSCC patients that had metastatic lesions, suggesting that it could be used as a predictor of lymph node metastasis [195]. In addition, it has been suggested that a higher CRP/albumin ratio might be an independent prognostic marker of poor outcomes in patients with OSCC [196]. Since CRP affects the metastatic ability of cancer cells this could represent another potential avenue whereby PD interacts with OSCC.

The expression of hypoxia inducible factor-1 (HIF-1) and vascular endothelial growth factor (VEGF) in periodontal patients was shown to be greater than that of healthy individuals [197]. VEGF, a fundamental growth factor that stimulates the proliferation of endothelial cells and increases vascular permeability, is regulated by HIF-1. The expression of both cytokines was found to correlate with the severity of the periodontal condition [197]. HIF-1 α also provokes invasion of OSCC cells, and VEGF-dependent angiogenesis was found to be vital for continuous vascular expansion during the transition from epithelial dysplasia to carcinoma [198, 199].

CONCLUSION

In an era where understanding the putative interconnectivity between cancer and other diseases, particularly inflammatory diseases, unveils new aspects and targets for cancer therapy, it has become clear that PD has the potential to exacerbate all the pathogenic characteristics of OSCC. From the earliest steps of the neoplastic process, PD may, in part, contribute to the induction of permanent genomic alterations, due to the sustained presence of bacterial-derived mutagens. Furthermore, primary and metastatic tumor cells can benefit from the weakened stromal elements due to PD-dependent tissue destruction, and their proliferation in this environment is sustained by its rich growth/survival factors. In addition to potentially mutagenic properties and stromal defects, the oral inflammatory environment in PD is permissive for tumor progression. This is characterized by increased inflammatory infiltrate, which is nevertheless associated with a blunted or suppressed immune response that contributes to the development and progression of OSCCs. PD can therefore aid the development of oral cancers that would otherwise be destroyed in a healthy oral environment by normal immune cell functions. Therefore, monitoring oral health and providing effective treatments for PD might hold promise in normalizing this misdirected immune response, restoring an inflammatory network capable of exerting anti-tumor properties.

AUTHOR CONTRIBUTIONS

OE designed and drafted the manuscript. AB, NF, and HT reviewed and edited the manuscript. MG organized, provided the frame for the manuscript, and critically revised the content. All authors contributed to the article and approved the submitted version.

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Increased Abundance of Tumour-Associated Neutrophils in HPV-Negative Compared to HPV-Positive Oropharyngeal Squamous Cell Carcinoma Is Mediated by IL-1R Signalling

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The incidence of human papillomavirus (HPV)-associated cancer is increasing and HPV is now implicated in the aetiology of more than 60% of all oropharyngeal squamous cell carcinomas (OPSCC). In OPSCC, innate immune cells such as neutrophils and macrophages generally correlate with poor prognosis, whilst adaptive immune cells, such as lymphocytes, tend to correlate with improved prognosis. This may, in part, be due to differences in the immune response within the tumour microenvironment leading to the recruitment of specific tumour-associated leukocyte sub-populations. In this study, we aimed to examine if differences exist in the levels of infiltrated leukocyte sub-populations, with particular emphasis on tumour-associated neutrophils (TAN), and to determine the mechanism of chemokine-induced leukocyte recruitment in HPV-positive compared to HPV-negative OPSCC. Immunohistochemical analysis showed that HPV-negative OPSCC contained significantly more neutrophils than HPV-positive tumours, whilst levels of CD68+ macrophages and CD3+ lymphocytes were similar. Using a 3D tissue culture model to represent tumour-stromal interactions, we demonstrated that HPV-negative tumour-stromal co-cultures expressed significantly higher levels of CXCL8, leading to increased neutrophil recruitment compared to their HPV-positive counterparts. HPV-negative OPSCC cells have previously been shown to express higher levels of IL-1 than their HPV-positive counterparts, indicating that this cytokine may be responsible for driving increased chemokine production in the HPV-negative 3D model. Inhibition of IL-1R in the tumour-stromal models using the receptor-specific antagonist, anakinra, dramatically reduced chemokine secretion and significantly impaired neutrophil and monocyte recruitment, suggesting that this tumour-stromal response is mediated by the IL-1/IL-1R axis. Here, we identify a mechanism by which HPV-negative OPSCC may recruit more TAN than HPV-positive OPSCC. Since TAN are associated with

poor prognosis in OPSCC, our study identifies potential therapeutic targets aimed at redressing the chemokine imbalance to reduce innate immune cell infiltration with the aim of improving patient outcome.

Keywords: oropharyngeal cancer, human papillomavirus, leukocytes, fibroblasts, chemokine, IL-1, neutrophils

INTRODUCTION

The worldwide increasing incidence of human papillomavirus (HPV)-driven oropharyngeal squamous cell cancer (OPSCC) has raised the profile of these tumours and intensified interest in this area of cancer research [1]. Of particular interest is the finding that HPV-positive OPSCC generally display improved prognosis and response to therapy than their HPV-negative counterparts, whose aetiology is generally linked to DNA damage by classical risk factors such as tobacco use and alcohol consumption rather than viral infection [2]. In addition to aetiology, the tumour microenvironment also has a profound influence on tumour progression. The tumour microenvironment consists of dynamic molecular interactions between cancer cells, fibroblasts, the extracellular matrix and immune cell populations, where pro-tumour factors outweigh those intended to inhibit disease.

In many malignant tumours, a pro-inflammatory tumour microenvironment drives the recruitment of tumour-infiltrating leukocytes that in turn have a major effect on tumour progression [3]. The presence of increased tumour-associated neutrophils (TAN) and tumour-associated macrophages (TAM) have been correlated with poor clinical outcome in many tumours, whilst on many occasions tumour-infiltrating lymphocytes (TIL) have been associated with improved prognosis [4]. There is good evidence to suggest that HPV-positive OPSCC contain abundant CD8+ T-cells that can recognise tumour cell-expressed HPV antigens, enabling activation of adaptive immune responses to eliminate cancer cells and impart improved outcome [5–7]. Although increased levels of TAM and TAN correlate with poor prognosis in oral squamous cell carcinoma (OSCC) [8, 9], the levels of TAM in HPV-positive/negative OPSCC are less well-characterised and to date there are no published studies correlating abundance of TAN in OPSCC with HPV status.

It has been known for many years that the increased gene expression and subsequent secretion of chemokines by cells at infected or inflammatory sites is mediated by pro-inflammatory cytokines, such as IL-1, that are present within the local environment [10]. There are 47 different human chemokines each with specific or overlapping affinities for different leukocyte populations [11]. Leukocytes are recruited to inflammatory sites and tumours from the circulation via chemotactic gradients of chemokines. Although OPSCC cells are known to over-express a number of chemokines, many now believe that the pro-inflammatory paracrine signalling between tumour cells and the surrounding tumour-associated fibroblasts is the driving force behind elevated chemokine expression in the tumour microenvironment [12]. The specific type and proportions of leukocytes recruited to tumours are directly related to the profile of chemokines released. We have recently demonstrated that HPV-negative OPSCC cells stimulate tonsillar fibroblasts to

secrete a distinct chemokine-rich profile compared to HPV-positive OPSCC cells. Moreover, this effect is mediated by the actions of tumour cell-secreted IL-1 on the IL-1R expressed by tonsillar fibroblasts [13]. It is therefore plausible that the chemotactic cues driven by the tumour microenvironment in HPV-negative OPSCC is different from those in HPV-positive OPSCC and this may directly account for any differences observed in tumour-associated leukocyte sub-populations. Here we examine the abundance of leukocyte populations in HPV-positive and HPV-negative OPSCC and show for the first time that TAN are preferentially recruited to HPV-negative OPSCC. Moreover, using a 3D culture system consisting of HPV-negative or HPV-positive OPSCC spheroids embedded in a tonsillar fibroblast-populated stromal matrix to mimic the tumour microenvironment, we show that both chemokine secretion and neutrophil recruitment are dependent on IL-1 β /IL-1R paracrine signalling. Our data point to possible intervention strategies to inhibit TAN recruitment to tumours that may be beneficial for patient prognosis.

MATERIALS AND METHODS

Human Samples

This study utilised patient samples and associated clinical data within the period of primary diagnosis 2002–2012. Patients were selected using the Chemocare database system (National Health Service, UK) and further cross-referenced against the histopathological database held at Sheffield Teaching Hospitals NHS Trust, UK in order to confirm diagnosis and to identify each tissue biopsy reference number. Patients were included in the study if there was sufficient tissue remaining after clinical histopathological diagnosis for TMA generation and if there was a reasonably complete dataset of associated clinicopathological information. All biopsy material was obtained before commencement of anti-cancer treatment. Paraffin-wax embedded tissue samples were retrieved and collated in a blinded fashion with respect to HPV status. HPV positivity using RNAScope[®] was determined as described in Hendawi et al. [14], whilst expression of p16 staining was assessed using the H-score system with a 300-point cut-off for positivity [14, 15]. Overall HPV status in the samples was found to be proportionate to the UK prevalence of HPV OPSCC, reflecting that a representative population sample was used in this study. Clinical data regarding tumour recurrence, clinical status and follow-up were retrieved from the patient's medical files at the Sheffield Teaching Hospital NHS Foundation Trust, UK. Overall survival was determined by the difference between the date of treatment and either the date of death due to the tumour or last follow-up. The study was

conducted with National Research Ethical Committee approval (UK 12/LO/2018).

Tissue Microarray Construction, Immunohistochemistry, and Image Analysis

Tissue microarrays (TMA) were constructed by selecting tumour regions displaying more than 70% cellularity with minimal necrosis and marked on haematoxylin and eosin-stained sections. TMA were constructed using a tissue arrayer with 3×1.0 mm diameter cores from each tissue block arranged at mapped locations into recipient paraffin blocks. TMA were sectioned ($5 \mu\text{m}$) by microtome onto SuperfrostTM adhesive glass slides (ThermoFisher Scientific) and automated immunohistochemical staining performed for CD3 (T lymphocytes, Agilent, clone F7.2.38), CD68 (macrophages, Agilent, clone KP-1) and myeloperoxidase (MPO, Agilent, code IS511,) by the Histology Department, Sheffield Teaching Hospitals NHS Foundation Trust. Stained TMA sections were imaged using an Aperio ScanScope CS slide scanner (Aperio Technologies, Vista, USA). Digital analysis was performed using QuPath software (<https://qupath.github.io>) [16]. Further details of the QuPath analytical approach is provided in **Supplementary Figure 1**. Cores with insufficient histology (<80% area) were not included in QuPath analysis. Each OPSCC case was represented by at least two cores in QuPath analysis and the image analysis data was calculated as the mean percent number of positively stained cells as a proportion of the total number of cells in each core. Leukocytes within blood vessels were excluded from the analysis.

Cell Culture

The OPSCC HPV-positive cell line UPCI-SCC90 was provided by Prof. Susanne Gollin, University of Pittsburgh and the HPV-negative cell line FaDu was purchased from the American Type Culture Collection. The authenticity of cell lines was verified by short tandem repeat analysis and their HPV status confirmed by the HPV Cytology Screening Unit using the cobas[®] qPCR HPV testing kit that detects a 200 bp region within the L1 region of the HPV genome (Sheffield Teaching Hospital NHS Foundation Trust, UK). Normal tonsillar fibroblasts (NTF) were isolated from biopsies obtained from tonsillectomies at the Sheffield Teaching Hospitals NHS Foundation Trust with written, informed consent (ethical approval 09/H1308/66) as described previously [17]. For this study, NTF isolated from one donor was used in all experiments to limit experimental variation. UPCI-SCC90 cells and NTF were cultured in Dulbecco's Modified Eagle's Medium and FaDu in RPMI-1640, both media were supplemented with 10% v/v foetal calf serum (FCS), 2 mM L-glutamine, 100 IU penicillin and 100 $\mu\text{g}/\text{ml}$ streptomycin, (all medium and supplements from Sigma-Aldrich) and cells cultured in a humidified incubator with 5% CO₂ at 37°C. All cells were confirmed mycoplasma-free before use in experiments.

Leukocyte Isolation

Human peripheral blood leukocytes were isolated from the venous blood of healthy donors with written, and informed

consent (University of Sheffield ethical approval, 012597) as previously described [18]. The donors were two male and one female, none had received the HPV vaccine, none were taking prescription medication or had been ill in the previous 2 weeks, and all were non-smokers. Blood was anti-coagulated using sterile 3.8% sodium citrate (Sigma-Aldrich, W302600) and centrifuged at 400 g for 20 min to separate the plasma from leukocytes. Mononuclear cells were isolated by Ficoll-Paque Plus (GE Healthcare, GE17-1440-02) density-gradient centrifugation, washed twice with Hank's balanced salt solution (HBSS, ThermoFisher Scientific, 14170112) and erythrocytes removed from neutrophils by hypotonic lysis. Total neutrophils and mononuclear cells were re-combined by re-suspension in RPMI-1640 supplemented with 10% v/v FCS and 2 mM L-glutamine then labelled with CellTrackerTM Deep Red dye (ThermoFisher Scientific, C34565) according to the manufacturer's instructions. Cell viability was assessed by trypan blue (Sigma-Aldrich, T8154) exclusion and was >95% by light microscopy.

3D Tumour—Stromal *in vitro* Culture Models

Multicellular tumour spheroids (MCTS) were generated as previously described [19]. Briefly, 100 μL of a 1×10^5 cells/mL suspension of either FaDu or UPCI-SCC90 cells were added to each well of a 96-well plate previously coated with 100 μL sterile 1.5% w/v type IV agarose (Sigma-Aldrich, 121852) in serum-free medium. Culture plates were incubated for 2 d in a humidified incubator with 5% CO₂ at 37°C to allow MCTS formation. To prepare 3D tumour-stromal *in vitro* models, type 1 rat-tail collagen (produced in-house) was mixed with $10 \times$ RPMI-1640, 10% FCS, 2 mM L-glutamine and reconstitution buffer (2.2% NaHCO₃, 4.8% HEPES, 0.25% NaOH in dH₂O, all from Sigma-Aldrich) and pH adjusted to 7.4. One millilitre collagen was added to 2×10^5 NTF and 60 FaDu or UPCI-SCC90 MCTS, the contents mixed to evenly disperse the NTF/spheroids and the hydrogel allowed to solidify for 1 h at 37°C, 5% CO₂ in a 24-well plate. A ratio of ~1:3 NTF to tumour cells was used in accordance with our previous 2D work [13]. Once set, 1 mL of serum-containing medium was added and models incubated for a further 24 h. Models were then washed twice with serum-free medium and incubated in the absence or presence of 1 or 10 $\mu\text{g}/\text{ml}$ anakinra (Trade name Kineret, Amgen) in 500 μL serum-free medium and further incubated for 24 h. Levels of anakinra were maintained throughout the experiment. Culture medium was then removed and stored at -20°C for further analysis by ELISA.

To generate immune cell-containing 3D tumour-stromal models, 200 μL of CellTrackerTM-labelled total leukocytes were added to the surface of either FaDu or UPCI-SCC90 3D co-culture models in the absence or presence of 10 $\mu\text{g}/\text{ml}$ anakinra, and incubated for 24 h. Models were washed twice with HBSS to remove non-infiltrating leukocytes then total cells dispersed from the models using type I collagenase (2 mg/mL in HBSS, Sigma-Aldrich, SCR103), washed in HBSS, sieved to remove cell aggregates and then fixed with 2% paraformaldehyde. Flow cytometry (FACSCaliburTM with associated CellQuestTM

TABLE 1 | Oropharyngeal squamous cell carcinoma patient demographics and clinical characteristics.

Characteristics (%)		HPV-positive (%)		HPV-negative (%)	P
Total Subjects	59 (100)	40 (68)	19 (32)		
Sex	Female	14 (24)	10 (25)	4 (21)	0.739
	Male	45 (76)	30 (75)	15 (79)	
Age (year)	Median	57	56		0.651
	Range	29-68	31-70		
Alcohol ^a	Never	3 (7.5)	0 (0)		0.018
	Moderate	22 (55)	6 (31.5)		
	Heavy	4 (10)	7 (37)		
	Unknown	11 (27.5)	6 (31.5)		
Smoking ^b	Smoker	13 (32.5)	9 (47)		0.032
	Non-smoker	11 (27.5)	0 (0)		
	Ex-smoker	9 (22.5)	7 (37)		
	Unknown	7 (17.5)	3 (16)		
Site	Tonsil	28 (70)	9 (47)		0.205
	Base of tongue	11 (27.5)	7 (37)		
	Post wall of pharynx	0 (0)	1 (5)		
	Soft palate	0 (0)	1 (5)		
	Oropharynx (not otherwise specified)	1 (2.5)	1 (5)		
Disease stage	Stage I	8 (20)	2 (11)		0.271
	Stage II	16 (40)	5 (26)		
	Stage III	5 (12.5)	6 (32)		
	Stage IV	10 (25)	5 (26)		
	Unknown	1 (2.5)	1 (5)		
T-Stage ^c	T1/T2	24 (60)	7 (37)		0.155
	T3/T4	15 (37.5)	11 (58)		
	Unknown	1 (2.5)	1 (5)		
N-stage ^c	N0	3 (7.5)	3 (15.7)		0.654
	N1-N2a	28 (70)	13 (68)		
	N2b-N3	7 (17.5)	3 (15.7)		
	Unknown	2 (5)	0 (0)		
M-Stage ^c		0 (0)	0 (0)		
Grade ^c	Poor	25 (62.5)	9 (48)		0.339
	Moderately	9 (22.5)	8 (42)		
	Well	2 (5)	1 (5)		
	Unknown	4 (10)	1 (5)		
Recurrence	Local	1 (5)	4 (21)		0.495
	Regional	0 (0)	2 (10.5)		
	None	39 (95)	13 (68.5)		

^aModerate alcohol consumption is defined as up to 10–25 units/week, heavy consumption is defined as >25 units/week.

^bEx-smoker is defined as an individual who has smoked at least 100 cigarettes in their lifetime but who had quit smoking within the last 12 months.

^cBrierly et al. [20].

Two-sided Chi-squared or Fisher's exact-test was used for comparison of categorical variables and two-tailed Student t-test was used for continuous variables. $P < 0.05$ are given in bold text.

software, BD Biosciences) was used to plot side scatter against fluorescence (650 nm emission) to determine the total number of infiltrating leukocytes into tumour-stromal models. These cells were further gated and side scatter plotted against forward scatter to determine the relative numbers of neutrophils, monocytes and lymphocytes according to their cell size and granularity (see **Figure 5** for gating strategy). Each experiment was performed using the leukocytes isolated from one donor with each test performed in technical triplicates and the entire experiment

was repeated three times ($n = 3$) using the blood from a different donor (two male, one female, all non-HPV-vaccinated and non-smokers) on each occasion.

Cell Viability

Cell viability as measured by metabolism of PrestoBlue™ (ThermoFisher Scientific, P50200) was performed according to the manufacturer's instructions. 3D models were incubated with serum-containing medium for 48 h at 37°C, 5% CO₂.

Models were washed with HBSS before addition of fresh medium containing PrestoBlue™ (1:10 v/v) and then incubated for a further 2 h. Medium was removed and the colour change measured by fluorescence excitation at 560 nm and emission at 590 nm.

Chemokine Level Quantification

Conditioned medium collected from 3D models in the absence or presence of anakinra was subjected to ELISA for CXCL8, CCL2 (BD Biosciences 555244 and 559017, respectively) and CCL5 (R&D systems, DRN00B) according to the manufacturer's instructions.

Statistics

All data are expressed as mean \pm SD of at least three independent experiments performed in triplicate unless otherwise stated. Statistical analysis was undertaken using GraphPad Prism (v8.4.3, GraphPad Software, San Diego, CA). For demographic and clinical data two-sided Chi-squared or Fisher's exact-test was used for comparison of categorical variables and two-tailed Student *t*-test was used for continuous variables. For TMA data pairwise comparisons were performed using Mann-Whitney *U*-test, and for ELISA data group-wise comparisons were made using one-way ANOVA with Tukey's multiple comparisons test. Flow cytometric data was analysed using one sample *t* and Wilcoxon-test. SPSS (v22, IBM Chicago, IL) was used to test for HPV-status effects in cumulative survival curves according to the Kaplan-Meier method with comparisons between survival curves made using the log rank test. Differences between groups was considered significant when $p < 0.05$.

RESULTS

HPV-Positive Status Is Associated With Improved 5-Year Survival in OPSCC

The patient demographic information is summarised in **Supplementary Table 1**. The median age was 57 years for HPV-positive and 56 years for HPV-negative patients. There was a statistically significant difference in the levels of alcohol ($p = 0.018$) and smoking ($p = 0.032$) between subjects with HPV-positive and HPV-negative OPSCC. However, there was no significant difference between any of the clinical parameters analysed (**Table 1**). OPSCC cases were stratified for HPV-status and overall survival over a 5-year follow-up period examined. Kaplan-Meier survival analysis showed that individuals with HPV-positive OPSCC correlated significantly ($p = 0.04$) with better overall 5-year survival than individuals with HPV-negative OPSCC (**Figure 1**).

HPV-Negative OPSCC Contain Elevated Numbers of Tumour-Associated Neutrophils Than HPV-Positive OPSCC but Levels of Other Tumour-Associated Leukocytes Are Similar

The number of tumour-infiltrating leukocytes present in HPV-negative or HPV-positive OPSCC was measured by

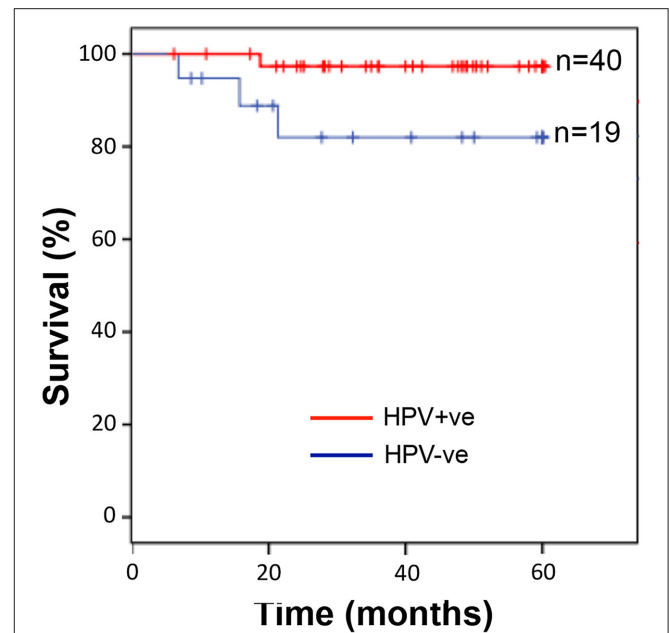
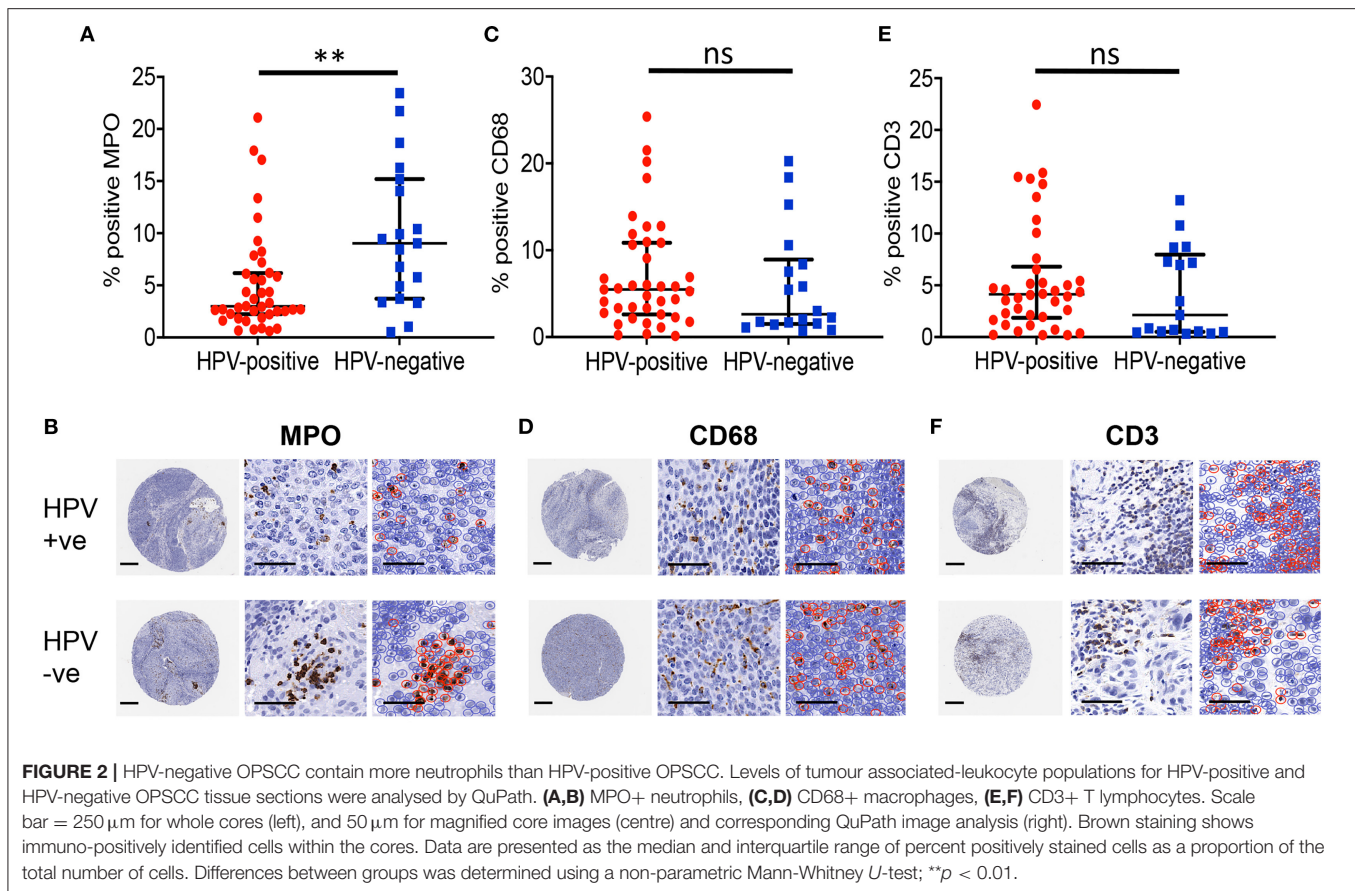


FIGURE 1 | Individuals with HPV-positive OPSCC display significantly better overall 5-year survival than those with HPV-negative OPSCC. Kaplan-Meier analysis followed by log rank-test showed that individuals with HPV-positive OPSCC ($n = 40$) correlated with significantly ($p = 0.04$) improved overall 5-year survival than individuals with HPV-negative OPSCC ($n = 19$).

immunohistochemical staining of TMA for myeloperoxidase (MPO; neutrophils), CD68 (macrophages) or CD3 (pan T cells) followed by QuPath image analysis and the percent number of positively stained cells as a proportion of the total number of cells in each core calculated (**Supplementary Figure 1**). There was a significant ($p = 0.003$) increase in the level of MPO-immunopositive staining in HPV-negative (median 9.04%, $n = 19$) compared with HPV-positive (median 2.98%, $n = 40$) OPSCC, indicating the increased prevalence of neutrophils in HPV-negative compared to HPV-positive OPSCC (**Figures 2A,B**). In contrast, similar levels of macrophages, identified by CD68-positive staining, were observed in both HPV-positive (median 5.49%, $n = 39$) and HPV-negative (median 2.64%; $p = 0.277$) OPSCC (**Figures 2C,D**). Likewise, the levels of T lymphocytes were similar in both HPV-positive (median 4.13%, $n = 38$) and HPV-negative (median 2.14%, $n = 17$; $p = 0.333$) OPSCC (**Figures 2E,F**). The tissue neutrophil to lymphocyte ratio (NLR) for HPV-negative OPSCC was significantly greater (median 2.60) than the ratio for HPV-positive tumours (median 0.773; $p < 0.01$). There were no significant differences observed in the levels of infiltrating leukocyte populations between HPV-positive and HPV-negative OPSCC at disease stage (**Supplementary Figure 2**) or T-stage (**Supplementary Figure 3**) examined. Taken together, these data show that HPV-negative OPSCC contained significantly more TAN compared to HPV-positive OPSCC whereas levels of CD68 and CD3-positive leukocyte populations were similar.



