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## **Identity matters: Cancer stem cells and tumour plasticity in head and neck squamous cell carcinoma**

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## 16 **Introduction**

17 Cellular plasticity is a phenomenon describes the ability of certain cells to adopt different phenotypes  
18 and functions, which is considered a characteristic feature of embryonic stem cells. However, such  
19 trait has also been observed in adult differentiated cells when challenged by chronic physiological or  
20 pathological conditions such as wound repair and tumorigenesis (Yuan et al., 2019). In the context of  
21 cancer, cell plasticity endows tumors with enhanced self-renewal and pro-invasiveness capacities.  
22 Further, by attaining different identities (phenotypes), tumor cells can bypass cell cycle arrest,  
23 apoptosis and circumvent the therapeutic insults (Boumahdi and de Sauvage 2020). Indeed, tumor  
24 microenvironment (TME) plays a crucial role in fueling tumor plasticity by exposing tumor cells to  
25 a wide variety of stimuli from substantially heterogeneous niche, thereby imposing a significant  
26 obstacle in cancer management (Yuan et al., 2019; da Silva-Diz et al., 2018).

27 Head and neck squamous cell carcinoma (HNSCC) encompasses a group of common and  
28 aggressive epithelial tumors with strong associations to smoking, alcohol dependence and infection  
29 with human papillomavirus (HPV) types 16 and 18 (Johnson et al., 2020). Recently, oral dysbiosis  
30 has been linked to HNSCC plus to certain oral potentially malignant lesions (Metsäniitty et al., 2021).  
31 These tumors arise more frequently in the oral cavity as oral SCC (OSCC), but also develop in  
32 oropharynx and larynx (Mehanna et al., 2010). Owing to their invasiveness and “metastability”,  
33 HNSCCs accounted for nearly one million new cases and over half a million deaths in 2018 alone  
34 (Ferlay et al., 2019; Bray et al., 2018). Currently, treatment options include surgery, chemo-radiation,  
35 targeted therapy, immunotherapy, or a combination of these modalities. Despite the remarkable  
36 improvement in HNSCC management, metastasis and drug resistance remain the main cause of  
37 mortality. Although survival can be prolonged with a multimodal approach, this can however induce  
38 drug toxicity and deteriorate the patients’ quality of life. Thus, the 5-year survival of these patients  
39 remains stagnant at approximately 50% (Johnson et al., 2020; Xing et al., 2021; Muzaffar et al.,  
40 2021).

41 Recent technical advances in single-cell genomics such as single-cell RNA sequencing  
42 (scRNA-seq) have revealed the complexity and heterogeneity of HNSCCs, which influence tumor  
43 plasticity and clinical response alike. Within such diverse ecosystem, tumor cells exhibit diverse  
44 expression of signatures related to cell cycle, stress, epithelial-to-mesenchymal transition (EMT),  
45 hypoxia, and epithelial differentiation (Puram et al., 2017). Importantly, TME also comprise a distinct  
46 subpopulation of cancer stem (or stem-like) cells (CSCs) with enhanced self-renewal, phenotypic  
47 plasticity (differentiation), tumorigenesis and metastability in multiple cancers including HNSCCs  
48 (**Figure 1**; Prince et al., 2007; Clay et al., 2010; Biddle et al., 2016). To develop more effective  
49 anticancer therapies, it will be critical to understand CSCs and how they can promote carcinogenesis

50 and multidrug resistance. Herein we review our current understanding of CSCs in HNSCC,  
51 highlighting some recently identified mechanisms that mediate their phenotypic plasticity and  
52 immune evasion. We also discuss critical factors governing their dynamic interplay within TME,  
53 including our evolving appreciation of the contribution of oral microbiota.

#### 54 **Intratumor heterogeneity in HNSCC**

55 Given the limited success of the traditional anticancer approaches, attention has been focused on  
56 identifying the genotype variations between patients to predict their response to targeted drugs.  
57 However, TME harbors, within the same patient, subpopulations of tumor cells with different  
58 phenotypes and mutations, referred to as intra-tumoral heterogeneity (Bedard et al., 2013). Intratumor  
59 heterogeneity drives the clinical resistance and poses a major challenge for designing effective  
60 therapies in solid tumors including HNSCC (Canning et al., 2019; Bedard et al., 2013). Initially, two  
61 models were proposed to explain the intra-tumoral heterogeneity. On the one hand, the stochastic  
62 model of clonal evolution postulates that every tumor cell with an appropriate set of somatic  
63 mutations can initiate and sustain a “metastable” tumor growth. However, this model speculates  
64 tumors as a homogeneous mass, hence falls short of explaining the variations in tumorigenic potential  
65 and multidrug resistance. On the other hand, according to the hierarchical cell model, cancer initiation  
66 and progression are driven mainly by a smaller subpopulation of cells—CSCs—that are intrinsically  
67 different from the majority, more differentiated, tumor cells (Shackleton et al., 2009; Fanelli et al.,  
68 2020).

69 In essence, CSCs were termed as such to highlight their stem cell-like properties including  
70 their self-renewal, transdifferentiation and migration abilities. In this regard, there has been an  
71 overwhelming evidence supporting this “stemness” model. CSCs were first characterized as a  
72 minority of CD34<sup>+ve</sup>/CD38<sup>-ve</sup> cells in acute myeloid leukemia (Lapidot et al., 1994). Thenceforward,  
73 CSCs with other surface markers have been identified in different cancers. For instance, CD44<sup>+ve</sup> and  
74 CD133<sup>+ve</sup> CSCs sustained the capacity to initiate new tumors in non-obese diabetic/severe combined  
75 immunodeficient (NOD/SCID) mouse models of breast and colorectal cancers, respectively (Al-Hajj  
76 et al., 2003; O'Brien et al., 2007). The first identification of CSCs in HNSCC was reported by Prince  
77 and colleagues, who showed that only CD44<sup>+ve</sup> cancer cells—comprising <10% of the tumors—  
78 initiated new malignant growths in NOD/SCID mice (Prince et al., 2007). Interestingly, as few as 5  
79 × 10<sup>3</sup> cells of early-passaged CD44<sup>+ve</sup> CSCs were able to produce new tumors *in vivo*, whereas CD44<sup>-ve</sup>  
80 cells failed to give rise tumors event at a 100-fold higher density. Of note, CD44<sup>+ve</sup> cell-derived  
81 tumors comprised phenotypically diverse cells of both CD44<sup>+ve</sup>/CD44<sup>-ve</sup> clones, suggesting that CSCs  
82 may also drive the intra-tumoral heterogeneity in HNSCC patients. These findings signify the role of

83 CD44 in identifying the CSCs in other tumors of epithelial origin (Prince et al., 2007). Thereupon,  
84 several cell surface receptors and intracellular proteins were reported as applicable CSC markers in  
85 HNSCC, as summarized in **Table 1**.

## 86 87 **CSC markers in HNSCC**

88 To date, Fluorescence Activated Cell Sorting (FACS) and the magnetic bead sorting are the most  
89 commonly applied approaches to detect and isolate CSCs from different tumor types. With these  
90 methods, various cell surface markers have been used either individually or in combination to detect  
91 HNSCC CSCs. Beside their importance to understand the complex behavior of CSCs, these markers  
92 start to emerge as valuable biomarkers and therapeutic targets in HNSCC. Here, we briefly outline  
93 recent findings of certain markers that are commonly applied in HNSCC. A list of other potential  
94 markers is found in **Table 1**.

