Pro-and Anti-inflammatory Biomarkers as Potential Prognosis Markers in Oral Squamous Cell Carcinoma

Biomarcadores Pro y Antiinflamatorios como Posibles Marcadores de Pronóstico en el Carcinoma Oral de Células Escamosas

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ABSTRACT: The most widely used method to classify prognostic factors in cancers today is TNM. However, Oral Squamous Cell Carcinoma (OSCC) often demonstrates different behaviors in relation to aggressiveness and therapeutic response at the same TNM stage. So, in such cases biomarkers can be used to identify the biological diversity of these tumors more reliably, leading to better therapeutic strategies and disease management. The presence of inflammatory immune cells in the tumor microenvironment can have pro or antitumor effects and the investigation of the expression of inflammatory markers in OSSC can be useful for designing immunotherapeutic interventions. The Transforming Growth Factor alpha is a potent stimulator of cell migration that acts on cell proliferation, invasion and metastasis of cancer, as well as immune suppression and angiogenesis. Inflammatory cytokines, such as Interferon-gamma, mediate macrophage differentiation. Macrophages are an important component of the OSCC microenvironment. The greater amount of tumor-associated macrophages, especially the M2 phenotype, may be associated with a more aggressive biological behavior of the OSCC and, consequently, with reduced survival.

KEY WORDS: oral squamous cell carcinoma, transforming growth factor-alpha, epidermal growth factor receptor, cd68 antigen, cd57 antigens, interferon-gamma, biomarkers, prognosis.

INTRODUCTION

Cancer will probably be the leading cause of death as well as the most important challenge for life expectancy worldwide in the 21st century (Bray et al., 2018). Oral squamous cell carcinoma (OSCC), the most prevalent malignant neoplasm in the oral cavity, has a high potential for local invasion and nodal metastasis. The overall 5-year survival rate of OSCC has not changed significantly over the last 30 years (Lampri et al., 2015), despite the discovery of new therapies and treatment options (Cervino et al., 2019). In 2018, 354,864 patients worldwide were diagnosed with OSCC and 177,384 of these patients died due to this disease (Bray et al., 2018). Previous studies have already estimated an incidence of 550,000 cases of OSCC in 2040 with 275,000 deaths (Bray et al., 2018). The main etiological and predisposing factors for OSCC include the use of tobacco products, drinking habits, ultraviolet radiation (specifically for lip cancer), human papillomavirus (HPV) infection, poor oral health, nutritional deficiencies, and genetic polymorphisms (McDermott & Bowles, 2019).

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Nowadays, the TNM staging system seems to be the most reliable prognostic factor for OSCC; however, OSCCs often have a diverse behavior especially regarding their aggressiveness and therapy responses at similar TNM stages. Therefore, TNM staging might benefit from the use of biomarkers that reflect the biological diversity of these tumors more reliably, leading to better therapeutic strategies and disease management (Hadler-Olsen & Wirsing, 2019). Biomarkers can be defined as biological molecules such as nucleic acids, proteins, peptides, enzymes, antibodies, metabolites, lipids, carbohydrates and growth factors able to mediate the interaction between neoplastic cells and their microenvironment (Santosh et al., 2016), which together form a self-sufficient biological structure (Peltanova et al., 2019).

Currently, a large number of biomarkers have been identified and are under investigation (Lampri et al., 2015). They can be used to estimate disease risk, track unknown primary cancer, distinguish benign neoplasms from malignant tumors, determine prognosis, monitor the disease status, detect recurrence as well as therapy effectiveness or failure (Santosh et al., 2016). Fortunately, considerable progress in the identification and validation of biomarkers with a high potential to improve cancer diagnosis and treatment has been made (Lampri et al., 2015).

The presence of inflammatory immune cells in the tumor microenvironment with functional plasticity and that can exert either pro- or anti-tumor effects (Takahashi et al., 2017) along with investigations of inflammatory marker expressions in OSCC might be helpful to design immunotherapeutic interventions. Since several tumor biomarkers have already been suggested to predict the prognosis of OSCC in patients, we decided to conduct a review to assess whether the expression of pro- (TGF-α, CD-68) and anti-inflammatory (IFN-γ, CD57) biomarkers can be used as a prognosis in OSCC.