HPV-Negative 3D Tumour-Stromal Culture Models Produce Significantly Higher Levels of Chemokines than their HPV-Positive Counterparts

Our previously published data using a 2D monolayer experimental culture system showed that when cultured with conditioned medium derived from several different HPV-negative OPSCC tumour cells, NTF are stimulated to secrete high levels of chemokines in an IL-1-dependent manner [13]. Here we used a 3D *in vitro* construct containing HPV-negative (FaDu) or HPV-positive (UPCI-SCC90) multi-cellular tumour spheroids (MCTS) (**Supplementary Figures 4A–F**) embedded in a NTF-populated stromal collagen matrix in an attempt to more accurately model the intimate cell-cell OPSCC tumour-stromal cell interactions within a 3D environment, similar to those occurring *in vivo*. Haematoxylin and eosin stained sections of the tumour-stromal 3D model demonstrated an evenly distributed fibroblast-populated matrix containing MCTS that often display a central necrotic core surrounded by several layers of tumour epithelium (**Supplementary Figures 4E,F**). The histological appearance of the tumour-stromal 3D model is comparable to that frequently observed with OPSCC tumours *in vivo* (**Supplementary Figure 4G**) although the density of the

fibroblasts within the *in vitro* models appears to be lower than observed *in vivo*.

Cell viability within collagen gels was measured for NTF, FaDu or UPCI-SCC90 spheroids alone or in combination. The mean fluorescence readings for all tests containing cells were increased compared to collagen alone showing that cells remained metabolically active and therefore viable whilst embedded in collagen. When in co-culture with NTF, both UPCI-SCC90 and FaDu displayed an additive and significant (*p* < 0.05) increase in fluorescence compared to when the spheroids or NTF were cultured alone, reflecting the synergistic nature of the co-culture system (**Supplementary Figure 4H**).

We next measured the levels of chemokines released in models containing NTF or MCTS alone or when in combination. We chose to measure CXCL8, CCL2 and CCL5, as these chemokines are well-recognised, potent chemoattractants for neutrophils, monocytes and lymphocyte populations, respectively. When cultured alone, NTF produced low levels for all three of the chemokines tested with 0.12 ± 0.007 ng/ml, 0.20 ± 0.02 ng/ml and 0.06 ± 0.005 ng/ml for CXCL8, CCL2 and CCL5, respectively (**Figures 3A–C**). This was also the case for UPCI-SCC90 MCTS when cultured alone (CXCL8— 0.09 ± 0.01 ng/ml, CCL2— 0.14 ± 0.02 ng/ml and CCL5— 0.13 ± 0.001 ng/ml; **Figures 3A–C**). Chemokine secretion was not significantly increased when NTF were co-cultured with UPCI-SCC90 MCTS (CXCL8— $3.52 \pm$

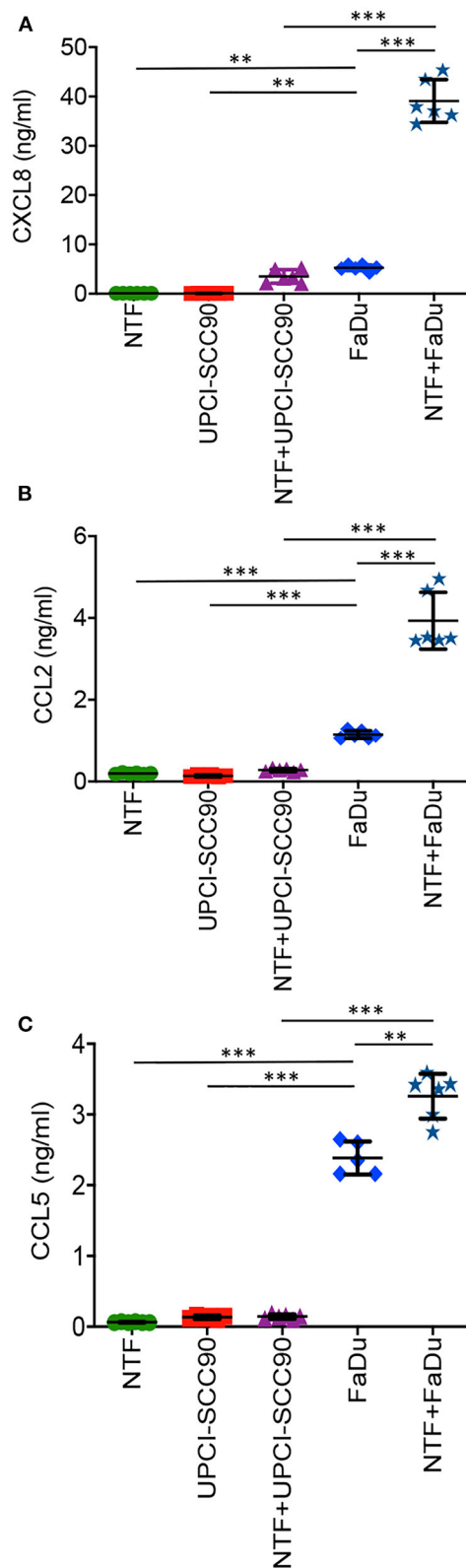


FIGURE 3 | FaDu HPV-negative OPSCC 3D tumour-stromal models display increased chemokine secretion compared to their UPCI-SCC90 HPV-positive (Continued)

FIGURE 3 | counterparts. Chemokine secretion of NTF-populated collagen alone, UPCI-SCC90 and FaDu MCTS alone or NTF/MCTS co-cultures for (A) CXCL8, (B) CCL2, and (C) CCL5. Data are mean \pm SD for at least 5 independent experiments. Statistics were performed using One-way ANOVA with Tukey's multiple comparisons test. ** $p < 0.01$, *** $p < 0.001$.

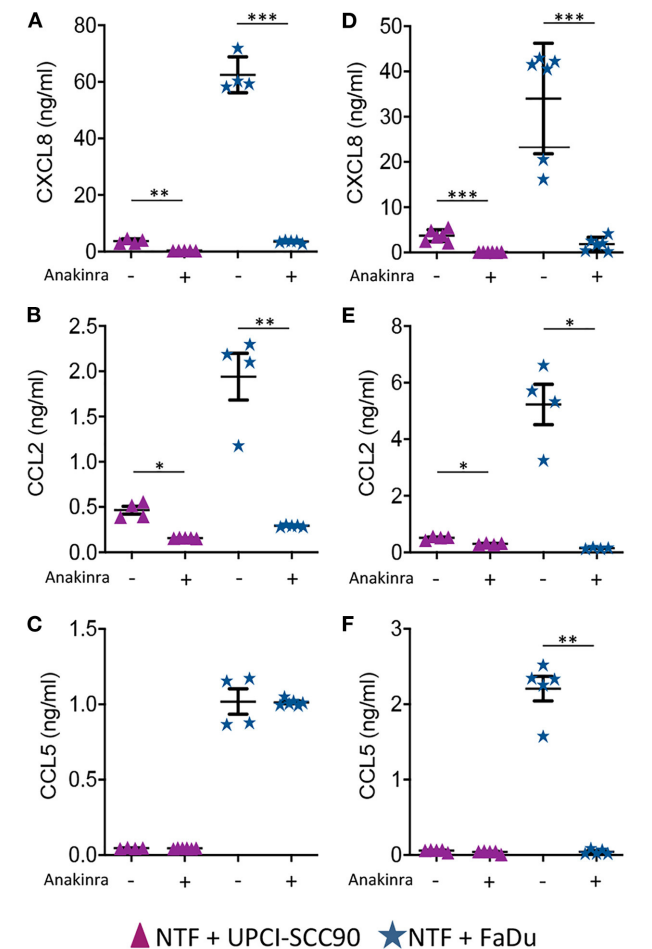


FIGURE 4 | Chemokine secretion by HPV-negative OPSCC 3D tumour-stromal models is reduced by anakinra. (A) CXCL8, (B) CCL2, and (C) CCL5 secretion from HPV-positive UPCI-SCC90/NTF or HPV-negative FaDu/NTF co-cultures in the absence or presence of 1 μ g/mL (A–C) or 10 μ g/mL (D–F) anakinra. Data are mean \pm SD for at least 4 independent experiments. Statistics were performed using Mann Whitney U-test. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

1.38 ng/ml, CCL2— 0.28 ± 0.04 ng/ml and CCL5— $0.14 \pm 0.004 \pm$ ng/ml; **Figures 3A–C**). In contrast, for CXCL8 (5.28 ± 0.6 ng/ml; $p < 0.05$) and CCL2 (1.15 ± 0.09 ng/ml; $p < 0.001$), FaDu MCTS alone secreted significantly more chemokine than NTF or UPCI-SCC90 MCTS alone, and for CCL5 (2.38 ± 0.23 ng/ml; $p < 0.001$) significantly more than NTF/UPCI-SCC90 co-culture models (**Figures 3A–C**). However, when FaDu MCTS were combined with NTF in a 3D tumour-stromal model, levels of CXCL8 increased 7-fold (39.1 ± 4.34 ng/ml; $p < 0.001$) and CCL2 by

3-fold (3.93 ± 0.69 ng/ml; $p < 0.001$, **Figures 3A,B**), showing that NTF and FaDu act synergistically in stimulating production of these chemokines. Levels of CCL5 also increased in the 3D tumour-stromal model compared to MCTS alone, although the difference between the amounts of chemokine released was much less [2.4 ± 0.2 ng/ml compared to 3.3 ± 0.3 ng/ml for FaDu MCTS alone and NTF + FaDu MCTS, respectively ($p < 0.01$); **Figure 3C**]. These data indicate that OPSCC cells within a 3D environment interact with NTF via paracrine signalling.

Synergistic Production of Chemokines by HPV-Negative 3D Tumour-Stromal Culture Models Is Mediated by IL-1/IL-1R

We next tested if the IL-1/IL-1R axis was the main paracrine signalling pathway in mediating elevated chemokine release by inhibiting this pathway using anakinra, a highly specific IL-1R antagonist. Here, 3D models containing either UPCI-SCC90 or FaDu MCTS co-cultured with NTF were pre-incubated with 1 or 10 μ g/ml anakinra and levels of CXCL8, CCL2 and CCL5 measured in the conditioned medium after 24 h. Pre-incubation with 1 μ g/ml anakinra dramatically reduced the production of CXCL8 and CCL2 but not CCL5 for both UPCI-SCC90 and FaDu 3D tumour-stromal models. Specifically, in FaDu-stromal 3D experimental models, CXCL8 was reduced 18-fold ($p < 0.001$) and CCL2 6-fold ($p < 0.01$) upon treatment with anakinra, whereas CCL5 levels remained the same as untreated models (**Figures 4A–C**). Inhibition of chemokine secretion was even more pronounced when models were pre-incubated with 10 μ g/ml anakinra, where levels of CXCL8, CCL2 and CCL5 were almost abolished in anakinra-treated FaDu stromal models ($p < 0.01$; **Figures 4D–F**).

HPV-Positive UPCI-SCC90 Tumour-Stromal Models Recruit Fewer Neutrophils than their HPV-Negative FaDu Counterparts Reproducing What Is Observed *in vivo*

Fluorescently labelled leukocytes isolated from whole blood were added to HPV-positive UPCI-SCC90 or HPV-negative FaDu tumour stromal models and the levels of total infiltrating leukocytes, as well as individual leukocyte subsets, quantified by flow cytometry using a gating strategy to identify neutrophils, monocytes and lymphocytes based on their well-characterised forward and side scatter profiles (**Figures 5A–D**). There were $36.8 \pm 14.9\%$ fewer total leukocytes infiltrating into HPV-positive UPCI-SCC90 tumour-stromal models compared to those infiltrating into the HPV-negative FaDu tumour-stromal models ($p = 0.05$; **Figure 5E**, data showing the actual numbers of total leukocytes or leukocyte subsets infiltrating into the tumour-stromal models for each individual experiment is provided in **Supplementary Table 1**). When broken down into leukocyte subsets, the proportion of neutrophils infiltrating into HPV-positive UPCI-SCC90 tumour-stromal models was $52.3 \pm 19.9\%$ less ($p = 0.045$) when compared to those infiltrating HPV-negative FaDu tumour-stromal models, whereas, although overall decreased, the proportion of infiltrating monocytes ($28.8 \pm 27.9\%$) and lymphocytes ($19.8 \pm 15.5\%$) were

not statistically different between UPCI-SCC90 and FaDu models (**Figures 5B,C,E**). Although these flow cytometric results have a relatively large standard deviation due to donor-to-donor variability, the data reflect those observed in the immunohistochemical analysis of leukocyte infiltration in the patient OPSCC tumour sections, where greater levels of tumour-associated neutrophils were observed in HPV-negative compared to HPV-positive tumours. Since pre-treatment with anakinra significantly reduced the levels of chemokines (CXCL8 and CCL2) in both FaDu and UPCI-SCC90 tumour-stromal models (**Figure 4**), we reasoned that these anakinra-treated tumour-stromal models would therefore also recruit fewer leukocytes. This was indeed the case with anakinra treatment reducing the numbers of infiltrating leukocytes for both UPCI-SCC90 and more dramatically for FaDu tumour-stromal models (**Supplementary Figure 4**). Here, anakinra-treated FaDu tumour-stromal models recruited $45.2 \pm 12.0\%$ ($p = 0.023$) fewer total leukocytes than untreated models (**Figures 5B,D,F**). At the leukocyte subpopulation level, the proportion of neutrophils and monocytes infiltrating FaDu tumour-stromal models was significantly reduced by $45.9 \pm 12.3\%$ ($p = 0.023$) and $52.9 \pm 16.4\%$ ($p = 0.030$) respectively, upon anakinra treatment, whereas the proportion of lymphocytes infiltrating into anakinra-treated FaDu tumour-stromal models was not significantly different ($40.3 \pm 17.5\%$; $p = 0.057$) from untreated models (**Figure 5F**).

DISCUSSION

The tumour microenvironment plays a major role in directing the course of tumour progression, and factors that regulate the immune response and direct the infiltration of tumour-associated leukocytes are key to this process [21]. It is important to understand the overall tumour-associated immune burden and mechanisms of how this is controlled because several lines of evidence show that the abundance of certain leukocyte subsets within tumours correlate with either poor or improved prognosis.

Although our patient cohort was relatively small, HPV status still stratified the patient groups in terms of outcome, where patients with HPV-positive OPSCC displayed significantly improved 5-year survival than those with HPV-negative tumours, as observed in several other studies [2, 6, 22, 23]. The percent 5-year overall survival for HPV-positive patients seen in this study is similar to those observed in previous studies, whereas we observed an increased 5-year overall survival for HPV-negative OPSCC subjects compared to previous studies [2, 6, 22, 23]. This is likely due to the relatively small sample size for the HPV-negative cohort used in this study compared to other larger studies as well as differences in local detection and/or treatment regimens. Upon leukocyte tumour burden assessment, we found TAN to be significantly more abundant in HPV-negative than HPV-positive tumours; the first time that differences in TAN levels in OPSCC has been shown to correlate with HPV status. We used a validated antiserum specifically raised against neutrophil MPO to detect the presence

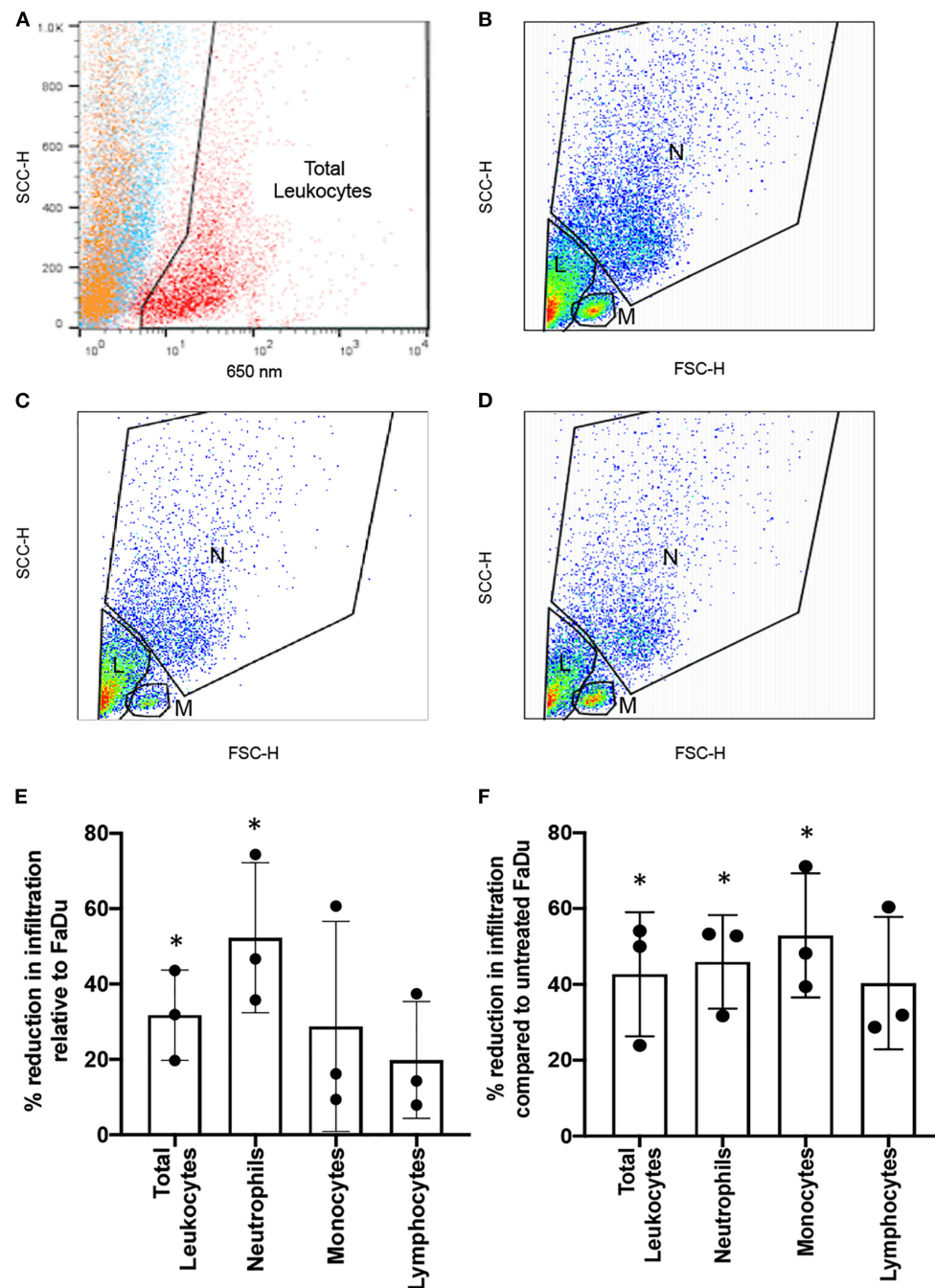


FIGURE 5 | Anakinra reduces leukocyte recruitment in an *in vitro* 3D model of OPSCC. Infiltration of leukocytes into 3D OPSCC tumour-stromal models in the absence or presence of 10 μ g/ml anakinra. **(A)** Fluorescence-based gating strategy to identify leukocyte population (red) compared to tumour (orange) or NTF (blue) cell populations. Total leukocytes identified in panel A were re-gated for their well-characterised side and forward scatter properties to determine the number of neutrophils (N), monocytes (M) and lymphocyte (L) populations infiltrating into **(B)** FaDu tumour-stromal models and **(C)** UPCI-SCC90 tumour-stromal models in the absence of anakinra, or **(D)** FaDu tumour-stromal models pre-treated with 10 μ g/ml anakinra for 24 h before addition of leukocytes. **(E)** Percent reduction in the number of leukocytes infiltrating HPV-positive UPCI-SCC90 tumour-stromal models relative to those infiltrating HPV-positive FaDu tumour-stromal models. **(F)** Percent reduction in the number of leukocytes infiltrating anakinra treated (10 μ g/ml) HPV-negative FaDu tumour-stromal models compared to untreated FaDu tumour-stromal model controls. Data in E and F are mean \pm SD for 3 independent experiments with each experiment being performed using the blood from an individual donor. Statistics were performed using one sample *t* and Wilcoxon-test. * $p < 0.05$.

of TAN, a biomarker commonly used by diagnostic pathology laboratories for the detection of neutrophils. MPO may not be as specific as less commonly used markers such as CD15 and CD66b, although these biomarkers too are expressed by other granulocytes. Unfortunately, we were unable to correlate TAN levels with prognosis for HPV status cases due to the sample size. However, similar data have been reported for OSCC [24], although this form of cancer rarely harbours oncogenic HPV [25]. Here, Li et al., observed increased abundance of CD15+ neutrophils in HPV-negative compared to HPV-positive OSCC, as well as finding that high levels of neutrophils correlated with poor 5-year survival, increased lymph node metastasis and were an independent prognostic factor for OSCC [24]. Using The Cancer Genome Atlas (TCGA) data set Chen et al., also found a higher neutrophil genetic imprint for HPV-negative compared to HPV-positive head and neck cancer [26].

In other tumour types, high levels of TAN have been shown to drive tumour progression by producing factors such as reactive oxygen species that initiate further DNA mutations [27], and by secreting potent pro-tumour factors such as vascular endothelial growth factor and matrix metalloproteinases that promote tumour angiogenesis [28, 29], and transforming growth factor beta (TGF- β) that induces myofibroblast formation [30]. Moreover, neutrophils that display an immunosuppressive phenotype upon stimulation by tumour micro-environmental cues [so called polymorphonuclear myeloid-derived suppressor cells (PMN-MDSC)] have been shown to accumulate in both patient biopsies and murine experimental models of head and neck squamous carcinoma (HNSCC), where they inhibit the tumoricidal functions of natural killer cells by secretion of TGF- β , nitric oxide and arginase-1 [31, 32]. Given these findings, it could be speculated that high TAN levels and their associated secreted factors are key in driving tumour immunosuppression, progression, metastasis and therefore poor outcome in HPV-negative OPSCC. Investigation of the TAN phenotypes in HPV-negative and HPV-positive OPSCC in future studies is warranted.

Similar to TAN, increased levels of TAM have been shown to correlate with poor prognosis in several tumours including HPV-negative OSCC [9, 33]. Although we observed high levels of TAM in tumours there was no significant difference in their abundance between HPV-positive and HPV-negative OPSCC. Our data is in line with other studies reporting similarities in overall TAM levels and HPV status in OPSCC and HNSCC [7, 26, 34]. In contrast, Seminerio et al., found increased prevalence of CD68+ macrophages in HPV-positive compared to HPV-negative OPSCC in the intra-epithelial but not stromal tumour component [33]. It is possible that different TAM phenotypes are recruited to OPSCC. Although we did not examine TAM polarisation status, a recent study found a higher M1/M2 TAM ratio in HPV-positive HNSCC that may account for differences [26].

Much attention has been recently paid to TIL that are correlated with improved prognosis in many tumours [35] and are the basis for several current immunotherapy approaches that have had variable success in treating head and neck cancers [36]. Using CD3, a pan T cell marker, we found no

difference in the levels of CD3+ lymphocytes in HPV-positive compared to HPV-negative OPSCC in our patient cohort, a similar finding previously observed by others [34, 37]. However, there is now compelling evidence that it is the recruitment of specific lymphocyte subsets that are crucial in driving anti-tumour responses, in particular CD8+ T cells, where the ability to control HPV-positive tumours is likely mediated by CD8+ T cell-specific recognition of HPV-derived antigens [38, 39]. Indeed, numerous reports have shown increased abundance of CD8+ T cells in HPV-positive compared to HPV-negative OPSCC where their presence is correlated with overall improved survival [5–7, 37, 40, 41]. In addition, CD20+ B cells [34, 40, 42] and FoxP3+Treg [5, 34] are also increased in HPV-positive compared to HPV-negative OPSCC, suggesting a complex interplay in adaptive immunity in response to HPV-driven oncogenesis. In light of this substantial evidence we did not pursue further lymphocyte characterisation at the sub-population level.

The ratio of circulating peripheral blood neutrophils in relation to lymphocytes has been suggested as a potential prognostic marker for many cancers including OPSCC [43, 44]. A high circulating neutrophil to lymphocyte ratio (NLR) has been found for both HPV-positive and HPV-negative OPSCC [45]. In HPV-positive OPSCC, a high NLR was associated with higher T classification, lower 5-year overall survival and disease-free survival [46]. Similarly, in a large cohort study, Huang et al. found higher levels of circulating neutrophils in HPV-negative compared to HPV-positive OPSCC, although both correlated with lower overall survival compared to patients with lower numbers of circulating neutrophils [47]. Contrary to this, high circulating lymphocyte levels were associated with improved recurrence-free survival in HPV-positive OSCC. However, following multivariate analysis the investigators found that a high circulating neutrophil count predicted for lower overall and recurrence-free survival for only the HPV-positive cohort [47]. In contrast, Rosculet et al. found that NLR was an indicator for both recurrence-free and overall survival in OPSCC but this association was lost when HPV-status was included in the analysis [48]. In support of this, a high NLR predicted for a worse 5-year overall survival compared to a low NLR in HPV-negative OPSCC [49]. Moreover, Rachidi et al. found that the circulating NLR was significantly lower in HPV-positive OPSCC compared to the HPV-negative counterparts [50].

This study showed that the tissue NLR is significantly greater for HPV-negative than HPV-positive OPSCC, which is supportive of some but not all of the current circulating NLR data. There may be a discourse between the numbers of circulating leukocytes and those recruited to the tumour micro-environment particularly for lymphocytes, as it appears that HPV-positive OPSCC contain greater numbers of specific subsets (CD8+ T cells, CD20-B cells and FoxP3+Treg) than their HPV-negative counterparts that are also associated with overall improved survival in HPV-positive OPSCC [5–7, 37, 40, 41]. Larger scale tissue-based immunohistochemical analysis in concert with measurement of circulating NLR is required to resolve the suitability of this type of analysis for prognostication of OPSCC with HPV-status.

Given the striking increase in TAN numbers in HPV-negative compared to HPV-positive tumours, we decided to examine the mechanisms by which the disparity in TAN abundance may be mediated. Recruitment of leukocytes to tumours is driven by chemokines; with specific chemokines responsible for the recruitment of particular leukocyte subsets and several studies have reported that OPSCC cells express a number of chemokines [13, 41, 51]. We reasoned that HPV-negative tumours would produce more neutrophil-specific chemokines than HPV-positive tumours as a mechanism to recruit increased numbers of TAN. Indeed, using a rudimentary 2D culture medium transfer model we previously showed that NTF were stimulated to secrete elevated levels of several cytokines in response to the culture medium from a number of HPV-negative but not HPV-positive OPSCC cell lines [13, 52]. Moreover, this increase was mediated in an IL-1-dependent manner with IL-1 liberated from HPV-negative OPSCC cell lines acting on the NTF IL-1R to stimulate chemokine production [13]. However, traditional 2D-based monolayer cell culture systems lack the 3D architecture and the spatial complexity that give solid tumours their characteristic features such as gradients for oxygen, pH, nutrition and waste products that give rise to areas of tumour necrosis and hypoxia, and so data generated in 2D often does not reflect what occurs in 3D. Most tumours grow as 3D masses closely surrounded by a fibroblast-populated stroma that communicate with tumour and other cells via paracrine signalling, driving tumour progression. *In vivo* orthotopic tumours cannot be used because the oropharyngeal cavity of rodents is small and any sizable tumour grown at this site would cause rapid asphyxiation and so *in vivo* models of OPSCC are limited to subcutaneously grown tumours that are far removed in terms of tissue structure and microenvironment than the tumours observed in humans. In addition, HPV is not a natural host of rodents and so an inappropriate immune response may ensue giving rise to false-positive data. We therefore endeavoured to recreate the tissue architecture using tumour spheroids [structures that are known to replicate many biophysical features of avascular tumours, [53]], embedded in a NTF-populated collagen matrix to more closely mimic the *in vivo* OPSCC microenvironment.