95  
96 **CD44:** The cluster differentiation CD44 is the key stem cell marker in solid tumors and the first used  
97 to study HNSCC-derived CSCs. CD44 is a multistructural and multifunctional transmembrane  
98 adhesion receptor that binds to several extracellular matrix (ECM) ligands, particularly to hyaluronic  
99 acid (HA; aka hyaluronan)—a glycosaminoglycan involved in pivotal tumorigenic events. CD44  
100 mediated cancer cell proliferation, migration, angiogenesis and stemness properties, which ultimately  
101 led to tumor progression and metastasis (Ludwig et al., 2019; Hujanen et al., 2021; Boxberg et al.,  
102 2018; Wang and Bourguignon 2011). Recently, Ludwig et al. analyzed the association of CD44 with  
103 the pro-angiogenic genotype in HNSCC using the Cancer Genome Atlas. Interestingly, they found  
104 that HNSCC has the second highest CD44 expression among all cancer types included in the Pan-  
105 Cancer Atlas. Moreover, using an orthotopic carcinogen-induced mouse model, CD44<sup>+ve</sup> expression  
106 was consistently upregulated at different stages of oral carcinogenesis, from dysplastic lesions to  
107 advanced carcinomas (Ludwig et al., 2019). Using primary human HNSCC samples and patient-  
108 derived xenografts, Lee et al. examined the immunogenicity of CSCs. Strikingly, CD44<sup>+ve</sup> CSCs in  
109 HNSCC revealed EMT features and were less immunogenic than other CD44<sup>-ve</sup> tumor cells when  
110 cultured with autologous CD8<sup>+ve</sup> tumor-infiltrating lymphocytes (TILs). Further, programmed death-  
111 ligand 1 (PD-L1) was selectively expressed on CD44<sup>+ve</sup> CSCs compared with the CD44<sup>-ve</sup> cells (Lee  
112 et al., 2016). In addition, HNSCC-derived spheroids, exhibited increased expression of CD44  
113 whereas the levels of other putative CSC markers, such as CD24 and CD133 were not notably  
114 increased (Byun et al., 2022).

115 Human CD44 is encoded by the highly conserved *CD44* gene on chromosome 11. Following  
116 extensive alternative splicing, it generates multiple variant isoforms including the standard (CD44s)

117 and variant (CD44v) forms, in which the latter represented a promising prognostic and therapeutic  
118 target in different cancers. In this regard, Wang and colleagues showed that HNSCC cells (HSC-3)  
119 expressed at least four CD44 isoforms (v3, v6, v10) and CD44s. Of note, these CD44 isoforms  
120 mediated cancer cell migration, proliferation, and cisplatin sensitivity. Importantly, the variant  
121 isoforms (v3, v6, v10), alone or in combination, showed a greater proportion of metastatic lymph  
122 nodes and tumor progression compared with the standard form (Wang et al., 2009). A meta-analysis  
123 study revealed a significant association between CD44 and worsening T stage, N status, higher tumor  
124 grades and 5-year overall survival (OS) rates in patients with HNSCC (Chen et al., 2014). However,  
125 in spite of its wide use in CSC studies, the increased levels of CD44<sup>+ve</sup> cells in some cohorts suggest  
126 that such cell subpopulation may not represent a pure mass of CSCs. Thus, combining multiple  
127 surface markers such as CD44 and aldehyde dehydrogenase (ALDH; CD44<sup>high</sup>/ALDH<sup>high</sup>) has been  
128 increasingly used for studying CSCs in HNSCCs (Kamarajan et al., 2017).

129  
130 **ALDH:** This family comprises a group of intracellular detoxifying enzymes that oxidize exogenous  
131 and endogenous aldehydes, hence mediating drug resistance in cancer patients (Januchowski et al.,  
132 2013). ALDH has been considered as a functional marker for human HNSCC-derived CSCs  
133 (Kamarajan et al., 2017; Chen et al., 2009; Clay et al., 2010). Among the first reports on this molecule  
134 in HNSCC, Chen et al. showed that ALDH1<sup>+ve</sup> tumor cells displayed EMT features and  
135 radioresistance and represented a reservoir for tumor initiation (Chen et al., 2009). Unlike the copious  
136 expression of CD44, most HNSCC cells had low ALDH activity; nevertheless, ALDH<sup>high</sup> cells (1.0%  
137 to 7.8%) clearly co-expressed CD44 and sustained high tumorigenic potential in NOD/SCID mice  
138 (Clay et al., 2010). In agreement with these studies, HNSCC ALDH1<sup>+ve</sup> CSCs exhibited higher cancer  
139 stemness properties including tumor spheres-forming capability than that of ALDH1<sup>-ve</sup> cells (Yu et  
140 al., 2011).

141 Indeed, these findings support the role of ALDH as a selective marker for HNSCC CSCs and  
142 hold a therapeutic and prognostic promise. In this regard, targeting ALDH with Aldi-6 (ALDH3A1  
143 inhibitor) sensitized HNSCC cells to cisplatin and reduced tumor growth burden *in vivo* (Kim et al.,  
144 2017). Prince et al. presented a feasible approach to prepare ALDH<sup>high</sup> CSC-based vaccines that can  
145 induce anti-HNSCC immunity, implying a clinical utility to treat cancer patients (Prince et al., 2016).  
146 Recently, a multifactorial analysis revealed that HNSCC patients with a negative immunoexpression  
147 of ALDH1A1 had 5.25 times higher OS compared with the ALDH1A1<sup>+ve</sup> group (P = 0.01).  
148 Furthermore, using univariate and multivariate analysis, only ALDH1A1 staining positivity showed  
149 a significant effect on OS in HNSCC patients compared with other CSC markers such as CD44  
150 (Szafarowski et al., 2020). Of interest, HNSCC-ALDH1<sup>+ve</sup> CSCs were found to possess high levels

151 of the transcriptional repressor Bmi-1, another putative marker of CSCs, which also regulated their  
152 stemness and drug resistance (Chen et al., 2009).

153  
154 **Bmi1:** The B-cell-specific moloney murine leukemia virus insertion site 1 (Bmi1) is a key factor  
155 responsible for self-renewal and enrichment of stem cells. In their seminal work on characterizing  
156 CSCs in HNSCC, Prince et al. reported a differential expression of Bmi1 in the tumorigenic CD44<sup>+</sup>  
157 population, indicating a potential role for this molecule in tumor plasticity (Prince et al., 2007).  
158 Interestingly, Bmi1 levels were abnormally upregulated in patients with HNSCC, which correlated  
159 positively with chemo- and radioresistance (Vormittag et al., 2009). Thus, these findings have made  
160 it an attractive target for CSC examination in HNSCC studies. Recently, a comparative study found  
161 that CSC markers Bmi1 and BCL11B were able to discriminate between healthy and HNSCC tissues,  
162 whereas ALDH1A1 and CD44 were both expressed to a comparable extent in healthy mucosa and  
163 cancerous tissues (Sharaf et al., 2021). Interestingly, Bmi1<sup>+</sup> cells were convincingly found as slow-  
164 cycled tumor-initiating CSCs that did not only initiate the tumor, but also mediated cervical lymph  
165 node metastasis in mouse model of chemically-induced HNSCC (4-nitroquinoline-1-oxide: 4-NQO).  
166 As congruous with CSC features, such Bmi1<sup>+</sup> tumor cells were highly tumorigenic and chemo-  
167 resistant, whereas a combination of Bmi1 inhibitor and cisplatin treatment potently inhibited HNSCC  
168 (Chen et al., 2017).

