

Review

Biological roles and clinical applications of EpCAM in HCC

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Epithelial cell adhesion molecule (EpCAM) is an important biomarker in tumors. In hepatocellular carcinoma (HCC), EpCAM+ cells exhibit high invasiveness, tumorigenic ability, therapeutic resistance, and self-renewal ability, often identified as liver cancer stem cells (CSCs). Detecting EpCAM+ cells in tumor lesions and circulation is valuable for predicting patient prognosis and monitoring therapeutic outcomes, emphasizing its clinical significance. Given its broad expression in HCC, especially in CSCs and circulating tumor cells (CTCs), EpCAM-targeting agents have garnered substantial research interest. However, the role of EpCAM in HCC progression and its regulatory mechanisms remains poorly understood. Furthermore, clinical applications of EpCAM, such as liquid biopsy and targeted therapies, are still controversial. This review summarizes the biological properties of EpCAM+ HCC cells, explores the regulatory mechanisms governing EpCAM expression, and discusses its clinical significance of using EpCAM as a prognostic marker and therapeutic target.

Keywords EpCAM · HCC · Circulating tumour cells · Biomarker · Cancer stem cells**1 Introduction**

HCC is a leading cause of cancer-related mortality worldwide. Despite advancements in treatment, including hepatic resection, liver transplantation, chemoembolization and systemic therapies, only surgical options, such as liver transplantation and hepatic resection, are considered potentially curative. However, their efficacy is limited due to high recurrence rates after resection and restricted patient eligibility, as most cases are diagnosed at advanced stages [1, 2]. Early diagnosis significantly improves prognosis, but current screening methods, such as alpha-fetoprotein (AFP) testing, lack sufficient sensitivity for early detection [3, 4].

HCC is marked by a predominant intratumoral heterogeneity, which correlates with worse clinical outcomes [5]. This heterogeneity, compounded by the lack of specific molecular signatures to guide personalized treatment regimens, hinders therapeutic efficacy [6]. Liver CSCs are thought to drive this heterogeneity in HCC [7]. Various biomarkers, including EpCAM, CD133, CD90, CD13, CD44, CD24, CD47, ICAM1, α2δ1, keratin19, OV6, and Lgr5, have been identified to define distinct HCC CSC populations [8, 9]. Each subpopulation may harbor unique oncogenic drivers, complicating efforts to develop effective molecularly targeted therapies. Understanding the cellular functions and regulatory mechanisms of these subpopulations, particularly those at the top of the cellular hierarchy, is critical for improving HCC treatment strategies.

Among these biomarkers, EpCAM stands out as a type I transmembrane glycoprotein expressed in epithelial tissues that was initially identified as a surface antigen in colorectal carcinoma [10]. Subsequent research, EpCAM has revealed

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its roles as a prognostic marker, therapeutic target, and anchor molecule for CTCs [11]. EpCAM is a multifunctional transmembrane protein involved in various cancer-related processes, cell proliferation, adhesion, stemness, metabolism, metastasis, chemo- and radio-resistance, angiogenesis, migration, and epithelial-mesenchymal transition (EMT) [11–13]. Its versatility makes it an attractive target for new diagnostic and prognostic approaches in cancer biology.

This review provides a comprehensive overview of EpCAM+ cells in HCC, focusing on their properties, interactions with other signaling pathways, and potential clinical applications. Additionally, the progress in EpCAM-based therapies is discussed, shedding light on their implications in HCC management.

2 Biological properties of EpCAM+ HCC cells

The expression of EpCAM in HCC is significantly correlated with higher tumor grades and elevated serum AFP levels. Downregulation of EpCAM gene expression significantly decreases the proliferation and invasiveness of HCC cells [14]. Research has shown that EpCAM+ cells express hepatic stem cell markers, efficiently form nonadherent spheroids, and demonstrate greater aggressiveness and tumorigenicity compared to EpCAM- cells, demonstrating their stem/progenitor cell-like characteristics [15, 16]. Furthermore, EpCAM-expressing proliferating ductal cells (PDC) in inflamed livers have been identified as potential cellular origins of HCC [17].

