



## Review

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# OCT4's role and mechanism underlying oral squamous cell carcinoma

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**Abstract:** Oral squamous cell carcinoma (OSCC), a common malignancy of the head and neck, ranks sixth worldwide in terms of cancers with the most negative impact, owing to tumor relapse rates, cervical lymphnode metastasis, and the lack of an efficacious systemic therapy. Its prognosis is poor, and its mortality rate is high. Octamer-binding transcription factor 4 (OCT4) is a member of the Pit-Oct-Unc (POU) family and is a key reprogramming factor that produces a marked effect in preserving the pluripotency and self-renewal state of embryonic stem cells (ESCs). According to recent studies, OCT4 participates in retaining the survival of OSCC cancer stem cells (CSCs), which has far-reaching implications for the occurrence, recurrence, metastasis, and prognosis of oral carcinogenesis. Therefore, we summarize the structure, subtypes, and function of OCT4 as well as its role in the occurrence, progression, and prognosis of OSCC.

**Key words:** Cancer stem cell (CSC); Octamer-binding transcription factor 4 (OCT4); Oral squamous cell carcinoma (OSCC); Prognosis; Signaling pathway

## 1 Introduction

Oral squamous cell carcinoma (OSCC) is the most common malignancy and accounts for more than 90% of oral cancers, with 300 000 new cases per year on average; thus, it has become a worldwide public health concern (Bray et al., 2018; Siegel et al., 2019; He et al., 2021; Pang et al., 2021). The main hazardous behaviors are smoking, drinking alcohol, and chewing betel quid (Huang et al., 2020). Treatment options include surgery, radiation, chemotherapy, or combined treatment, based on cancer location, tumor type, and stage (Tahmasebi et al., 2020). Despite considerable improvements in gauging and treatment protocols, five-year survival remained at approximately 50% in 2020, unchanged from the previous years

(Moro et al., 2018; Zhang et al., 2019; Mishra et al., 2020). Low treatment response, high recurrence rate, and local metastasis are the major causes of therapeutic failure and bleak prognosis. Consequently, finding the molecular mechanism of OSCC occurrence and development and searching for specific tumor markers have already become urgent matters.

With advances in basic research on tumors, it has been discovered that tumor progression is associated with cancer stem cells (CSCs), which are a portion of tumor tissue with stem-cell nature and possessing the ability to proliferate infinitely, self-renew, as well as initiate and promote tumors (Cai et al., 2016; Olivares-Urbano et al., 2020; Oshimori, 2020). The CSC theory originated from leukemia (Griffin and Lowenberg, 1986), and multiple studies have demonstrated its prognostic role in solid organ malignancies such as glioblastoma (Lathia et al., 2015; Gimple et al., 2019; Sharifzad et al., 2019), non-small-cell lung cancer (Heng et al., 2019; Deng et al., 2020), breast cancer (Yang et al., 2017; Bai et al., 2018; Quaglino et al., 2020), hepatocellular carcinoma (Liu YC et al.,

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2020; Dai et al., 2021; Wong et al., 2021), esophageal squamous cell carcinoma (Wu et al., 2019), and oral cancer (Rodini et al., 2017; Liu YF et al., 2020; Ma et al., 2020; Al-Magsoosi et al., 2021; Feng et al., 2021). According to the theory, CSCs are a unique subset of cancer cells with high tumorigenicity and potential for metastasis. In addition, they largely determine the biological properties of cancer, contributing to fast growth, invasion, and metastasis (Reya et al., 2001; Baillie et al., 2017). CSCs are also resistant to most forms of chemoradiotherapy, which explains the failure and repetition of anticancer therapy in many cancer patients, including OSCC patients (Nichols et al., 1998; da Silva et al., 2012; Rodini et al., 2017; Mishra et al., 2020; Sun et al., 2020).