169 Using a multicolor lineage tracing method in 4-NQO-induced mouse model of OSCC, Tanaka  
170 and colleagues reported that Bmi1<sup>+</sup> cells could serve as oral CSCs. They showed that Bmi1<sup>+</sup> cells  
171 were scattered in the developing tumors, which then proliferated to produce new patches, fueling the  
172 tumor growth and maintenance. However, some Bmi1<sup>+</sup> cells remained single and gradually  
173 disappeared from the malignant tissue, implying that Bmi1 was also expressed by differentiated cells,  
174 which have limited capacity to self-renew and maintain tumor growth (Tanaka et al., 2016). This also  
175 signifies the importance of using multiple surface markers for better characterization of CSCs.  
176 Importantly, a recent study showed that Bmi1 inhibition not only helped to abolish Bmi1<sup>+</sup> CSCs in  
177 HNSCC, but also augmented PD1 blockade by activating tumor cell-intrinsic immunity, which  
178 hindered the metastasis and prevented tumor relapse (Jia et al., 2020).

### 179 180 **CSC plasticity—a partial phenotypic transition?**

181 In addition to the aforementioned patterns of intra-tumoral heterogeneity, a newer more nuanced  
182 model was recently proposed as “CSC plasticity”, whereby CSCs reversibly switch between stemness  
183 and differentiated cell states. Such transition is mediated by genetic and epigenetic instabilities

184 together with cues from key processes, particularly EMT and mesenchymal-to-epithelial transition  
185 (MET; Ghuwalewala et al., 2016; La Fleur et al., 2012; Biddle et al., 2016; Fanelli et al., 2020).

186 During embryogenesis, cells undergo a highly dynamic and reversible shift between epithelial  
187 and mesenchymal states. When the shift is toward the mesenchymal phenotype, cells undergo EMT  
188 and obtain potent migratory and invasive characteristics. The main EMT transcription factors include  
189 the Snail family (Snail 1 and 2), the Twist family (Twist 1 and 2), and the ZEB family (ZEB1 and 2)  
190 of transcription factors (Yeung and Yang 2017). Opposite to EMT, cells may however start losing  
191 these migratory features and shift towards an epithelial state by acquiring junctional attachments and  
192 apico-basal polarization—a process referred to as MET (Thiery et al., 2009). Although the role of  
193 MET/EMT in cancer plasticity is still under investigation, it is nevertheless widely accepted that  
194 much of the intra-tumoral heterogeneity, invasion, metastasis and drug resistance are driven by these  
195 processes. CSCs can employ EMT to dissociate from the primary tumors, intravasate into the  
196 circulation and initiate new locoregional/distant metastatic colonies. Upon reaching a preferable  
197 metastatic niche, cells therein revert to an epithelial state (MET) to terminate migration, promote  
198 proliferation and seed new heterogeneous tumor colonies (Nieto et al., 2016).

199 In HNSCC, CSCs were mainly localized to the tumor invasive front, wherein both EMT and  
200 metastasis are executed, in contrast to the upper layers of the tumor bulk which remains largely  
201 epithelial (Sterz et al., 2010). Consistently, Chowdhury et al. showed that the tumor leading edges in  
202 a subset of OSCC were enriched by CD44<sup>high</sup>/ALDH<sup>high</sup> CSCs that demonstrated greater proliferative  
203 and invasive activities. Notably, CD44<sup>high</sup> CSCs from HNSCC tumors revealed clear EMT-related  
204 features including migration and invasiveness. Further, CD44<sup>high</sup> cells formed bilateral lung  
205 metastases in NOD-SCID mice, in contrast to CD44<sup>low</sup> which failed to generate similar metastatic  
206 growths (Davis et al., 2010). When analyzed the expression of EMT-associated genes in twenty-five  
207 HNSCC-derived cell lines, Johansson et al. found that EMT program-expressing cells were CD44<sup>high</sup>  
208 with an enhanced motility. Moreover, the expression of Twist1, a key inducer of EMT, was correlated  
209 with radioresistance in HNSCC (Johansson et al., 2016). Of interest, such CD44<sup>high</sup>, EMT-expressing  
210 cells had low levels of the epidermal growth factor receptor—a pattern associated with stemness  
211 (Johansson et al., 2016; La Fleur et al., 2012). In support of these reports, Twist1 directly regulated  
212 the expression of the potential CSC marker Bmi1. Furthermore, Twist1 and Bmi1 were mutually  
213 essential to promote EMT and tumour-initiating capability and associated with unfavorable clinical  
214 outcomes in HNSCC (Yang et al., 2010). In OSCC, EMT characteristics such as ZEB1  
215 overexpression and the loss of E-cadherin were remarkably higher in CD44<sup>high</sup>/CD24<sup>low</sup> CSCs,  
216 signifying the fact that tumor cell stemness concur with EMT in HNSCC (Ghuwalewala et al. 2016).  
217 Recently, 16 canonical EMT markers were surveyed in pan-cancer cohort collected from various

218 tumors, which confirmed the presence of EMT features in HNSCC patients (Gibbons and Creighton  
219 2018).

220         Recent emerging evidence has shown that tumor cells do not necessarily undergo a complete  
221 phenotypic transition. Intriguingly, studies on various cancer types indicated that tumor cells tend to  
222 execute partial (p-EMT) or hybrid EMT by concurrently bearing epithelial and mesenchymal  
223 phenotypes (Bakir et al., 2020). Supporting the “CSC plasticity” model, transcriptional profiles of  
224 ~6000 single cells from HNSCC patients revealed that pEMT-expressing cancer cells were localized  
225 to the leading edge of the primary tumors (Puram et al., 2017). Interestingly, these cells were in  
226 proximity with cancer-associated fibroblasts and their pEMT program was concluded as an  
227 independent predictor of nodal metastasis, grade, and adverse pathologic features in patients with  
228 HNSCC (Puram et al., 2017). In this regard, tumor-initiating cells can enhance their mesenchymal  
229 gene repertoire at the tumoral front to invade and disseminate distally; while clearly maintaining  
230 certain epithelial characteristics to reseed and establish new metastatic growths. Such plasticity is  
231 influenced by many TME-related factors including hypoxia (Mimeault et al., 2013).

232

### 233 **Role of hypoxic TME**

234 Hypoxia, either persistent or temporary, is a hallmark of most solid tumors. Accumulating  
235 experimental data suggests hypoxia as a crucial inducer of EMT and CSC plasticity, wherein hypoxia-  
236 inducible factors (HIFs) associate with tumor cell stemness, metastasis, angiogenesis and drug  
237 resistance (Mimeault et al., 2013). Of note, recent studies indicated that CSCs favor hypoxic niches  
238 for their growth and maintenance of stemness (Lee and Simon 2012). Like other solid tumors,  
239 hypoxia ensues in HNSCC when the blood supply becomes insufficient due to tumor growth, vascular  
240 disturbances or metabolic stress. Importantly, hypoxia had anti-apoptotic effects, predicted poor  
241 therapeutic response and OS, correlated with tumor aggressiveness and promoted the formation of  
242 functional tumor cell invadopodia in HNSCC (Sasabe et al., 2005; Moreno Roig et al., 2018; Beasley  
243 et al., 2002; Díaz et al., 2013; Wiechec et al., 2022).