A small proportion of EpCAM+ cells present in advanced cirrhosis possesses self-renewal capabilities mediated by autocrine Wnt signaling, making them prone to progression into HCC [18]. Follow-up studies of patients with compensated HCV-related cirrhosis showed that EpCAM expression is an independent predictor of HCC occurrence [19]. Additionally, Ogasawara et al. revealed that EpCAM+ hepatocellular-cholangiocarcinoma (CHC) cells exhibit stem cell-like features, high tumorigenicity, and the ability to develop tumors with CHC-like tumors, suggesting CHCs may originate from EpCAM(+) cells [20].

EpCAM+ HCC CSCs have also been shown to resist natural killer (NK) cell-mediated cytotoxicity by up-regulating carcinoembryonic antigen-related cell adhesion molecule 1 (CEACAM1) expression [21]. Studies found that EpCAM frequently co-expresses with other markers, with these co-expressing cells potentially representing a more precise CSC phenotype. For example, CD133+ EpCAM+ cells in Huh7 cells exhibit enhanced self-renewal, differentiation, drug resistance, and tumorigenesis [22]. Liao et al. identified a subset of Wnt-activity^{high} ALDH1+ EpCAM+ triple-positive cells as the most tumorigenic, stem cell-like, and phenotypically plastic subpopulation of cells in HCC, referred to as "superpotent CSCs" (spCSCs) [23]. Similarly, EpCAM+ AFP+ cells, a highly aggressive subgroup associated with metastasis, treatment resistance, and poor prognosis, have been designated hepatic stem cell-like HCC (HPSC HCC) due to their stemness and tumorigenic properties [24].

3 Regulatory mechanisms of EpCAM expression

3.1 Key molecules of EpCAM+ HCC cells discovered by Omics techniques

To investigate the regulatory mechanisms of EpCAM+ HCC cells, various omics approaches have identified several key molecules. Using GeneNet h50K shRNA library and RNA interference (RNAi) screening, Takai et al. identified PMPCB as a top candidate gene with a synthetic lethal interaction with EpCAM. Blocking PMPCB inhibits EpCAM expression and Wnt/ β -catenin signaling by inducing mitochondria-related reactive oxygen species and FOXO activities [25].

Whole exome sequencing of sorted EpCAM+ and EpCAM- HCC cells revealed that protocadherin 18 (PCDH18) is functionally suppressed by somatic mutations in a subset of EpCAM+ HCC cells, potentially playing an important role in their development [26]. Transcriptomic analysis by Zhao et al. identified YY1-associated protein 1 (YY1AP1) as a critical regulator of EpCAM+ AFP+ HCC cell survival, with YY1 binding to EpCAM promoter to drive its transcription [27].

Single-cell RNA sequencing (scRNA-seq) by Ho et al. provided detailed transcriptomic landscape of HCC EpCAM+ and EpCAM- cells, showing similar mutational profiles between these subtypes. This suggests that mutation acquisition may not be the main factor driving subtype emergence. Notably, scRNA-seq data revealed that EpCAM+ cells were enriched in lipid metabolism-related genes, while EpCAM- cells showed higher expression of genes related to the translation and RNA processing [28].

Transcriptomic sequencing also identified epidermal growth factor receptor kinase substrate 8-like protein 3 (EPS8L3) as associated with CD24/CD13/EpCAM-triple positivity in liver CSCs. Akt signaling-driven SP1 upregulated EPS8L3

expression, promoting advanced tumor stages in HCC [29]. Microarray analysis by Zeng et al. found that the Spalt Like Transcription Factor 4 (SALL4) is upregulated in EpCAM + HCC cells, underscoring its important role in maintaining their stemness [30]. These findings collectively provide a deeper understanding of the biological properties and regulatory mechanisms of EpCAM + HCC cells, offering insights into their potential as therapeutic targets.

3.2 miRNAs and EpCAM + HCC cells

Using small RNA deep sequencing, Ji et al. identified miR-155 as overexpressed in EpCAM + HCC cells and demonstrated its critical role in maintaining stemness. They further demonstrated that miR-155 plays an important role in the maintenance of EpCAM + HCC cell stemness [31]. Microarray-based global miRNA profiling methods revealed that members of the miR-181 family are upregulated in EpCAM + HCC cells. Elevated miR-181 expression supports stem cell properties in these cells, while its blockade reduces the proportion of EpCAM + HCC cells and induces their differentiation [32]. The enrichment of miR-429 in EpCAM + HCC cells promotes liver CSC properties by targeting retinoblastoma-binding protein 4 (RBBP4) [33]. Additionally, miR-26b-5p has been shown to maintain EpCAM + cells stemness by targeting HSPA8 [34]. miR-30e-3p directly targets EpCAM, contributing to its role in stemness maintenance [35].