The self-renewal capacity of CSCs can be sustained through certain endogenous signaling pathways, for instance wingless/integrated (Wnt), Notch, Hedgehog, B-cell-specific Moloney murine leukemia virus integration site 1 (BMI1), phosphatase and tensin homolog (Pten), bone morphogenetic protein (Bmp), and transforming growth factor- $\beta$  (TGF- $\beta$ ) (Shin and Kim, 2018); when these pathways are out of balance, tumorigenesis can occur. Activation of Notch and Hedgehog has been found in leukemia and other cancers (Unden et al., 1996; Diévert et al., 1999; Nam et al., 2002; Nickoloff et al., 2003; Benson et al., 2004; Karhadkar et al., 2004; Olsen et al., 2004), and hematopoietic stem cells (HSCs) can undergo self-renewal by Bmp and Notch signaling (Karanu et al., 2000; Varnum-Finney et al., 2000; Bhardwaj et al., 2001). In addition, elevated levels of  $\beta$ -catenin and Wnt proteins enhance protein stability, which is activated in colorectal, melanoma, breast, and oral cancers (Gat et al., 1998; Iwai et al., 2010; Liu et al., 2010; Fujii et al., 2011; Ravindran and Devaraj, 2012; Zhan et al., 2017).

To identify CSCs, one can use cell surface markers; familiar CSC biomarkers in OSCC include octamer-binding transcription factor 4 (OCT4), cluster of differentiation 44 (CD44), sex-determining region Y-box 2 (SOX2), Nanog homeobox (NANOG), and aldehyde dehydrogenase 1 (ALDH1) (Curtarelli et al., 2018; Gliagias et al., 2019). OCT4, as a considerable regulatory factor maintaining stem-cell pluripotency, is specifically expressed in embryonic stem cells (ESCs) and is inextricably associated with the relapse and drug resistance of various solid tumors in the human body. It may be a key gene for the potential regeneration and differentiation of OSCC. Therefore, this article

reviews the function and possible mechanism of OCT4 in OSCC.

## 2 OCT4 overview

### 2.1 Structure of OCT4

#### 2.1.1 Structure of the *OCT4* gene

*OCT4* (encoded by POU class 5 homeobox 1 (*POU5f1*), also called *OCT3*, *OCT3/4*) belongs to subgroup V of the POU transcription-factor family (Chiou et al., 2008; Sawant et al., 2016; Khan et al., 2018), whose members regulate transcription of the target gene by specifically integrating with an octameric sequence motif AGTCAAAT, and hence are named *OCT4* (Bourguignon et al., 2012). *OCT4* is oriented on chromosomes 6p21.31 and 17B1 in the human and mouse genomes, respectively, with a length of 16.4 kb. Moreover, *OCT4* isoform 1 is one of the major isoforms of transcription, with five exons and four introns (Zhao et al., 2020).

#### 2.1.2 Structure of the OCT4 protein

The relative molecular weight of the OCT4 protein is 18 kDa, and it is composed of three functional domains: the POU-binding domain, N-terminal transcriptional activation domain, and C-terminal cell-type-specific transactivation domain (Herr and Cleary, 1995; Pesce and Scholer, 2001). The POU-binding domain includes two subunits: the N-terminal and the C-terminal. An acidic and proline-rich conserved domain resides at the N-terminus of the POU family (POUs), while the C-terminus is a conventional homeodomain (POUh), which is full of proline, serine, and threonine residues; POU and POUh are linked by connecting peptides.

### 2.2 Subtypes of the *OCT4* gene

OCT4 has three isoforms in human tissues: OCT-4A, OCT-4B, and OCT-4B1 (Wang et al., 2011; Kong et al., 2014). OCT-4A and OCT-4B consist of 360 and 265 amino acids, respectively, of which 225 amino acids at the C-terminus are the same, but different sequences are formed at the N-terminus. The N-terminus of OCT-4A can bind to DNA and activate transcription, while the N-terminus of OCT-4B inhibits binding to DNA and the activity of the OCT4 activator to activate its transcription. Therefore, the biological functions

of OCT-4A and OCT-4B are different. A transcription factor known as OCT-4A is located in the nucleus of ESCs, controlling a number of stem-cell genes, while OCT-4B is located in ESC cytoplasm and is insufficient to maintain an undifferentiated state and activate transcription of the *OCT4* gene (Cauffman et al., 2006; Lee et al., 2006; Chiou et al., 2008; Kotoula et al., 2008; Reers et al., 2014). OCT-4B1 is mainly expressed in pluripotent cells (Liu et al., 2017), and it shares the same amino terminal and partial POU-binding region with OCT-4B, while the rest of the amino-acid sequence is different. OCT-4B1 can enhance the anti-apoptotic functions of cells and regulate their pluripotent potential, which may be related to tumor progression.