Using these 3D tumour-stromal models we observed that HPV-negative FaDu tumour/NTF co-cultures produced substantially more chemokines than NTF or FaDu MCTS cultured alone, and importantly, much more than UPCI-SCC90 HPV-positive tumour-stromal models. Furthermore, expression of the neutrophil-specific chemokine CXCL8 was produced at significantly higher levels than CCL2 or CCL5 in HPV-negative tumour-stromal models, suggesting that neutrophil-specific chemokines may out-weigh those for monocytes and lymphocytes, potentially skewing leukocyte subset recruitment in these tumours. We were unable to produce reliable and consistent MCTS from other HPV-positive cell lines and so our 3D analysis is limited to FaDu and UPCI-SCC90 cell lines. However, the chemokine profiles detected using these MCTS directly correlated with the profiles observed for other HPV-positive/negative cell lines in our previous 2D study [13], providing some evidence that these phenomena is not cell line

specific but may be a general occurrence for HPV status. In support of this, analysis of the Gene Expression Omnibus (GEO) and TCGA databases showed significantly elevated levels of CXCL8 in HPV-negative compared to HPV-positive tumours [24], consistent with our *in vitro* 3D model data. In addition to CXCL8, increased abundance of other neutrophil-specific chemokines such as CXCL1, CXCL5 and CXCL6 is likely, as evidenced by our previous cytokine array analysis [13], and this may further skew the imbalance in leukocyte recruitment in favour of preferential neutrophil recruitment.

Blocking IL-1R using the highly specific antagonist anakinra almost completely abolished chemokine production, providing further support to the notion that IL-1/IL-1R paracrine signalling between HPV-negative tumour cells and NTF is of paramount importance for chemokine production. In support of this, increased levels of IL-1 β have been found in HPV-negative compared to HPV-positive OPSCC patient samples [13, 41].

Tonsillar [54] and oral keratinocytes [55] constitutively express IL-1 at basal levels, but levels significantly increase upon DNA-induced malignant transformation [56, 57] and this appears to be important in tumour progression, as pharmacological inhibition of IL-1 β interrupts chemically-induced oral carcinogenesis in rodent models [57]. HPV infection appears to ablate the ability of keratinocytes to express IL-1 β ; indeed we previously observed low levels of IL-1 α and IL-1 β in HPV-positive compared to HPV-negative cell lines and tumour biopsies [13]. Moreover, a complete lack of IL-1 β gene expression has also been observed in HPV-positive cervical carcinoma cell lines [56]. In HPV infected cervical keratinocytes, Niebler et al., demonstrated that IL-1 β is continually degraded in a HPV-16, E6 driven proteasome-dependent process via ubiquitin ligase, leading to complete loss of the cytokine as HPV-induced malignancy develops [56]. It is plausible that such a mechanism also occurs in HPV-positive OPSCC cells. Since IL-1 β is known to drive NF- κ B-induced chemokine expression in many cell types, it is logical that HPV-negative OPSCC are driven to secrete high levels of chemokines and therefore recruit increased numbers of TAN, whereas chemokines are much less abundant in HPV-positive OPSCC and so TAN recruitment is reduced. Li et al. overexpressed HPV18 E7 in the HPV-negative adenocarcinoma OSCC cell line Cal27 and showed that this directly reduced CXCL8 gene expression and protein secretion, suggesting that HPV gene products may have a more direct effect on chemokine production [24], although such a mechanism has not been shown for OPSCC cells. HPV infection may act to suppress TAN recruitment to HPV-positive OPSCC, although more research is required to further define this link.

Given the high levels of chemokines produced by the paracrine tumour-stromal interactions in HPV-negative OPSCC models it was no surprise that these co-cultures exhibited substantially more overall leukocyte recruitment than HPV-positive 3D models. However, it is remarkable that we observed significantly more neutrophil infiltration into HPV-negative tumour-stromal models than their HPV-positive counterparts, mirroring that observed in human patient tumour

samples. Treatment with anakinra significantly reduced the recruitment of both neutrophils and monocytes into both HPV-positive and HPV-negative tumour-stromal models, although the treatment was far more pronounced for HPV-negative tumour-stromal models, once again underscoring the importance of IL-1 β in immune cell recruitment to tumours. These data are encouraging and validate the usefulness of human 3D *in vitro* models to study complex tumour microenvironment interactions with multiple cell types that may negate some of the problems experienced in the differences between human and murine immune systems encountered during *in vivo* animal experiments and also with 2D culture.

The use of anakinra to inhibit immune cell infiltration is an interesting concept. Indeed, anakinra was found to reduce circulating levels of CXCL8, tumour growth and the number of infiltrating TAM into mice bearing erlotinib-resistant adenocarcinoma OSCC (Cal27) and laryngeal carcinoma (SQ20B) xenografts grown subcutaneously. Overall survival in these mice was increased further when they were treated with the epidermal growth factor receptor (EGFR) tyrosine kinase inhibitor, erlotinib, indicating that this adjunct therapy may be effective at overcoming EGFR inhibitor tumour resistance [58]. Anakinra has also been shown to reduce the levels of CXCL8 and number of TAM as well as reducing lymph node metastasis in a murine model of lung cancer [59]. Whereas, in breast cancer blocking IL-1 activity with anakinra or the IL-1 β specific antibody, canakinumab, reduced breast cancer metastasis by inhibiting epithelial to mesenchymal transition and preventing metastatic outgrowth of disseminated tumour cells via inhibition of wnt signalling pathways [60–62]. Since blockade of IL-1R by anakinra reduced leukocyte levels in both HPV-positive and HPV-negative OPSCC *in vitro*, it could be argued that this antagonist may be effective for both types of tumour, however, the increased numbers of leukocytes recruited to HPV-negative OPSCC suggests that the treatment would be most effective for this cancer type. Therefore, blockade of the IL-1/IL-1R axis may be a promising adjunct anti-tumour therapy that would particularly affect HPV-negative OPSCC, although there may be inherent side effects in the blocking of this key inflammatory pathway, such as potential changes to inflammatory signalling pathways leading to dysregulated host inflammatory responses to infection or alterations to the activation of important immune cells types such as natural killer and cytotoxic T cells that are crucial in host anti-cancer responses [63, 64].

In summary, our human *in vivo* and 3D tumour-stromal *in vitro* data show, for the first time, that HPV-negative OPSCC contain significantly more TAN than HPV-positive OPSCC. Additionally, the mechanism of neutrophil recruitment appears to be via IL-1-mediated CXCL8 release by NTF. HPV infection appears to prevent IL-1 expression by tumour cells thereby suppressing TAN recruitment. Since TAN have been linked with poor prognosis, their apparent reduced recruitment to HPV-positive tumours may partially explain the improved outcome imparted by HPV-infection in OPSCC. Targeting the IL-1/IL-1R

axis may be a viable consideration for the treatment of HPV-negative OPSCC.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation.

ETHICS STATEMENT

The studies involving human participants were reviewed and approved by National Research Ethical Committee approval (UK 12/LO/2018). Written informed consent for participation was not required for this study in accordance with the national legislation and the institutional requirements.

AUTHOR CONTRIBUTIONS

CM, KH, and RB conceived and designed the research. SA-S, NH, BO, and CM performed experiments, analysed the data, conducted statistical analysis, and interpreted the results. The manuscript was written and figures prepared by CM, SA-S and BO, and further edited by all the authors. PO contributed essential reagents and expert knowledge. All authors are aware of the content and have read and approved the manuscript for publication.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/froh.2021.604565/full#supplementary-material>

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Inflammatory Mediators in Oral Cancer: Pathogenic Mechanisms and Diagnostic Potential

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Approximately 15% of cancers are attributable to the inflammatory process, and growing evidence supports an association between oral squamous cell carcinoma (OSCC) and chronic inflammation. Different oral inflammatory conditions, such as oral lichen planus (OLP), submucous fibrosis, and oral discoid lupus, are all predisposing for the development of OSCC. The microenvironment of these conditions contains various transcription factors and inflammatory mediators with the ability to induce proliferation, epithelial-to-mesenchymal transition (EMT), and invasion of genetically predisposed lesions, thereby promoting tumor development. In this review, we will focus on the main inflammatory molecules and transcription factors activated in OSCC, with emphasis on their translational potential.

Keywords: oral cancer, inflammation, oral carcinogenesis, biomarker, OPMD

INTRODUCTION

The links between cancer and chronic inflammation are well-established. In this process, pro-inflammatory mediators act by stimulating inflammation to either abrogate tumor progression or facilitate tumor growth and metastasis [1, 2]. Approximately 15% of cancers are attributable to the inflammatory process [3]. Such cancers include lung, pancreatic, esophageal, bladder, gastric, cervical, colorectal, and prostate [4]. During the oral malignant transformation process [from non-dysplastic hyperkeratosis, through oral dysplasia to the development of oral squamous cell carcinoma (OSCC)], there is a progressive increase of the inflammatory infiltrate (quality and density) [5], and growing evidence supports an association between OSCC and chronic inflammation [6, 7]. Different oral inflammatory conditions, such as OLP, submucous fibrosis, and oral discoid lupus, are all predisposing for the development of OSCC [8]. The microenvironment of these conditions contains activated cytokines and chemokines, prostaglandins, reactive oxygen species, and various transcription factors. Some of these mediators have the ability to induce proliferation, epithelial-to-mesenchymal transition (EMT), and invasion [9] of genetically predisposed lesions (with mutations in tumor-suppressor genes and/or oncogenes), thereby promoting tumor development. In established OSCC, chronic inflammation is also a common feature, being involved in tumor progression, invasion, and metastasis [5, 6, 10]. Thus, many studies have assessed the utility of different inflammatory molecules as prognostic biomarkers and treatment targets for OSCC.

The aim of this review is to outline the main inflammatory molecules and transcription factors activated in OSCC, with special focus on their translational potential.

INFLAMMATORY MEDIATORS INVOLVED IN ORAL CARCINOGENESIS

There are different inflammatory mediators reported to have a role in the development and progression of OSCC (Table 1). In this review, we will focus on the most commonly investigated.

NF- κ B

Nuclear factor kappa-beta (NF- κ B) is a key inflammatory transcription factor frequently expressed in tumors that regulates the expression of a variety of genes involved in inflammation, proliferation, tumorigenesis, and cell survival [47–49]. NF- κ B is canonically activated by tumor necrosis factor alpha (TNF- α), interleukin (IL)-1, and lipopolysaccharide (LPS) [48], and when activated, it enhances the expression of different cytokines, including IL-1, IL-6, and IL-8 [50]. Its aberrant expression is linked to carcinogenesis [51] and EMT induction [52] and is associated with worse survival in solid cancers [53]. In OSCC, NF- κ B is constitutively activated and is associated with the upregulation of different inflammatory genes, including *IL-6*, *IL-8*, *CCL5*, and *CXCL10* [6], and is considered a major factor responsible for the inflammatory infiltrate observed in the tumor microenvironment (TME) [54]. NF- κ B has an important role in the malignant phenotype of oral cancers, as it participates in the modulation of bone invasion [48]; enhances angiogenesis [55], invasion [40, 56], and metastasis [40, 41]; and induces EMT [52]. The EMT process is a crucial step for the development of OSCC metastasis [57]. It involves the repression of E-cadherin (an important epithelial adhesion molecule) *via* Snail expression, which depends on NF- κ B activation *via* AKT [52]. IL-8 and EGF are able to induce EMT *via* NF- κ B activation, and IL-8- and EGF-induced EMT can be reversed by blocking AKT or NF- κ B [58, 59]. NF- κ B importance during OSCC development is well-exemplified by its inactivation, as this inhibits cell survival and growth; expressions of IL-1 α , IL-6, and IL-8 [60]; and metastases [41]. Because of this, NF- κ B inhibition has been proposed as a possible treatment for head and neck squamous cell carcinoma (HNSCC).

AP-1 Pathway

Activator protein 1 (AP-1) is a transcription factor complex composed of either homodimers of Jun protein or heterodimers of Jun and Fos proteins [61] that orchestrates the expression of different genes involved in inflammation, embryonic development, lymphoid proliferation, oncogenesis, and apoptosis [62] and is reported to be essential for DNA synthesis [63]. AP-1 activation seems to be of clinical significance in cancer, as high expression levels have been associated with drug resistance [64]. AP-1 is activated during oral keratinocyte carcinogenesis [37], and its expression increases with oral tumor progression [38]. Similar to NF- κ B, it can also be activated by IL-1 [65], which induces IL-8 secretion and promotes the cell survival and growth of HNSCC cells [39]. A recent study suggested that AP-1 induces bcl-2 expression (a proto-oncogene related to apoptosis suppression implicated in resistance to chemoradiation therapy in OSCC) in recurrent chemo- and radioresistant oral tumors [38], which suggests that targeting

TABLE 1 | Inflammatory pathways and mediators reported to have a role in oral carcinogenesis.

Pro-inflammatory cytokines	References
IL-1	[7, 9, 11, 12]
IL-1R1	[13]
IL-6	[6, 11, 14]
IL-8	[6, 11, 14, 15]
TNF- α	[5, 11, 16]
TGF- β	[17–19]
Immunosuppressive Cytokines	
IL-1RA	[20, 21]
IL-2	[22]
IL-4	[22, 23]
IL-10	[24–26]
IL-12	[27]
IL-13	[24]
IFN- γ	[14, 28]
Chemokines	
CCL	[29]
CXCL1	[30]
CXCL2	[29, 31]
CCL4	[32]
CCL7	[33]
CXCL3	[29]
CXCL10	[34]
CXCL12	[31]
CXCR1	[35, 36]
CXCR2	[36]
Transcription factors	
AP-1	[37–39]
NF- κ B	[6, 40–42]
Enzymes	
COX2	[43–45]
Prostanoids	
PGE2	[46]

the AP-1 pathway might contribute to overcome resistance to chemoradiation therapy in OSCC. As AP-1 can be activated by IL-1, targeting IL-1 could be beneficial for oral cancer treatment, as this could reduce the activation of NF- κ B and AP-1 pathways with subsequent reduction of bcl-2, but this hypothesis needs to be corroborated.

TNF- α

TNF- α is a multifunctional cytokine identified as an important mediator of cancer development [66], as well as induces EMT [67] and enhances tumor angiogenesis [68] and invasion [56]. Therefore, it is considered an important regulator of proliferation, invasion, and metastasis of many cancers [69]. TNF- α is expressed in some oral potentially malignant disorders (OPMDs), such as OLP [70], and is endogenously expressed in oral carcinomas [71]. In OSCC, TNF- α promotes a pro-invasive and pro-inflammatory phenotype in a paracrine manner

[5, 16] by upregulating genes that are associated with neutrophil recruitment, invadopodia, and invasion. The upregulation of these genes was also associated with reductions in both the overall survival and disease-free survival of patients with OSCC [5]. Elevated TNF- α receptor-1 (TNFR-1) signaling has also been associated with metastasis of OSCC [41, 72], attributable to the ability of TNF- α to stimulate the invasion of OSCC cells by enhancing matrix metalloproteinase (MMP)-2 and MMP-9 production [41, 56], which is regulated by the NF- κ B, AKT, and PI3K signaling pathways [5, 41, 72]. It has been demonstrated that MMPs play critical roles in OSCC, as elevated expression of MMPs is associated with increased OSCC invasion, metastasis, and poor prognosis [73–75]. MMPs are also reported to have a prominent role in the EMT process [76], as MMP-2, MMP-9, and MMP-7 are able to enhance EMT [77–79]. NF- κ B is an important regulator of MMPs [80], and TNF- α can activate NF- κ B *via* TNFR1, which results in enhanced MMP secretion [81]. TNF- α is also able to induce EMT *via* p38 MAPK activation [82], and TNF- α -induced EMT has been related to the induction of cancer stem cells (CSCs) [67]. The presence of CSCs in OSCC is of importance as this has been linked to therapy resistance and worst prognosis. In OSCC, the expression of CD44 (a well-known CSC marker) has been associated with increased cell invasion, cell migration, and therapy resistance *via* a mechanism that includes the activation of PI3K/Akt/GSK3 β and Raf-MEK-ERK signaling networks [83], and silencing CD47 (a molecule involved in the generation of CSCs in OSCC) has shown to reduce EMT and the presence of CSCs [84]. The activation of the PI3K/Akt/GSK3 β signaling pathway has also been associated with increased proliferation, invasion [85], the development of EMT, and distant metastasis [86].

Due to all the beneficial effects of TNF- α during cancer development, targeting TNF- α might be a useful strategy for OSCC treatment. *In vitro* experiments have shown anti-TNF- α therapy to reduce growth and metastasis of OSCC cells [87], but this needs to be investigated further before it can be translated into the clinic.

IL-6 and IL-8

Both IL-6 and IL-8 are considered “oncogenic cytokines,” as they are able to cause EMT [88], stimulate angiogenesis and tumor growth [89, 90], disrupt cell–cell communication, impede macrophage function, and promote epithelial and endothelial cell migration and invasion [91]. IL-6 and IL-8 levels are elevated in patients with OPMDs and OSCCs [6, 14, 92, 93], which is likely to be a consequence of aberrant NF- κ B activation [94]. IL-6 and IL-8 can be produced by malignant oral keratinocytes themselves, or by other cells of the TME, such as tumor-associated macrophages (TAMs). TAMs are an important source of both of these cytokines, and thus many attempts have been done to target TAMs to restrict their secretion [95]. IL-8 is reported to act as an autocrine growth factor in HNSCC and other cancers [15] and has been proposed as a potential mediator of the development of OSCC. It is constitutively expressed in malignant oral keratinocytes, and its inhibition decreases viability, proliferation [6], and invasion of OSCC cells [16] and enhances the proliferation, angiogenesis, and survival rate

of cancer cells [96]. Similarly, IL-6 overexpression in patients with HNSCC is associated with poor prognosis, probably by enabling an immunosuppressive TME by increasing the presence of myeloid-derived suppressor cells and PDL-1 expression, and is considered a significant predictor of treatment outcome [97]. In OSCC, the expressions of IL-6 and IL-8 are associated with a more invasive mode of growth [11].

IL-1 Family Members

IL-1 is the prototype of a pro-inflammatory cytokine and includes IL-1 α and IL-1 β . IL-1 α and IL-1 β are both constitutively expressed in OSCC [9, 12, 98, 99], can be found in the saliva of patients with OSCC [100, 101], and have been reported to have important functions in OSCC carcinogenesis and tumor progression [7, 10].

IL-1 α expressed by OSCC promotes autocrine activation of NF- κ B and AP-1 and upregulates the expression of IL-8 [39] and IL-6 [98]. OSCC cells produce IL-1 α [12], which induces the proliferation and cytokine secretion by cancer-associated fibroblasts (CAFs) (CCL7, CXCL1, and IL-8), promoting tumor progression [33]. IL-1 α seems to be important for the development of distant metastases, as IL-1 α is highly expressed in metastatic HNSCC tumors compared to non-metastatic HNSCC tumors. This is probably achieved by the capability of IL-1 α to induce transmigration of tumor cells across the endothelium and to enhance the expression of metastatic genes, such as *MMP-9*, *PGE2*, *VEGF*, and *IL-8* [10]. It has also been reported that IL-1 α can act as an oncoprotein by itself, as intranuclear IL-1 α has been shown to induce malignant transformation of cells from the bone marrow and perivascular area [102].

IL-1 β increases the levels of IL-6 and IL-8 expressed by OD and OSCC cells and promotes the invasiveness of OSCC by inducing EMT [9]. IL-1 β has also been identified as a key node gene in the TME of OSCC *in vivo* [7]. The expression of precursor IL-1 β mRNA is correlated with the presence of malignant changes (from normal, to mild, through severe dysplasia to OSCC) [9], and elevated IL-1 β expression has been related to lymph node metastasis of OSCC [103]. IL-1 produced by HNSCC can also stimulate the production of different cytokines by CAFs and normal fibroblasts, such as CCL-7, CXCL1, IL-8, and CCL-5 [33, 104]. These findings strongly suggest a possible role of IL-1 β in the oral carcinogenesis process, which is supported by the fact that IL-1 β silencing can reduce tumor size *in vivo* [7].

The IL-1 agonist receptor, IL-1R1, is also overexpressed in OSCCs and, together with IL-1 β , was shown to promote cancer growth and metastasis by upregulating CXCR4, which could be reversed by inhibiting IL-1R1 by overexpressing the interleukin 1 receptor antagonist (IL-1RA) [13]. Interestingly, IL-1RA has been reported to be downregulated in OD and in OSCC [20] and is reported to regulate IL-1-induced secretion of IL-6 and IL-8 by inhibiting the p38 MAPK and NF- κ B pathways [50, 105].

COX-2

Cyclooxygenase (COX)-2, an inflammation-induced enzyme that converts arachidonic acid into prostaglandins [e.g., prostaglandin E2 (PGE2)], is frequently expressed in many types of cancers. COX-2 is able to induce CSC-like activity and to promote

angiogenesis, proliferation, apoptotic resistance, inflammation, invasion, and metastasis of cancer cells [106]. Importantly, COX-2 inhibition has been shown to reverse cancer progression [107, 108]. COX-2 is induced by a variety of molecules, including IL-1 [109], epithelial growth factor (EGF) [110], transforming growth factor-beta (TGF- β) [111, 112], and TNF- α . COX-2 expression is induced early in the process of oral carcinogenesis [43]. Its level is associated with the degree of dysplasia [44], is overexpressed in OSCC [113, 114], and is correlated with advanced tumor stage, high risk of distant metastasis [115], and worse prognosis in patients with OSCC [116]. In oral cancer, COX-2 is of importance for maintaining a chronic inflammatory state [117], influencing different processes, such as cell migration by upregulating the expression of intercellular adhesion molecule-1 (ICAM-1) *via* PGE2 [46], and lymphoangiogenesis by regulating VEGF production [45, 118, 119]. VEGF is commonly overexpressed in OSCC, and COX-2/VEGF-C co-expression is correlated with lymphoangiogenesis, lymph node metastasis, and TNM stage and is reported as an independent factor for survival [45]. Increased VEGF expression in oral cancer is also a consequence of tumor-associated hypoxia, as VEGF is upregulated in decreasing concentrations of oxygen [120, 121]. In reduced oxygen concentrations, hypoxia-inducible factor-1 α (HIF-1 α) binds to hypoxia response elements and upregulates VEGF, promoting angiogenesis [122]. In OSCC, HIF-1 α and HIF-2 α correlate positively with clinical-pathological parameters, such as tumor size and micro vessel density, and *in vivo* experiments have shown their knockdown to reduce tumor angiogenesis and tumor growth [123]. In addition, hypoxia will also promote an inflammatory state, as VEGF is able to induce COX-2 expression, which will result in the production of PGE2 and the activation of NF- κ B [124].

TGF- β

TGF- β is a multifunctional pro-inflammatory cytokine that can either inhibit or promote tumor formation and progression of many cancers, whether by inducing apoptosis and growth arrest and by inhibiting proliferation or by stimulating angiogenesis, inflammation, EMT, and immune suppression, respectively [125]. If TGF- β acts as a tumor suppressor or tumor promoter depends on the regional and cellular context [126]. In OSCC, TGF- β is reported to promote tumorigenesis [17]. This is supported by the fact that OPMDs [18] and OSCC [19, 127] express higher levels of TGF- β than healthy controls and that high TGF- β levels are associated with disease recurrence and poor prognosis in patients with OSCC [19]. There are different mechanisms by which TGF- β could act as a tumor promoter in oral cancer. TGF- β is probably the most important factor involved in the differentiation of CAFs, and the accumulation of CAFs is reported as an independent prognostic factor in OSCC. CAFs are able to modulate the TME, facilitating cancer progression [128]. An *in vivo* mouse model in which TGF- β 1 was transgenically induced revealed that TGF- β 1 induced epithelia hyperproliferation, severe inflammation, and angiogenesis at similar levels to those observed in HNSCCs, suggesting that TGF- β 1 provides a tumor-promoting microenvironment [17]. In OPMDs, TGF- β promotes a more malignant phenotype by

increasing cell motility *via* the protein phosphatase 1 (PP-1) signaling pathway [129]. TGF- β seems to be important for EMT development, as TGF- β induces EMT in endothelial cells, and endothelial cells cultured with TGF- β are able to induce EMT in OSCC cells [130]. Also, TGF- β is able to induce EMT by stimulating the expression of ADAM12 (a desintegrin and metalloprotease associated with cancers) [131].

Immunosuppressive Cytokines

Anti-inflammatory cytokines also have a role in the oral carcinogenesis process. They can act as a double-edged sword, they can counteract the tumorigenic potential of their pro-inflammatory counterpart, and they can act as immunosuppressive molecules by decreasing the anti-tumor immune response [132]. Different immunosuppressive cytokines have been reported to have different roles in OSCC development (Table 1), with IL-1RA, IL-4, IL-10, and IL-13 being the most commonly investigated. IL-1RA decreases during the oral carcinogenesis process [20] and *IL1RN* (the gene that codes for IL-1RA) is downregulated in HNSCC [133, 134]. This in theory would allow higher IL-1 activity with the aforementioned effects. Nevertheless, high IL-1RA expression has been reported in advanced and poorly differentiated OSCCs [20, 24], suggesting that IL-1RA expression could increase tumor progression, but this needs further investigation. IL-4, IL-10, and IL-13 have also been reported to increase in OSCC patients compared to healthy controls [24, 25, 135], and high IL-10 expression has been associated with a more aggressive OSCC phenotype [136]. IL-4 induces immune deviation from T_H1 to T_H2 responses, which prevents tumor rejection [137]; IL-10 suppresses the anti-tumor immunity and contributes to tumor immune escape [135] and IL-13 compromises the anti-tumor response by inhibiting IFN- γ secretion and CD8+ T lymphocyte activity [138].

SOURCES OF INFLAMMATION

Within the TME, cancer cells are not the only source of inflammatory molecules. Tumors are complex systems composed not only of neoplastic cells but also of stromal cells, which form the TME. These cells are not innocent bystanders and can interact with tumor cells and modify the extracellular matrix, facilitating and promoting proliferation, invasion, angiogenesis, and metastasis [49, 139]. Single cell profile of 5,578 samples obtained from 18 OSCCs revealed the presence of nine clusters of cells based on known marker genes, such as epithelial cells (malignant and non-malignant, based on CNV and their karyotypes), T cells (four sub-clusters), B/plasma cells, macrophages, dendritic cells, mast cells, endothelial cells, fibroblasts (three sub-clusters), and myocytes [140], which shows how heterogeneous tumors are.

As discussed previously, malignant oral keratinocytes (which are genetically unstable) activate different transcription factors, such as AP-1 and NF- κ B, leading to the activation of oncogenes (which induces proliferation by the regulation of apoptosis, angiogenesis, and cell growth), and inflammatory genes [6]. The latter results in the constitutive production of different inflammatory factors, such as IL-1, IL-6, IL-8, TNF- α , and

TGF- β [141], among many others, that can activate the same transcription factors, creating a positive feedback loop.

TAMs, T lymphocytes, neutrophils, and mast cells are also considered important sources of inflammatory mediators [5]. TAMs promote proliferation and invasion in OSCC [142, 143], and their presence correlates with disease progression and is considered an adverse prognostic factor [144]. They act as an important source of cytokines, metalloproteinases, and growth factors [95]. T lymphocytes are considered the most abundant inflammatory cells among the inflammatory infiltrate observed in OSCCs and can be beneficial or detrimental for oral carcinogenesis depending on their secretion profile [145]. They can secrete molecules that favor tumor progression (IL-6, IL-17, IL-23, TNF- α , and TGF- β) or molecules that exhibit an anti-tumor effect (IL-12 and IFN- γ) [49]. Neutrophil infiltration increases OSCC invasion by inducing matrix degradation and invadopodia formation through a paracrine TNF- α -induced mechanism [5, 16]. Mast cells have been associated with angiogenesis and are able to secrete numerous cytokines, chemokines, and angiogenic factors [146, 147], but their role in the development of OSCC is still debatable.

Cancer-associated fibroblasts, the most dominant components of the TME, are recipients of many of these factors (e.g., TGF- β), as well as directly contributing to tumor progression and an inflammatory TME *via* the secretion of VEGF, IL-6, IL-8, PGE2, TGF- β , and activation of NF- κ B [148]. The presence and activity of CAFs are associated with poorer prognostic outcomes for OSCC [149] and are involved in bone invasion [150].