3.3 HBx and EpCAM + HCC cells

Chronic viral hepatitis B is a major risk factor for hepatocarcinogenesis, and HBV X protein (HBx) encoded by hepatitis B virus (HBV) is implicated in HCC pathogenesis and HCC CSC maintenance. HBx induces EpCAM expression via RelA-dependent demethylation [36]. Furthermore, HBx activates β -catenin signaling and upregulates miR-181, enhancing EpCAM expression [37]. It also induces EpCAM expression in HCC by activating histone demethylase KDM5B [38]. Wang et al. demonstrated that HBx promotes HCC formation by promoting the expansion and tumorigenicity of EpCAM + hepatic progenitor cells (HPCs) in a DDC-induced mouse model, suggesting a potential origin for HCC arising from chronic hepatitis infection [39].

3.4 Other regulators

Yamashita et al., identified two Tcf binding elements in the EpCAM promoter, showing that EpCAM is a direct transcriptional target of Tcf/ β -catenin in HCC cells. They also found that EpCAM + HCC cells are more sensitive to Tcf/ β -catenin binding inhibitors compared to EpCAM- HCC cells, further confirming this regulatory relationship [40]. Zinc finger protein X-linked (ZFX) enhances the maintenance of EpCAM + CSCs by promoting nuclear translocation and transactivation of β -catenin [41].

NK cell-derived IFN- γ upregulates EpCAM expression through the STAT1 pathway, inducing epithelial-mesenchymal transition (EMT) and promoting liver inflammation and HCC development [42]. Compared with EpCAM- cells, EpCAM + HCC cells exhibit longer telomeres, higher expression of human telomerase reverse transcriptase (hTERT) and the shelterin complex, as well as increased chromosomal instability [43]. Additionally, NDRG1 stabilizes EpCAM through protein-protein interactions and prevents its ubiquitination [44].

4 EpCAM expression in HCC and prognostic value

EpCAM is overexpressed in various human malignant tumors and is recognized as an important prognostic factor [45, 46]. Its prognostic value in HCC has been extensively studied. Survival analysis has demonstrated that EpCAM overexpression is significantly associated with lower overall survival rates and higher recurrence rates in HCC patients [47–51]. In hepatocellular-cholangiocarcinoma (CHC), EpCAM is highly expressed in 80% of cases and is strongly correlated with poor prognosis [52]. Additionally, overexpression of EpCAM in HCC is associated with other clinicopathological features, including high AFP levels and poorer tumor differentiation [53, 54].

The anatomical distribution of EpCAM expression in tumors also influences postoperative recurrence rates. Patients with peritumoral EpCAM expression exhibit higher recurrence rates and worse prognoses compared to those with pan-tumoral EpCAM expression [21]. Clinical data indicate that recurrent tumors following treatments such as radiofrequency ablation (RFA) or transarterial chemoembolization (TACE) treatment have a higher proportion of EpCAM + cells compared

to primary tumors. This suggests that residual tumors enhanced EpCAM expression may drive aggressive phenotypes and local recurrence [55–59].

However, the spatial heterogeneity of EpCAM expression in HCC adds complexity to its prognostic value. Homogeneous EpCAM expression is significantly associated with early recurrence, while heterogeneous EpCAM expression and EpCAM negativity are linked to similar clinical outcomes [60].

Yamashita et al. hypothesized that EpCAM + HCC can be further subclassified based on AFP expression [24]. EpCAM + AFP + HCC typically occurs in younger patients with advanced TNM stages and portal vein invasion, whereas EpCAM– AFP– HCC is predominately found in older patients with early TNM stages. EpCAM + AFP– HCC also develops in younger early TNM stages and low frequencies of portal vein invasion [24]. Another study showed that EpCAM + AFP + and EpCAM– AFP + HCC are associated with advanced TNM stages and high frequencies of venous invasion, whereas EpCAM + AFP– and EpCAM– AFP– HCC are associated with early TNM stages and low frequencies of venous invasion. Furthermore, EpCAM + AFP + exhibits higher microvessel density (MVD) and vascular endothelial growth factor (VEGF) expression levels of EpCAM + AFP + HCC compared to other subtypes, indicating a more angiogenic tumor phenotype [61]. Thus, the relationship between EpCAM expression profiles and different clinical outcomes is complex, influenced by factors such as tumor subtype, stage, and distribution of EpCAM expression. While EpCAM expression is a significant marker in HCC, its prognostic value is not fully understood and warrants further investigation.