### 2.3 Function of the *OCT4* gene

As a transcription factor, OCT4 exists in the inner cell mass of blastocysts and has a marked effect in retaining the pluripotency and self-renewal of ESCs, germ cells, and adult stem cells (Chiou et al., 2008; Sawant et al., 2016; Tegginamani et al., 2020; Han et al., 2022). The *OCT4* gene, a significant ESC marker, regulates the growth and development of the body in the early stage, but its expression is weakened after cell differentiation and maturation (Rizzino and Wuebben, 2016). In addition, OCT4, SOX2, and NANOG work together in regulating the cell reprogramming of CSCs and somatic cells (Naini et al., 2019). These key transcription factors can reprogram human somatic fibroblasts into ESC-like pluripotent cells, which are called induced pluripotent stem cells (iPSCs) (Ghazi et al., 2020; Cao et al., 2022; Shen et al., 2022; Ilia et al., 2023). In OSCC, OCT4 produces a marked increase in tumor transformation, tumorigenicity, invasion, and metastasis (Chang et al., 2008; Chiou et al., 2008; Kim and Nam, 2011; Huang et al., 2014). Some studies have also proposed that OCT4 may promote tumorigenesis by regulating epithelial-mesenchymal transition (EMT), so it is conjectured to be a potential marker of CSCs (Baillie et al., 2017).

## 3 Expression and prognostic assessment value of OCT4 in OSCC

Because of its complex structure and reprogramming function in CSCs and somatic cells, OCT, as a marker of ESCs, is also expressed in primordial germ

cells and their tumors, as well as various somatic tumors. In addition, reactivation of OCT4 has been observed in many cancers, such as lung cancer (Li et al., 2019; Lu CS et al., 2020), esophageal cancer (Vijayakumar et al., 2020), gastric cancer (Chen et al., 2019; Basati et al., 2020), breast cancer (Lu HQ et al., 2020), and bladder cancer (Lu et al., 2017). It plays a role as a tumor biomarker and promoter, as well as a key role in the occurrence and development of multiple malignancies. Therefore, we probed the expression of OCT4 and its prognostic assessment value in OSCC.

### 3.1 Expression of OCT4 in OSCC and correlation with clinicopathological features

Numerous studies have revealed that OSCC expresses OCT4. Rodrigues et al. (2018) showed that in tongue squamous-cell carcinoma samples, only 3.33% (2/60) were devoid of OCT4 expression, 36.66% (22/60) were considered weakly positive, and 60.00% (36/60) were considered strongly positive. Vijayakumar et al. (2020) performed immunohistochemical staining on 20 cases of OSCC, 20 cases of oral epithelial dysplasia (OED), and 25 normal oral mucosa (NOM) samples. Although less expressed in OSCC (3.97%) or OED (8.66%), OCT4 was significantly different compared to NOM (0.00%). Studies by Baillie et al. (2017), Lee et al. (2019), and Mishra et al. (2020) have shown similar increases in OCT4 expression in oral cancers. Compared with OED, Rao et al. (2020) found OSCC to express significantly higher levels of OCT4, and negative and weak expression was found in 60% (24/40) and 40% (16/40) of OED cases, respectively; while in OSCC, there were 45% (18/44) weakly positive cases, 35% (14/44) strongly positive cases, and 20% (8/44) negative cases for OCT4. The expression of OCT4 in OSCC samples was not related to the clinicopathological parameters of age, sex, history of habits, or histology grade, but showed a relationship to tumor site, lymph-node metastasis, and tumor node metastasis (TNM) stage. Lymph-node metastatic cases with strongly positive staining accounted for 70% of all cases (14/20), whereas positive staining was absent in all nonmetastatic cases.