Senescent cells (which are more prevalent in older individuals, same as cancer) also contribute to chronic inflammation. When cells senesce, they develop an inflammatory secretory phenotype known as the senescent-associated secretory phenotype (SASP) [151], characterized by the secretion of high levels of “pro-oncogenic cytokines,” such as IL-1, IL-6, and IL-8 [152]. In fact, the SASP is currently recognized as a cancer promoter mechanism, as it can induce EMT, invasion, and metastasis [151, 153], and its regulation has been proposed as anti-cancer treatment [154, 155].

DIAGNOSTIC POTENTIAL

Due to the advantages of using saliva samples (non-invasive and cost-efficient) for diagnostic and disease screening purposes, different studies have explored the possibility of using salivary inflammatory factors as biomarkers for the development and progression of OSCC. The most studied inflammatory proteins are TNF- α [5, 14, 42, 141, 156–159], IL-1 [5, 14, 141, 160, 161], IL-6 [5, 14, 34, 42, 92, 141, 158, 159, 162–164], and IL-8 [2, 5, 14, 42, 141, 160, 161, 164] (NF- κ B-dependent cytokines), which have been found to be increased in the saliva of patients with different OPMDs (including OLP, oral leukoplakia, verrucous proliferative leukoplakia, and oral submucous fibrosis) and OSCC in comparison to healthy controls. Other cytokines, such as MIP-1 β and IFN γ [14], and the anti-inflammatory cytokines IL-10 and IL-13 [24] have also been found to be increased in the saliva of patients with OSCC.

Using an array that analyzed the expression of 50 cytokines present in the saliva of patients with stage I OSCC before and after surgical treatment, Kamatani et al. [101] showed a significant decrease in salivary IL-1 β after surgical resection. Similar to this, higher salivary levels of IL-8, IL-6, IL-1 β , MIP-1 β , and IP-10 before surgical intervention in patients with stage I OSCC were recently reported [165]. These results suggest that salivary inflammatory cytokines might be useful to monitor disease relapse.

A proteomic analysis of 60 saliva samples from healthy individuals and patients with OPMD and OSCC detected 21 proteins differentially expressed in OSCC compared to those in the other groups. Among those, three proteins were selected for further validation using ELISA, which included the interleukin-1 receptor antagonist (IL-1RA). Salivary IL-1RA was significantly decreased in patients with OPMD and control individuals compared to that in patients with OSCC but, alone, was suboptimal for distinguishing patients with OPMDs and healthy controls from patients with OSCC. In combination with other biomarkers (SLC3A2 and S100A2), IL-1RA was able to distinguish patients with OSCC from both healthy individuals and patients with OPMD with a sensitivity and specificity of 83.33/83.33% and of 93.33/70%, respectively [21]. Salivary IL-1 β and IL-8 have also been found to discriminate between healthy individuals and patients with OSCC [160, 166] and high sensitivity and specificity values have been reported (86/97% for IL-8 and 83/76% for IL-1 β) [166, 167]. Nevertheless, a recent systematic review reported average sensitivity and specificity values of 41/69% for IL-8 and of 26/46% for IL-1 β [94], which are suboptimal. Both cytokines performed better when used in combination with other markers [161, 166], so it is likely that their future use will be as part of a panel of salivary biomarkers, rather than as single markers.

IL-6 is also a promising biomarker for the development of OSCC. IL-6 salivary levels are reported to increase with the severity of oral dysplasia [34], to differentiate between OPMD and OSCC (sensitivity and specificity values of 96 and 99%, respectively) [163], and to predict treatment outcomes in patients with OSCC [11, 97]. High salivary expression of TNF- α , IL-1 α , and IL-8 has also been associated with a decreased survival rate in tongue squamous cell carcinoma (TSCC) [11].

FUTURE DIRECTION

The understanding of the role and origin of the different inflammatory molecules involved during tumor initiation, promotion, and progression of oral cancers provides an opportunity to target inflammation to improve patient outcomes. This can be done by selectively targeting transcription pathways (e.g., NF- κ B), cytokines (e.g., IL-1), or cell types known to contribute to the inflammatory secretome (e.g., CAFs and senescent cells). There are several research lines in this field, but little has been translated into the clinics, especially with regard to OSCC. Although all of the aforementioned reports are pointing in the direction that salivary cytokines could be used for diagnostic

and prognostic aims in patients with oral cancer, more prospective studies are needed before they could be used in clinical settings.

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AUTHOR CONTRIBUTIONS

SN performed the review and wrote the manuscript.

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At the Crossroads of Molecular Biology and Immunology: Molecular Pathways for Immunological Targeting of Head and Neck Squamous Cell Carcinoma

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Background: Recent advances in immunotherapy for head and neck squamous cell carcinoma (HNSCC) have led to implementation of anti-programmed death receptor 1 (PD-1) immunotherapy to standard of care for recurrent/metastatic HNSCC. However, the majority of tumors do not respond to these therapies, indicating that these tumors are not immunogenic or other immunosuppressive mechanisms might be at play.

Aim: Given their role in carcinogenesis as well as in immune modulation, we discuss the relation between the STAT3, PI3K/AKT/mTOR and Wnt signaling pathways to identify potential targets to empower the immune response against HNSCC.

Results: We focused on three pathways. First, STAT3 is often overactivated in HNSCC and induces the secretion of immunosuppressive cytokines, thereby promoting recruitment of immune suppressive regulatory T cells and myeloid-derived suppressor cells to the tumor microenvironment (TME) while hampering the development of dendritic cells. Second, PI3K/AKT/mTOR mutational activation results in increased tumor proliferation but could also be important in HNSCC immune evasion due to the downregulation of components in the antigen-processing machinery. Third, canonical Wnt signaling is overactivated in >20% of HNSCC and could be an interesting pleiotropic target since it is related to increased tumor cell proliferation and the development of an immunosuppressive HNSCC TME.

Conclusion: The molecular pathology of HNSCC is complex and heterogeneous, varying between sites and disease etiology (i.e., HPV). The in HNSCC widely affected signaling pathways STAT3, PI3K/AKT/mTOR and Wnt are implicated in some of the very mechanisms underlying immune evasion of HNSCC, thereby representing promising targets to possibly facilitate immunotherapy response.

Keywords: head and neck cancer, molecular targets, immune microenvironment, immunotherapy, signaling pathways

INTRODUCTION

In 2018, 700,000 patients were diagnosed with head and neck squamous cell carcinoma (HNSCC) worldwide, and 350,000 patients died of the disease [1]. HNSCC develops from squamous epithelial cells in the upper-aerodigestive tract, most frequently in the oral cavity, oropharynx, hypopharynx and larynx. The development of HNSCC is caused by alcohol and tobacco use [2]. Besides this, infection with human papillomavirus (HPV) is related to formation of a specific type of HNSCC tumors (HPV⁺) which are predominantly localized in the oropharynx and have distinct clinical, molecular and immunological characteristics when compared to HPV-unrelated (HPV⁻) tumors [3].

From a molecular point of view HNSCCs are very heterogeneous. Besides mutational changes in oncogenes and most particularly tumor suppressor genes, also epigenetic changes and chromosomal instability add to the overall molecular heterogeneity [3, 4]. This variable genetic background translates into a variety of tumor characteristics, challenges treatment efficacy and demands personalized approaches. Likewise, heterogeneity is observed in the immune composition of the tumor microenvironment (TME) of HNSCC, depending on etiology and/or localization of the tumor as recently reviewed by us and others [5–7]. In general, HPV⁺ HNSCC often display a more immune inflamed TME compared to HPV⁻ HNSCC, which are frequently immunologically cold or immune excluded. In addition, tumors with these separate etiologies seem to use different immune escape mechanisms [6, 7].

Despite advances in treatment, the survival rates for HNSCC have improved very moderately over the past five decades, with the average 5-year overall survival (OS) stabilizing at 40–60% for advanced stage disease [8]. Immunotherapy has been at the forefront of translational cancer research for the last decade and has provided great therapeutic benefits in the treatment of various cancer types [9], and also emerged as novel modality for HNSCC.

The currently available immunotherapies for treatment of HNSCC are nivolumab and pembrolizumab, which are both immune checkpoint inhibitors (ICIs) targeting the programmed death receptor 1 (PD-1). Nivolumab was approved in platinum refractory, recurrent/metastatic (R/M) HNSCC on basis of the results of the Checkmate-141 trial showing superior overall survival (OS) of the nivolumab treated arm when compared to investigator's choice of therapy (7.5 vs. 5.1 months; HR 0.70; 97.73% CI 0.51–0.96; $p = 0.01$) [10]. Pembrolizumab was first approved for platinum refractory R/M HNSCC based on the Keynote-012 trial that showed objective responses in 16% (95% CI 11–22) of patients, of which 5% were complete and 82% were durable (≥ 6 months) [11, 12]. The Keynote-048 trial has led to the approval of pembrolizumab as monotherapy or in combination with chemotherapy as first-line treatment for programmed death-ligand 1 (PD-L1) positive R/M HNSCC [13].

Many studies are underway investigating the use of these ICIs, and evaluating other immunotherapy regimens [14]. Recently promising results have been reported for pembrolizumab and nivolumab with or without ipilimumab [anti-cytotoxic T-lymphocyte-associated antigen 4 (CTLA-4)] neoadjuvant to

surgery with curative intent in oral cavity squamous cell carcinoma [15, 16].

Currently, anti-PD-1 immunotherapy is effective in only a minority of HNSCC patients [17], and evidence accumulates that HNSCC can indeed be highly immune-evasive [18]. One approach is to study expression of immune-related genes in HNSCC that might relate to immune cell infiltration, predict patient outcome and could be applied to guide treatment choice [19]. Another approach to overcome immune-evasion might be to apply targeted therapies directed at molecular pathways known to be affected in HNSCC and that specifically relate to its immunological characteristics. To develop such targeted therapies, it is crucial to understand the specific pathways involved. In this review we relate the molecular landscape of HNSCC to its immunological characteristics, focusing on three of the most frequently affected pathways in HNSCC STAT3, PI3K/AKT/mTOR and Wnt, besides the EGFR pathway as a known target.

IMMUNOLOGICAL IMPLICATIONS OF THE HNSCC MOLECULAR LANDSCAPE

EGFR

One of the major hallmarks of cancer is sustained proliferative signaling [20]. Growth factor signaling is commonly mediated by the family of receptor tyrosine kinase (RTK) cell-surface receptors, of which epidermal growth factor receptor (EGFR) is the most prominent in HNSCC [21]. It signals through the RAS-MAPK-, PI3K/AKT/mTOR-, phospholipase C-gamma-, signal transducers and activators of transcription (STAT)- and Src family kinase pathways [22]. Activation of EGFR promotes cell proliferation, angiogenesis, invasiveness and metastatic potential and has a prominent role in tumor initiation and maintenance. Activation of EGFR is seen in up to 80–90% of HNSCC cases as a result of *EGFR* amplifications or autocrine loops [23]. It should be noted, however, that *EGFR* does not show the typical activating mutations in HNSCC that are found in lung cancer, and whether HNSCC cells are really oncogene addicted remains elusive.

Cetuximab, a monoclonal antibody targeting EGFR, was the first new drug in decades, and the first targeted therapy, to be FDA approved for treatment of HNSCC [24]. Initially, cetuximab seemed quite promising with a favorable toxicity profile compared to chemotherapeutics, but recent phase III trials have demonstrated its inferiority to cisplatin in terms of primary disease control [25]. Cetuximab remains one of the cornerstones in the treatment of patients unfit to receive cisplatin and in the R/M setting [26].

While framed as a targeted drug and not introduced as an immunotherapy agent, cetuximab appeared to have an additional immune-related mode-of-action through the mediation of antibody-dependent cellular cytotoxicity (ADCC) [25]. Cetuximab stimulates the CD16/Fc receptor of natural killer (NK) cells resulting in their activation and the release of granzymes and perforins leading to tumor kill [25]. Increased interferon gamma (IFN γ) production by NK cells can induce PD-L1 expression on tumor cells and immune cells within

the TME, providing a rationale for the possible synergistic potential of combining cetuximab with anti-PD-1 therapy [27–29]. Response to cetuximab treatment in HNSCC was shown to be hampered by treatment-induced recruitment of PD-1⁺ and TIM-3⁺ dysfunctional tumor-infiltrating T cells [30]. Also, PD-L1 expression on tumor cells hampered the cytolytic abilities of PD-1⁺ activated NK cells, reducing cetuximab efficacy in patients [31]. Preliminary data of a phase II trial evaluating the combination of PD-1 and EGFR inhibitory therapy showed promising results in 33 R/M HNSCC patients unfit for or refractory to cisplatin, with an overall response rate of 41% and few adverse events [32]. Results on other trials investigating the potential of this combinational regimen are to be awaited (Supplementary Table 1) [33].

STAT3

STAT3 is part of the STAT protein family that regulates the transcription of various proliferative and cytokine-related genes [34]. It is of particular interest in HNSCC because of its near-universal signaling activation, already during early oral carcinogenesis [35], and its ability to be directly activated by EGFR [34]. As STAT3 mutations in HNSCC, leading to gain-of-function, have not been described, activation of STAT3 is presumably the result of enhanced signaling through its positive regulators (cytokines, growth factors and non-receptor TKs), or decreased signaling through its negative regulators (protein tyrosine phosphatase receptors) [36]. There are differences reported between HPV⁺ and HPV[−] HNSCC with regards to STAT3 mutations and activation (Figure 1). Gaykalova et al. reported significantly more activated STAT3, as well as activated NF- κ B, in HPV[−] HNSCC [37].

In addition to supporting tumor cell proliferation, STAT3 activity is related to a variety of immunosuppressive mechanisms and is a key regulator of immune processes (Figure 2) [43]. STAT3 inhibition could thus hit two birds with one stone. It is implicated in inhibition of pro-inflammatory mediators production such as IFN γ , antigen presentation, and accumulation and anti-tumor potential of effector T cells [44]. In myeloid-derived suppressor cells (MDSCs), STAT3 activation leads to expression of cyclin D and the S100A9 receptor, resulting in the suppression of cellular maturation and increased MDSC survival, respectively [45]. In the treatment of HNSCC, radiotherapy was shown to cause immune modulation by activating STAT3 in MDSCs [46]. Furthermore, STAT3 has the ability to increase expression of the PD-1/PD-L1/L2 and CTLA-4 checkpoints [44, 47].

Altogether, these data provide a rationale for combining STAT3 inhibitors with ICIs, which has already led to various pre-clinical and clinical studies [36, 44, 48]. AZD9150, a small DNA oligonucleotide which competitively blocks the binding site of STAT3 on its promotor has been tested in a phase I dose escalation study [49]. Results showed stable disease in 44% ($n = 11/25$) of all patients, and tumor shrinkage in 50% ($n = 3/6$) of treatment refractory lymphoma patients. In a follow-up study in treatment refractory lymphoma a clinical benefit was observed in 13% of patients [50]. A large study

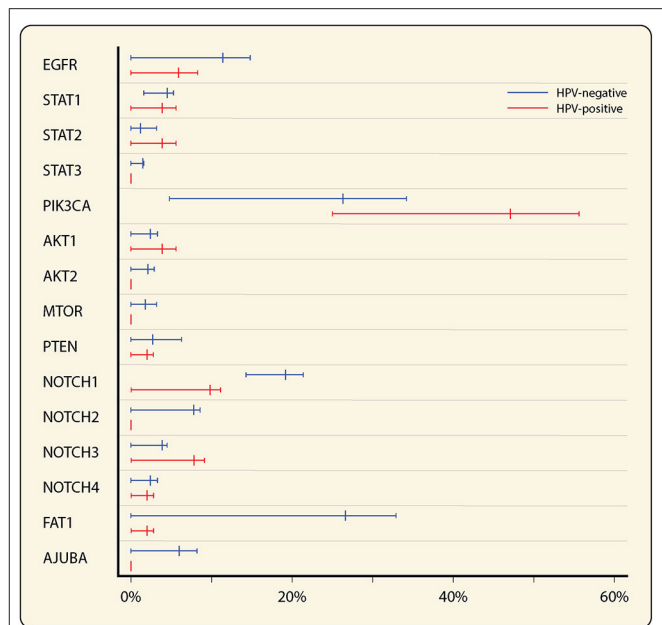
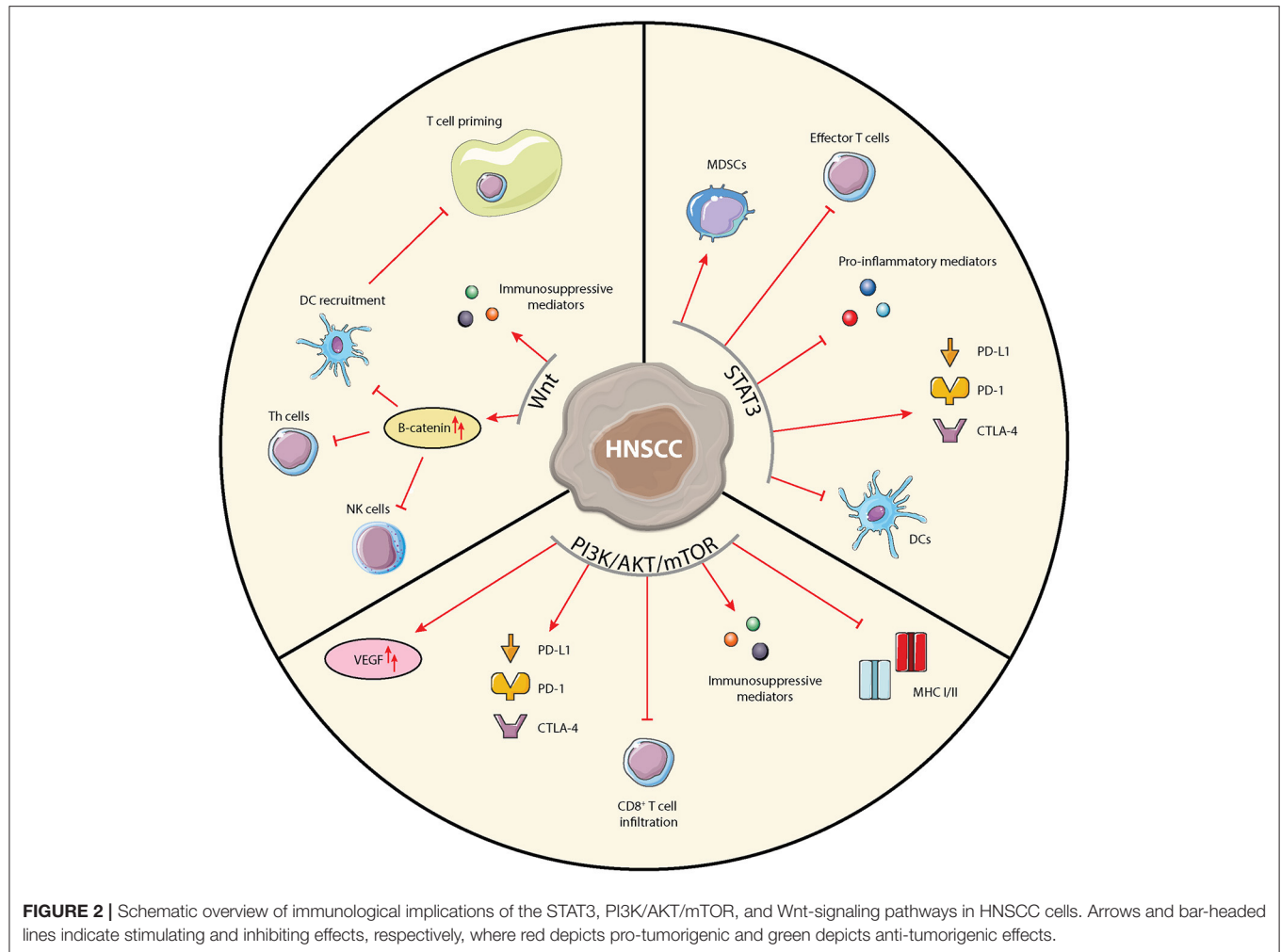


FIGURE 1 | Forest plot of mutation rates of most frequent affected genes in EGFR, PI3K/AKT/mTOR and Wnt-signaling pathways in HNSCC, stratified by HPV status (total $n = 385$, 334 HPV[−] and 51 HPV⁺). Mean mutation rates were estimated from the mutation rates in three HNSCC datasets [38–40], queried through cBioPortal [41, 42]. Minimum and maximum reported mutation rates are represented by the error bars.

investigating AZD9150 combined with durvalumab anti-PD-L1 immunotherapy in patients with solid tumors including HNSCC is underway [51]. In a recent *in vitro* study in breast cancer sentinel lymph nodes (SLN), van Pul *et al.* showed that STAT3 inhibition in immune cells, combined with immune stimulation through TLR9 using CpG-B, could activate dendritic cell (DC) subsets in SLN cultures and increased tumor-specific T cell responses [52]. Using *in vivo* HNSCC mouse models, Moreira et al. showed that a STAT3-inhibiting oligonucleotide linked to CpG specifically targeted to myeloid cells, increased tumor sensitivity to radiotherapy and increased the anti-tumor immune response, suggesting that this could be a valid pathway to target in HNSCC [53]. In a syngeneic carcinogen-induced immune competent HNSCC mouse model, a small molecule inhibitor HNC0014, targeting cMET/STAT3/CD44 and PD-L1, was shown to reduce tumor growth, pSTAT3 and PD-L1 levels in tumors and increase T cell frequencies in the circulation most efficiently when combined with anti-PD-L1 treatment [48]. Of note, STAT3 inhibition was shown to reduce PD-L1 expression in HNSCC cell lines [47]. Potentially, STAT3 inhibition by itself might already reduce the inhibitory effect of the PD-1/PD-L1 axis, especially when tumor PD-L1 expression is regulated through oncogenic pathway activation often seen in HPV[−] HNSCC. Combination therapy with ICIs targeting other immune checkpoints like TIM-3, LAG-3 or TIGIT might prove even more effective [54]. However, little is known at the moment about the effect of STAT3 on the expression of those immune checkpoints.



PI3K/AKT/mTOR Pathway

The PI3K/AKT/mTOR pathway is involved in many cellular processes including cell cycle, survival, proliferation and motility [55]. Phosphatidylinositol 3-kinases (PI3Ks) are heterodimeric kinases formed by a regulatory and catalytic subunit and are activated by RTKs. The p110 α catalytic subunit is encoded by a variety of genes of which *PIK3CA* is most important and harbors alterations in 26 and 47% of HPV⁻ and HPV⁺ HNSCC, respectively (Figure 1) [38–40]. Upon RTK activation, the regulatory subunit binds the catalytic subunit resulting in lipid phosphorylation and a cascade of events leading to activation of AKT, one of the major effectors of PI3K.

AKT is a serine-threonine kinase comprising three isoforms that are encoded by the *AKT1*, *AKT2*, and *AKT3* genes. Alterations in these genes are uncommon but overexpression of AKT in HNSCC has been reported as the result of a variety of factors such as microenvironmental stimuli, mutations in *PIK3CA* and diminished expression of *PTEN* [56–59]. *PIK3CA* and *PTEN* serve as central regulators of the PI3K/AKT/mTOR pathway and are known as bona fide HNSCC cancer genes.

The serine-threonine kinase mTOR comprises mTORC1 and mTORC2 and is an important downstream effector of AKT. It regulates critical biological functions including growth factor signaling and metabolism [55]. Genetic alterations in *EGFR*, *PIK3CA*, *PTEN*, and *HRAS* are known deregulators of mTOR signaling and are amongst the most frequently affected genes in HNSCC.

Various agents targeting PI3K, AKT, or mTOR have been studied in pre-clinical and clinical studies [60]. Although some studies in HNSCC have shown promising results, no trials have made it to phase III thus far due to unsatisfying efficacy and challenging tolerability. These early clinical trials have, however, provided valuable insights into the various physiological roles of the PI3K/AKT/mTOR pathway. It has become increasingly clear that apart from its functions in cancer cells, the PI3K/AKT/mTOR pathway also regulates many processes within the TME [61]. In various cancer types the PI3K/AKT/mTOR pathway has been implicated in the expression of immunosuppressive chemokines and cytokines [62, 63], expression of the immune suppressive vascular endothelial growth factor (VEGF) [64], reduced tumor CD8⁺ T cell

infiltration [65], expression of immune checkpoints [66–68], and expression of MHC classes I and II (**Figure 2**) [69, 70]. In HNSCC the association of activated PI3K signaling with suppression of MHC expression was demonstrated using IHC, showing an inverse staining of MHC-I and phospho-AKT [71]. Moore et al. reported that co-inhibition of mTOR and PD-L1 enhanced anti-tumor efficacy in an oral cancer mouse model [72]. Since the PI3K/AKT/mTOR pathway is overactivated in over 90% of HNSCC, through various mechanisms, it is a highly interesting pathway to target in HNSCC, especially combined with ICIs [60].

Wnt-Signaling

The Wnt-signaling cascade is an evolutionary highly conserved cascade important in (embryonic) cell growth, migration and differentiation [73]. About half of breast cancer tumors involve an activated Wnt-signaling pathway and hereditary colon cancer is often induced by a mutation in the adenomatous polyposis coli (*APC*) gene, part of the Wnt-signaling cascade [73]. Also in HNSCC, Wnt-signaling has been recognized as a central player [74].

Canonical Wnt-signaling depends on the APC destruction complex that regulates β -catenin levels, whereas non-canonical Wnt-signaling does not involve the APC complex. Binding of Wnt ligands to the Frizzled receptors leads to activation of the signaling pathway. When the Frizzled receptors are not stimulated by Wnt, cytoplasmic β -catenin levels are regulated by a destruction complex that includes amongst others APC, Axin and glycogen synthase kinase 3 β (GSK3 β) [73]. β -catenin is phosphorylated by GSK3 β and subsequently degraded by the proteasome. Upon Frizzled receptor activation, however, Axin, APC and GSK3 β are recruited to the membrane leading to inactivation of the destruction complex. Hence, β -catenin is able to translocate to the nucleus where it drives expression of target genes. These in turn regulate diverse cellular functions including cell proliferation, -survival and -migration [2].

β -catenin levels can be regulated by other processes as well, forming a source of non-canonical pathways. In HNSCC, several genes involved in Wnt-signaling are mutated or inactivated. The Cancer Genome Atlas (TCGA) data showed inactivating *FAT1* mutations in 23% of HNSCCs [38]. *FAT1* is a cadherin-related adhesion receptor which can form cellular adhesion structures and therefore plays a role in cell-cell contact. Cadherin receptors can sequester β -catenin to the plasma membrane, thus preventing its translocation to the nucleus [75]. *FAT1* knockdown in glioblastoma cell lines resulted in promotion of cell cycle progression and cellular growth and in a breast cancer xenograft model *FAT1* knockdown resulted in the progression of ductal carcinoma *in situ* to invasive breast cancer [75, 76]. In HNSCC cell lines the effect of *FAT1* knockdown was inconsistent between studies, being associated with both increased [77] and decreased [78] migration and tumorigenesis. In HNSCC patients, *FAT1* mutations and downregulation are independent predictors of shorter disease-free survival [77]. Further studies are required to clarify the role of *FAT1* in HNSCC carcinogenesis, including its effect on Wnt signaling.

AJUBA is a scaffold protein which stimulates the phosphorylation and degradation of β -catenin by activating

GSK3 β . Inactivating *AJUBA* mutations could result in a lower rate of β -catenin phosphorylation which in turn increases β -catenin-mediated gene transcription. Inactivating mutations in *AJUBA* are relatively infrequent in HNSCC with a prevalence of 6% and seem more common in HPV[−] disease [38].

Also implicated in the Wnt-signaling pathway is Notch signaling. The Notch family comprises the Notch 1, Notch 2, Notch 3, and Notch 4 receptors, which are cleaved upon binding to their ligand through cell-cell contact, leading to the transfer of their intracellular domain into the nucleus to regulate the expression of target genes. The overall role of Notch signaling in cancer development is still highly debated. Mutational inactivation of Notch has been associated with tumor development, but overexpression has been associated with tumor progression and immune evasion [79]. *Notch 1* mutations are reported in 19% of HNSCC, most common in HPV[−] tumors (**Figure 1**), and are correlated to worse outcome [80].