5 The application of EpCAM in liquid biopsy of HCC

Liver biopsies provide valuable insights into tumor biology but are rarely performed due to their invasiveness and the risk of tumor seeding. Blood-based tests, such as AFP, offer limited sensitivity for the diagnosis or prognosis of HCC. Liquid biopsy, an emerging method for early detection and monitoring of cancer, has gained significant attention in recent years [62]. In HCC, liquid biopsies mainly include circulating tumor cells (CTCs), circulating tumor DNA (ctDNA), and extracellular vesicles (EVs) [63, 64].

5.1 EpCAM-based CTC detection

CTCs are tumor cells derived from the original tumor and extravasate into circulation [65]. Analyzing the characteristics and genomic heterogeneity of CTCs provides critical insights into HCC prognosis and treatment response [66]. Platforms for CTC detection often rely on immunoaffinity methods with the EpCAM being the most commonly used biomarker in HCC and other cancers [66–68].

Studies have reported that EpCAM + CTCs were present in 66.7% of HCC patients, with counts ranging from 1 to 34 per 7.5 mL of blood. A preoperative CTC count of $\geq 2/7.5$ mL was identified as an independent prognostic factor for tumor recurrence after surgery [69]. Schulze et al. used the CellSearch™ system to detect ≥ 1 CTC/7.5 mL in 18 of 59 HCC patients but only 1 of 19 patients with cirrhosis or benign hepatic tumors. Compared with CTC-negative patients, CTC-positive patients had a significantly shorter overall survival (OS) [70]. In patients undergoing chemoembolization, CTC counts were also identified as independent predictors of both OS and progression-free survival (PFS) [71]. HCC patients with ≥ 1 CTC/7.5 mL were more likely to have AFP levels ≥ 400 ng/mL and vascular invasion [70, 72]. Similarly, using fluorescence-activated cell sorting (FACS), Hao et al. demonstrated that HCC patients with ≥ 3.5 CTCs/10 mL experienced higher recurrence rates than those with < 3.5 CTCs/10 mL [73].

The association between EpCAM + CTCs and HCC recurrence after liver transplantation has also been highlighted. Hwang et al. reported that preoperative and postoperative EpCAM + CTC counts were significantly correlated with recurrence [74]. Additionally, Jin et al. enriched CTCs using anti-EpCAM nanoparticles and detected AFP mRNA levels in EpCAM-positive CTCs from HCC patients before hepatectomy by AFP nested RT-PCR. Their findings indicated that positive AFP mRNA expression in EpCAM-positive CTCs could be a pivotal predictor for HCC metastasis before and after hepatectomy [75]. Similarly, Zheng et al. used an integrated immunomagnetic-microfluidic platform (iMAC), which demonstrated significantly higher sensitivity in detecting EpCAM + CTCs in the blood samples from HCC patients compared to the CellSearch system [76].

RT-PCR-based platforms have proven to be sensitive, rapid, and cost-effective for identifying CTCs [77–79]. Guo et al. developed a CTC detection platform using negative enrichment and quantitative real-time PCR (qRT-PCR). This platform exhibited high specificity and sensitivity for detecting EpCAM^{mRNA+} CTCs in small blood samples. Their study revealed that pre-treatment EpCAM^{mRNA+} CTCs significantly correlated with higher recurrence rates or worse PFS.

Notably, EpCAM^{mRNA+} CTCs also showed diagnostic value in HCC subgroups with AFP < 20 ng/ml and early-stage HCC [80]. Kocheise et al. also detected CTCs by negative enrichment and qRT-PCR-based CTC detection platform and found that combining EpCAM + CTCs with serum AFP levels improved the identification of HCC patients with poor outcomes after surgical resection [81]. Zhou et al. found that elevated EpCAM^{mRNA+} CTCs and Treg/CD4 + cell levels were associated with postoperative HCC recurrence, suggesting that combined detection of these biomarkers could enhance prognostic accuracy [82].