244         The tumorigenic and pro-stemness effects of hypoxia could in part be mediated through EMT.  
245 In this context, co-expression of hypoxic and EMT markers (Twist 2/ Snip1 and HIF-1 $\alpha$ , respectively)  
246 served as an independent prognosticator for both OS and disease-free survival in patients with tongue  
247 SCC (TSCC; Liang et al., 2011). Furthermore, hypoxia induced the expression of key transcriptional  
248 factors regulating EMT and promoted pulmonary metastasis in OSCC (Huang et al., 2009; Wiechec  
249 et al., 2022). A recent study found that hypoxia-related genes were enriched in CD44<sup>+ve</sup> CSCs from  
250 patients with HNSCC. Interestingly, functional assays indicated that HIF-1 $\alpha$  promoted stemness, drug  
251 resistance and EMT in these CD44<sup>+ve</sup> CSCs. Noteworthy, inhibition of HIF1 $\alpha$ -driven pathways

252 reversed the CD44-mediated chemoresistance *in vivo*, implying new therapeutic opportunities in  
253 HNSCC (Byun et al., 2022).

254 Collectively, these reports denote that hypoxia is not only a promoter of tumor stemness and  
255 EMT but can also regulate the therapeutic response to anticancer agents. Additional evidence on the  
256 impact of hypoxia on tumorigenesis and stemness can be found in these detailed reviews (Yeo et al.,  
257 2016; Mimeault and Batra 2013; Lee and Simon 2012). Another important aspect of hypoxia-induced  
258 stemness is the induction of a new pattern of tumor vasculature, termed vascular mimicry (VM),  
259 which will be discussed in the next section.

260

## 261 **Plasticity underlies tumor cell mimicry**

### 262 *i. Endothelial-like cell mimicry*

263 Angiogenesis is a key hallmark of cancer. However, the limited success of antiangiogenic strategies  
264 remains a daunting challenge in treating many solid tumors including HNSCCs (Ribatti et al., 2019).  
265 In fact, despite the growing number of clinical trials, targeting the classical angiogenic pathways (e.g.  
266 vascular endothelial growth factor, VEGF) showed a modest improvement in the OS of cancer  
267 patients. In addition, inhibiting the VEGF pathway has been associated with persistent tumor  
268 invasiveness, increased distant metastasis and worsening treatment outcome (Ebos et al., 2009; Pàez-  
269 Ribes et al., 2009). Questions have therefore emerged, not only how tumor cells can survive such  
270 harsh hypoxic conditions but also how they become more “metastable” and resistant following the  
271 treatment with angiogenic inhibitors.

272 Tumor vasculature has long been assumed to arise from preexisting endothelial cells (ECs).  
273 However, a significant number of studies suggest that CSCs utilize their plasticity to acquire  
274 differentiation programs of distinct cell types, including EC-like phenotype (Seftor et al., 2012).  
275 Indeed, the CSC marker CD44 has been implicated in promoting several tumor proangiogenic events  
276 (Wang and Bourguignon 2011). In this regard, VM represents an alternative pattern of tumor  
277 microcirculation, in which aggressive tumor cells mimic ECs by initiating perfusable networks of  
278 vessel-like structures *in vitro* (Salem and Salo 2021). Notably, tumor cells capable of VM share  
279 considerable molecular similarity with that of CSCs (Seftor et al., 2012; Fan et al., 2013). For  
280 instance, up to 90% of CSCs were able to transdifferentiate into functional ECs in glioblastoma, the  
281 most common and aggressive brain tumor, implying that a significant part of tumor vasculature has  
282 a neoplastic origin (Ricci-Vitiani et al., 2010). Recently, we showed that metastatic OSCC cells co-  
283 express the endothelial marker CD31 *in vitro*. Furthermore, tissue samples from OSCC patients  
284 revealed distinct CD31<sup>+ve</sup> mosaic VM lumens that also contained red blood cells (Almahmoudi et al.,  
285 2021; Hujanen et al., 2021). Interestingly, and unlike VM-free regions, such VM-competent cells

286 display CD44<sup>high</sup>/E-cadherin<sup>low</sup> phenotype, denoting a common stemness-related state (Hujanen et al.,  
287 2021).

288         Beside angiogenesis, tumor lymphatics play a pivotal role in cancer progression. In a recent  
289 study on basal-like breast cancer, CSCs were capable to undergo lymphatic cell differentiation via  
290 the activation of VEGF-C pathway, by which lymphatic vessel-like channels were initiated. Further  
291 *in vivo* and *in vitro* experiments revealed that lymphangiogenic mimicry (LM) served as conduits for  
292 CSCs to the lymphatic vessels and accelerated lymphatic metastases (Wang et al., 2018). Our group  
293 has recently demonstrated that the lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1), a  
294 homologue of the CSC-marker CD44, is expressed by OSCC cells and promoted their dissemination  
295 and vessel-like formation (Karinen et al., 2021). Notably, patients with tumors expressing high levels  
296 of LYVE-1 tend to suffer more lymph node metastasis and worse survival (Karinen et al., 2021;  
297 Karinen et al., 2022). Of interest, LYVE-1 is a receptor for HA—a key component of ECM that  
298 influences, directly and indirectly, the self-renewal and maintenance of CSCs (Chanmee et al., 2015).  
299 Thus, targeting LYVE-1 or VEGF-C pathways (or both) may represent a novel therapeutic approach  
300 to conquer CSC-driven lymphatic metastasis in HNSCC. Notwithstanding, the potential clinical  
301 applications of LM remain unclear and warrant further in-depth investigations.

302  
303 *ii. Immune and neuronal cell mimicry*

304 In addition to the vascular cell phenotype, several recent studies uncovered more intriguing  
305 differentiation programs of CSCs including the acquisition of immune and neuronal cell states to  
306 facilitate tumor progression (Gangoso et al., 2021; Gao et al., 2021; Zeng et al., 2019). However, a  
307 conventional bulk transcriptomic profiling can be ineffective in distinguishing such tumor-intrinsic  
308 programs from other TME-infiltrating cells.

309         Based on scRNA-seq datasets and experimental models, an elevated immune-like  
310 transcriptional program was recently seen in cells of multiple cancer types, which was progressively  
311 acquired during the course of malignant transformation. Specifically, an enrichment of B cell, T cell  
312 and myeloid cell signatures was revealed in tumor cells from lung, breast, kidney, and pancreatic  
313 cancers. The score was, however, lower in tumor cells than in immune cells, implying a partial  
314 acquisition of this immune mimicry during progression from normalcy to neoplasm (Gao et al., 2021).  
315 Of note, such mimetic profile might adversely influence the prognostic value of immune cell  
316 signatures in cancer studies. Hence, through the exclusion of tumor cell-related immune genes, a new  
317 optimized immune response signature was proposed, which offered more reliable prognostic  
318 estimates (Gao et al., 2021). These findings are consistent with a recent work showing a striking gain  
319 in the immune evasion capabilities of CSCs following the acquisition of a transcriptional module that

320 hampered the immune response in glioblastoma multiforme (Gangoso et al., 2021). In primary  
321 HNSCC, Lee et al. provided a mechanism by which long-lived CD44<sup>+</sup> CSCs can selectively evade  
322 host immune responses. Interestingly, CD44<sup>+</sup> cells expressed higher levels of PD-L1 compared with  
323 the CD44<sup>-</sup> cells, which was associated with constitutive phosphorylation of STAT3 and decreased  
324 immunogenicity. Importantly, PD-1/PD-L1 blockade partially reversed the weakened  
325 immunogenicity and activated the TILs response against CD44<sup>+</sup> CSCs (Lee et al., 2016). Indeed,  
326 these data highlight the complex genetic and phenotypic changes of CSCs and their infinite ability to  
327 hijack the immune response and remodel TME. Although this is still a new area of research, it will  
328 be paramount to investigate whether the immune mimicry is implicated in HNSCC, wherein  
329 mechanisms underpinning its immunosuppressive TME remain an enigma.