However, there have been contradictory conclusions. In the study by Fu et al. (2016), OCT4 expression was slightly, but not significantly, higher in patients

without lymph-node metastasis. Based on 45 OSCC samples and 15 OED samples, Ghazi et al. (2020) discovered that OCT4 expression differed significantly with age in OSCC tumor groups. Expression of OCT4 in young patients (<60 years old) was substantially higher than in elderly patients (>60 years old) ( $P=0.032$ ). It was also significantly higher in OSCC grade III patients than in grade I or II cases, but the relationship was insignificantly different ( $P=0.84$ ). Experiments by Chiou et al. (2008) showed a positive correlation between increased OCT4 expression and progression of oral cancers, as well as medium to poor differentiation, but not with lymph-node metastasis. In addition, more OCT4 nuclear staining was observed in grades III and IV oral cancer tissues than in grades I and II tissues. In summary, we can conclude that OCT4 is highly expressed in OSCC, but its relationship with patient age and lymph-node metastasis remains to be further explored.

### 3.2 Prognostic assessment value of OCT4 in OSCC

The prognostic significance of OCT4 has been noted in cervical carcinomas, renal-cell carcinomas, and breast cancer (Rasti et al., 2018; Tulake et al., 2018; Zhang et al., 2018). Kaplan-Meier analysis was used to evaluate the impact of OCT4 on survival of OSCC patients, and the results indicated that the overall survival rate for OCT4 immunohistochemical positive cases was significantly worse than that for negative ones (Chiou et al., 2008; Rao et al., 2020). Kaplan-Meier analysis by Chiou et al. (2008) and Singh et al. (2018) also predicted that the survival rate for patients with triple-positive OSCC (OCT4/NANOG/CD133) would be the worst. Fan et al. (2017) also confirmed that high expression of OCT4 and NANOG was related to lower overall survival (OS) in head and neck squamous-cell carcinoma (HNSCC) patients. Sawant et al. (2016) and Roy et al. (2019) found that an increase in OCT4 expression was relevant to poor prognosis and cisplatin resistance in OSCC. According to Pandian et al. (2022), gastric diffuse, poorly differentiated, and stage III tumors consistently express 84 genes that correlate positively with the activation pattern of the available *OCT4* gene sets. Therefore, positive expression of OCT4 has a significant effect on the chemotherapy response and survival rate of OSCC patients, shows independent prognostic value, and may provide a new observation metric for OSCC clinical treatment.

In summary, OCT4 is highly expressed in OSCC tissues, and its expression level is tightly related to lymph-node metastasis and pathological stage. When highly expressed, OCT4 can promote the occurrence and development of tumors, resulting in poor prognosis and a low survival rate.

## 4 Important regulatory signaling pathways related to OCT4 in OSCC

Relevant studies have found that the mechanism by which OCT4 maintains stem-cell self-renewal and multipotential differentiation may be regulated by Wnt, TGF- $\beta$ , Hedgehog, and other signaling pathways (Pandian et al., 2022). In OSCC, we found activation of the Wnt/ $\beta$ -catenin, Lin28/hsa-Let-7 (Let-7), and nuclear factor of activated T-cells (NFAT) pathways (Chien et al., 2015; Nguyen et al., 2022; Yang et al., 2022). We will elaborate on these pathway mechanisms of OCT4 in OSCC below (Fig. 1).

### 4.1 Wnt/ $\beta$ -catenin signaling pathway

The Wnt signaling pathway is a complicated protein-interaction network that is closely linked to embryonic development, as well as tumor formation and development. It is well known that Wnt signaling is classically mediated by Wnt signaling transmission to glutathione (GSH) after entering the cell, and that activating GSH inhibits the activity of the compound (Axin/ $\beta$ -catenin/adenomatous polyposis coli (APC)/glycogen synthase kinase 3 (GSK3)/casein kinase-1 (CK1)) (Zhan et al., 2017). Because of this,  $\beta$ -catenin cannot be phosphorylated by GSK-3 $\beta$ ; it accumulates in the cytoplasm, migrates to the nucleus, and combines with T-cell factor/lymphoid enhancer-binding factor (TCF/LEF) transcription factors to regulate gene expression by activating TCF transcriptional activity. The Wnt pathways are normally closed, but when they are activated, abnormal cell proliferation and differentiation occur, eventually leading to the formation of tumors. Observations were made by Ravindran and Devaraj (2012) regarding Wnt/ $\beta$ -catenin reactivation in oral cancers. Ravindran et al. (2015) revealed that the expression patterns of  $\beta$ -catenin and OCT4 have a significant positive correlation in oral carcinoma, based on Spearman correlation analysis. Wang et al. (2021) found that Wnt/ $\beta$ -catenin signaling was abnormally activated in OSCC SCC-55 cells, while *OCT4* gene