Loganathan et al. performed a CRISPR-Cas study in a HNSCC mouse model, in which they induced mutations in a wide-array of the so-called “long tail” genes [81], genes that are significantly mutated in tumors, but at very low frequency. Strikingly, mutational inactivation of p53 itself did not induce HNSCC, but introduction of mutations in these long tail genes did induce HNSCC tumor growth [81]. When evaluating the specific long tail genes it was found that knockout of *AJUBA* resulted in tumor growth but more importantly, it resulted in a significant decrease in Notch signaling [81]. Induction of Notch expression reversed the increased tumor growth of *AJUBA*-deficient mice, implicating Notch as the tumor-suppressive factor. Upon investigating the entire long tail gene panel, the authors ultimately concluded that in 67% of HNSCC cases, oncogenic mutations often impact Notch signaling, proposing decreased Notch signaling as a new hallmark of HNSCC [81].

The immunomodulatory role of the Wnt-signaling pathway in cancer has been reviewed extensively [82–85]. In line with its ubiquitous expression and involvement in many diverse cell functions, the Wnt pathway impacts many of the immunological players in the TME (**Figure 2**). Through activation of the Wnt-signaling pathway, DCs are pushed into a regulatory, tumor tolerant state. A recent study by Lopez-Gonzalez *et al.* showed that inhibition of Wnt-signaling through introduction of a constitutively active form of GSK3 β restored human DC activation in the presence of immune suppressive cytokines and in an *in vivo* melanoma mouse model resulted in DC recruitment and activation and promoted tumor control [86]. Wnt-pathway activation in tumor cells negatively regulates the production of the chemokine CCL4, inhibiting the recruitment of cross-presenting DCs into the TME [87]. Consequently, infiltration of effector T cells into the TME is impaired, as no nodal T cell priming occurs. In melanoma cells, increased β -catenin expression was shown to even further hamper T cell priming through upregulation of IL-10 [88]. Indeed, analysis of TCGA data indicated that activation of the Wnt-pathway correlated with an immune-excluded TME in 90% of 31 included tumor types [89]. Additionally, upregulated β -catenin expression has been associated with impaired development and function of Th cells, impaired maturation of NK cells, and increased Treg survival

[90]. Colombo et al. reviewed how cancer cells can use Notch signaling to change to cytokine milieu by secreting immune suppressive factors such as TGF- β , IL-10, CXCL12, thereby shaping a pro-tumorigenic microenvironment via cross-talk with stromal cells [91].

Hence, targeting Wnt-signaling seems a promising treatment strategy to augment ICI in HNSCC given its role in carcinogenesis as well as in shaping the TME [92]. Multiple small molecule inhibitors have been developed and some have already entered clinical trials also for HNSCC (**Supplementary Table 1**). LGK974 was shown to effectively inhibit *in vitro* HNSCC tumor growth and metastasis [93] and ICG001 was shown to downregulate HNSCC cancer stem cells and tumor growth *in vitro* [74]. Several other inhibitors of the Wnt-pathway are currently under clinical investigation [94].

Clinical trials targeting the Notch pathway have been performed and are currently ongoing [95]. However, inhibition of Notch is often associated with high toxicity possibly related to the notion that Notch signaling influences a wide array of processes [79, 81]. Clearly these issues need to be addressed, potentially by local rather than systemic inhibition of Notch, before Notch inhibitors could safely make their way to the clinic. To our knowledge, there are currently no targeted therapies available for *FAT1* or *AJUBA* mutated tumors. Obviously the notion that all these genes display inactivating mutations in HNSCC, hampers the exploitation as druggable target, and detailed functional characterization of the signaling pathways is crucial.

CONCLUSION AND FUTURE PERSPECTIVES

We aimed to outline potential targets to aid HNSCC immunotherapy response by linking selected molecular pathways, widely-affected in HNSCC, to their immunological implications. STAT3 and the PI3K/AKT/mTOR- and Wnt-pathways are of particular interest, because they are implicated in some of the very mechanisms believed to be responsible for primary or acquired resistance to ICI therapy. Interfering with the immunomodulatory functions of these pathways could provide a means to boost the response to ICI therapies. Especially for HPV⁻ HNSCC, which is considered an immunologically “cold” tumor, such strategies may have promise. Cold tumors, characterized by an immune-excluded or -desert phenotype, are known to respond poorly to ICI [96], and could be pushed toward a more inflamed or “hot” phenotype by enabling CD8⁺

T cell infiltration through inhibition of the PI3K/AKT/mTOR or Wnt-pathways. Inhibiting these pathways would on the one hand inhibit the tumor cells, and on the other hand stimulate the immune cells. Moreover, the milieu of cytokines and other mediators including IFN γ and VEGF seems tailorable through the proposed pathways, as well as the expression of MHCII and immune checkpoints like PD-1/L1 and CTLA-4. The TME could additionally be organized into a more pro-inflammatory state through regulating the migration of immunosuppressive players, such as Tregs or MDSCs into the TME as well as directly mitigating their modulatory functions by targeting STAT3 both in the tumor cells and the immune cells. An overview of recent trials investigating agents targeting the discussed pathways is given in **Supplementary Table 1**. Given the difference in prevalence of alterations in particular molecular pathways between HPV⁺ and HPV⁻ HNSCC (**Figure 1**), certain targets might be more relevant for one of the etiologies. Interference with the STAT3 pathway could hold more clinical relevance for HPV⁻ disease, while in HPV⁺ disease the PI3K/AKT/mTOR pathway might be a more suitable target. Future clinical studies should consider building in a comparison between HPV⁺ and HPV⁻ HNSCC when evaluating the efficacy of drugs interfering with these molecular pathways. Moreover, it remains crucial to consider the fact that the functional consequences of targeting the discussed pathways could be unpredictable due to the complex composition of the HNSCC TME [97]. Dissecting the impact of targeted and combination therapies on the various cell populations involved in HNSCC may help explain the success or failure to potentiate an anti-tumor immune response.

AUTHOR CONTRIBUTIONS

NW and DN wrote the manuscript. JP, CL, RB, and RV guided and revised the manuscript. RV conceptualized and guided the project. All authors contributed to the article and approved the submitted version.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/froh.2021.647980/full#supplementary-material>

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Adrenergic-Angiogenic Crosstalk in Head and Neck Cancer: Mechanisms and Therapeutic Implications

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Head and neck squamous cell carcinomas (HNSCC) are loco-regionally aggressive tumors that often lead to debilitating changes in appearance, speech, swallowing and respiratory function in patients. It is therefore critical to develop novel targeted treatment strategies that can effectively target multiple components within the tumor microenvironment. In this regard, there has been an increased recognition of the role of neural signaling networks as mediators of disease progression in HNSCC. Here, we summarize the current knowledge on the mechanisms of adrenergic signaling in HNSCC specifically focusing on neurovascular crosstalk and the potential of targeting the adrenergic-angiogenic axis through repurposing of FDA-approved drugs against HNSCC.

Keywords: HNSCC, adrenergic signaling, angiogenesis, drug repurposing, propranolol

INTRODUCTION

Head and neck squamous cell carcinomas (HNSCC) are loco-regionally aggressive tumors that result in debilitating functional and esthetic sequelae in approximately half a million individuals worldwide [1, 2]. Although chemoradiation and immunotherapy-based approaches have led to improved therapeutic benefit, treatment resistance remains a significant clinical challenge [2]. Additionally, a majority of these patients experience prolonged treatment-induced morbidities including severe xerostomia, dysphagia, loss of dentition, and mandibular osteoradionecrosis [3]. Clearly, there is a need to investigate novel therapies that can exhibit improved therapeutic efficacy against HNSCC with reduced toxicities and treatment-related complications in this patient population.

One strategy to accomplish this goal involves assessing the anticancer activity of existing Food and Drug Administration (FDA) approved drugs used for non-oncologic indications, a concept termed as drug repurposing or repositioning [4, 5]. Given the significant costs associated with drug development, an informed approach focused on identifying and evaluating existing FDA-approved agents that target critical pathways implicated in development, progression or treatment resistance in HNSCC would be beneficial. In this context, there has been an increased recognition of the role of neural signaling networks as mediators of disease progression and therapeutic resistance in several solid tumors including HNSCC [6–8]. In this article, we summarize the current knowledge on the neurovascular talk in HNSCC specifically focusing on the adrenergic signaling within the head and neck tumor microenvironment. The rationale for targeting the adrenergic-angiogenic axis through repurposing of FDA-approved neuroscience drugs against HNSCC is presented.

NEURAL REGULATION OF CANCER

The role of nerves in cancer patients, particularly in the context of cancer pain, has been long recognized [9, 10]. Sympathectomy (localized surgical interruption or removal of nerve fibers/ganglions) has been used to alleviate pain in cancer patients since the 1940s [9]. A study by Batkin et al. in 1970 showed that denervation of sciatic nerves resulted in a reduction in take of neuroblastomas in mice [10]. The infiltration of tumors by growing nerves termed as neoneurogenesis or axonogenesis has been linked to tumor progression [6, 7]. Recent landmark publications in prostate, pancreas and gastric cancers have demonstrated that nerves are not just passive players in carcinogenesis or tumor progression but an integral part of the tumor microenvironment [11–13]. Sympathectomy has been shown to prevent growth and metastasis of transplanted tumors and transgenic models of prostate cancer [11]. Surgical or pharmacologic denervation has been shown to reduce tumor incidence and progression in gastric cancer and enhance chemotherapeutic efficacy [12]. However, the role of nerves in tumor initiation or progression in HNSCC has not been systematically examined until recently.

NEURAL SIGNALING AND ADRENERGIC STRESS IN HNSCC

Head and neck cancers were among the first set of cancers that showed propensity to grow along nerves [14, 15]. Perineural invasion (PNI) is a distinct route of tumor spread that is recognized as a key pathologic feature of many cancers including HNSCC [16]. Over the last decade, experimental studies have implicated the autonomic nervous system, specifically, adrenergic signaling axis in oral cancer progression [17–21]. Chronic stress induced through physical restraint has been shown to promote cancer progression in a mouse model of HNSCC through increased norepinephrine (NE) which upregulates vascular endothelial growth factor (VEGF) and matrix metalloproteinase (MMP2) levels [17, 18]. Adrenergic stimulation has been shown to upregulate interleukin-6 (IL-6) in HNSCC via β -adrenergic receptor (ADRB) activation [19]. Activation of ADRB signaling has also been shown to promote tumor progression and epithelial-to-mesenchymal transition (EMT) in HNSCC [20]. Using the 4NQO carcinogen-induced model of oral squamous cell carcinoma (OSCC), Valente et al. have shown that baseline levels (prior to 4NQO exposure) of NE, cortisone and neurotrophins such as brain-derived neurotrophic factor (BDNF) in normal tongue can be predictive of cancer occurrence in rats exposed to 4NQO [22]. Amit et al. have recently examined the significance and mechanisms involved in neuron reprogramming in head and neck cancer [8]. Using *Krt5^{Cre}Trp53^{flox/flox}* mice, the authors demonstrated increased nerve density in p53 deficient tumors compared to wild type p53 controls implicating the loss of p53 in epithelial cells with neuritogenesis during oral carcinogenesis. The authors showed that loss of *TP53* leads to phenotypic trans-differentiation

of sensory nerves to adrenergic nerves and regulates cancer associated neurons via extracellular vesicle derived signals [8].

In the clinical setting, HNSCC patients have increased circulating levels of NE associated with their bio-behavioral symptoms and anxiety levels [23]. Multiple studies have shown that β -adrenergic receptor-2 (ADRB2) is highly expressed in HNSCC compared to normal epithelium and has been associated with alcohol and tobacco use [24, 25]. The prognostic implications of ADRB2 expression, however, are unclear. Shang and colleagues examined ADRB2 expression in 65 human OSCC specimens and 10 normal oral mucosa samples and observed a higher expression of ADRB2 in OSCC that was positively correlated with tumor size, clinical stage and lymph node metastasis [24]. Similarly, increased TH+ nerve density was associated with lower recurrence-free survival in OSCC [8]. In contrast, strong ADRB2 expression in Brazilian OSCC patients was associated with improved overall survival and cancer-specific survival compared to patients with weak/negative ADRB2 expression [25]. Perhaps due to the global epidemiology of OSCC (higher prevalence in Asia and South East Asia compared to North America or Europe), the prognostic significance of ADRB2 expression in North American or European HNSCC patients has not been reported. However, Amit et al. have reported on the role of adrenergic signaling in 70 head and neck cancer patients treated at MD Anderson Cancer Center (Texas, United States). Although ADRB2 staining was not performed, the authors showed that increased TH+ nerve density was associated with lower overall and recurrence free survival in their patient population [8].

ADRENERGIC-ANGIOGENIC CROSSTALK IN THE TUMOR MICROENVIRONMENT

Angiogenesis is one of the hallmarks of cancer and initiation of the angiogenic switch is recognized as an early and critical event in head and neck cancer [26, 27]. Several studies have shown that overexpression of vascular endothelial growth factor (VEGF) has been associated with poor prognosis in HNSCC [28–31]. Although a considerable body of literature exists on the mechanism(s) of interactions between tumor cells and blood vessels, the literature on reciprocal neurovascular interactions in tumors, especially in HNSCC is limited.

The cross talk between tumor cells, endothelial cells and nerves is mediated by growth factors such as nerve growth factor (NGF) which can regulate VEGF and matrix metalloproteinases (MMPs) within the microenvironment [32–35]. NGF is one of the well-characterized neurotrophins that can serve as autocrine factor to tumor cells [36, 37]. NGF binds to its low affinity receptor, NGFR (p75NTR) or the high affinity receptor, Tropomyosin-related kinase (TrkA) [38, 39]. Work by Ye et al. and Kolokythas et al. has shown that NGF is a critical factor that contributes to oral carcinogenesis [40, 41]. Expression of NGF can induce neovascularization around the nerves in turn promoting tumor growth and proliferation [42]. Conversely, VEGF can induce endothelial cells to secrete collagenase contributing to degradation of the basement membrane, a critical

step in PNI, vascular invasion and metastatic dissemination [16, 42]. Common to these interactions is adrenergic signaling as ADRB2 is expressed both on tumor cells and endothelial cells and activation of adrenergic signaling promotes tumor cell survival, drive angiogenesis through several downstream signaling pathways (**Figure 1A**). ADRB2-mediated signaling (through local release of NE from SNS nerve fibers or from circulation) in tumor cells can upregulate NGF production which in turn can stimulate NGFR/TrkA signaling in an autocrine loop to promote cell survival by preventing apoptosis [13]. Chronic stress-induced release of neurotransmitters can activate ADRB2 and upregulate VEGF levels resulting in enhanced tumor vascularization and aggressive tumor growth [17, 43]. Activation of β -adrenergic signaling through NE has been shown to promote epithelial to mesenchymal transition (EMT) through upregulation of MMP2/9 and VEGF thereby enhancing the invasive and metastatic properties of tumor cells [17, 20]. β -adrenergic signaling is also involved in the regulation of hypoxia [44, 45]. It has been shown that β -adrenergic receptors are fundamental regulators of hypoxia and necessary for hypoxia-inducible factor 1 alpha (HIF-1 α) accumulation [44]. In pancreatic cancer cells, binding of NE to ADRB2 has been shown to upregulate HIF-1 α expression through Akt and ERK pathways [45]. While the interplay between tumor angiogenesis and hypoxia is well-known, the role of ADRB2 in and regulating tumor hypoxia especially through HIF-1 α signaling has not been extensively studied in head and neck cancer and warrants further research. Nevertheless, these observations highlight the cross talk between the vascular and neural components within the HNSCC tumor microenvironment.

TARGETING THE ADRENERGIC-ANGIOGENIC AXIS IN HNSCC

Repurposing Neuroscience Drugs—A Case for Propranolol

Given the role of adrenergic signaling in HNSCC, it would be reasonable to postulate that directly targeting adrenergic signaling in tumor cells or indirectly targeting neuro-vascular interactions (e.g., ADRB2-NGF-VEGF signaling) within the tumor microenvironment could have significant therapeutic benefit in HNSCC. However, safety concerns with anti-NGF antibodies [46] have hampered their clinical use in HNSCC patients. Given the huge cost and time-constraints associated with pharmaceutical development of novel agents, drug repurposing is an attractive approach that can enable successful identification and development of agents that can target the adrenergic-angiogenic axis in head and neck cancer. The availability of pharmacologic and toxicology data of these FDA-approved agents in humans can accelerate clinical evaluation of promising agents [4, 47]. In this regard, the non-selective beta-blocker, propranolol (PRO) is currently being investigated for its therapeutic potential against cancer [48]. PRO is FDA-approved for treating patients with variety of conditions ranging from hypertension and cardiac failure to neurological

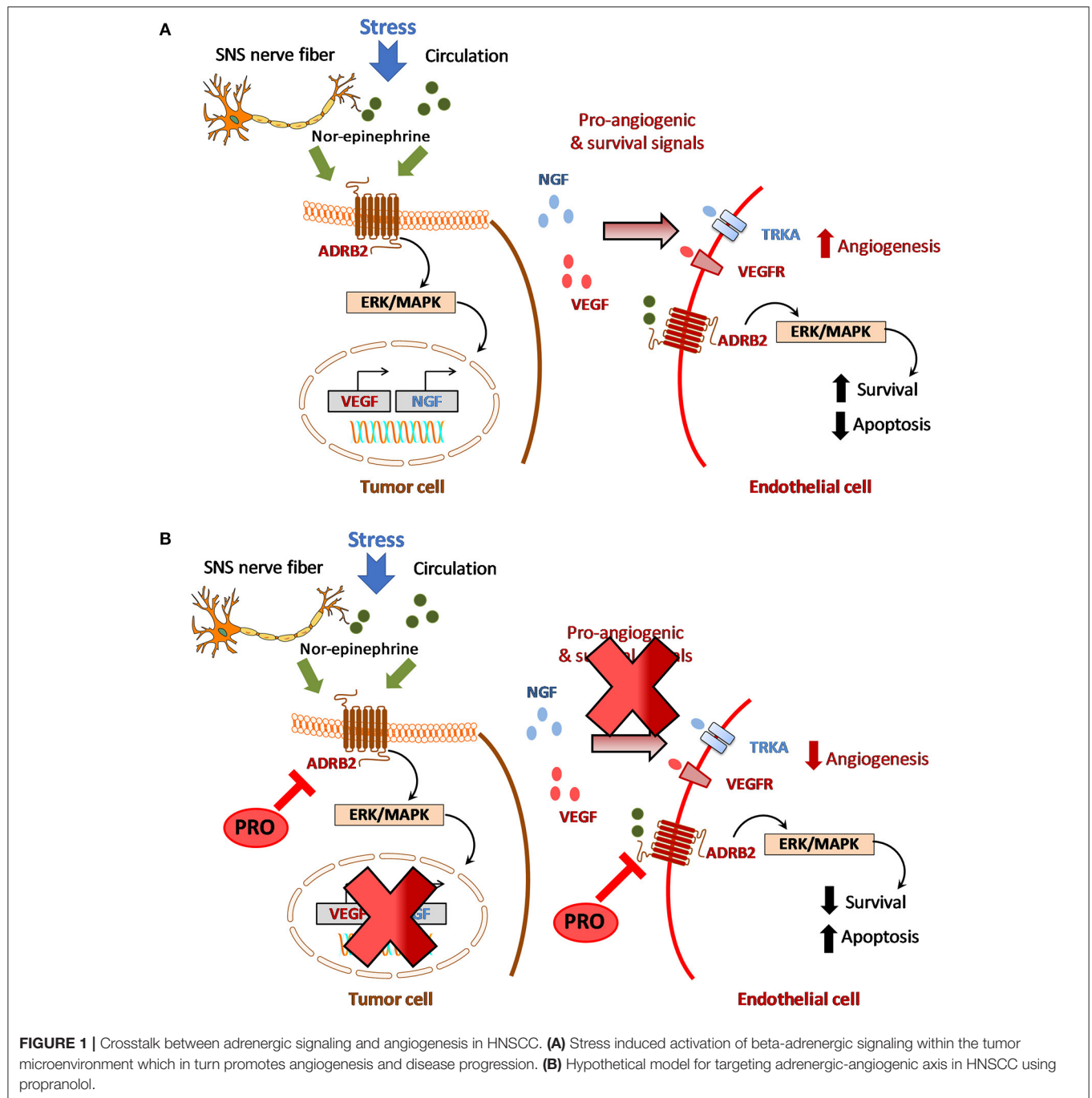
disorders including anxiety, migraines, tremors and glaucoma [49, 50]. In this section, we summarize the current preclinical and clinical evidence on the effects of PRO on adrenergic signaling and angiogenesis in HNSCC.

PRO has been shown to inhibit NE stimulated migration and invasion of HNSCC *in vitro* [20]. In nasopharyngeal carcinoma (NPC) cell lines, PRO has been shown to inhibit NE-induced MMP-2/9 and VEGF [17]. In Epstein-Barr virus (EBV) associated nasopharyngeal carcinoma, latent membrane protein 1 (LMP1) is the viral oncogene that promotes invasion and metastasis through effects on MMP-2/9 [51, 52]. Using EBV positive (clone 13) and EBV negative (clone 39) of LMP1 expressing HONE-1 cells, Yang et al. showed that NE stimulated the release of VEGF, MMP-2, and MMP-9 in both NPC cells independent of their EBV status. While the direct effects of EBV oncoproteins including LMP1 on adrenergic signaling is unclear, the study showed that both clones of the NPC cell line expressed ADRB2 and were inhibited by PRO through downregulation of MMP-2/9 expression [17]. Similarly, the forkhead box (FOXA) family of transcription factors have been implicated in the biology of NPC [53, 54]. Overexpression of FOXA1 has been shown to suppress proliferation, migration, and invasion of NPC cells in culture [53]. In NPC patients, FOXA1 expression has been correlated with prolonged disease-free survival and overall survival [54]. However, the effects of PRO on FOXA1 signaling has not been previously reported.

Preclinical studies have also examined the interaction between PRO and standard of care chemo- and radiation therapy in HNSCC. Wolter et al. have shown that PRO reduces HNSCC viability, inhibits VEGF production and can enhance the efficacy of cisplatin and radiation against HNSCC cells [55]. Recently, Lucido et al. have shown that PRO exhibits potent antitumor activity against human papillomavirus positive (HPV+) HNSCC that is mediated by a reduction of mitochondrial oxidative phosphorylation [56]. In the study, PRO in combination with chemoradiation resulted in inhibition of primary tumor growth and reduction in metastases.

And finally, studies have also demonstrated the antiangiogenic effects of PRO in experimental tumor models. PRO has been shown to suppress angiogenesis by inhibiting proliferation, migration and differentiation of endothelial cells *in vitro* [57]. Blockade of ADRB2 signaling by PRO inhibits VEGF induced phosphorylation of VEGFR2, extracellular signal-regulated kinase-1/2 (ERK) and pro-MMP2 secretion. PRO exhibits antiangiogenic effects at non-toxic concentrations (<50 μ M) and potentiates the antiangiogenic and therapeutic efficacy of chemotherapeutic agents, 5FU and taxol [58]. PRO has been shown to inhibit growth, decrease vessel density and lower VEGF, MMP2/9 levels in neuroblastomas [59] and repress tumor growth in hemangiomas through hypoxia-inducible factor-1 alpha (HIF-1 α) and STAT3 signaling [60]. Collectively, these preclinical observations highlight the therapeutic potential of PRO in targeting adrenergic-angiogenic signaling in HNSCC (**Figure 1B**).

Repurposing PRO for use in HNSCC patients presents an attractive strategy considering the cost of the drug and wealth



of pharmacologic and toxicologic data that exists in humans. However, the existing clinical evidence from epidemiologic or retrospective analyses regarding PRO use in HNSCC is conflicting. Chang et al. have shown that long-term PRO use (>1,000 days) was associated with a reduction in risk of HNSCC (HR: 0.58; CI: 0.35–0.95) [61]. In contrast, an observational study in 1,274 patients conducted in South Korea showed that post diagnosis beta-blocker use was associated with decreased survival and increased recurrence in HNSCC patients [62]. A recent meta-analysis of epidemiologic and perioperative studies

suggests that benefits associated with beta-blockers are likely to vary across patients with different tumor sites [63].

CONCLUSIONS

In summary, neuronal programming and neurovascular interactions represent relatively understudied mechanisms that contribute to malignant progression in HNSCC. The literature presented in this review highlight the importance and therapeutic potential of targeting adrenergic signaling

pathways within the head and neck tumor microenvironment. However, additional investigation to better understand the role of adrenergic-angiogenic cross talk in head and neck cancer and the potential of targeting this axis using PRO in the current treatment paradigm for HNSCC is warranted. In this regard, 3D organoid models and organoid co-culture systems can serve as a useful platform to dissect the mechanisms of interaction between tumor cells, neurons and endothelial cells and to screen therapeutic agents that can effectively target the adrenergic-angiogenic axis in head and neck cancer. Although limited, the published preclinical evidence on the activity of PRO against HNSCC is encouraging. Studies should therefore investigate the activity of PRO in combination with chemoradiation and immune checkpoint blockade using clinically relevant orthotopic models of HNSCC. Given the known effects of PRO on tumor cells, neural signaling, and blood vessels, such studies could employ clinically relevant imaging methods (e.g., MRI, PET) to assess the metabolic, vascular and hypoxic profiles of tumors. Integration of imaging phenotypes with genomic data and response to PRO would enable identification of patients that

could benefit from the addition of PRO to existing standard of care regimens. Investigation into the potential chemopreventive effects of PRO in carcinogen-induced models of HNSCC could also be insightful. Such studies could serve to accelerate the clinical translation of a relatively inexpensive and a readily available drug to treat these esthetically and functionally debilitating cancers.

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MS designed and drafted the manuscript. VKV-C and MS edited the manuscript, critically revised the content, and approved the final submitted version of the manuscript. All authors contributed to the article and approved the submitted version.

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Cancer-Associated Fibroblasts in Oral Cancer: A Current Perspective on Function and Potential for Therapeutic Targeting

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The role of the tumour microenvironment (TME) in cancer progression and resistance to therapies is now widely recognized. The most prominent non-immune cell type in the microenvironment of oral cancer (OSCC) is cancer-associated fibroblasts (CAF). Although CAF are a poorly characterised and heterogenous cell population, those with an “activated” myofibroblastic phenotype have been shown to support OSCC progression, promoting growth, invasion and numerous other “hallmarks of malignancy.” CAF also confer broad resistance to different types of therapy, including chemo/radiotherapy and EGFR inhibitors; consistent with this, CAF-rich OSCC are associated with poor prognosis. In recent years, much CAF research has focused on their immunological role in the tumour microenvironment, showing that CAF shield tumours from immune attack through multiple mechanisms, and particularly on their role in promoting resistance to anti-PD-1/PD-L1 checkpoint inhibitors, an exciting development for the treatment of recurrent/metastatic oral cancer, but which fails in most patients. This review summarises our current understanding of CAF subtypes and function in OSCC and discusses the potential for targeting these cells therapeutically.

Keywords: oral cancer, head & neck squamous cell carcinoma, tumour microenvironment, cancer-associated fibroblasts, myofibroblasts

INTRODUCTION

Historically, the search for novel therapies has focused on tumour cells, attempting to inhibit oncogenic pathways that drive tumour progression; targeting the EGFR pathway for example. Although such targeted therapies can produce dramatic initial results, acquired resistance, where tumours progress after initial response, seems an almost inevitable consequence of this approach. In recent years, and particularly following the success of anti-PD-1/PD-L1 (programmed cell death protein 1/programmed death ligand 1) checkpoint immunotherapy, there has been a realisation that a tumour is a complex mixture of different cell types that interact to promote tumour progression, and this has generated significant interest in developing therapies that target the tumour microenvironment (TME) [1].