330 In order to survive and initiate metastatic colonization in the brain, tumor cells must render  
331 their new neural niche to an amenable microenvironment. In this context, Neman et al. showed that  
332 HER2<sup>+</sup>, breast-to-brain metastatic (BBM), CSCs can attain neuronal phenotype by expressing and  
333 metabolizing Gamma-aminobutyric acid (GABA)—the chief inhibitory neurotransmitter in  
334 mammalian brains. GABA was utilized by tumor cells to promote their proliferation and GABAergic  
335 neuronal properties. Further, BBM cells expressed Reelin, a critical neuronal glycoprotein for brain  
336 development, which was directly associated with HER2 (Neman et al., 2014). Supporting these  
337 observations, a recent preprint (not peer-reviewed) study showed that small-cell lung cancer (SCLC)  
338 cells undergo a neuronal mimicry—a transition towards neuronal phenotype during tumor  
339 progression and metastasis. More importantly, this neuronal mimicry was critical for establishing  
340 SCLC growth in the brain, whereby tumor cells secrete neuronal pro-survival factors (e.g. Reelin) to  
341 recruit astrocytes and promote brain metastases (Fangfei et al., 2021). In essence, although brain  
342 metastasis in HNSCC is a rare event comprising <1% of all cases (Barrett et al., 2018), these reports  
343 further assert the concept of CSCs and urge the need for more studies in this exciting area that has  
344 much more to reveal.

345

### 346 **Oral microbiota and CSCs: Emerging evidence**

347 The “polymorphic microbiome” has recently been proposed as a new hallmark of cancer (Hanahan  
348 2022). Indeed, dysbiosis of the commensal microbiota can contribute, both positively and negatively,  
349 to the initiation and progression of cancer and, through immunomodulation, to anticancer drug  
350 response. Recent research has now advanced our understanding of the interactions between  
351 microbiota and tumor cells and there is a growing appreciation of their potential to transform  
352 treatment strategies for cancer patients. This review briefly outlines a few examples of microbiota  
353 commonly involved with HNSCC, to then focus on their possible role in tumor plasticity.

354 Oral cavity hosts diverse microbial communities inhabiting different sites such as teeth,  
355 saliva, tongue and other mucosal surfaces. Using germ-free animal models, particular  
356 microorganisms, chiefly but not exclusively bacteria, were shown to impact key features associated  
357 with tumor cell stemness such as EMT, proliferation, migration and invasion. Among these, two  
358 prominent oral bacteria, *Porphyromonas gingivalis* (*P. gingivalis*) and *Fusobacterium nucleatum* (*F.*  
359 *nucleatum*) influenced oral carcinogenesis and/or cancer progression. For example, infection with *P.*  
360 *gingivalis*, a major anaerobic Gram-negative periodontopathogen, induced EMT-driven  
361 morphological changes in OSCC cells and augmented their migratory and invasive capacities.  
362 Importantly, *P. gingivalis*-infected tumor cells exhibited evident plasticity features including the  
363 upregulation of CSC markers (CD44 and CD133) and chemotherapeutic resistance (Ha et al., 2015).  
364 Using a murine model of periodontitis-associated oral TSCC (OTSCC), infection with both *P.*  
365 *gingivalis* and *F. nucleatum* markedly enhanced the tumors' size and invasiveness. Furthermore,  
366 administration of these periodontopathogens significantly induced the activation of Signal  
367 Transducer and Activator of Transcription 3 (STAT3)—an important regulator of CSCs in HNSCC  
368 (Binder Gallimidi et al., 2015). In agreement, exposure to *P. gingivalis*, *F. nucleatum* or *E. coli*-  
369 derived lipopolysaccharide resulted in a strong upregulation of EMT transcripts (vimentin, Snail, and  
370 Twist) in OSCC cells. In contrast, the epithelial adhesion molecule, E-cadherin, was downregulated,  
371 implying shifting towards a mesenchymal state. Of interest, infected tumor cells showed  
372 morphological changes resembling that of fibroblasts, while unstimulated cells maintained a classical  
373 epithelial cobble-stone morphology (Abdulkareem et al., 2018).

374 Epstein–Barr virus (EBV) is a human herpesvirus that is associated with several malignancies  
375 including the nasopharyngeal carcinoma (NPC). Lun et al. (2012) found that CSC markers (CD44  
376 and SOX2) were overexpressed in a minor population of EBV<sup>+ve</sup> NPC cells. Notably, these CSCs  
377 were resistant to chemotherapy and showed high spheroid formation efficiency. Consistent with CSC  
378 properties, authors revealed that the sorted CD44<sup>+ve</sup> cells generated heterogeneous population of both  
379 CD44<sup>+ve</sup> and CD44<sup>-ve</sup> cells (Lun et al., 2012). The exact mechanisms by which EBV, and other  
380 pathogenic microbiota, induce tumor cell stemness are still being elucidated. For instance, the latent  
381 membrane protein 1 (LMP1) constitutes a key oncoprotein of EBV. Interestingly, Kondo et al. (2011)  
382 revealed that EBV instigates the development of CD44<sup>high</sup>/CD24<sup>low</sup> phenotype of CSCs and cancer  
383 progenitor cells in NPC via LMP1. Moreover, LMP1 induction in nasopharyngeal epithelial cells  
384 resulted in high tumorigenicity, rapid proliferation and enhanced self-renewal abilities.  
385 Morphologically, LMP1-expressing cells changed into fibroblast-like, spindle-shaped cells.

386 HPV-induced oropharyngeal HNSCC represents one of the most rapidly increasing cancers  
387 in high-income countries which also affects younger individuals (Lechner et al., 2022). Despite the

388 evident prognostic value of HPV status in HNSCC patients, its impact on CSCs and tumor cell  
389 stemness remains poorly understood and requires more research. Tang et al. (2013) showed that HPV  
390 status in HNSCC does not correlate with the proportion of ALDH<sup>high</sup> CSCs since their proportion was  
391 not significantly different between the HPV<sup>+ve</sup> and HPV<sup>-ve</sup> cell lines. On contrary, another study  
392 showed that HPV16<sup>+ve</sup> HNSCC had a 62.5-fold greater intrinsic CSC pool than HPV<sup>-ve</sup> cells (Zhang  
393 et al., 2014). Further, transfecting HPV<sup>-ve</sup> tumor cells with HPV16 genome enhanced CSC features  
394 including ALDH activity, tumor growth, migration/invasion and self-renewal capacity (Lee et al.,  
395 2015). In fact, it is difficult to explain how HPV<sup>+ve</sup> tumors—characterized by substantially better  
396 prognosis and outcome—harbor higher levels of CSCs, which render tumors more aggressive and  
397 drug resistant. Nevertheless, more recent studies suggested that HPV status in HNSCC could impact  
398 CSC populations after initiating the therapeutic regimen. In this sense, Reid et al. (2020)  
399 demonstrated that HPV<sup>-ve</sup> tumors had significant elevations in CD44<sup>+ve</sup>/ALDH<sup>+ve</sup> CSCs following  
400 irradiation, with more increasing escalation, compared to the HPV<sup>+ve</sup> cell lines.

401 Collectively, although these illustrative examples are rather limited and comprise small  
402 sample sizes, they encourage further research to uncover the relationship between oral microbiota  
403 and CSCs and how it can influence carcinogenesis in the head and neck tissues.