transcription in SCC-55 cells was significantly down-regulated when  $\beta$ -catenin was silenced, resulting in reduced efficiency of tumor cell proliferation, invasion, and colony formation.

#### 4.2 Lin28/Let-7 signaling pathway

Lin28 is a structurally highly conserved RNA-binding protein in advanced eukaryotes, exerting a major role in normal development of the human body and in some disease states. Let-7 microRNAs (miRNAs) are known to target many important oncogenes as tumor suppressors in head and neck cancers (HNCs) (Thomaidou et al., 2022). In human cells, Lin28 negatively regulates transcription of Let-7, inhibits synthesis of Let-7 in mature cells, upregulates the cell cycle, and promotes stem-cell proliferation. In human tumor stem cells, Lin28 can selectively inhibit the processing and synthesis of mature Let-7 cells, thereby promoting tumor stem-cell proliferation and inhibiting apoptosis, which ultimately leads to tumorigenesis. In human tumor cells, Lin28 is highly expressed, while Let-7 is expressed at low levels. It is generally believed that Lin28 and Let-7 are a pair of mutually inhibiting and negatively regulating factors, so they are known as the double-negative feedback loop or regulatory loop. When Lin28 is normally expressed, it can combine with OCT4, SOX2, and NANOG to reprogram human fibroblast cells into multifunctional stem cells, but its overexpression can cause malignant transformation of cells, which has been confirmed by researchers in hepatocellular carcinoma, lung cancer, and other tumors. Chien et al. (2015) also demonstrated that the Lin28B/Let-7 pathway, as a driving mechanism, promotes ESC stemness properties by positively regulating OCT4 and SOX2 expression and inducing reprogramming in OSCC cells.