**Pro-inflammatory Biomarkers**

**Transforming Growth Factor α (TGF-α).** TGF-α was described by Roberts et al. (1981), and was initially called the epidermal growth factor-potentiated TGFs. TGF-α is a potent cell migration stimulator that also acts on cell proliferation, cancer invasion and metastasis, as well as inducing immune suppression, and angiogenesis (Sherbet et al., 2011; Le et al., 2019). The biologic importance of this growth factor in head and neck cancer progression is supported by the demonstration that the survival rate of patients correlates significantly with the expression levels of TGF-α in the primary tumor, independent of other clinical and pathological parameters. This led us to believe that this protein is probably involved in the development and progression of cancer.

TGF-α is a small mitogenic peptide with 50 amino acid residues and three disulfide bridges (Sherbet et al., 2011). TGF-α belongs to the endothelial growth factor family and is encoded by the TGFA gene, which is expressed during craniofacial development (Le et al., 2019). The secondary structure is very similar to the epidermal growth factor (EGF) and has a sequence homology of 40 % with this (Sherbet et al., 2011). Because of its structure, TGF-α can bind by competition to EGF through Phe15 and Leu48, which resemble Tyr13 and Leu47 of EGF giving comparable binding interactions (Sabbah et al., 2020).

TGF-α is produced by transformed cells, embryonic cells, and tumor cells, and is closely involved in both normal and aberrant cell development and differentiation (Wong, 1993; Sherbet et al., 2011). Under normal conditions, epithelial cells are the major producers of this peptide (Wong, 1993), so that they can act physiologically in tissue regeneration and bone homeostasis (Sun et al., 2018). Levels of TGF-α, EGFR and EGFR mRNA in tissues can be measured by several molecular techniques, including radiolabeled ligand binding, protein blotting, RNA blotting, in situ hybridization, quantitative reverse transcription-polymerase chain reaction (rt-PCR) and immunohistochemical analysis (Grandis et al., 1998).

The overexpression of TGF-α deregulates cell proliferation and promotes the development and progression of the tumor (Endo et al., 2000; Sherbet et al., 2011; Sabbah et al., 2020). This overexpression has been observed in a wide range of human tumors, such as gastric, bladder, lung, brain, breast, colon, prostate, ovary, renal, liver, pancreas, bone metastasis, and head and neck (Sun et al., 2018; Le et al., 2019).

TGF-α also facilitates the epithelial-mesenchymal transition (EMT), which is crucial for the metastasis process and consequently a poor prognosis (Le et al., 2019; Yokokawa et al., 2020). The epithelial tumor cells leave a primary tumor from the disruption of tight junctions and adherent junction complexes, delocalization of tight junction proteins (zonula occludens-1, claudin-1, and occluding), and the
occurrence of reorganization of the actin cytoskeleton anchored to the focal adhesion complexes (Furue, 2011). Thus, the silencing of the TGF-α expression may be a potential therapeutic approach in cancer treatment (Le et al., 2019).

Currently, no alternative receptor protein able to bind TGF-α has been described in the literature other than EGFR (Endo et al., 2000; Ekblad et al., 2015). EGFR is a member of the tyrosine kinase receptor family, which generates an intracellular signaling cascade that results in cell proliferation (Lampri et al., 2011; Shahsavari et al., 2020). Cells that acquire the ability to overexpress this ligand increasing the number of EGFR on their surface can create an autocrine growth pathway, resulting in uncontrolled growth with cellular proliferation and inhibition of apoptosis (Lampri et al., 2015). Cells showing EGFR overexpression acquire growth advantages, especially when this is accompanied by increased expression of TGF-α (Diniz-Freitas et al., 2007).

Both EGFR and TGF-α are frequently overexpressed in tumor specimens of patients with head and neck squamous cell carcinoma (HNSCC) (Endo et al., 2000; Byeon et al., 2019). The binding of TGF-α to EGFR activates the Signal Transducer and Activator of Transcription (STAT) 1, and STAT 3, phosphatidylinositol 3-kinase (PI3k)/AKT/mTOR, PLCg/PKC, and the Ras-MAPk/ERk pathways to cell survival and proliferation in HNSCC (Lampri et al., 2015; Byeon et al., 2019). This suggests that the maintenance of an autocrine loop in HNSCC is dependent on the elevated levels of EGFR and the presence of TNF-α (Endo et al., 2000).