404

#### 405 **A need for new models?**

406 Besides the *in vivo* models, the characteristics of CSCs are traditionally assessed using  
407 plentiful three-dimensional (3D) techniques (comprehensively reviewed in: Langhans 2018; Zhang  
408 et al., 2020). Among these, the sphere (or spheroid-like) formation assay is commonly used to assess  
409 the ability of CSCs to grow in extremely low attachment/serum conditions and form tumorspheres.  
410 These tumorspheres are also termed “orospheres” when formed by HNSCC CSCs, indicating their  
411 origin from oral cavity and head and neck tumors (Krishnamurthy and Nör 2013). Typically,  
412 tumorspheres are generated using scaffold-free (e.g., Hanging drop cultures and low adhesion plates)  
413 and scaffold-based models. The latter scaffold-based 3D cultures provide more physiologically  
414 relevant conditions, particularly when incorporating biologically-derived hydrogels such as collagen,  
415 fibrin or Matrigel. These matrices facilitate cell-to-cell and cell-to-ECM interactions, thereby  
416 allowing more reliable assessment of CSC tumorigenicity, stemness and drug response including  
417 possible chemo-/radioresistance. In particular, Matrigel, a matrix secreted by Engelbreth–Holm–  
418 Swarm (EHS) mouse sarcoma cells, has been broadly used to assess CSC features (e.g., invasion)  
419 due to its high content of ECM proteins, growth factors and proteoglycans (Zhang et al., 2020;  
420 Langhans 2018; Aramini et al., 2022). However, animal-derived matrices such as Matrigel exhibit  
421 several limitations, making them suboptimal for human CSC research, including non-human origin,

422 inter-patch variations, and the presence of several undefined factors (Pamarthy and Sabaawy 2021).  
423 Therefore, the safety and efficacy of 85% of the drugs identified in such models are not translated to  
424 early clinical trials (Ledford 2011).

425 In order to provide a reliable alternative to animal-derived matrices, our group has developed  
426 “Myogel”, a matrix isolated from human leiomyoma that provides a physiologically relevant 3D  
427 milieu for *ex vivo* cancer modelling. Although its proteome is substantially different from other EHS-  
428 based matrices, yet, Myogel comprises key ECM proteins such as laminin, collagen (types IV, XII  
429 and XIV), tenascin-C, heparan sulfate proteoglycans, nidogen and epidermal growth factor (Salo et  
430 al., 2015). Indeed, balance in the physiological pH environment is important to the regulation and  
431 maintenance of stem cell activities including proliferation, viability and differentiation (Teo et al.,  
432 2014). In this context, Myogel pH is neutral and more stable during cell culture than that of Matrigel,  
433 hence providing a good control of CSC experiments. Importantly, key CSC-related properties were  
434 more efficiently represented in Myogel, including tumor cell migration, invasion and response to  
435 targeted anti-HNSCC therapy (Salo et al., 2015; Tuomainen et al., 2019). Furthermore, primary  
436 HNSCC cell lines showed a greater tendency to form VM in Myogel, whereas human endothelial  
437 cells formed consistent and dense tubes throughout the matrix, suggesting that ECM is an important  
438 modulator of the tumor cell-derived tubulogenesis (Hujanen et al., 2021). Thus, when selecting a 3D  
439 scaffold for CSC studies, it is important to consider matrices that sustain stemness traits and faithfully  
440 recapitulate the structural and molecular features of human TME.

441 Tumor-initiating capacity is considered to be the gold standard for identifying and confirming  
442 CSC-like cells. Currently, most *in vivo* studies of CSCs rely upon tumor engraftment into an  
443 immunocompromised mouse model—typically the NOD/SCID mice. These mice are B cell- and T  
444 cell-deficient model and exhibit defective activity of dendritic cells, macrophages and natural killer  
445 cells, thus enhancing the chances of successful xenotransplantation (Skidan and Steiniger 2014).  
446 However, in addition to cost and labor challenges, these traditional models do not reliably represent  
447 the complex TME interactions in the patients including the lack of specific cytokines necessary for  
448 the activities of CSCs. To overcome such constraints, Morton et al. (2016) developed a humanized  
449 xenochimeric mouse model of HNSCC (XactMice) comprising human hematopoietic stem and  
450 progenitor cells (HSPCs) that can home into the transplanted tumor and replicate its natural TME.  
451 Following the harvesting of HSPCs from either donated cord blood or adult peripheral blood, cells  
452 were expanded *ex vivo* and injected into sub-lethally irradiated NOD/SCID gamma mice to generate  
453 XactMice, wherein HNSCC cells were later engrafted. Interestingly, XactMice tumors showed  
454 epithelial, stromal and immune gene signature that aligns more closely to the original TME observed  
455 clinically—an effect partly mediated by HSPC-/tumor cell-driven cytokines (Morton et al., 2016).

456 Additionally, the same group has developed a dual infusion protocol of HSPCs and mesenchymal  
457 stem cells, resulting in higher degrees of “humanization” of the HNSCC mouse model. This includes  
458 incremental human bone marrow engraftment, excessive increase in human immune cells and  
459 intratumor homing with better lineage reconstitution. This optimized model is more closely  
460 resembling that of the originating patient's tumor, suggesting an enhanced capability to accurately  
461 recapitulate a human TME (Morton et al., 2018).

462 Another potential *in vivo* model for CSC research is Zebrafish, which has been increasingly  
463 used as an anticancer screening platform. Recently, our group has utilized zebrafish larvae as  
464 xenograft model of human HNSCC to evaluate tumor cell metastasis, VM formation and personalized  
465 drug response (Karinen et al., 2021; Hujanen et al., 2021; Wahab et al., 2021; Al-Samadi et al., 2019).  
466 Indeed, zebrafish has several advantages over murine models considering its efficiency, feasibility  
467 plus to the associated cost- and labor-effectiveness. However, similar to mice, zebrafish model is  
468 devoid of critical cytokines, chemokines and other TME factors released in human patients. To  
469 alleviate this limitation, Rajan and colleagues (2020) pioneered the first “humanized” zebrafish that  
470 expresses multiple human hematopoietic-specific cytokines. By transplanting primary HSPCs and  
471 leukemia cells, they showed that their model exhibits hematopoietic niche homing that more precisely  
472 represent the behavior of human leukemia. Further, such humanized zebrafish promoted survival,  
473 self-renewal and multi-lineage differentiation of HSPCs (Rajan et al., 2020). Although this platform  
474 has not yet been harnessed for HNSCC CSCs, the findings pave the way for a new modelling  
475 paradigm in humanized animal-based research.

476 Taking together, developing physiologically relevant *ex vivo* and *in vivo* models that closely  
477 recapitulate CSCs’ niche and enable their characterization and therapeutic targeting will definitely  
478 facilitate the translation of basic discoveries to the clinical practice in a timely manner. Such  
479 approaches are paramount for the development of novel drugs that can selectively target and destroy  
480 CSCs.

481

## 482 **Conclusions and future perspectives**

483 HNSCCs encompass highly heterogeneous tumors, wherein CSCs seem to play pivotal and  
484 multifaceted roles in their initiation, progression, metastasis, clinical resistance and possible relapse.  
485 Recent technological advances, such as scRNA-seq and tumor modelling, have led to unprecedented  
486 understanding of CSCs and their intricate interplay with other TME factors. However, much work  
487 remains to be undertaken before this understanding can be translated into successful anticancer  
488 therapies, since the prognosis for HNSCC patients remains generally dismal. To this end, several  
489 areas need to be further elucidated including, inter alia, pathways involved in CSC signaling including

490 with local microbiota; the molecular underpinning of CSC-driven drug resistance; and immune cell  
491 mimicry. Another challenge is to developing better cancer models for CSC research. Despite the  
492 tremendous progress brought by humanized animal platforms, yet they remain relatively immature  
493 with several shortcomings. For instance, besides cost and labor intensiveness, the possibility to  
494 develop xenogenic graft versus host disease (GVHD) mediated by engrafted human T-cells is a major  
495 obstacle in such models. GVHD not only affects the number of viable experimental animals but also  
496 complicates data interpretation by overlaying a second set of diseases (Greenblatt et al., 2012).  
497 Nevertheless, the humanized animal models remain a promising approach with a high potential for  
498 improvement to catalogue the diverse range of cellular activities in head and neck carcinogenesis.