#### 4.3 NFAT signaling pathway

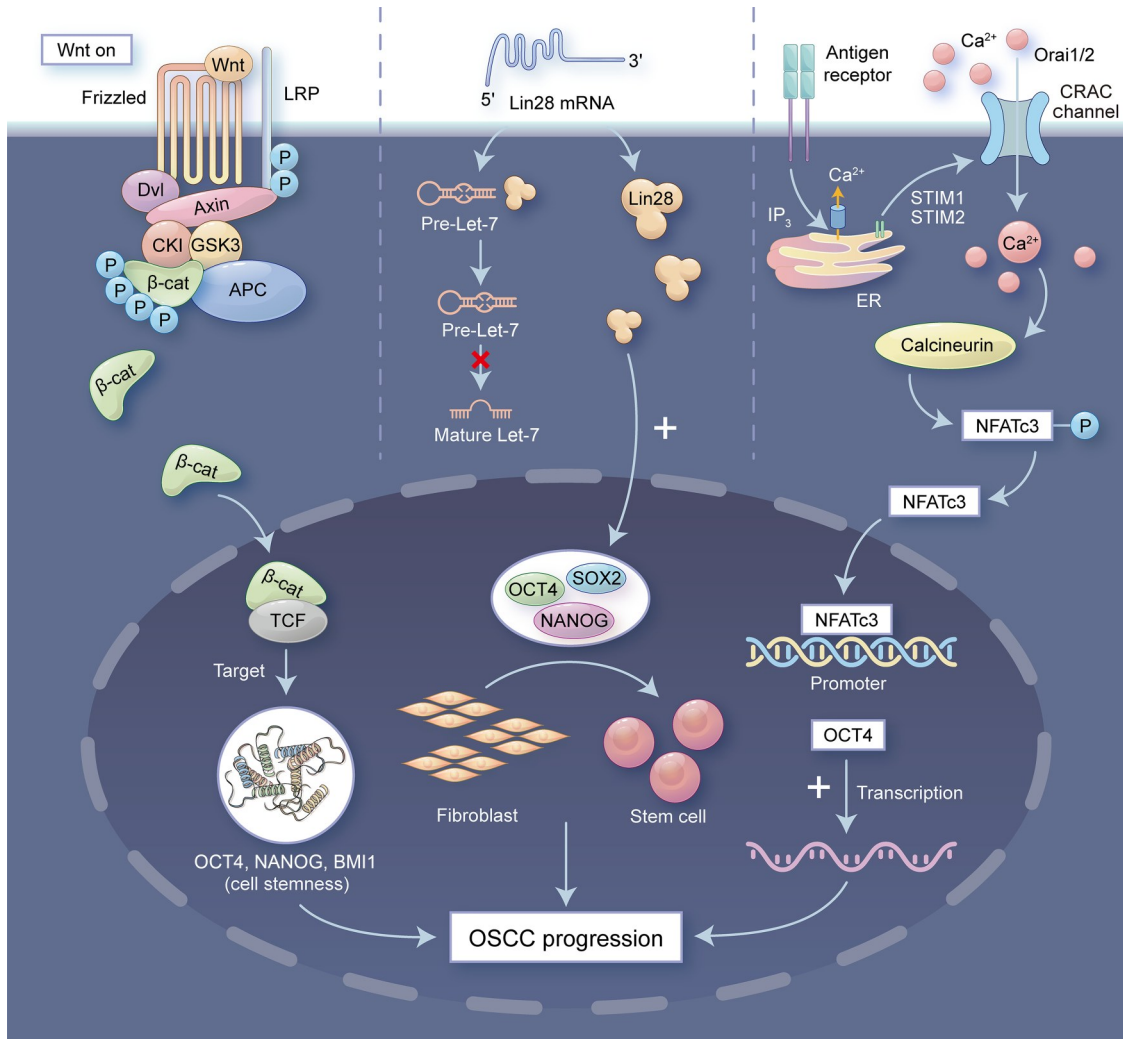
NFAT family is a group of transcription factors that are dependent on calcium/calcineurin. Hyperphosphorylation of NFAT is confined to the cytoplasm during the resting state. When the  $\text{Ca}^{2+}$  channel on the cell membrane is opened and the intracellular  $\text{Ca}^{2+}$  concentration remains at a high level, a conformational change in NFAT occurs, and dephosphorylation exposes the nuclear localization sequence. Subsequently, it binds to the target promoter element and regulates transcription of specific response genes which regulate

a wide variety of life activities of cells. Studies have shown that regulation of NFAT is not limited to neuro-development or the immune system, but also plays a significant role in various tumor-cell activities and malignant transformation. For example, NFATc3 plays a pivotal role in the pathophysiological process of diseases with a high degree of malignancy, including esophageal cancer, triple-negative breast cancer, and glioblastoma. Lee et al. (2019) found that NFATc3 also exerts its action in OSCC. NFATc3 is located upstream of OCT4, and regulates CSC characteristics such as migration and chemical resistance through up-regulation of OCT4, showing that the NFATc3–OCT4 axis may become a necessary therapeutic target for OSCC.

In summary, Wnt/ $\beta$ -catenin signaling is currently a hotspot for research. Yuan et al. (2010) found that OCT4 plays an important role in hepatocellular carcinoma through the TGF- $\beta$  signaling pathway. Another group (Wen et al., 2013) found that OCT4's involvement in keeping drug-resistant colon cancer cells alive may be related to the signal-transducer and activator of the transcription-3 (STAT3)/survivin signaling pathway. Pandian et al. (2022) found that OCT4 is positively associated with dysregulation of the TGF- $\beta$ , glioma-associated oncogene homolog (GLI), polycomb repressive complex 2/enhancer of zeste homolog 2 (PRC2/EZH2), Wnt, Kirsten rat sarcoma viral oncogene homolog (KRAS), serine/threonine-kinase 33 (STK33), and Yes-associated protein (YAP) signaling pathways in diffuse subtype gastric cancer. OCT4, however, has yet to be explored in relation to the occurrence, development, and prognosis of OSCC via these pathways.