Tobacco smoke, a classic etiological factor for HNSCC, can increase TGF-α production, and consequently resulting in direct EGFR activation (Byeon et al., 2019). The high expression of EGFR is a negative prognostic factor often associated with nodal or distant metastasis, poor survival (Grandis et al., 1998; Lampri et al., 2015), local treatment failure (Byeon et al., 2019) and increased resistance to radiotherapy and chemotherapy in patients with HNSCC (Yokokawa et al., 2020). However, Shahsavari et al. (2020) did not find any significant correlation between EGFR expression and the TNM stage of OSCC.

TGF-α seems to be overexpressed in areas of mild dysplasia compared to normal mucosa, but no additional expression of this factor can be seen in more aggressive stages of dysplasia or even in carcinoma. However, EGFR levels increase progressively accompanying aggressiveness of dysplasia until they reach the maximum expression in HNSCC (Grandis et al., 1998). Similar to what happens in other cancers, the levels of EGFR expression seem to be upregulated in the normal mucosa of HNSCC patients, suggesting that increased EGFR expression is an early event in the development of HNSCC (Lampri et al., 2015). In fact, previous studies have already determined that about 80 % of OSCC specimens overexpress EGFR, with rare events of EGFR mutations or EGFR amplifications (Byeon et al., 2019; Shahsavari et al., 2020; Yokokawa et al., 2020).

Several agents that are known to trigger mechanisms of EGFR nuclear translocation in HNSCC are: EGFR ligands, Cetuximab, Epstein Barr Virus, radiation, and Src family kinase (SFK). The therapeutic resistance and cancer progression may be caused by increased activity of EGFR, which induces cell proliferation and repair of DNA damage caused by chemoradiotherapy (Byeon et al., 2019).

The efficacy of EGFR in HNSCC is at an advanced research stage, currently in the Phase III clinical trial investigation (Santos et al., 2016), and the aim of these researchers is to find specific inhibitors of EGFR. Two classes of EGFR inhibitors have already been developed and approved for various cancer therapies; they are the reversible tyrosine kinase inhibitors (TKI) (gefitinib, erlotinib), and the EGFR blocking antibodies (cetuximab, panitumumab) (Ekblad et al., 2015). Cetuximab is a monoclonal antibody that acts as a competitive inhibitor at the ligand-binding site of EGFR in HNSCC (Ekblad et al., 2015), which consequently results in the abrogation of EGFR dimerization (Byeon et al., 2019). The administration of Cetuximab in radiotherapy or chemotherapy has enhanced tumor control (Ekblad et al., 2015), and its association with platinum-based and 5-fluorouracil chemotherapy are the first-line in recurrent, unresectable or metastatic HNSCC treatment (National Comprehensive Cancer Network, 2020). Meanwhile, the cetuximab monotherapy as second-line therapy for platinum resistant recurrent/metastatic HNSCC had a poor response rate. The reversible action of TKI on EGFR has not shown any clinical benefit in HNSCC, but multi target TKIs (lapatinib, afatinib, dacomitinib) have shown promising results in recent clinical trials (Byeon et al., 2019).
Cancer tissues form a complex structure composed by malignant cells, nonmalignant cells, and inflammatory cells in a tumor microenvironment (Santosh et al., 2016). Ekblad et al. (2015) investigated the effect of the EGFR ligand TGF-α and cetuximab, alone and in combination, on HNSCC cell lines. They showed that TGF-α can have both growth-stimulating and growth-inhibiting effects in the same cell line just like cetuximab that can have a similar behavior, and which can be explained by the influence of tumor microenvironment.

The initial response rates to cetuximab monotherapy are far from therapeutically encouraging, mainly because responses seem to decline rapidly after a short period of effect. The major mechanisms of resistance of EGFR-targeted monoclonal antibodies has been identified as: EGFR and TGF-α overexpression, deregulation of EGFR internalization and its degradation by ubiquitination, the intracellular binding of MDG1 to EGFR that avoids extracellular targeting, EGFR nuclear translocation, enhanced SFK-mediated signaling, constitutively activated EGFR in a ligand-independent manner, KRAS mutation with constant activation of EGFR downstream signals, PI3K/AKT signal activation, increased heterodimerization of EGFR or HER2 with HER3, crosstalk with HGF-MET or VEGF-VEGFR1, and EMT (Byeon et al., 2019).