EpCAM expression is heterogenous and can be absent in certain tumor stages or altered phenotypes, especially during EMT. This limitation can result in undetected CTCs and lead to inaccurate results [65, 83–87]. To address this issue, researchers have investigated combining EpCAM with other biomarkers to improve the sensitivity in HCC. For example, Huang et al. used EpCAM/vimentin/Glypican-3(GPC3) antibody-modified lipid magnetic spheres (LMS) to detect CTCs with epithelial, mesenchymal, and GPC3 phenotypes. This system demonstrated high capture efficiency, low toxicity, high sensitivity and strong specificity [88]. Wu et al. created a dual-targeting functionalized reduced graphene oxide (rGO) film (DTFGF) for HCC CTC detection. By simultaneously targeting EpCAM and HCC cell-specific asialoglycoprotein receptor (ASGPR) to capture and enumerate CTCs in one operation step, the system achieved outstanding selectivity and sensitivity in a single-operation step [89]. An imaging flow cytometry method that incorporates multiple biomarkers, including immunofluorescence of cytokeratin, EpCAM, AFP, glypican-3 and DNA-PK, along with size, morphology, and DNA content analyses, has also enhanced CTC detection sensitivity in HCC [90]. Using the Amnis ImageStreamX Mark II flow cytometer, Debnath et al. employed a biomarker panel (EpCAM, CK, and AFP) that demonstrated strong performance in detecting CTCs in early-stage and AFP-negative HCC patients with high sensitivity and specificity [91]. Xia et al. designed a novel strategy involving Fe₃O₄ magnetic nanobeads co-assembled with EpCAM antibodies and a tumor cell-specific enzyme, aminopeptidase N (APN). This strategy significantly improved the efficacy of CTC capture while maintaining cell viability [92].

5.2 EpCAM-based EVs detection

Extracellular vesicles (EVs) are cell-derived membranous structures present in biological fluids that facilitate intercellular communication by enabling the exchange of proteins, lipids, and genetic material between cells. This exchange enables EVs to play crucial roles in various physiological and pathological processes [93]. Tumor-secreted EVs are vital mediators of cell-to-cell communications between tumor cells and stromal cells in local and distant microenvironments [94]. EpCAM has been used as a marker of EVs isolation in many tumors [95–98]. However, Similar to tumor cells, tumor-derived EVs are also highly heterogeneous, necessitating the integration of multiple surface markers to enhance the sensitivity and specificity of EVs detection. Julich-Haertel et al. identified AnnexinV + EPCAM + CD147 + tumour-associated microparticles (taMPs), a class of large EVs, as being significantly elevated in HCC. Their study demonstrated that AnnexinV + EpCAM + ASGPR1 + CD133 + taMPs can differentiate HCC from chronic liver disease without liver tumors, suggesting high HCC using this biomarker combination [99]. Similarly, Sun et al. reported that EpCAM + CD63 + HCC EVs are strongly associated with HCC diagnosis. They developed a logistic regression model, named HCC EV ECG score, calculated from the readouts of three HCC EV subpopulations: EpCAM + CD63 +, CD147 + CD63 +, and GPC3 + CD63 + HCC EVs. This model shows significant potential for the early detection of HCC [100].

6 Therapeutic strategies targeting EpCAM in HCC

EpCAM is a key cancer biomarker in primary tumor cells, CTCs, CSCs, and recurrent tumor cells, making it an attractive target for antitumor strategies. Numerous promising anti-tumor strategies targeting EpCAM are widely studied [101–103]. Zhou et al. developed an EpCAM-specific aptamer (EpCAM-apt) for drug delivery in HCC. They conjugated EpCAM-apt with doxorubicin (Dox) to create EpCAM-apt-Dox, which selectively delivered Dox to EpCAM + HCC cells. This approach achieved high drug retention and significant therapeutic effects in HCC organoid xenograft models, extending survival without adverse side effects on major organs [104]. Mitoxantrone (MX), an antitumor drug and photosensitizer, has been integrated into anti-EpCAM antibody-grafted micelle for dual-modality magnetic resonance/upconversion luminescence (MR/UCL)-guided synergetic chemotherapy and photodynamic therapy (PDT). These micelles demonstrated good biocompatibility, high specificity to HCC cells, and effective synergetic antitumor efficacy [105]. Xue et al. developed a nanocomplex comprising 5'-deoxy-5-fluorouridine(5'-DFUR), an EpCAM aptamer, and plasmid DNAs encoding miR-122 through hydrogen bonding. These nanocomplexes specifically targeted EpCAM + HCC cells, releasing 5-FU and