CAF HETEROGENEITY

The most prominent non-immune cells within cancers are cancer-associated fibroblasts (CAF); these can account for up to 80% of tumour mass in late stage head & neck cancers (HNSCC) and are generally assumed to be tumour-promoting [2, 3]. CAF remain a poorly characterised and heterogeneous cell population; most studies have focused on myofibroblastic CAF and the terminology within the literature has been confusing with “cancer-associated fibroblast,” “myofibroblast” and “peritumoral fibroblast” variably used, and only recently is the term myofibroblastic CAF (myCAF) starting to be used consistently in the literature. These contractile, α -SMA-positive cells are generated principally through TGF- β signalling/mechanotransduction [4], and secrete extracellular matrix (ECM) analogous to myofibroblasts found in healing wounds and fibrotic disorders. In tissue sections these are usually identified using immunohistochemistry for α -SMA, although this protein is also expressed by pericytes [5] and smooth muscle cells [6]. Indeed, there is no specific single marker that accurately identifies CAF; other markers such as FAP- α (fibroblast activation protein α), FSP1 (fibroblast specific protein 1) and PDGFRB (platelet derived growth factor receptor β) have been used to identify CAF, but also are not CAF specific [7]. Moreover, and despite extensive research, the myCAF cell of origin also remains inconclusive, and, although it is thought that most myCAF originate from local fibroblasts–pericytes, adipocytes, endothelial cells and bone marrow-derived mesenchymal stem cells have all been shown to be potential myCAF progenitors [8, 9]. In recent years, macrophages and cancer stem cells have also been highlighted as potential myCAF precursors [1, 10, 11], and it remains unclear whether cell of origin affects the final myCAF phenotype.

The advent of single cell transcriptomic sequencing (scRNA-seq) is beginning to characterise CAF heterogeneity within HNSCC and other cancers, and it is now accepted that not all CAF subpopulations are characterised by high expression of α -SMA, and conversely, not all α -SMA-positive CAF are myofibroblastic. Elyada et al. [12] and Öhlund et al. [13] analysed pancreatic cancers using scRNA-seq and identified two main CAF populations; myCAF and a subpopulation characterised by expression of inflammatory genes, which were termed iCAF. iCAF subpopulations have subsequently also been identified in breast cancer [14]. Puram et al. [15] used scRNA-seq to characterise HNSCC and described two main fibroblast groups which were termed “myofibroblasts” and “CAF.” The latter group could be further divided into two subclusters through differential expression of immediate early response genes, mesenchymal markers, ligands and receptors, and ECM proteins, suggesting further potential subdivisions. It is not yet clear whether iCAF are found in HNSCC as a distinct subpopulation. Patel et al. [16] performed transcriptomic analysis on CAF cultures from oral cancers (OSCC) and also identified two main subgroups: CAF1 (α -SMA^{low}) and CAF2 (α -SMA^{high}). CAF1 was associated with increased proliferation of cancer cells but with suppressed self-renewal growth of oral stem-like cancer cells (oral-SLCCs).

Conversely, CAF2 correlated positively with frequency of oral-SLCCs but negatively with tumour cell proliferation. BMP4 (bone morphogenetic protein 4) was differentially expressed between the two CAF populations and was suggested to be at least partially responsible for exerting the suppressive effect on cancer cells’ stemness. Costea et al. [17] compared heterogeneity of OSCC CAF with normal fibroblasts, performing transcriptomic analysis on CAF cultured in 2D and 3D-matrices. This study also identified two CAF populations; CAF-N, motile fibroblasts whose transcriptome and secretome were more similar to normal fibroblasts, and CAF-D subpopulation, which had a more divergent expression pattern and secreted high levels of TGF- β 1. Both CAF subtypes resulted in higher tumour incidence and deeper invasion in murine models, though intriguingly, CAF-N was best at supporting tumour formation. The two subpopulations were not compared in terms of their α -SMA expression, however 50% of the upregulated genes compared with normal fibroblasts were TGF- β targets, suggesting differentiation towards a myofibroblast-like phenotype. The authors suggest that the two populations may be a spectrum in CAF development, with CAF-N representing an earlier stage of differentiation.

Fibroblast phenotype may also vary according to molecular phenotypes of HNSCC. Hassona et al. [18] compared CAF from genetically stable OSCC (GS-OSCC; maintaining wild-type p53) and genetically unstable OSCC (GU-OSCC) and found that cultured CAF from GU-OSCC were significantly more senescent. They found that malignant keratinocytes from GU-OSCC produce high levels of reactive oxygen species (ROS), associated with increased production of TGF β 1 and TGF β 2, and (myo)fibroblast activation. Consistent with this observation, senescent fibroblasts commonly express α -SMA, are contractile and tumour promoting [19, 20] but differ from myofibroblasts in their ability to deposit ECM [19, 21]. Notably, the generation of intracellular reactive oxygen species plays a major role in CAF (and myofibroblast) differentiation, with the ROS-producing enzyme, NADPH oxidase 4 (NOX4), central to this process [22, 23].

However, despite the progress made in identifying different CAF subtypes in oral cancer (Table 1) characterisation of CAF heterogeneity remains incomplete; studies have identified CAF-secreted inflammatory factors as promoting OSCC progression, but it is not yet clear whether iCAF are a distinct subpopulation in HNSCC or whether myCAF also acquire inflammatory properties in certain situations. As novel CAF subgroups are identified, their effect on OSCC progression will be an intriguing area of research, and in order to study function it will be necessary to modify *in vitro* culture conditions to maintain these phenotypes. Standard 2D-tissue culture techniques tend to skew CAF to a myCAF-like phenotype [24], meaning that studies have tended to focus, either deliberately or inadvertently, on myCAF. Future experimental work will require a more detailed characterisation of CAF phenotypes given increasing understanding of CAF heterogeneity and plasticity.

TABLE 1 | Heterogeneity of CAF in oral cancer.

Source	Tumour	CAF subpopulations	Description/Markers
Puram et al. [15]	HNSCC (oral cavity)	Myofibroblasts CAF	ACTA2, MCAM, MYLK, MYL9, IL6, PDGFA FAP, THY1, PDPN, MMP2, MMP11, PDGFRA/L, TGFB3. Could be further divided into CAF1 and CAF2
Patel et al. [16]	Gingivobuccal–oral tumour	Resting fibroblasts	Lack of activation markers
		CAF1 (α -SMA ^{low} BMP4 ^{+ve})	Increased proliferation of cancer cells; suppressed self-renewal growth of oral-SLCC
Costea et al. [17]	OSCC	CAF2 (α -SMA ^{high} BMP4 ^{-ve})	Negative correlation with cancer cells' proliferation; increased frequency of oral-SLCC
		CAF-N	Motile; high production of hyaluronan; promoted invasion; secretome similar to the secretome of normal fibroblasts;
Hassona et al. [18]	GS-OSCC	CAF-D	Less motile; high expression of TGF- β 1; promoted invasion and EMT; secretome different from the secretome of normal fibroblasts
	GU-OSCC	Non-senescent CAF	Non-senescent CAF failed to promote keratinocytes' invasion <i>in vitro</i>
		Senescent CAF	Malignant keratinocytes induced fibroblast activation and senescence through ROS and TGF- β ; senescent CAF promoted keratinocytes' invasion <i>in vitro</i>

CAF AND OSCC SURVIVAL

Numerous studies have shown that CAF-rich OSCC are associated with significantly shorter patient survival. In the largest study of this type, Marsh et al. [25] performed a retrospective analysis of 282 OSCC patients, analysing a number of tumour cell and stromal cell molecular markers by IHC. They found that the best independent risk factor of early OSCC death was high stromal α -SMA expression, which produced the highest adjusted hazard ratio (HR 3.06, 95% CI 1.65–5.66; $p = 0.002$), and likelihood ratio (3.6; Detection rate: False positive rate) of any feature examined, and was strongly associated with mortality regardless of disease stage. A recent meta-analysis examined correlations between myCAF (assessed by α -SMA immunohistochemistry) and risk of OSCC death, analysing 1,328 patients from 12 studies [26]. The combined results showed that myCAF predicted poor overall survival (HR 2.16 95% CI 1.60–2.92; $P < 0.00001$) and shortened disease-free survival (HR 3.32 95% CI 2.09–5.26; $P < 0.00001$). The presence of high levels of stromal myCAF was associated with pathological features related to tumour aggressiveness, including depth of invasion, lymphatic invasion and extra-nodal metastatic spread [26].

CAF AND MALIGNANT TRANSFORMATION

Oral potentially malignant disorders (PMDs) include leukoplakia, erythroplakia and oral submucous fibrosis (OSMF) [27]. Approximately 1% of potentially malignant disorders give rise to cancer but the mechanism of the transformation is poorly understood [28]. Changes in stroma, such as myofibroblast activation, are considered as potential promoters of the transformation of pre-malignant lesions. Several studies, using immunohistochemistry staining for α -SMA, have compared the number of myofibroblasts in potentially malignant disorders and OSCC. Generally, studies report a lack of myofibroblasts in leukoplakias and erythroplakias, including a meta-analysis that analysed 19 articles [28, 29]. However, some studies

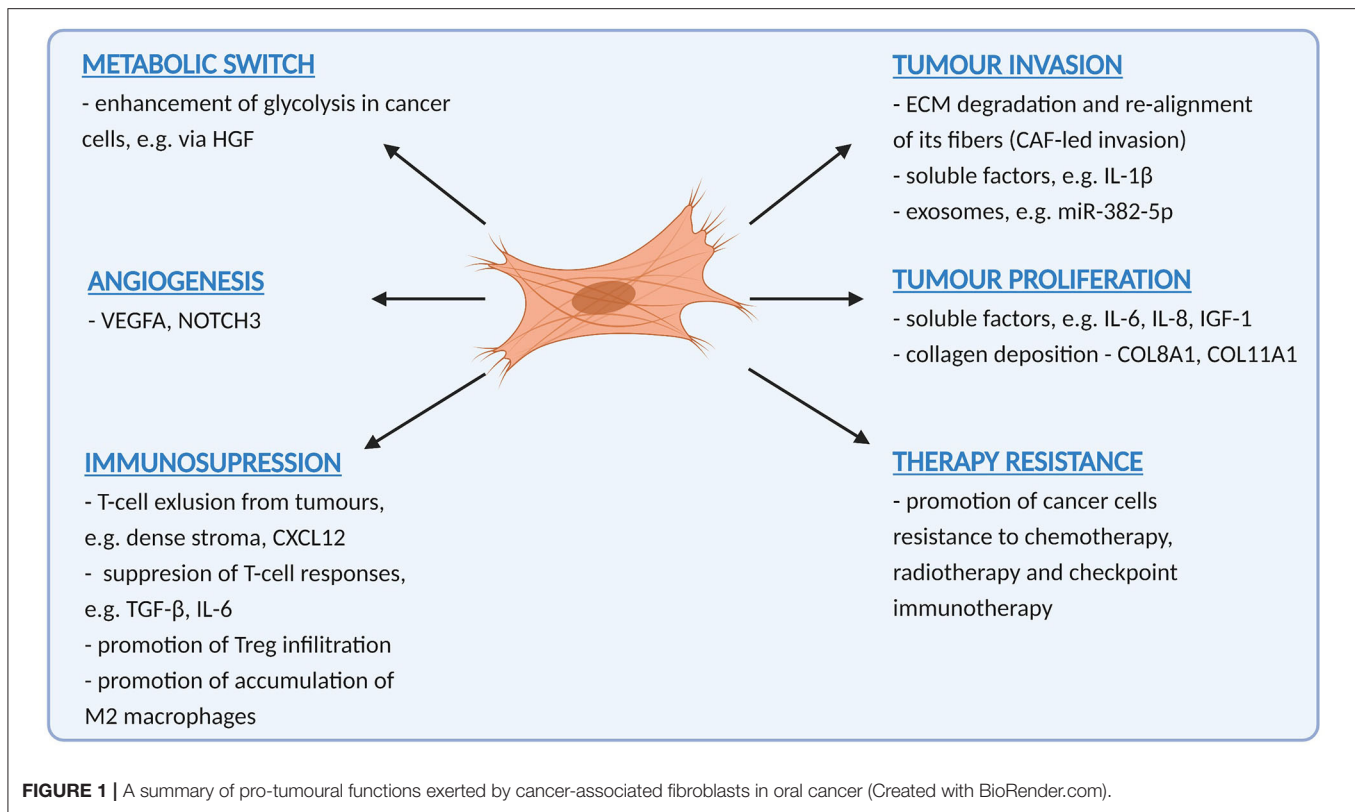
have reported increased myofibroblasts in high-risk epithelial dysplasia [30]. Conversely, studies have consistently reported increased myofibroblasts in OSMF compared to healthy oral mucosa [28, 31–33], with late-stage OSMF reported to contain more myofibroblasts than early-stage OSMF [32]. These findings are perhaps not surprising given that OSMF is a fibrotic disorder, and whether myofibroblasts play an active role in the malignant transformation of this disease remains to be determined.

CAF FUNCTION IN OSCC

Clues as to how CAF function to promote OSCC progression can be found in clinic-pathological correlates. The fact that CAF correlate with many features of tumour aggressiveness, including invasion, metastasis, absence of T-cells and therapy resistance suggest that their role is multifactorial, and this is borne out in numerous functional studies that show that CAF promote many, if not all of the “hallmarks of malignancy” [34]. Understanding these functions will help develop CAF-targeting strategies for OSCC treatment. Tumour promoting functions of CAF in OSCC are summarised in **Figure 1**.

CAF AND TUMOUR CELL INVASION

CAF promote tumour invasion through multiple mechanisms, including deposition and remodelling of ECM, a central myCAF function. Tumour ECM forms a dense meshwork, generally difficult for cells to penetrate. Gaggioli et al. [35] found that CAF create “tracks” in ECM through which tumour cells invade and are led by CAF. Generation of tracks was dependent on a combination of protease- and force-mediated matrix remodelling mechanisms. Expression of integrins $\alpha 3$ and $\alpha 5$, and activity of Rho and ROCK (Rho-associated protein kinase) (drivers of a force-mediated remodelling) in fibroblasts were shown to be crucial for the remodelling process. More recently, Chen et al. [36] demonstrated that HNSCC cell invasion is facilitated by fibroblast-dependent degradation of dense ECM. By varying



collagen concentration in co-culture experiments, they found in lower concentrations of collagen (2 mg/ml), that both tumour cells and fibroblasts remodel the matrix and invade into the surrounding collagen independently. However, tumour cells growing in more concentrated collagen (8 mg/ml) were unable to penetrate the matrix unless fibroblasts were present. Similar to the Gaggioli study, fibroblasts were seen to lead cancer cells through the matrix. Both studies suggest that cancer cells require fibroblasts to remodel dense extracellular matrix in order to invade into surrounding tissues and disseminate.

A similar mechanism has been reported to regulate OSCC invasion into bone [37], where a fibrous CAF stroma characterised by a high expression of α -SMA was observed to sit between tumour cells and bone. Notably, α -SMA-positive CAF were commonly seen infiltrating bone ahead of cancer cells, again suggesting that they are the leading cells in cancer invasion. Two proteins associated with regulation of bone resorption: RANKL (receptor activator of NF κ -B ligand) and OPG (tumour necrosis factor receptor superfamily member 11B) were expressed in OSCC cells and bone-adjacent stroma. Moreover, treatment with conditioned media from both experimentally generated CAF and OSCC-tumour-derived CAF could induce osteoclastogenesis in macrophages – i.e., a transdifferentiation of macrophages into bone-resorbing osteoclasts. CAF induced osteoclastogenesis in macrophages to a greater extent than cancer cells, suggesting they may be the main orchestrators of bone invasion in OSCC, modulating macrophages as well as tumour cells in this process.

CAF produce numerous ECM proteins and the composition of the matrix can significantly affect cancer invasion. For example, CAF in OSCC express high levels of hyaluronan synthetase 2 (HAS2), an enzyme producing hyaluronan, which is a major component of ECM. HAS2 promotes invasion of OSCC cells, and its expression correlates with advanced clinical stages and cervical lymph node metastases [38]. The mechanism underlying HAS2-dependent invasion of cancer cells was suggested to depend on regulation of the balance between ECM-degrading matrix metalloproteinases (MMPs) and their inhibitors (tissue inhibitors of metalloproteinases; TIMPs). HAS2⁺ CAF expressed higher levels of MMP1 and lower levels of TIMP1 than normal fibroblasts, and knockdown or inhibition of HAS2 in CAF not only reduced OSCC invasion but also reversed the ratio between MMP1 and TIMP1 expression, reducing expression of MMP1 and upregulating TIMP1. HAS2 has also been reported to play a role in regulating the fibroblast response to TGF- β . Dermal fibroblasts and fibroblast from the oral mucosa respond differently to TGF- β 1 treatment [39, 40], which promotes proliferation in dermal fibroblasts but suppresses proliferation in fibroblasts from the oral mucosa. Overexpression of HAS2 in oral fibroblasts resulted in a pro-proliferative response to TGF β 1 stimulation. The presence of hyaluronan in the TME is also known to promote cancer cell and CAF motility [41]. A subtype of hyaluronan-producing CAF could represent a promising drug target.

CAF also modulate tumour cell invasion via secreted soluble factors. Various CAF-secreted factors, have been implicated in

promoting HNSCC invasion and/or proliferation, including IL-1 β (interleukin 1 β) [42], activin A [43], HGF (hepatocyte growth factor) [44] and EREG (epiregulin) [45], which has additionally been suggested to play an autocrine role in CAF activation [45]. In recent years there has also been significant interest in CAF-tumour cell communication via exosomes. These secreted extracellular vesicles contain proteins, lipids and nucleic acids, such as messenger RNA (mRNA), micro RNA (miRNA), long non-coding RNA (lncRNA) and others [46], and exosomal miR-382-5p and MFAP5 have been shown in separate studies to promote OSCC cell migration and invasion [47, 48]. Intriguingly, Li et al. [49] showed miR-34a-5p could suppress proliferation and metastasis of OSCC cells and that CAF exosomes contained reduced levels of this miRNA, suggesting that the cancer-promoting features of exosomes might not only be due to a transfer of pro-tumoral factors but also due to the lack of suppressive factors.

CAF AND TUMOUR PROLIFERATION

CAF have been shown to promote proliferation of cancer cells in multiple tumour types [50–52]. Co-injection of CAF with HNSCC cells *in vivo* enhances tumour growth [53], and similar observations have been made in 3D co-culture models, where CAF increase proliferation of tumour spheroids [54]. Conditioned medium from CAF promotes HNSCC cell proliferation *in vitro* [53] and consistent with this a number of secreted cytokines and growth factors have been shown to stimulate tumour growth. For example, interleukin-6 (IL-6) has been shown to upregulate expression of osteopontin (SPP1) in HNSCC cells and to increase their proliferation via integrin/NF- κ B signalling [55]. Osteopontin may play an important role in bi-directional communication between CAF and HNSCC cells, and in breast cancer models has been shown to induce transformation of mesenchymal stem cells into CAF, in a MZF1(myeloid zinc finger 1)-TGF β 1-dependent manner [56]. Plasma osteopontin has also been suggested as a potential prognostic biomarker in HNSCC patients; negatively correlating with overall and relapse-free survival [57].

Another example of a reciprocal paracrine interaction between tumour cells and CAF was shown by Bae et al. [58], who observed that tumour volume of orthotopic tumours correlated with numbers of CAF co-injected with tumour cells. They found that interleukin-1 α (IL-1 α) secreted by OSCC cells increased proliferation of CAF and upregulated expression of secretory cytokines, including CCL7 (chemokine ligand 7), CXCL1 (C-X-C motif chemokine 11) and IL-8 (interleukin 8). In turn, these cytokines increased tumour cell proliferation *in vitro*.

Fibroblasts have also shown to be a source of IGF-1 (insulin growth factor 1) in OSCC, which promotes tumour cell proliferation through activation of PI3K-AKT and Hedgehog signalling pathways [59]. The matrix-remodelling capabilities of CAF may also affect tumour proliferation [60]; CAF-secreted collagens, collagen8A1 and collagen11A1 [61], have been shown to modulate tumour cell growth through interaction with

DDR1 (Discoidin domain receptor 1), which is overexpressed in HNSCC tissues.

CAF, ANGIOGENESIS, AND THE METABOLIC SWITCH

Rapidly growing tumours create a hypoxic microenvironment and CAF play a major role in neo-angiogenesis, producing angiogenic factors such as VEGFA (vascular endothelial growth factor), and also attracting other cells, such as macrophages, which also contribute to the angiogenic process [62].

In OSCC, CAF are thought to be the main source of interleukin-6, which acts through an autocrine signalling loop to induce the secretion of VEGFA in CAF and also in OSCC cells [63]. Kayamori et al. [64] suggested that Notch signalling in CAF could also promote tumour angiogenesis; around one third of tongue OSCC cases were found to have CAF expressing NOTCH3 (neurogenic locus notch homolog protein 3) which correlated positively with tumour size and was associated with increased micro-vessel density.

CAF can also show metabolic adaptations to meet the energetic demands of tumour cells. In a phenomenon termed the “reverse Warburg effect,” CAF and tumour cells are metabolically coupled, whereby CAF metabolism is corrupted to undergo aerobic glycolysis, producing metabolites such as lactate and pyruvate that can be used by cancer cells in oxidative phosphorylation. Lactate also has other pro-tumour effects, promoting angiogenesis, metastasis, and generating an immune-suppressive microenvironment [65–68]. Conversely, CAF have also been shown to promote glycolysis in tumour cells. Kumar et al. [3] reported that CAF-secreted HGF induces glycolysis in HNSCC cells and promotes expression of bFGF (basic fibroblast growth factor), which induces oxidative phosphorylation in fibroblasts creating another type of metabolic loop between the cells.

CAF, RADIOTHERAPY, AND CHEMOTHERAPY

Radiotherapy with or without chemotherapy is commonly used in the treatment of OSCC. These treatments can modulate the tumour microenvironment in various ways. Notably, radiotherapy induces a wound healing response, promoting inflammation, CAF modulation/myofibroblast activation and ECM remodelling [69], and while CAF are considered relatively radioresistant [70], the DNA damage induced by radiation can result in a senescent phenotype, which can also be tumour promoting [71]. Kamochi et al. [72] showed that irradiated fibroblasts promote invasive growth of OSCC cells, upregulating expression of TGF- β 1, that promote invasion and also potentiate further myofibroblasts differentiation. Indeed, irradiation is a potent activator of latent TGF- β and myofibroblasts which results in the fibrosis which is a well-recognised complication of radiotherapy [73]. CAF may also protect cancer cells from radiation. Huang et al. [74] found that radioresistant nasopharyngeal carcinoma had a higher infiltration of CAF

compared with radiosensitive tissue, and showed that this radioprotective effect was modulated via IL-8/NF- κ B signalling. This effect was diminished following treatment with Tranilast – a drug known to inhibit fibrosis and TGF- β signalling.

Chemotherapy, similar to radiotherapy, has been shown to promote the acquisition of CAF phenotype in breast [75], colorectal [76], and head and neck cancer [77]. A number of studies have also reported CAF-mediated chemotherapy resistance in HNSCC. CAF are associated with mediating resistance to cisplatin in head and neck cancer cells, and are generally more intrinsically resistant to this drug. Qin et al. [78] found that CAF transfer an exosomal miR-196a to cancer cells which renders them resistant to cisplatin through a downregulation of CDKN1B and ING5. Resistance to cisplatin has also been shown to be mediated by CAF-secreted collagens [61]; HNSCC cells pre-treated with collagen (or gelatin) prior to cisplatin treatment display significantly reduced cisplatin-induced apoptosis. In the presence of a DDR1 (Discoidin domain receptor 1; collagen receptor expressed by HNSCC cells) inhibitor, this protective effect was abolished.

Yegodayev et al. [79] also demonstrated that resistance to cetuximab is partially mediated by CAF. They found that TGF- β -activated CAF positively correlate with resistance to cetuximab both, *in vitro* and *in vivo*, and inhibiting TGF- β signalling improved cetuximab treatment efficacy. In a separate study, CAF were shown to be non-sensitive to cetuximab, but their conditioned medium protected HNSCC cells from cetuximab in a dose-dependent manner [80]. This CAF-mediated resistance was suggested to be partially driven by an upregulation of metalloproteinases (MMPs) in both, CAF and HNSCC cells, following co-culture. MMP1 was the most upregulated protease, and use of its inhibitor partially restored the sensitivity of the HNSCC to cetuximab. Notably however CAF with silenced MMP-1 could still mediate cetuximab resistance, and the conclusion drawn from the study was that other MMPs (such as MMP-2, -3, -7, -13) were also likely involved in modulating this effect.

CAF AND TUMOUR IMMUNE SUPPRESSION

The microenvironment of HNSCC is immunosuppressive and pro-inflammatory, and is associated with T-cell and NK-cell dysfunction, as well as accumulation of Tregs and pro-tumoral macrophages [81]. In recent years, the role of fibroblasts in promoting this suppressive microenvironment has generated much interest, particularly in the context of resistance to anti-PD-1/PD-L1 checkpoint immunotherapy. CAF contribute to tumour immune evasion through multiple mechanisms, affecting both innate and adaptive immunity [82]. Takahashi et al. [83] found that HNSCC CAF express elevated amounts of PD-L1 (also known as B7H1) and PD-L2 (B7DC); both molecules interact with PD-1 receptor on T-cells to suppress effector functions [84, 85]. CAF also suppress infiltration of CD8 T-cells into tumours; in part this may result from T-cell interactions with the extracellular matrix “barrier” secreted by myCAF [86]. The

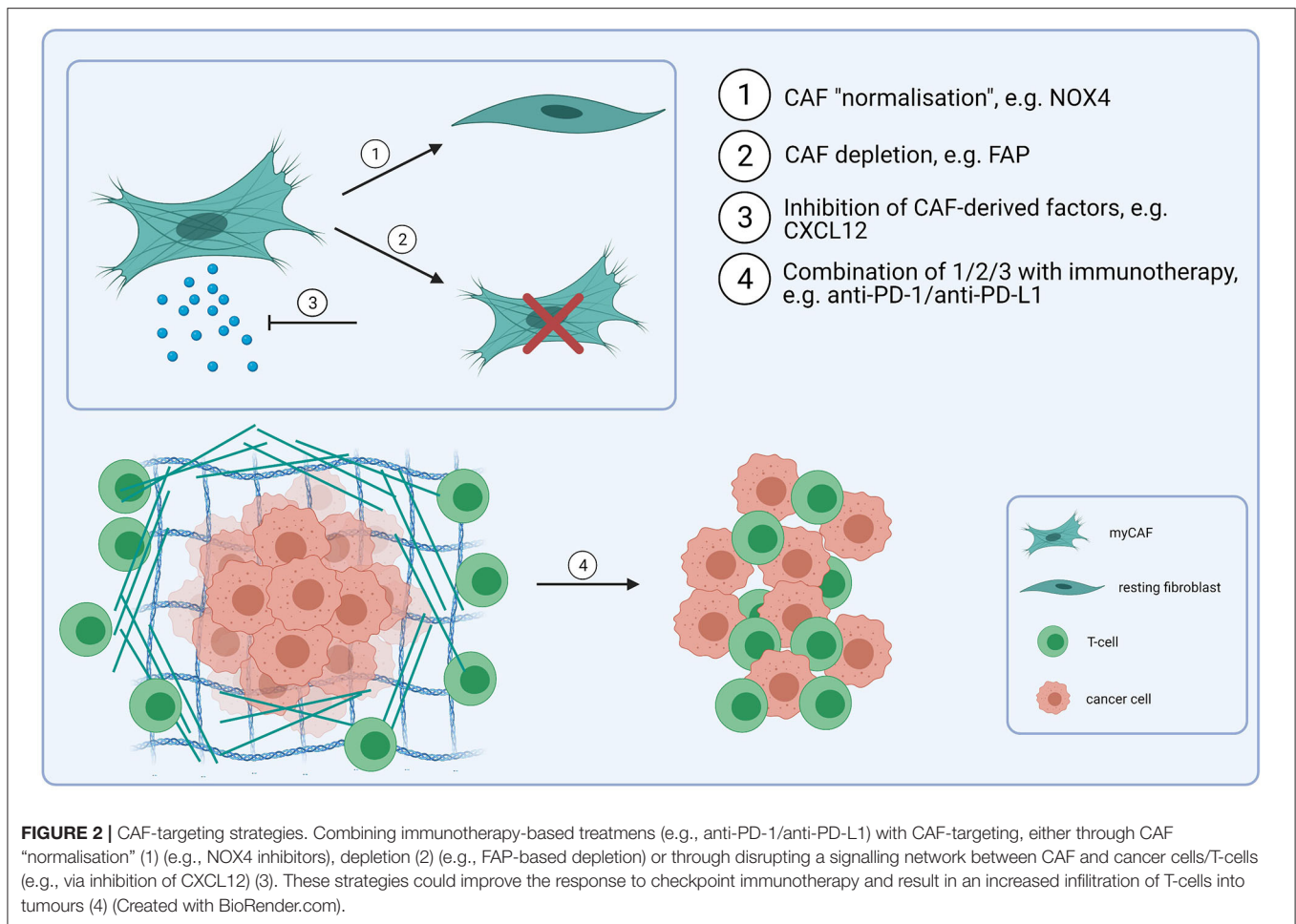
desmoplastic stroma produced by myCAF is rich in collagen, fibronectin and various proteoglycans (hyaluronan, versican), which have been shown to “trap” T-cells and inhibit T-cell motility [87]. A dense meshwork of collagen fibres has also been shown to limit T-cell penetration into tumours [88] and enhance matrix density; the protease-independent nature of T-cell amoeboid migration leads to contact guidance where T-cells follow a path-of-least-resistance along collagen fibres [89]. CD8 T-cells in myCAF-rich murine and human tumours have been shown to upregulate expression of CTLA-4, which may play a role in modulating T-cell interactions with ECM [23]. In a murine model of pancreatic cancer, CXCL12 (C-X-C motif chemokine ligand 12) produced by CAF has also been shown to inhibit T-cell infiltration into tumour islets [90]. CAF-derived TGF- β and IL-6 also have recognised roles in suppressing T-cell responses [91]. Recently, a novel subpopulation of antigen presenting CAF that interact with CD4 T-cells have been identified in pancreatic carcinoma, suggesting even more complex CAF interactions in shaping the adaptive T-cell response [12].