The proto-oncogene Src is currently being investigated for apparently promoting resistance to EGFR inhibitors. This proto-oncogene is a non-receptor tyrosine kinase, expressed in several cancers and correlates with tumor progression and metastasis development (Simatou et al., 2020). Once activated, Src phosphorylates the intracellular domain of EGFR facilitating the interaction between STAT 3 and 5 and EGFR forming a multiple molecular kinase complex able to transduce EGFR signals to STATs (Xi et al., 2003). Phase I/II clinical trials with Dasatinib, a src inhibitor including several members of the SFK family, are underway for EGFR-resistant HNSCC (Stabile et al., 2017).

Cluster of Differentiation 68 (CD68)

CD68 is a type I transmembrane glycoprotein with advanced glycation, composed of 354 amino acids, associated with an endosomal/lysosomal compartment. CD68 can be found in several types of non-hematopoietic cells, umbilical cord mesenchymal stem cells, fibroblasts, endothelial cells, various tumor cell lines and in smooth muscle cells of human arteries. This glycoprotein is highly expressed in the lineage of mononuclear phagocytes, such as macrophages, microglia, osteoclasts and myeloid dendritic cells (Chistiakov et al., 2017; Zhao et al., 2020). In studies using immunohistochemistry, CD68 is a marker for macrophages as well as for subsets of lymphocytes, fibroblasts and endothelial cells (Wirsing et al., 2018).

Tumor cells express immune markers to escape macrophage-mediated phagocytosis and effects of CD8 + cytotoxic T cell damage during invasion of a normal non-tumor tissue environment (Chistiakov et al., 2017). Macrophages, derived from circulating monocytes, play an important role in both innate and adaptive immunity (Ni et al., 2015). These tumor-associated macrophages (TAMs) become activated after infiltrating the tumor microenvironment due to their phenotypic plasticity, and can exhibit two states of functional polarization; either the pro-inflammatory M1 phenotype (anti-tumorigenic) or the anti-inflammatory M2 (protumorigenic) phenotype. TAMs acquire immunosuppressive properties and inhibit the cytotoxic activity of CD8 + T cells in tumors. CD68 is a pan macrophage marker that can express both phenotypes (M1 and M2) (Ni et al., 2015; Fang et al., 2017; Kikuchi et al., 2021).

The CD68 expression has been related to a higher expression of vimentin and lower expression of E-cadherin, which are important markers of EMT (Zhang et al., 2016). Based on this, TAMs can induce tumor cell EMT, resulting in the progression of OSCC and participating in the carcinogenesis process by activating the Gas6/Axl-NF-kB signaling pathway (Wei & Hujie, 2018).

A high density of CD68 TAMs is accompanied by high levels of stromal and high serum levels of the vascular endothelial growth factor (VEGF), which favor angiogenesis. Possibly, there is a positive regulation of VEGF in macrophages exposed to ionizing radiation that decreases the antitumor efficacy of radiotherapy. Therefore, CD68 could be used as an indicator to monitor radiotherapy treatment (Yu et al., 2015).

Overexpression of CD68 in tumor tissue may indicate a prometastatic state, be correlated with the degree of tumor differentiation, the chance of lymph node metastasis and a poor prognosis (Hu et al., 2016; Zhao et al., 2020). In the study by Dantas et al. (2019), the CD68 expression in patients with OSCC was higher in the primary tumor, compared to the surgical margin and lymph nodes, however they found no association.
between the CD68 expression and prognosis. In contrast to the previous study, Wirsing et al. (2018) found an association between CD68 and survival in OSCC patients.

The conflicting results of survival may be due to differences in the immunohistochemical procedures, in the scoring system, in the marker used (Wirsing et al., 2018), in the location of the TAM infiltration (Zhao et al., 2020) and by the decrease of the patient’s immune response (Wei & Hujie, 2018). TAMs at different tumor sites can have different effects on cancer prognosis (Kikuchi et al., 2021) but the impacts of CD68 micro locations on the clinical outcomes of patients with OSCC are limited (Ni et al., 2015). CD68 staining does not differentiate between M1 and M2 macrophages when using immunohistochemistry; therefore, some researchers have suggest combining CD68 and CD163 to generate more specificity for the M2 macrophages (Hu et al., 2016; Wei & Hujie, 2018).