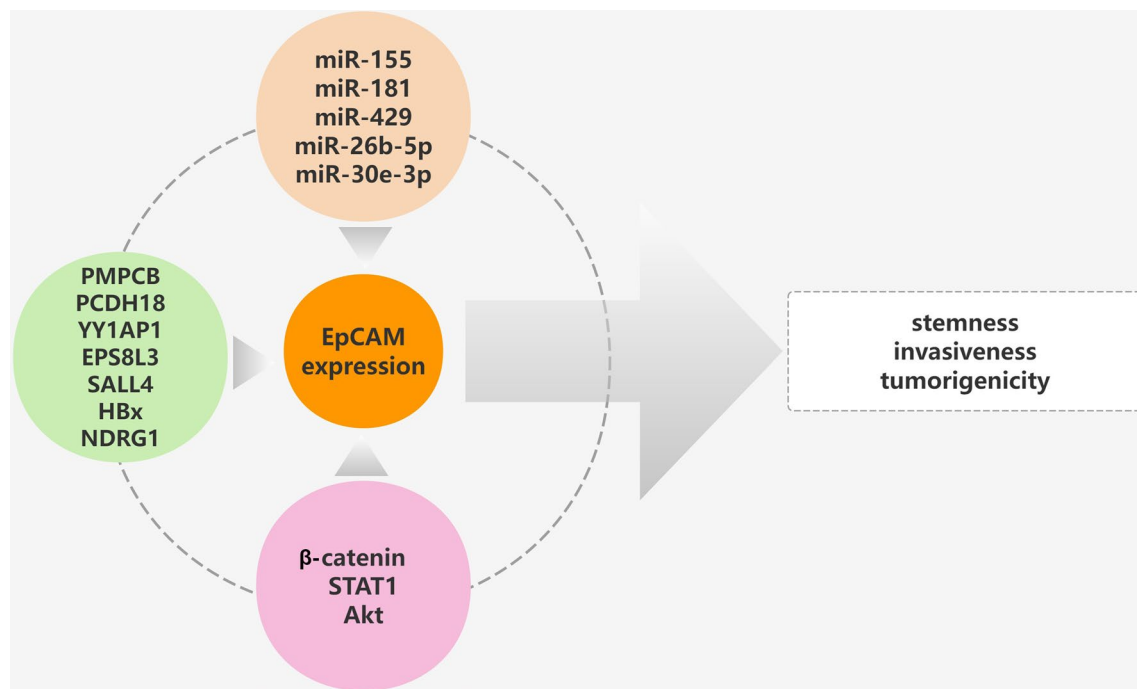


Fig. 1 The molecular mechanism that regulates the expression of EpCAM in HCC

miR-122 into tumor cells and exhibiting potent antitumor effects [106]. Chen et al. synthesized biological porous nanospheres using RNA as a building block and cyclodextrin as an adhesive. These nanospheres delivered EpCAM siRNA and sorafenib to EpCAM + HCC cells, where cytoplasmic degradation by Dicer enzymes released their therapeutic payloads for synergistic therapy [107]. Using RNA nanotechnology, Ishiguro et al. engineered nanoparticles decorated with RNA aptamers against EpCAM. These nanoparticles delivered siRNA targeting β -catenin to EpCAM + liver CSCs, resulting in β -catenin downregulation and effective HCC treatment [108]. Huang et al. developed multicomponent and multifunctional nanoparticles (ICG-CuS-Gd@BSA-EpCAM) for high-sensitivity optical molecular imaging to achieve the purpose of high-sensitivity, noninvasiveness, and high-efficiency photothermal therapy, offering a non-invasive and efficient method for early HCC detection and treatment [109].