CAF have also been reported to mediate T-cell suppression in OSCC indirectly through attraction and polarisation of macrophages [92]. Clinicopathological analysis has revealed a positive relationship between numbers of CAF and TAMs (tumour-associated macrophages) in OSCC tumour samples, and both cell types correlate with vascular invasion and TNM stage [92]. Several CAF-derived factors have been shown to recruit macrophages into tumours and polarise them towards an M2 tumour promoting phenotype, including CXCL12 and MCP-1 (monocyte chemotactic protein 1) [93, 94], with M2 macrophages having suppressive effect on T-cells mediated by increased expression of arginase I, interleukin-10 and TGF- β [92]. Similarly, CAF-secreted CCL7 that has been shown to increase invasion of OSCC cells is also chemotactic for macrophages [95].

The recruitment of immune cells by CAF is usually described in terms of soluble immunomodulatory factors, such as CXCL10 (C-X-C motif chemokine ligand 10), IL-6, MCP-1 [96], but recently a novel mechanism for recruitment of macrophages was proposed by Pakshir et al. [97], who demonstrated that macrophages can sense ECM deformation resulting from myofibroblast contraction, and migrate towards them. This mechanosensing mechanism could potentially attract macrophages into CAF-rich tumours independent of chemotactic factors.

CAF-TARGETING STRATEGIES

In addition to their tumour-promoting functions, CAF have been shown to confer resistance to different types of cancer therapy, including cetuximab and anti-PD-1/PD-L1 checkpoint immunotherapy, as well as radiotherapy and cisplatin chemotherapy [77–80, 98–101], suggesting that therapeutic CAF targeting could increase response rates for a diverse range of treatments. Potential strategies for CAF-directed therapy include inhibiting CAF activation or function, “normalizing” CAF or killing CAF within the tumour microenvironment



(Figure 2), although clinical testing has generally yielded disappointing results [102, 103]. Given the myriad tumour promoting functions regulated by CAF, the specific context in which a particular pathway is targeted is clearly important. For example, FAP-expressing CAF have been shown to exclude T-cells from tumours through secretion of CXCL12 [90]; targeting the CXCL12/CXCR4 signalling axis using plerixafor (a CXCR4 inhibitor) has been shown to overcome this exclusion effect and promote response to anti-PD-1 [104]. Inhibiting CAF activation has also been investigated as a possible therapy; TGF- β signalling/mechanotransduction pathways are the primary signalling pathway regulating myCAF activation, although other growth factors and signalling molecules, including lysophosphatidic acid, PDGF, FGF, IL-6 and TNF (tumour necrosis factor) have also been implicated in the differentiation process. Targeting TGF- β is potentially problematic for several reasons; in the early stages of tumorigenesis it acts as a tumour suppressor; it also plays an important role in tissue homeostasis, and early testing of small molecule TGF- β 1 inhibitors highlighted on-target cardiac toxicities and development of cutaneous carcinomas [105]. However, recognition of its role in promoting resistance to anti-PD-1/PD-L1 checkpoint immunotherapy through both CAF-dependent and independent mechanisms, has led to a resurgence in interest

in targeting the pathway [106], including use of neutralising antibodies, receptor inhibitors and ligand traps [107]. With the identification of different fibroblast phenotypes and the recognition of CAF plasticity, "normalizing" CAF is an attractive concept, particularly since certain fibroblast phenotypes may be tumour suppressive [108]. In pancreatic cancer, vitamin D receptor has been shown to act as a master repressor of stellate cell activation, and treatment with calcipotriol (a synthetic derivative of calcitriol) reduces fibrosis and improves response to gemcitabine in tumour-bearing KPC mice [109]. Hanley et al. [22] identified NOX4 as a critical regulator of myCAF activation in multiple tumour types, including HNSCC, and found that inhibiting NOX4 using Setanaxib (GKT137831), a drug developed to treat organ fibrosis, suppressed myCAF activation and also "normalized" established myCAF. More recently, Ford et al. [23] developed myCAF-rich murine tumour models and showed that Setanaxib could be used to effectively overcome myCAF-mediated T-cell exclusion from tumours and potentiate response to anti-tumour vaccination and anti-PD-1 immunotherapies [23]. Grauel et al. [110] also examined the effect of TGF- β inhibition on the CAF phenotype *in vivo*, and found that TGF- β neutralisation reduced myCAF development and promoted an immunomodulatory phenotype characterised by strong response to interferon. CAF depletion could also

be a therapeutic approach. Depletion of fibroblast activation protein (FAP)-positive CAF in murine models has been shown to enhance anti-tumour immunity [111]; Duperret et al. [112] used a DNA vaccine targeting FAP, which induced CD8+ and CD4+ T-cells and synergised with other tumour antigen-specific DNA vaccines to enhance anti-tumour immunity. However, FAP is widely expressed on different cell types [113] and there is still lack of a CAF-specific target that could make this approach effective.

CONCLUSIONS

CAF support HNSCC progression and promote treatment resistance and have emerged as an attractive therapeutic target. Treatments designed to target CAF however, have not been successful clinically, and the identification of specific CAF targets has proven problematic, mostly due to a limited understanding of

the molecular and functional phenotypes within a heterogeneous CAF population and compounded by murine models that do not accurately recapitulate the stromal microenvironment of human tumours. However, the advent of new technologies, particularly single-cell RNA-sequencing, is unpicking CAF complexity and there is great optimism in the field that effective CAF-targeted therapies are on the near horizon.

AUTHOR CONTRIBUTIONS

KB, CH, and GT wrote the manuscript. All authors contributed to the article and approved the submitted version.

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IL-1/IL-1R Signaling in Head and Neck Cancer

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Decades ago, the study of cancer biology was mainly focused on the tumor itself, paying little attention to the tumor microenvironment (TME). Currently, it is well recognized that the TME plays a vital role in cancer development and progression, with emerging treatment strategies focusing on different components of the TME, including tumoral cells, blood vessels, fibroblasts, senescent cells, inflammatory cells, inflammatory factors, among others. There is a well-accepted relationship between chronic inflammation and cancer development. Interleukin-1 (IL-1), a potent pro-inflammatory cytokine commonly found at tumor sites, is considered one of the most important inflammatory factors in cancer, and has been related with carcinogenesis, tumor growth and metastasis. Increasing evidence has linked development of head and neck squamous cell carcinoma (HNSCC) with chronic inflammation, and particularly, with IL-1 signaling. This review focuses on the most important members of the IL-1 family, with emphasis on how their aberrant expression can promote HNSCC development and metastasis, highlighting possible clinical applications.

Keywords: head and neck cancer, squamous cell carcinoma, oral cancer, tumor microenvironment, IL-1, Anakinra (PubChem CID: 90470007)

INTRODUCTION

The association between chronic inflammation and cancer has been reported for many years. Fifteen percent of all cancers are attributed to inflammation [1], with a well-recognized association in lung, pancreatic, esophageal, bladder, gastric, cervical, colorectal and prostate cancers [2]. Pro-inflammatory cytokines present in the tumor microenvironment (TME) can have dual effects; they can stimulate inflammation to decrease tumor progression; or they can stimulate inflammation favoring carcinogenesis, tumor growth and metastasis [3]. Cytokines are produced by host cells in response to factors secreted by the tumor cells or by the tumor itself [4, 5]. Interleukin-1 (IL-1) is commonly found at tumor sites and is considered one of the most important cytokines of the TME, where it plays a key role in carcinogenesis and tumor progression [6], and its expression has been associated with poor prognosis in cancer patients [7]. There is a growing association linking head and neck squamous cell carcinoma (HNSCC) with chronic inflammation [8, 9], in which IL-1/IL-1R signaling seems to be a key player [10]. Cumulating evidence suggests that the effects of IL-1 autocrine and paracrine signaling within the TME is central to HNSCC development. This signaling axis not only leads to increased expression of proteases and factors that dramatically alter the extracellular matrix, aiding tumor cell invasion and metastasis [2, 3], but also increases the production of leukocyte chemoattractants [11]. These molecules selectively recruit both innate and adaptive immune cells to the TME that have both anti- and pro-tumorigenic properties.

Innate immune cells, such as macrophages and neutrophils, are recruited in large numbers to the HNSCC TME where they secrete tumor promoting and pro-angiogenic factors that exacerbate inflammation, and increase the supply of nutrients and oxygen that drives tumor progression. It is no surprise that high numbers of macrophages and neutrophils in the TME are associated with poor prognosis in HNSCC patients [12, 13]. In contrast, and particularly for HPV-positive HSNCC, increased numbers of T lymphocytes have been observed and these have been associated with improved prognosis due to direct anti-tumor cell targeting by these cells [14].

Here, we review the most important members of the IL-1 family, with emphasis on how their aberrant expression can promote HNSCC development and metastasis, highlighting possible clinical applications.

IL-1 FAMILY MEMBERS

The IL-1 family consists of several different ligands and receptors (Table 1) [16]. The most studied ligands are IL-1 α and IL-1 β , commonly known collectively as IL-1, and the interleukin-1 receptor antagonist (IL-1RA), which antagonizes the effects of IL-1 α and IL-1 β [17]. These ligands bind to IL-1 receptor 1 (IL-1R1) and IL-1 receptor 2 (IL-1R2) that are expressed by several cells. IL-1R1 is a biologically active receptor with the ability to bind to either form of IL-1 [18], while IL-1R2 is non-biologically active and acts as a decoy receptor, inhibiting the effects of IL-1 [19, 20].

IL-1 α

IL-1 α is produced initially as a 31–33 kDa precursor protein (preIL-1 α) that is cleaved into its 17 kDa mature C-terminal component (mIL-1 α) and a 16 kDa N-terminal propiece (ppIL-1 α) by the calcium-activated cysteine protease, calpain [5, 21–23]. All forms of IL-1 α are biologically active [24]. PreIL-1 α lacks a leader peptide and therefore cannot be secreted and remains intracellular [17, 25]. Despite not being secreted, preIL-1 α can localize on the cell surface of macrophages, endothelial cells, fibroblasts and dendritic cells [26] where is referred to as membrane-bound IL-1 α . Here it acts in a juxtacrine manner by activating the IL-1R1 receptor of surrounding cells [17]. Both preIL-1 α and mIL-1 α are expressed constitutively in epithelial

and endothelial cells and are considered to act in an autocrine or paracrine manner [27–29]. IL-1 α plays an important role in inflammation acting in a juxtacrine manner [17] and has been related with several other cellular functions, such as onset of senescence [30–32], cell growth, cell differentiation [28, 33], immune response [34] and regulation of gene expression [35–37].

To exert its biological function, mIL-1 α binds to IL-1R1 to trigger different cellular functions, but preIL-1 α and ppIL-1 α can also interact directly with the DNA without binding to IL-1R1 in a variety of cells [28, 38]. This is because ppIL-1 α contains a canonical nuclear localization sequence (NLS) that enables it to interact directly within the nucleus in a non-IL-1R1-dependent manner [39, 40]. PreIL-1 α , via ppIL-1 α , interacts with histone acetyltransferases Gcn5, p300, PCAF and with the adaptor component Ada3, inducing protein transcription without activating IL-1R1 [41], and in doing so exerts different intracellular functions, such as NF- κ B and AP-1 activation [38], modulation of endothelial proliferation [28], migration [42] and cytokine production [43].

IL-1 β

IL-1 β is the classic inflammatory secreted cytokine produced in response to inflammatory signals and other stimuli and can act in a paracrine or systemic manner [44, 45]. IL-1 β is mainly produced by monocytes by intracellular cleavage from its 31 kDa precursor protein (pIL-1 β) into a 17.5 kDa mature form (mIL-1 β) by caspase-1 or IL-1 β converting enzyme (ICE) [5, 46]. The precursor form of IL-1 β is considered to be an inactive immature form of the protein [18]. Unlike preIL-1 α , pIL-1 β is not expressed in health [47]. Many microbial products are able to stimulate IL-1 β secretion, and when produced, IL-1 β , together with IL-1 α , has the ability to upregulate its own gene expression *in vitro* and *in vivo* [48]. IL-1 β expression is mainly restricted to inflammatory cells, where it is regulated in response to external stimuli [49]. IL-1 β is 25–50-fold more abundant than IL-1 α in stimulated human peripheral mononuclear cells [50], and upon activation, around 70% of IL-1 β is secreted by these cells after 24 h stimulation [51].

The main functions of IL-1 β are to induce upregulation of cytokines, chemokines, adhesion molecules, acute phase proteins and tissue remodeling enzymes [17, 49, 52]; it may also act as an angiogenic factor in tumors [53], inducing the production of vascular endothelial growth factor (VEGF) *via* cyclooxygenase (COX)-2 activation [54]. IL-1 β has been associated with the pathobiology of many diseases, such as familial periodic fever syndromes [55], multiple organ failure in sepsis [56], rheumatoid arthritis, type II diabetes [57], chronic obstructive pulmonary disease [58] and growth, vascularization and metastasis of malignant tumors [53].

IL-1 Receptors

IL-1R1

IL-1R1 is the main receptor through which IL-1 exerts its effects and is found on T cells, keratinocytes, fibroblasts, synovial cells, endothelial cells, chondrocytes, and hepatocytes [17, 51]. All active forms of IL-1 (pIL-1 α , mIL-1 α and mature IL-1 β) bind with similar affinity to IL-1R1, triggering biological actions [49, 59]. IL-1R1 is an 80 kDa molecular weight protein and

TABLE 1 | IL-1 family of ligands and receptors (adapted from Dinarello, [15]).

IL-1 family member	Receptor	Function
IL-1 α	IL-1R1/IL-1R2	PI/AI
IL-1 β	IL-1R1/IL-1R2	PI/AI
IL-1RA	IL-1-R1	AI
IL-18	IL-1R5	PI
IL-33	IL-1R4	PI
IL-36 α , β , γ	IL-1R6	PI
IL-36RA	IL-1R6	AI
IL-37	IL-1R5	AI
IL-38	IL-1R6	AI

belongs to the immunoglobulin (Ig) super family. It has a single transmembrane portion with a cytosolic region and an extracellular segment that contains three domains homologous to Igs, with seven N-linked glycosylation sites. To be active, the IL-1R1/IL-1 extracellular complex requires the additional binding of a co-receptor, the IL-1 receptor accessory protein (IL-1RAcP) or IL-1R3, forming a trimeric complex [60, 61]. IL-1RAcP is essential for signal transduction, as murine fibroblasts deficient in IL-1RAcP showed no response after IL-1 stimulation [62]. After IL-1 binds to the extracellular domain, the Toll/interleukin-1 receptor (TIR) domain of the cytoplasmic portion of IL-1R1 triggers a cascade of intracellular signaling events that result in the phosphorylation and degradation of inhibitor nuclear factor κ B (I κ B) [63]. This releases p50 and p65 NF- κ B subunits that upon phosphorylation are transported into the nucleus and bind to specific DNA promoter sequences, initiating gene transcription [49, 64]. Although it is generally accepted that IL-1R1 is localized on the cell membrane, recent reports have shown that the receptor is also present on the nuclear membrane of malignant oral keratinocytes [65, 66], although the relevance of this nuclear localization is unknown.

IL-1R2

IL-1R2 is an inactive IL-1 receptor that acts as a molecular trap, capturing IL-1 on the plasma membrane or within the extracellular space when membrane IL-1R2 is cleaved and present as a soluble receptor, without triggering agonist activity [61, 67]. Together with IL-1RA, these IL-1R2 forms act as IL-1 inhibitors [68]. IL-1R2 is also a member of the Ig super family, consisting of three Ig-like domains in the extracellular portion and a transmembrane segment. It is found on B and T helper 2 cells, neutrophils, monocytes, bone marrow and microglial cells [15]. The main difference between the two IL-1R forms is that, unlike IL-1R1, IL-1R2 has no TIR domain, and is therefore unable to trigger intracellular signaling, rendering it biologically inactive [69].

IL-1RA

IL-1RA blocks the binding of IL-1 α and IL-1 β to IL-1R1, having no cross-reactivity with IL-1 α and IL-1 β [70]. When binding to IL-1R1, IL-1RA does not recruit IL-1RAcP. Thus, IL-1RA has no agonist action, acting as a pure antagonist molecule [71]. IL-1RA mainly binds IL-1R1, having little effect on IL-1R2, which is in agreement with their action as IL-1 inhibitor molecules [72]. As IL-1RA competes with IL-1 for the same receptor, it is found in higher concentrations than IL-1. For example, in the skin, IL-1RA expression has been found to be \approx 100-fold higher than IL-1 α [27]. Similarly, a study with recombinant IL-1RA showed that in order to have 50% inhibition of IL-1-induced actions, IL-1RA had to be present in 5–100-fold excess over both IL-1 α and IL-1 β [73]. This is because IL-1R1 is very sensitive to small amounts of IL-1. Even 5% IL-1 receptor occupancy is able to trigger a complete biological response [63]. So, for IL-1RA to efficiently block the effects of IL-1, it must be in abundance [15].

Two main forms of IL-1RA are now recognized; a secreted form (sIL-1RA) [74] and an intracellular form (icIL-1RA) [75]. Intracellular IL-1RA has the same amino acid structure as

the secreted form, but lacks a leader peptide that prevents its secretion. The intracellular variant is transcribed by alternate splicing of the same gene as sIL-1RA [75]. Three isoforms of the intracellular form have been reported (icIL-1RA1 or transcript variant 3, icIL-1RA2 or transcript variant 2 and icIL-1RA3 or transcript variant 4) [76–78], with icIL-1RA1 being the most studied. Both secreted and intracellular IL-1RA forms are tissue specific. icIL-1RA is constitutively expressed in tissue sites exposed to environmental factors, such as epithelial cells of the skin, oral cavity, vagina, ovaries and upper respiratory tract [65, 75, 79, 80], while sIL-1RA is found in monocytes, neutrophils and other cells [77].

Other IL-1 Family Members

The IL-1 family of proteins comprises of several other members in addition to IL-1 (Table 1). IL-18, whose actions are mediated by binding to IL-1R5, is considered an immunomodulatory cytokine important for IFN γ production and is up-regulated by keratinocytes in response to contact sensitizers [81, 82]. IL-33 is a pro-inflammatory cytokine that binds to IL-1R4, but similarly to IL-1 α , can also exert its actions directly to the nucleus [83]. IL-36 is an inflammatory protein associated with the development of psoriasis and acts by binding to IL-1R6. Decreased levels of its specific antagonist, IL-36RA, have also been related with the development of pustular psoriasis [84]. Similar to IL-18, IL-37 also binds to and activates IL-1R5. However, unlike IL-18, IL-37 is considered an anti-inflammatory cytokine, where low levels are thought to contribute to disease severity [61]. IL-38 also has predominantly anti-inflammatory actions that are mediated by binding to IL-1R6 [85] where it has been shown to reduce clinical manifestations of systemic lupus erythematosus and arthritis [86].

IL-1 IN KERATINOCYTE BIOLOGY

IL-1 α and IL-1RA are constitutively expressed by skin and oral keratinocytes [34, 65, 80, 87]. IL-1 β can be found intracellularly [87], but because keratinocytes lack ICE, pIL-1 β cannot be cleaved into its 18 kDa mature form and remains inactive and is not reported to be secreted [87, 88]. However, it has been recently reported that normal oral keratinocytes do secrete IL-1 β (although in very low levels) that significantly increases with cell aging, although the underlying mechanism is unknown and might be related with the culture conditions (co-culture with irradiated fibroblasts) [65]. To counteract the action of IL-1, keratinocytes mainly express icIL1-RA1 [79, 89], which is localized both in the cytoplasm and inside the nucleus [65], whereas the secreted isoform (sIL-1RA) is either absent or found in very low levels [65, 90]. This makes biological sense as keratinocytes mainly express IL-1 α , which is considered an intracellular cytokine, thus an intracellular antagonist is needed to regulate its activity. Although the main actions of icIL1-RA are attributed to its ability to block IL-1R1, icIL1-RA1 is also able to decrease IL-6 and CXCL8 levels by inhibition of the p38 MAPK and NF- κ B signaling pathways in an IL-1R1-independent manner [89, 91]. Thus, it is likely that the main icIL-1RA1 functions are related to the regulation of intranuclear

IL-1 α . Keratinocytes also express IL-1R2 at higher levels than IL-1R1 (resting and when activated). So, both IL-1R2 and icIL-1RA have synergistic roles in regulating IL-1 action on keratinocytes, protecting these cells from excessive autocrine activation of IL-1 α [92].

IL-1 α and icIL-1RA may have an important role in keratinocyte growth, differentiation, and aging. An *in vitro* study testing the growth conditions for different epithelial cells found that IL-1 α inhibited the proliferation of stratified squamous epithelial cells, whereas IL-1RA enhanced it. Moreover, significant growth promotion in normal epidermal keratinocytes was observed upon addition of exogenous IL-1RA [93]. Changes in the ratio of icIL-1RA:IL-1 α might help to control growth and differentiation of human skin, as icIL-1RA accumulates in more differentiated cells and IL-1RA expression in oral keratinocytes is positively correlated with the expression of involucrin (a marker of cell terminal differentiation that is restricted to the granular cell layer) [94], whereas IL-1 α is uniformly expressed in all keratinocyte maturation stages [33]. icIL-1RA1 is reported to be an important factor in the regulation of oral keratinocyte senescence and the development of the senescence-associated secretory phenotype (SASP) [65]. Cellular senescence corresponds to a cellular state characterized by permanent cell growth arrest in response to different stressors in order to avoid propagation of genetically damaged cells [95]. When cells senesce, they remain metabolically active and develop a SASP characterized by the presence of multiple pro-inflammatory factors which have been related with the development of age-related disorders, including cancer [96]. Oral keratinocytes lacking icIL-1RA1 have been shown to senesce prematurely when compared with keratinocytes expressing icIL-1RA1, and icIL-1RA1 was found to regulate the expression of two important SASP factors, IL-6 and CXCL8 [65], which have been associated with the development of malignancies [96].

IL-1 SIGNALING IN HEAD AND NECK SQUAMOUS CELL CARCINOMA

IL-1 α , IL-1 β , and IL-1R1 have been reported to be constitutively expressed in HNSCC [66, 97–99] whilst decreased IL-1RA expression has been observed early in the oral carcinogenesis process [65]. As different members of the IL-1 signaling pathway have reported to have important functions in HNSCC carcinogenesis and tumor progression, we will review them separately.

IL-1 α

IL-1 α expression in HNSCC contributes to cell growth and survival and has been considered by some authors as a prognostic factor. In the study of Leon et al. [100], patients with metastatic HNSCC displayed higher expression of IL-1 α than patients without metastases. Constitutive IL-1 α over-expression was correlated with that of IL-1 family genes, such as IL-1 β and IL-1RA. IL-1 α expression also correlated with increased cell transmigration of tumor cells across the endothelium, which was inhibited by addition of IL-1RA. IL-1 α expression also correlated

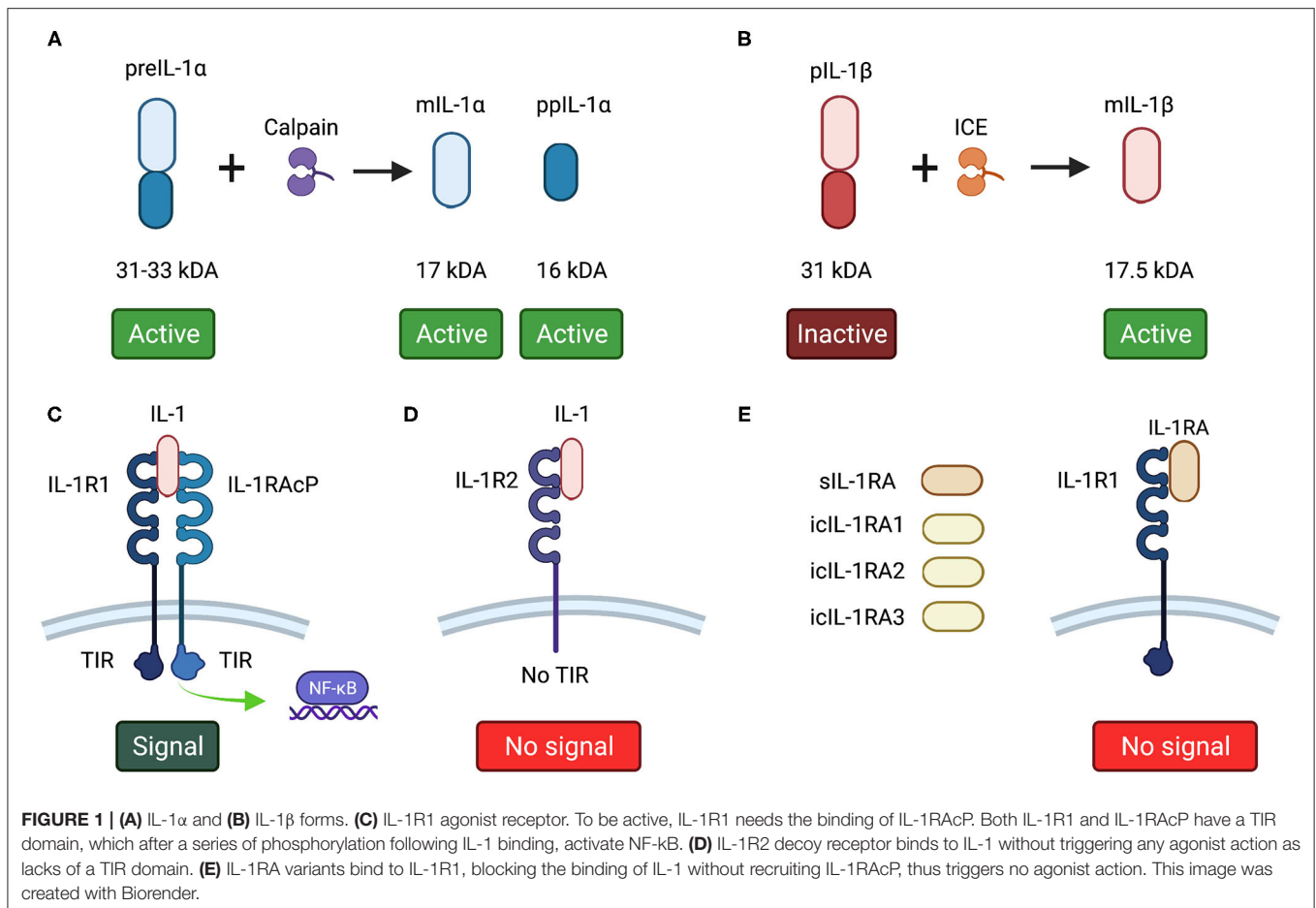
with different genes that have been associated with metastasis, particularly MMP-9 (a matrix metalloproteinase associated with EMT), PGE₂ (a product of COX-2 activation associated with metastases of OSCC), VEGF (the most important angiogenic factor in HNSCC) and CXCL8 [100]. The five-year distant metastasis-free survival was 70% for patients with high tumor levels of IL-1 α in contrast to 95% for patients with low expression of IL-1 α . Patients with increased levels of IL-1 α had a 5.3-fold higher risk of developing metastasis and patients with distant metastases had also a significant increase in secreted IL-1 α [100].