Kikuchi et al. (2021), found a high density of CD68 in the intratumor region related to poor survival rates; however, in the stroma region this relationship was not true. On the other hand, in the study by Ni et al. (2015), the greatest expression of CD68 appeared in the tumor stroma, a place that also has a relationship with low survival rates of patients with high tumor staging and with lymph node metastasis. Hu et al. (2016), found this association between the expression of CD68 in the "tumor nest" and the prognosis, but did not show any relationship in the tumor stroma and the tumor cells.

In contrast to previous research, Zhao et al. (2020) identified that patients with high CD68 expression in cancer-associated fibroblasts (CAF) revealed low postoperative recurrence and better prognosis, with greater overall survival (OS), disease-free survival (DFS) and recurrence-free survival (RFS). However, after multivariate analyzes, CD68 expression was not considered an independent risk factor for OS, RFS and DFS in the tumor center or on the invasive front of patients with OSCC. Thus, TAMs and CAFs may show a distinct expression pattern of CD68 in the OSCC tumor microenvironment.

**Anti-Inflammatory Markers**

**Interferon-gamma (IFN-γ).** IFN-γ, which is the only representative of the type II interferon family, is a cytokine that plays a key role in mediating the immune response to different stimuli, such as microbial agents, viruses and tumors. Furthermore, as a pleiotropic agent, it is involved in the immunomodulation of innate and adaptive responses (Mendoza et al., 2019). Its production occurs mainly in natural killer cells (NK) and in CD4+ and CD8+ T-lymphocytes (Jorgovanovic et al. 2020).

Although the role of IFN-γ in the antitumor immune response remains controversial, it has demonstrated high physiological importance in immunomodulation against pathogens. A significant amount of evidence suggests that IFN-γ mediates several tumor suppressive effects, such as: induction of apoptosis by upregulation of the JAK-STAT/caspases pathway; inhibition of metastases by the FN-1 expression; stimulation of tumor senescence via the p16INK4a-Rb pathway and tumor dormancy by regulating the IDO1-Kyn-Ahr-p27 pathway (Jorgovanovic et al. 2020). On the other hand, there is evidence to indicate that IFN-γ also has a pro-tumorigenic role that is directly related to its concentration in the tumor microenvironment (Jorgovanovic et al., 2020). Low doses of IFN-γ tend to increase the metastatic potential, while the reverse effect is observed at high doses (Chen et al., 2011). However, the accumulation of IFN-γ in the peritumoral lymphatic vessels is also able to increase the expression of PD-L1, which reduces the migration of T-lymphocytes to the tumor microenvironment and severely affects the immune response (Lane et al., 2018).

A low expression of IFN-γ in OSCC associated with high levels of IL-10 and low levels of CD163 are linked to lower overall survival and tumor progression (Wang et al., 2014). Lower levels of IFN-γ were found in metastatic OSCC than in non-metastatic OSCC and in tissues used as controls (Costa et al., 2013). Interestingly, the lowest levels of IFN-γ were not associated with macrophages, which suggests that they are associated with other cell types such as CD4+ Th1 T-lymphocytes (Costa et al., 2013). Consistent with these findings, Boxberg et al. (2019) used in situ hybridization to confirm that tumor-infiltrating lymphocytes in OSCC had high levels of IFN-γ, which would correspond to a T-cell inflamed tumor microenvironment. These phenotypes demonstrate great responsiveness, including to immunotherapy (Trujillo et al., 2018).

**Cluster of differentiation 57 (CD57).** CD57 is an epitope that contains a sulfated carbohydrate (glycoepitope). It was first identified in 1981 as a marker...
of NK cells (Nielsen et al., 2013). This marker is recognized by murine monoclonal antibodies, Human Natural Killer 1 (HNK-1) and Leu-7. Initially CD57 was considered an exclusive marker of NK cells, however, it was also found in cells derived from the neural crest (Lipinski et al., 1983) and in CD8+ T-lymphocytes (Markey & McDonald, 1989). In this latter cell population, persistent immune stimulation has already been shown to induce a change in the expression pattern of CD28+CD57- to CD28-CD57+ (Vallejo et al., 2005). CD57+ T lymphocytes have shorter telomeres, low telomerase activity and reduced capacity for proliferation, in addition to being highly cytotoxic (Nielsen et al., 2013; Vallejo et al., 2005). Therefore, CD8+CD57+ T-lymphocytes are considered terminally differentiated oligoclonal populations (Nielsen et al., 2013). A similar maturation process involving CD57 was also observed in NK cells, which show the CD56dimCD57+ phenotype after stimulation with IL-2 or co-culture with target cells (Lopez-Vergès et al., 2010).