499 Lastly, but importantly, we need to identify specific (i.e. exclusive) markers for CSCs in  
500 HNSCC. To date, there are no available universal markers that can label CSCs alone. On contrary,  
501 many of the current markers are also expressed by other cell types such as normal stem cells. Thus,  
502 combining different putative labels of CSCs is recommended. Importantly, novel therapies should be  
503 carefully designed to exclusively targeting this subpopulation of tumor cells and to minimize possible  
504 elimination of tissue stem cells or disrupting vital functions (Skidan and Steiniger 2014; Prince et al.,  
505 2016). Additionally, anti-cancer vaccines targeting CSCs through dendritic cells and other immune  
506 cell types showed promising results in HNSCC and could be further elaborated in future (Prince et  
507 al., 2016). In sum, tumor cell plasticity and CSCs represent an exciting and expanding battleground  
508 with great implications for cancer therapy that are only beginning to be appreciated in head and neck  
509 oncology.

510

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515

#### 516 **Conflict of interest**

517 The authors declare no conflict of interest.

518

#### 519 **Figure legend**

520 **Figure 1. Cancer Stem Cells (CSCs) in head and neck squamous cell carcinomas.** CSCs are a  
521 small subpopulation of tumor cells which exhibit the following main capabilities: **a)** self-renewal; **b)**  
522 differentiation into multiple types of cancer cells; and **c)** tumor-initiation (tumorigenesis) when  
523 transplanted into an animal host.

524 **Figure 2. Examples of models used to assess cancer stem cells (CSCs) features. a)** Ex vivo models  
525 are broadly categorized to scaffold-free cultures (e.g. low attachment plates and hanging drops) and  
526 scaffold-based models (e.g. Matrigel and Myogel) that used to assess CSC features such as  
527 tumorspheres formation and invasion. **b)** In vivo models are mainly used to assess the capacity of  
528 CSC-like cells to initiate new tumors (tumorigenicity and metastability) using different models,  
529 particularly non-obese diabetic/severe combined immunodeficient mice and humanized models.

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940 **Table 1. Cancer stem cell markers in head and neck squamous cell carcinoma**

CSC Marker	Protein type and localization	Main tumorigenic potential in HNSCC	References
ALDH	Enzyme; cytoplasmic	<ul style="list-style-type: none"> <li>▪ ALDH<sup>+ve</sup> cells (as few as <math>5 \times 10^2</math>) initiated visible malignant growths <i>in vivo</i> that resembled the original tumors.</li> <li>▪ ALDH activity in HNSCC involved its isoforms ALDH1-3; and it was associated with increased levels of several tumorigenic properties, e.g., sphere formation, enhanced migration and drug resistance.</li> <li>▪ ALDH had therapeutic and prognostic potential; and ALDH<sup>high</sup> CSC-based vaccines induced anti-HNSCC immunity.</li> </ul>	Clay et al., 2010; Prince et al., 2016; Chen et al., 2009; Yu et al.; 2011; Chen et al., 2010; Kim et al., 2017; Szafarowski et al., 2020
Bmi1 (PCGF4)	Binding protein; nuclear	<ul style="list-style-type: none"> <li>▪ Bmi1 mediated metastasis in mouse model of chemically-induced HNSCC, while Bmi1<sup>+ve</sup> cells showed features of tumor-initiating CSCs</li> <li>▪ Bmi1<sup>+ve</sup> cells were chemoresistant and fueled tumor growth and maintenance. ▪ Bmi1 targeting augmented immunotherapeutic drugs and reduced metastasis.</li> </ul>	Prince et al., 2007; Chen et al., 2017; Vormittag et al., 2009; Sharaf et al., 2021; Tanaka et al., 2016; Jia et al., 2020
CD133 (PROM1)	Transmembrane protein; cell surface protrusions	<ul style="list-style-type: none"> <li>▪ CD133<sup>+ve</sup> cells represented &gt; 5% of OSCC cells and showed properties of CSCs including chemoresistance, self-renewal, clonogenicity, proliferation and differentiation <i>in vitro</i> and <i>in vivo</i> compared with the CD133<sup>-ve</sup> cells.</li> <li>▪ CD133<sup>+ve</sup> cells had higher levels of pluripotency-associated genes</li> <li>▪ Targeting CD133 ameliorated the drug resistance while combining anti-CD133 and cisplatin led to the maximal inhibition of tumor initiating properties</li> <li>▪ CD133<sup>+ve</sup>/CD44<sup>+ve</sup> immunophenotype predicted poor prognosis of early-stage OSCC patients.</li> </ul>	Yu et al., 2016; Oliveira et al., 2014; Zhang et al., 2010