## 5 Current situation and prospects

Surgical resection combined with neck dissection is the most common treatment regimen for oral cancer, followed by radiotherapy and chemotherapy. However, as a result of tumor recurrence and drug resistance, the prognosis is still not optimistic (Swain et al., 2020). The existence of heterogeneous subsets of CSCs is considered one of the leading causes for the failure of OSCC treatment (Gupta et al., 2021). CSCs are resistant to chemoradiotherapy drugs such as cisplatin (Okamoto et al., 2009; Noto et al., 2013; Nör et al., 2014; Tsai et al., 2014), paclitaxel (Okamoto et al., 2009; Zhang et al., 2010), and etoposide (Song et al.,



**Fig. 1** Three important pathway mechanisms of OCT4 in OSCC. OCT4: octamer-binding transcription factor 4; OSCC: oral squamous cell carcinoma; Wnt: wingless/integrated; LRP: leucine-responsive regulatory protein; Dvl: dishevelled; CK1: casein kinase-1; GSK3: glycogen synthase kinase 3; β-cat: β-catenin; APC: adenomatous polyposis coli; TCF: T-cell factor; NANOG: Nanog homeobox; BMI1: B-cell-specific Moloney murine leukemia virus integration site 1; mRNA: messenger RNA; SOX2: sex-determining region Y-box 2; CRAC: Ca<sup>2+</sup> release-activated Ca<sup>2+</sup>; IP<sub>3</sub>: inositol 1,4,5-trisphosphate; ER: endoplasmic reticulum; STIM: stromal interaction molecule; NFATc3: nuclear factor of activated T-cells c3; P: phosphorylated.

2010). Accordingly, oral cancer treatment targeting tumor stem cells may prove to be an important new approach (Satpute et al., 2013).

As a core transcription factor that enables ESCs to maintain self-renewal and differentiation potential, OCT4 shows high expression in OSCC and plays a considerable role in maintaining tumorigenicity, invasiveness, and drug resistance. In addition, it regulates and acts together with multiple factors and multiple signaling pathways, which offers a new direction for further investigation of oral CSCs. These cells may become a research hotspot of molecular targeted therapy

for oral cancer in coming years. *OCT4* gene knock-down can reduce the self-renewal ability and stem-cell transformation of HNSCC (Nathansen et al., 2021), inhibit the proliferation, migration, and invasion of cancer cells, and exert antitumor effects (Xie et al., 2022). Specific targeted molecules such as transient-receptor-potential melastatin-subfamily member 7 (TRPM7) (Chen et al., 2022) and 3-photonoinoside-dependent kinase 1 (PDK1) (Pai et al., 2021) can inhibit the metastasis and chemo/radioresistant resistance of cancer cells by downregulating the expression of OTC4 and regulating multiple signaling pathways;

this may provide effective treatment ideas and strategies to enhance antitumor efficacy. However, most current oral cancer research is based on cell experiments, and cell research involves many factors such as personal operation and laboratory conditions, as well as the existence of pseudogene transcription, DNA contamination, and *OCT4* subtypes. The false-positive rate of *OCT4* was obviously increased, which makes determining the nature of the tumor complicated. Therefore, the clinical use of *OCT4* as an indicator of OSCC cannot be the sole basis for diagnosis or treatment planning. Further studies on the isolation and identification of *OCT4* subtypes are needed, as well as clinical trials.

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### Author contributions

Yuwei DAI contributed to the conception of the study; Ziqiong WU and Yitong CHEN contributed significantly to analysis and manuscript preparation; Xinjian YE performed the data analysis and wrote the manuscript; Chaowei WANG provided ideas and financial support for the review; Huiyong ZHU helped perform the analysis with constructive discussions and provided substantive guidance on the paper's ideas and the entire writing process. All authors have read and approved the final manuscript.

### Compliance with ethics guidelines

Yuwei DAI, Ziqiong WU, Yitong CHEN, Xinjian YE, Chaowei WANG, and Huiyong ZHU declare that they have no conflict of interest.

This article does not contain any studies with human or animal subjects performed by any of the authors.

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