The role of NK cells in immune recognition of cancer has been well established by a significant amount of evidence (Narendra et al., 2013). Higher frequencies of peripheral or tumor-associated NK cells in cancer patients have been associated with better results (Nielsen et al., 2013).

Research found a greater expression of CD57 in OSCC tissues was correlated with a better overall survival of patients (Taghavi et al., 2016), and was associated with greater differentiation of tumor squamous cells (Aganwal et al., 2016) and early clinical stages (Fang et al., 2017). The study by Fang et al. (2017) also found that the higher expression of CD57 was correlated with the absence of metastasis in the lymph nodes.

Conversely, a recent retrospective, case-control study by Elahi & Rakshan (2020) found that the upregulation of CD57, CD16 and MED15 were associated with poor prognoses. This worsening of prognosis was accentuated mainly in older patients with a high TNM stage (Elahi & Rakshan, 2020). Furthermore, this recent study differs from its predecessors due to the use of quantitative PCR (qPCR) to analyze the expression of the tumor markers, whereas those previously mentioned used less accurate methods, such as immunohistochemistry (IHC). However, other previous IHC-based studies have also found a negative association between survival and CD57 expression. Zancope et al. (2010) found no prognostic value in the expression of CD57 in NK cells infiltrated in tumors; however, this study used a small sample size. Fraga et al. (2012) found that CD57 could not be considered an independent prognostic variable, even though they found an association between the frequency of locoregional metastases and the density of CD57+ cells.

Nevertheless, there are many methodological differences between studies that have proven to be paradoxical. In addition, the immune-tumor interaction appears to be more complex than is currently known. The accumulation of CD8+CD57+ T-lymphocytes, for example, is associated with reduced survival of patients with different tumors, such as lymphomas, myelomas and melanomas (Nielsen, 2013). This seems to have a relation with the prolonged stimulation of this population, in a scenario in which the antitumor response is ineffective. Therefore, further studies are still needed to clarify the role of CD57 as a tumor marker in OSCC, especially with techniques that provide more accurate results.

**CONCLUSION AND FUTURE PROSPECT**

OSSC is the most prevalent malignant neoplasm in the oral cavity with a 5-year survival ratio ranging from 5 to 80 %, depending on the stage of the disease. The TNM classification system alone or in combination with histological grading is not sufficient to predict the prognosis of OSCC. These facts highlight the urgent need to identify novel prognostic parameters, such as biomarkers for improving patient survival, life expectancy and quality-of-life. The application of new therapeutic agents such as anti-EGFR monoclonal antibodies or multi-target tyrosine kinase inhibitors is promising as an alternative strategy for OSCC therapy. Nevertheless, the inclusion of EGFR inhibitors in the treatment protocols has already come up against tumors that are unresponsive to this therapy. However, the latest strategies for the treatment of OSCC are focused on alternative drugs which are able to downstream signals (such as src) to improve the prognosis of these tumors. Such research is already undergoing clinical trials.

There is suggestive evidence that TGF-α overexpression may occur in mild dysplastic lesions. Abnormal expression of this protein can be considered potential endpoints and molecular prognostic factors for chemoprevention studies mainly in the presence of
en el microambiente tumoral puede tener efectos pro o antitumores y la investigación de la expresión de marcas- dores inflamatorios en COCE puede ser útil para diseñar intervenciones inmunoterapéuticas. El factor de crecimiento transformante α es un potente estimator de la migración celular que actúa sobre la proliferación celular, la invasión y metástasis del cáncer, así como la inmunosupresión y la angiolíisis. Las citocinas inflamatorias, como el IFN-γ, median en la diferenciación de macrófagos. Los macrófagos son un componente importante del microambiente COCE. La mayor cantidad de macrófagos asociados a tumores, especialmente el fenotipo M2, puede estar asociada a un comportamiento biológico más agresivo del COCE y, en consecuencia, a una menor supervivencia.

**PALABRAS CLAVE:** carcinoma oral de células escamosas, factor de crecimiento transformante alfa, receptor del factor de crecimiento epidérmico, antígeno 68; antígeno 57, interferón-gamma, biomarcadores, pronóstico.

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