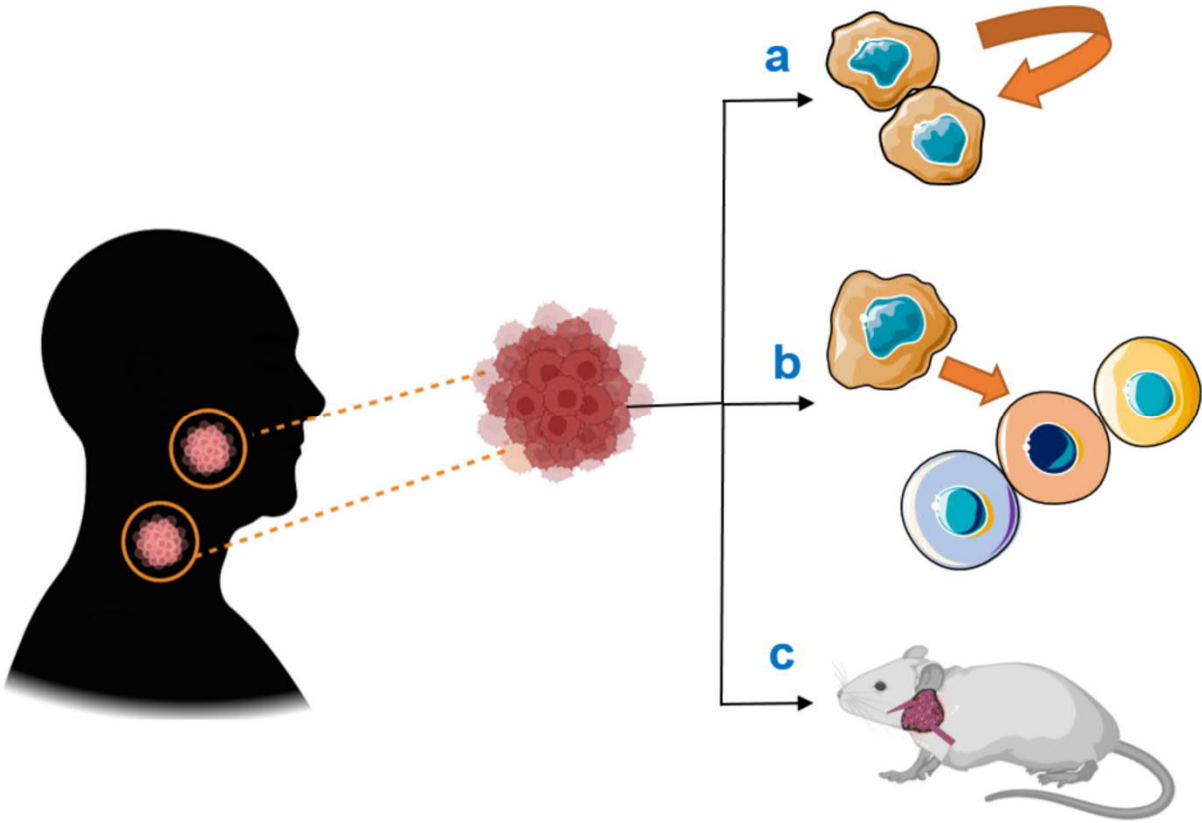
CD24	Membrane receptor; cell surface	<ul style="list-style-type: none"> <li>▪ CD24 expression level directly affects cisplatin sensitivity as well as the expression of key apoptotic, stem and drug resistance genes in LSCC cells</li> <li>▪ CD24<sup>high</sup> LSCC tumors had unfavorable response to cisplatin treatment</li> <li>▪ CD24<sup>+ve</sup> OSCC cells showed a significantly higher functional angiogenic capillary density in NOD/SCID mice compared with CD24<sup>-ve</sup> cells</li> <li>▪ CD24<sup>+ve</sup>/CD44<sup>+ve</sup> cells possessed stemness characteristics of self-renewal and differentiation, higher cell invasion and clonogenicity <i>in vitro</i> and generated larger tumors in nude mice</li> <li>▪ CD24<sup>+ve</sup>/CD44<sup>+ve</sup> cells were chemoresistant to gemcitabine and cisplatin.</li> <li>▪ In contrast, Ghuwalewala et al. showed that OSCC-derived CSCs are CD44<sup>high</sup>/CD24<sup>low</sup> cells, which had EMT characteristics, increased clonogenicity, sphere forming ability, invasion and elevated chemoresistance.</li> </ul>	Modur et al., 2016; Zimmerer et al., 2017; Han et al., 2014; Ghuwalewala et al. 2016
CD271 (NGFR)	Transmembrane protein; cell surface	<ul style="list-style-type: none"> <li>▪ CD271<sup>+ve</sup>/CD44<sup>+ve</sup> subpopulation was highly tumorigenic cells and showed higher cell proliferation, sphere/colony formation, chemo- and radio-resistance</li> <li>▪ Targeting CD271 inhibits tumor cell proliferation and tumorigenicity</li> <li>▪ CD271-overexpressing cells resulted in a more invasive and metastatic phenotype including the upregulation of EMT-related transcription factors</li> <li>▪ CD271 expression correlated with greater nodal metastasis and shorter disease-free survival <i>in vivo</i>.</li> </ul>	Murillo-Sauca et al., 2014; Elkashty et al., 2020; Chung et al., 2018
CD44 (HCAM)	Transmembrane protein; cell surface	<ul style="list-style-type: none"> <li>▪ It is the most frequently studied CSC marker in cancer including in HNSCC.</li> <li>▪ CD44<sup>+ve</sup> cells comprised &lt;10% of the cells in HNSCC and gave rise to new tumors <i>in vivo</i>, which reproduced the original tumor heterogeneity and could be serially passaged</li> </ul>	Prince et al., 2007; Wang and Bourguignon 2011; Boxberg et al., 2018; Joshua et al., 2012; Chen et al., 2014; Ludwig et al., 2019; Hujanen et al., 2021;

		<ul style="list-style-type: none"> <li>▪ CD44<sup>+ve</sup> cells were less immunogenic; had a higher EMT features and elevated potential for 3D sphere-forming ability, migration and drug resistance</li> <li>▪ CD44 signaling pathway promoted tumor growth, metastasis, cell survival, drug resistance, tumor-related angiogenesis and VM.</li> <li>▪ CD44 expression was correlated with poorer clinicopathological parameters of HNSCC patients</li> <li>▪ CD44 isoforms enhance migration, proliferation, and cisplatin sensitivity and hold prognostic potential in HNSCC</li> </ul>	Irani and Dehghan 2018; Lee et al., 2016; Byun et al., 2022; Wang et al., 2009
c-Met (HGFR)	Transmembrane receptor tyrosine kinase; cell surface	<ul style="list-style-type: none"> <li>▪ c-Met<sup>+ve</sup> HNSCC cells showed CSC properties <i>in vivo</i>, which was suggested superior to CD44 and only slightly inferior to ALDH.</li> <li>▪ c-Met<sup>+ve</sup> HNSCC cells have higher self-renewal, chemoresistance and colony-forming ability <i>in vitro</i>; while enhanced metastatic ability <i>in vivo</i></li> <li>▪ c-Met<sup>+ve</sup> staining strongly correlated with neck metastasis and increased depth of tumor invasion in OTSCC</li> <li>▪ c-Met activation enhanced migration and invasion of OTSCC cells <i>in vitro</i></li> <li>▪ c-Met overexpression in OSCC cells was significantly associated with lymphangiogenesis including higher peritumoral lymphatic vessel, higher incidence of peritumoral lymphatic invasion, and positive lymph node status</li> <li>▪ c-Met targeting may have therapeutic effect in HNSCC via radiosensitization</li> <li>▪ c-Met overexpression in HNSCC was significantly correlated with poor overall survival and unfavorable clinicopathological features.</li> </ul>	Sun and Wang 2011; Lim et al., 2012; Zhao et al., 2011; Lüttich et al., 2021; Vsiansky et al., 2018; Zhou et al., 2007
Oct4 (POU5F1)	Transcription factor; nuclear	<ul style="list-style-type: none"> <li>▪ Oct4 promoted conversion of differentiated HNSCC cells into CSCs</li> </ul>	Koo et al., 2015; Routila et al., 2022; Nathansen et al., 2021

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- Oct4<sup>high</sup> CSCs have more stem cell-like traits including self-renewal, chemoresistance, invasion capacity and tumorigenicity *in vitro* and *in vivo*.
  - Oct4 expression served as a potent prognostic marker in HNSCC patients.
  - Using several independent patient cohorts, Oct4 expression predicted impaired survival in the radiotherapy-only HNSCC patients
  - Oct4 positivity served as a biomarker of benefit from DNA damaging chemotherapies; it was implicated in the irradiation-induced DNA damage response in HNSCC and contributes to the regulation of the radioresistant CSCs
  - Oct4 overexpression in the HNSCC cell line resulted in apoptosis resistance

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941 3D, three-dimensional; ALDH, aldehyde dehydrogenase; Bmi1, B-cell-specific moloney murine leukemia virus insertion site 1; CD, cluster of differentiation; c-Met, c-  
942 mesenchymal–epithelial transition factor; CSC, cancer stem cell; EMT, epithelial-mesenchymal transition; GPR49, G-protein coupled receptor 49; HCAM, homing cell adhesion  
943 molecule; HGFR, hepatocyte growth factor receptor; HNSCC, head and neck squamous cell carcinoma; Lgr5, Leucine-rich repeat-containing G-protein coupled receptor 5;  
944 LSCC, laryngeal squamous cell carcinoma; NGFR, nerve growth factor receptor; NOD/SCID, non-obese diabetic/severe combined immunodeficient; Oct4, octamer-binding  
945 transcription factor 4; OSCC, oral squamous cell carcinoma; OTSCC, oral tongue squamous cell carcinoma; PCGF4; polycomb group RING finger protein 4; POU5F1; Pic-1,  
946 Oct1,2, Unc-86 transcription factor 1; PROM1, prominin-1; VM, vascular mimicry



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