IL-1 α has also been reported to induce the overexpression of IL-6 [97] and CXCL8 in HNSCC cell lines, the latter by inducing NF- κ B and AP-1 pathways [36]. This is of importance as IL-6 and CXCL8 are considered important “oncogenic cytokines”, as they are able to cause EMT [101], stimulate angiogenesis and tumor growth [102, 103], disrupt cell-cell communication, impede macrophage function and promote epithelial and endothelial cell migration and invasion [104]. NF- κ B is considered a key factor in the regulation of the inflammatory infiltrate observed in the TME [105] and has been associated with the acquisition of a malignant phenotype of HNSCC, as is associated with tumor angiogenesis [106], EMT [107], invasion [108, 109] and metastasis [110]. In addition, inactivation of NF- κ B in HNSCC suppressed cell survival and expression of IL-1 α , IL-6, CXCL8 and GM-CSF in a murine model of head and neck cancer [111] and its aberrant expression is associated with poor prognosis in solid cancers [112]. AP-1 expression increases with HNSCC progression and induces bcl-2 expression that is associated with suppression of apoptosis and resistance to chemoradiation therapy [113] (Figure 3).

IL-1 β

The mechanism by which IL-1 β is constitutively overexpressed in HNSCC is not clear, but a single nucleotide polymorphism of the IL-1 β gene could explain this. In fact, IL-1 β -511 polymorphism has been reported to be a significant risk factor for the development of OSCC [114]. IL-1 β is identified as a key node gene in the tumor microenvironment (TME) of OSCC *in vivo* [115]. Keratinocytes lack ICE and therefore should not be able to produce the mature active form of IL-1 β . However, other proteases are able to cleave IL-1 β precursor form, suggesting that pIL-1 β can be processed after secretion by other proteases that are present in the TME [116]. In agreement with this, IL-1 β produced by oral keratinocytes and HNSCC cells is biologically active. Interaction of IL-1 β with the TME leads to monocyte recruitment that then differentiate into tumor-associated macrophages (TAMs) whose increased levels in HNSCC are associated with poor prognosis [12, 117]. Also, stimulates the production of numerous cytokines by different cell types, such [116] as cancer-associated fibroblasts (CAFs), normal fibroblast, endothelial cells, neutrophils as well as oral dysplastic and cancer cells, among others [10, 11, 98, 118], through an IL-1-dependent innate immune response.

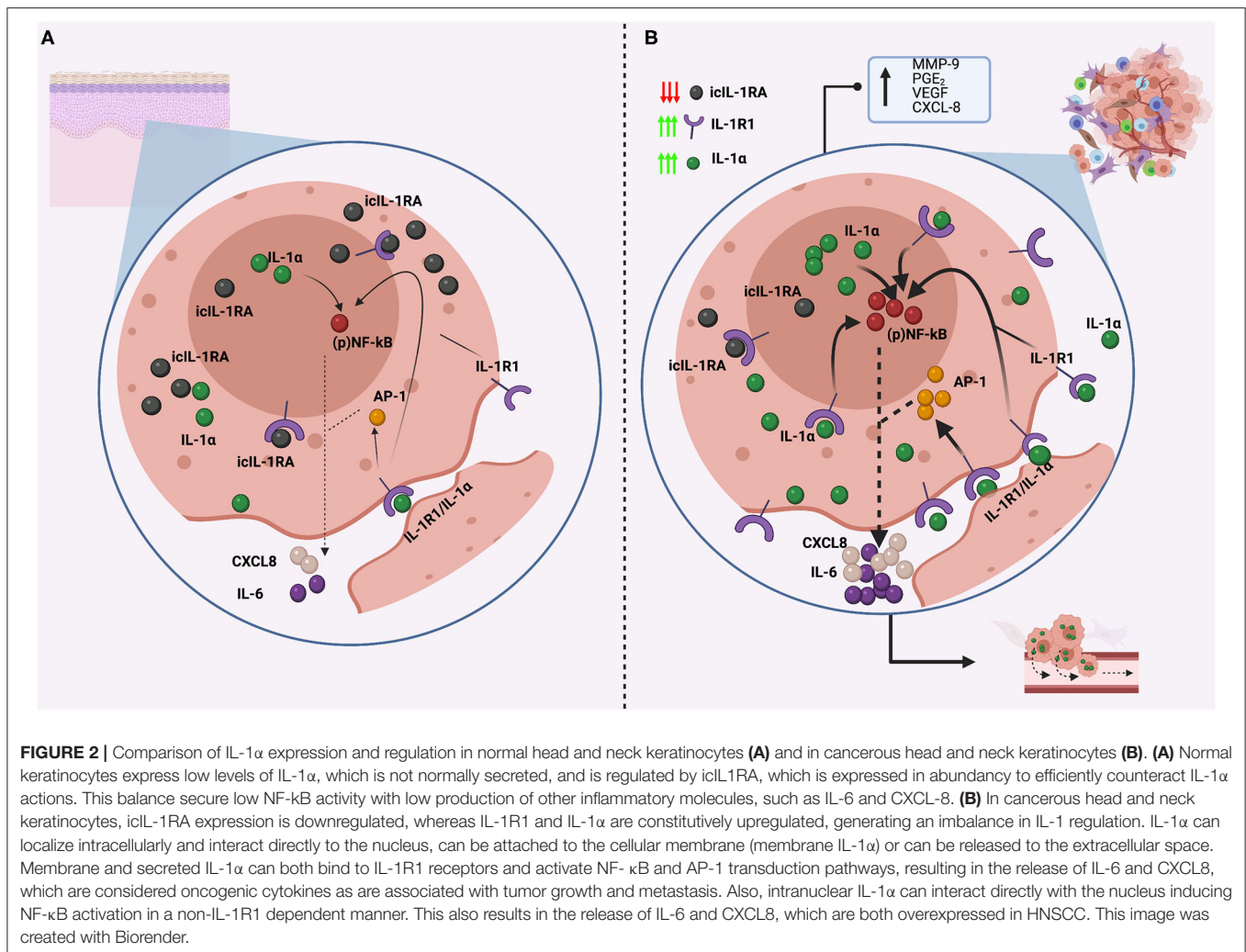
The IL-1 β found in the TME is also produced by other cells in addition to HNSCC cells. A recent report demonstrated that IL-1 β produced by CAFs induces CCL22 mRNA overexpression in oral cancer cells. CCL22 is implicated in the recruitment of



T regulatory cells, and its expression in oral cancer patients has been associated with a reduced disease-free survival [119]. Tumor-associated macrophages (TAMs) also secrete IL-1 β , which, together with the actions of TNF- α stimulate tumor angiogenesis by inducing the release of VEGF and CXCL8 by HNSCC cells [120]. This creates an inflammatory TME that can predispose to tumor progression [121] (**Figure 1**). For example, in HNSCC IL-1 signaling drives neutrophil and monocyte recruitment [10], and accumulation of these tumor-associated leukocytes has been associated with poor prognosis [13, 122]. The IL-1/IL-1R axis mediates chemokine release from normal tonsillar fibroblasts (NTF) induced by HPV-negative oropharyngeal carcinoma (OPC) cells, which can be reverted with IL-1 inhibition [11]. This is of significance, as for example, CXCL1 and MMP-1 produced by CAFs in response to IL-1 β from OSCC cells, increased the invasion and migration capabilities of OSCC cells [123]. Also, IL-1 released from HNSCC cells has been shown to stimulate COX-2 production by CAFs [124] that correlated with lymphangiogenesis [125] and E-cadherin regulation, important factors for epithelial-to-mesenchymal transition (EMT) development [126], and increased risk of distant metastases [127]. In OSCC, IL-1 β produced by tumor cells can act in a paracrine manner, inducing the expression of fascine

that is associated with ECM degradation and tumor cell invasion [128] (**Figure 2**).

The oncogenic properties of IL-1 β have also been demonstrated using *in vivo* models. In a mouse oral cancer model in which carcinogenesis was induced by mimicking tobacco and areca nut carcinogens, an increase in pIL-1 β mRNA positively correlated with the presence of malignant change (from normal, to mild, through severe dysplasia to OSCC). In agreement with these findings, OSCC and dysplastic cell lines from smokers and/or betel quid chewers had higher IL-1 β levels than controls, with inflammasome components constitutively expressed in OSCC cells that allows the cleavage of pIL-1 β into mL-1 β . IL-1 β might have an important role in the induction of EMT in OSCC, as in the same study, OSCC cells treated with IL-1 β showed upregulation of Snail and Slug (two repressors of E-cadherin expression), increased vimentin expression, and downregulation of E-cadherin. This was also correlated with a change in cell morphology, from a squamous cell-like shape, in cells not exposed to IL-1 β , to a spindle-like shape in OSCC cells exposed to IL-1 β . The migration capacity of OSCC cells treated with IL-1 β increased significantly after 48 hours, compared to untreated OSCC. These findings strongly suggest a role of IL-1 β in EMT in OSCC [98], which has also been reported by



others [126, 129, 130]. This is also supported by the fact that IL-1 β silencing reduces OSCC tumor size *in vivo* [115] and that elevated IL-1 β expression has been related with lymph node metastasis of OSCC [131].

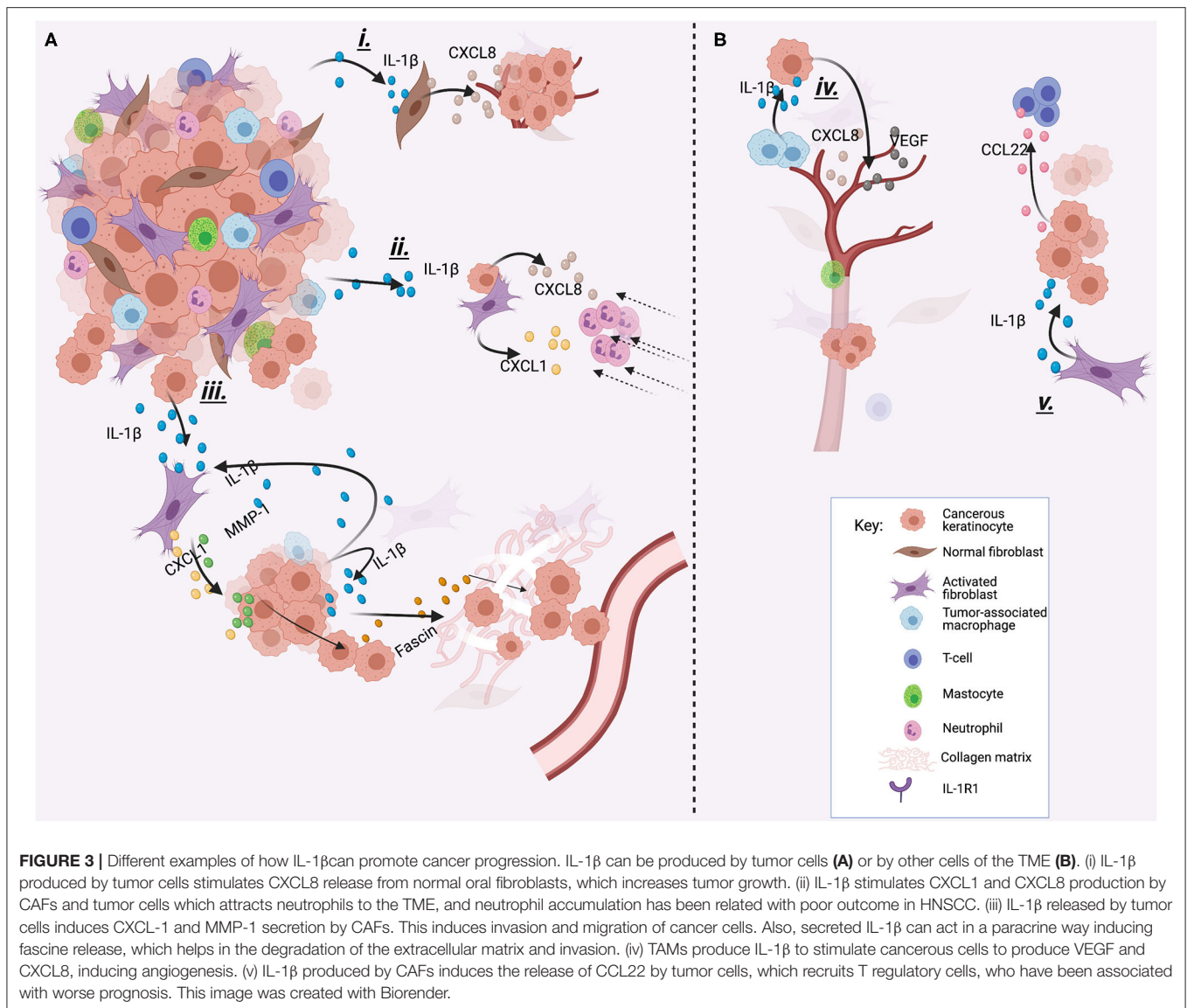
IL-1RA

Several gene expression profiles of HNSCC have shown that *IL-1RN* is downregulated in HNSCC when compared to matched normal oral mucosa [132–139]. In addition, *IL-1RN* was reported to be a reliable marker when predicting the presence or absence of HNSCC in tissue samples in a cohort of 46 patients with HNSCC, with sensitivity and specificity of 93.5 and 95.7%, respectively [138]. Despite this, very little is known about the role of IL-1RA in HNSCC.

Von Biberstein et al. [99] reported an imbalance in the IL-1:IL-1RA ratio in HNSCC when compared to healthy patients, that was attributed mainly to an increase in the levels of IL-1 α and IL-1 β , but also to a decrease in the levels of IL-1RA. These authors also reported higher expression of IL-1RA in the more differentiated epithelial cells within the tumors. IL-1RA protein expression decreases progressively during oral

carcinogenesis and in HNSCC [65], which is in agreement with a previous report [80] and IL-1R2, the other IL-1 inhibitor, is not able to compensate for IL-1RA lack of expression [65]. Also, IL-1RA levels decrease significantly in immortal normal and dysplastic oral keratinocytes when compared to their mortal counterparts. This suggest that IL-1RA downregulation during the carcinogenic process might be an important step for the acquisition of a malignant phenotype, primarily because the binding of IL-1 to IL-1R1 is not inhibited, allowing dysregulated activation of the IL-1/IL-1R1 axis that can predispose to the carcinogenesis process in different ways (**Figures 1, 2**). Moreover, In oral keratinocytes, icIL-1RA1 regulates IL-6 and CXCL8 secretion, most likely by interfering with NF- κ B activation [65]. Both IL-6 and CXCL-8 secretion is canonically regulated by NF- κ B, and icIL-1RA1 is able to regulate NF- κ B activation wheter by inhibiting IL-1 binding to IL-1R1, or by directly interfering with the NF- κ B signaling pathway (see below). Thus, a downregulation of IL-1RA would allow overexpression of these cytokines (**Figure 3**).

There has been much debate about the specific functions of icIL-1RA. icIL-1RA is able to bind to IL-1R1, but as a strictly intracellular molecule, it is more likely that the



main functions of icIL-1RA are not related to IL-1R1 binding. IL-1R1 is located on the membrane surface, thus, icIL-1RA would require secretion into the extracellular space for it to block IL-1R1, although IL-1R1 intranuclear localization in oral dysplastic and cancer cells has been recently described [65]. It has been proposed that the main function of icIL-1RA is to counteract the intranuclear action of IL-1 α . icIL-1RA may act intracellularly by binding to other cytoplasmic proteins in order to interfere with the downstream cascade. In fact, icIL-1RA has been reported to interact with the third component of the COP9 signalosome (CSN3) inhibiting CSN-associated kinases [91]. The signalosome (CSN) is found in the cytoplasm and nucleus of all mammalian cells, and among other functions, it has kinase activity that induce phosphorylation of proteins involved in signal transduction. When interacting with CSN3, icIL-1RA1 inhibits phosphorylation of p53, c-Jun and I κ B thereby inhibiting IL-1 α -mediated IL-6 and CXCL8 transcription. These inhibitory

actions may also affect the p38 MAPK signal transduction pathway, as transfected keratinocytes with icIL-1RA1 showed no detectable phosphorylated p38 MAPK when stimulated with IL-1 α [91]. Similar icIL-1RA1 inhibitory mechanisms have also been reported in intestinal epithelial cells [89]. Böcker et al. [140] also reported inhibition of IL-1-induced CXCL8 expression by icIL-1RA1, but did not specify the mechanism underlying this inhibition. It has been proposed that the role of CSN3 is to bring icIL-1RA1 close to a kinase in order to inhibit its action. So, icIL-1RA1 would block an upstream kinase in the p38 MAPK or NF- κ B pathways, indirectly inhibiting p38 MAPK or NF- κ B phosphorylation and consequently, its downstream products, such as IL-6 and CXCL8 [91].

It can be hypothesized then, that downregulation of icIL-1RA in HNSCC could lead to de-regulated expression of pro-inflammatory cytokines related to cancer development by allowing the un-controlled activation of IL-1 α and

NF- κ B (**Figure 3**). This speculation is based on the finding that OSCC constitutively express higher levels of IL-1 α and NF- κ B than healthy controls [8, 100, 118, 141] and that levels of IL-6 and CXCL8 are elevated in OSCC [142, 143]. In addition, IL-1 α can interact directly with nuclear DNA and induce malignant transformation [40]. Thus, if endogenous levels of IL-1 α are constitutively overexpressed, and its main inhibitor (icIL-1RA) is downregulated, there could be more chances for icIL-1 α to induce malignant transformation. In agreement with this hypothesis, a recent study comparing nuclear and cytoplasmic IL-1 α expression in OSCC showed that the high expression of nuclear IL-1 α in combination with EGFR, was associated with perineural invasion and high risk of recurrence and worse progression-free survival, compared to OSCC expressing none or moderate nuclear IL-1 α in combination with EGFR [144]. These studies suggest that uncontrolled nuclear IL-1 α activity might be of clinical importance.

There is some controversy about the role of IL-1RA in HNSCC. Shiiba et al. [80] reported an increase of IL-1RA (T3/T4) compared to early OSCC cases (T1/T2), suggesting that IL-1RA expression could increase tumor progression. Similar observations have been reported by other authors in gastric [145] and cervical carcinomas [146], reporting a more aggressive behavior from IL-1RA expressing tumors. A possible explanation to this could be that over time, endogenous IL-1 antagonism (which is likely to be beneficial in antagonizing disease progression) changes the tumor phenotype to one that is less susceptible to IL-1 inhibition. Thus, the disease progresses, and IL-1RA levels remain high [71]. Also, most of the aforementioned studies measured sIL-1RA, so the increase in sIL-1RA may be due to a decrease in icIL-1RA levels. Nevertheless, these contradictory functions of IL-1RA in different cancers only highlights the multiple functions that IL-1RA displays in relation to the specific tissue, cell type or the microenvironment in which it is present.

IL-1R1

A number of different polymorphisms of the *IL1R1* gene have been related with a reduced (rs956730) or increased (rs3917225) risk for developing HNSCC [147]. IL-1R1 is overexpressed by oral dysplastic and OSCC cells compared to normal oral keratinocytes [65], which seems to provide phenotypic advantages. IL-1R1 promotes oral cancer growth and metastasis by upregulating CXCR4 (a chemokine receptor involved in tumor progression, angiogenesis and metastasis) after IL-1 β stimulation, and IL-1R1 inhibition with recombinant IL-1RA has shown to reverse these effects [66]. IL-1R1 is also constitutively expressed by normal oral fibroblasts [11]. This is of importance as HNSCC cells are able to secrete IL-1 β which stimulates other cells of the TME (such as fibroblasts) to generate chemokines and other inflammatory molecules creating an inflammatory TME with cancer promoting properties [11].

TRANSLATIONAL POTENTIAL

Utility as a Saliva Biomarker

The discovery that saliva contains molecules that are able to translate the presence or activity of local or systemic diseases has opened a new diagnostic field known as salivary diagnostics

[148]. The use of saliva as a diagnostic method is very practical, as saliva can be collected in an easy, non-invasive way. As there is evidence suggesting that IL-1 α , IL-1 β , and IL-1RA are involved in the pathogenesis of HNSCC and can be detected in the saliva of cancer patients [149–151], different studies have explored their possible use as diagnostic or prognostic biomarkers for this cancer.

IL-1 β is overexpressed in the saliva of oral cancer patients compared to oral leukoplakia and control patients [152, 153] and IL-1 β salivary levels have been shown to discriminate between OSCC subjects and controls [154–156], but not between oral potentially malignant disorder (OPMD) patients and healthy subjects [155]. The reported AUC of salivary IL-1 β to differentiate between OSCC and control individuals varies between 0.729 and 0.7724 [154, 155] but increases to 0.901 when considering only late stage OSCC [155]. Also, the discriminatory power of salivary IL-1 β increases when used with other markers, such as CXCL8, SAT1 and DUSP1 [156]. In the study by Singh et al. salivary IL-1 β failed to distinguish between post-treatment OSCC individuals and healthy subjects, suggesting a normalization of IL-1 β salivary levels after tumor removal [155]. In agreement, a study in which the authors analyzed the expression of 50 cytokines (including IL-1 β , IL-1 α , and IL-1RA) in the saliva of 16 OSCC patients before and after surgical intervention, showed a significant decrease in salivary IL-1 β levels after tumor resection. No significant changes in other cytokine levels were reported [150]. Similar results were also reported elsewhere [157]. IL-1 α expression is also reported to be increased in the saliva of tongue SCC (TSCC) patients compared to controls and has also been associated with tumor growth pattern [9, 158]. Patients presenting with endophytic TSCC exhibited significantly higher IL-1 α levels compared to exophytic TSCC, which correlated with a decreased survival rate in the group of endophytic tumors [158].

IL-1RA can also be detected in the saliva and its expression is reported to be significantly decreased in the saliva of OPMD and OSCC patients compared to healthy controls [151]. Opposite to salivary IL-1RA, plasma circulating IL-1RA levels have been shown to be increased and OSCC patients and correlated with tumor size, but were not related with different outcome measures [159]. By itself, salivary IL-1RA displayed a poor performance in diagnosing OSCC, but in combination with other proteins (SLC3A2 and S100A2), it was able to distinguish between individuals with OSCC from healthy controls and OPMD patients, with AUC of 0.89 and 0.87 respectively [151].

The use of salivary IL-1 α , IL-1 β , and IL-1RA as HNSCC biomarkers is promising, but as there are many local and systemic diseases that can give rise to elevated salivary IL-1 or decreased IL-1RA levels (e.g., periodontal disease, oral lichen planus, Sjögren's syndrome) [94, 160, 161], which increases the likelihood of false positives, more clinical studies are needed before translating this into clinical practice.

Therapeutics

Many beneficial functions of IL-1 inhibition have been described in different cancers, thus, targeting IL-1 has been proposed as a possible therapy for IL-1 expressing tumors, such as melanoma, gastric and breast cancers, among others [162]. In gastric

cancer, recombinant IL-1RA inhibited tubule formation [163] and reduced proliferation and migration of endothelial cells *in vitro* in a dose-dependent manner [164]. Similar results have been reported in breast cancer. A murine experimental breast cancer model showed that treatment with anakinra (a recombinant form of IL-1RA with FDA approval for the treatment of rheumatoid arthritis and cryopyrin-associated periodic syndromes) reduced the size and number of bone metastases as well as tumor angiogenesis [165]. Taken together, these data suggest that rIL-1RA could be a beneficial alternative for the inhibition of tumor-dependent angiogenesis, probably by reducing the production of VEGF, CXCL8, endothelin-1, IL-1 β and hepatocyte growth factor (HGF) [164–166].

Anakinra has been used in clinical trials for the treatment of some cancers. The first study to use anakinra as a cancer treatment was a phase II clinical trial of pre-multiple myeloma. Anakinra in combination with dexamethasone was found to increase the progression-free survival as well as overall survival in patients at high risk of progressing to multiple myeloma, by targeting the IL-1/IL-6 pathway [167]. In refractory metastatic colorectal cancer, anakinra in combination with fluorouracil (an anti-metabolite) and bevacizumab (anti-EGF monoclonal antibody) showed good efficacy with low toxicity. Currently, there are several clinical trials where recombinant IL-1RA is being tested either as a monotherapy or in combination for the treatment of different cancers, including multiple myeloma, prostate, breast, pancreatic, and colorectal cancers (<https://clinicaltrials.gov/ct2/results?cond=Cancer&term=termIL1RA+OR+Anakinra&cntry=&state=&city=&dist=>). Nevertheless, care must be taken when considering IL-1RA therapy for HNSCC treatment, as recombinant IL-1RA is likely reduce the innate immunity response in already ill patients, which in theory, could worsens the disease. Thus, IL-1RA replacement therapy may be only appropriate for IL-1 producing tumors [162].

Exogenous IL-1RA (i.e., anakinra) corresponds to the secreted isoform of IL-1RA, which is present in very low levels in oral keratinocytes, as oral keratinocytes constitutively express icIL-1RA1. It is not entirely clear how exogenous IL-1RA works. It is thought that exogenous IL-1RA acts in a similar manner to sIL-1RA, by blocking IL-1R1 on the cell membrane. Nevertheless, exogenous IL-1RA has been shown to be incorporated into the cytoplasm of cardiac myocytes during ischemia, mimicking the intracellular form of IL-1RA, at least in terms of intracellular distribution [168]. Whether exogenous IL-1RA can replace icIL-1RA (which expression is lost during the malignant transformation process of oral keratinocytes and OSCC) functions is not known.

Despite the data supporting an oncogenic role of the IL-1/IL-1R1 axis in HNSCC, there is a lack of studies that have

explored the use of IL-1 inhibition for HNSCC treatment. A recent study [115] showed that exogenous IL-1RA can inhibit the growth of Cal27 cells (a tongue squamous adenocarcinoma cell line) *in vitro*, but more importantly, can potentially interrupt the oral carcinogenesis process *in vivo*. Submucosal injections of IL-1RA into the tongue of mice during 4NQO-induced oral carcinogenesis interrupted the malignant transformation process. This was done presumably by downregulating genes that were upregulated during the 4NQO-induced carcinogenesis process, such as the oncogene Myc and COX-2 [115]. In addition, anakinra has been shown to overcome erlotinib (an EGFR inhibitor) resistance in a HNSCC mouse xenograft cancer model, suggesting its use as a possible strategy to overcome EGFR inhibitor resistance for HNSCC treatment [169]. Although these initial data are promising, there are no clinical trials that have assessed anakinra for HNSCC treatment and more research in this area is warranted.

CONCLUSION

There is compelling evidence that the IL-1 signaling pathway is deregulated in HNSCC, with overexpression of agonistic molecules and downregulation of inhibitory factors. This results in a dysregulated signaling pathway that mediates the development of a pro-inflammatory microenvironment prone to tumor development, progression and metastasis. Oral carcinogenesis is a multistep process which includes three phases: initiation, promotion, and progression. The available evidence suggests IL-1 signaling to influence the promotion and progression phases of the malignant transformation process. The increased presence of IL-1 in HNSCC support the idea that salivary IL-1 could be of use as a screening tool for the early detection of cancer, probably as part of a biomarker panel rather than as a single marker. Early data shows promise, although more rigorous studies are needed before this can be translated into clinical practice. IL-1 inhibition is already being tested as a possible treatment alternative for different cancers, such as myeloma, breast, pancreatic and colorectal cancers, and there are *in vivo* animal studies showing promising results for HNSCC treatment. However, there is still a long way to go before this can be applied in a clinical setting.

AUTHOR CONTRIBUTIONS

All three authors contributed equally to the writing of this review. The concept and outline were agreed upon by all. SN wrote the initial draft and constructed the figures. All authors agree on the final version for submission.

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