Immunotherapies targeting EpCAM have emerged in recent years as promising strategies for anticancer treatments, including vaccines against EpCAM [110, 111], EpCAM-targeting CAR-T cell [112, 113] and anti-EpCAM [114, 115]. VB4-845 (Opportuzumab monatox), a conjugated recombinant antibody and immunotoxin targeting EpCAM, has demonstrated antitumor effects [116, 117]. Ogawa et al. showed that VB4-845 suppressed HCC CSC properties and tumor growth when combined with 5-FU in subcutaneous and orthotopic liver xenograft models [118]. Choi et al. showed that activating dendritic cells (DCs) with EpCAM peptides enhanced T cell stimulation, leading to HCC cell cytotoxicity and tumor growth suppression [119]. An anti-EpCAM BiTE (bispecific T cell engager), 1H8/CD3, has been constructed and was shown to eradicate HCC cells as well as CSCs of HCC in vitro and in vivo [120]. These preclinical studies suggest that EpCAM-targeted therapy may offer a promising approach for the treatment of HCC, but there is still a long way to go before it can be clinically applied.

7 Conclusion

EpCAM is overexpressed on the cell surface of many cancers, including HCC, where it plays diverse roles in cancer progression, such as proliferation, CSC stemness, invasiveness, and therapy resistance (Fig. 1). Its expression pattern in HCC lesions holds significant potential for prognostic evaluation. EpCAM has received considerable attention in liquid biopsy applications, including the detection and isolation of CTCs and EVs from the blood of patients with HCC. However, some CTCs and EVs have low or negative EpCAM levels, necessitating the integration of additional markers to improve

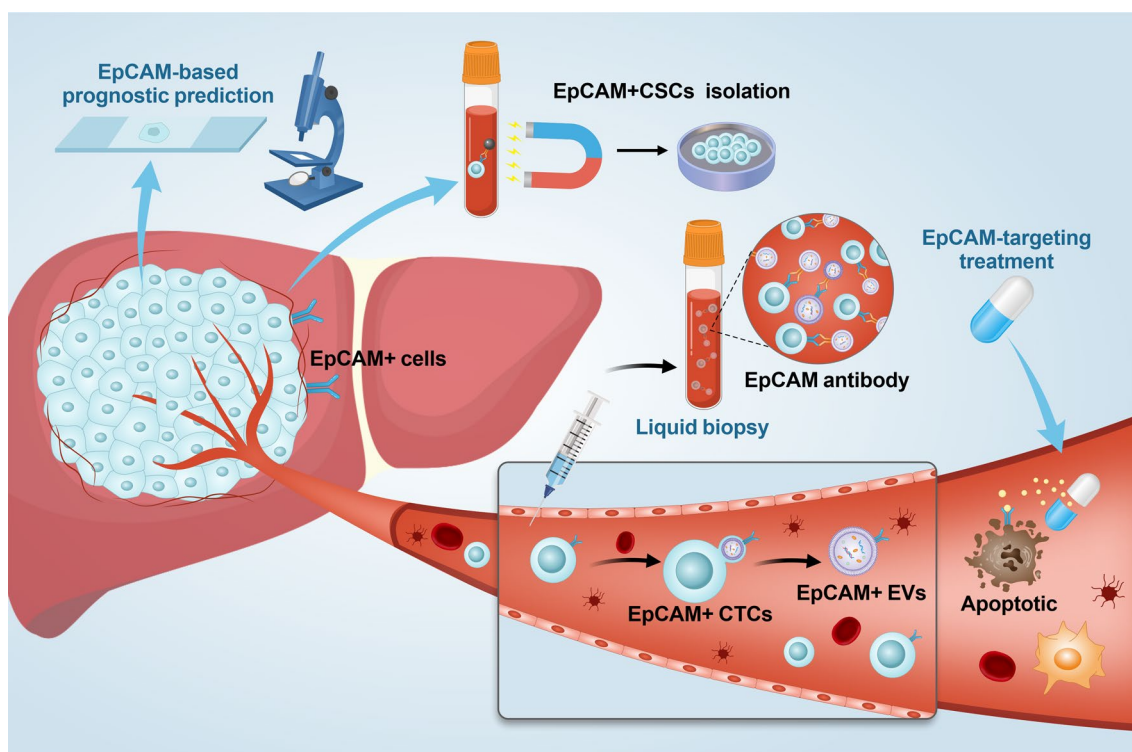


Fig. 2 Applications of EpCAM in HCC. The expression pattern of EpCAM in HCC lesions holds significant potential for prognostic evaluation. EpCAM has received considerable attention in liquid biopsy applications, including the detection and isolation of CTCs and EVs from the blood of patients with HCC. Given its consistent expression in tumor-initiating cells and CTCs, EpCAM remains a promising therapeutic target for HCC

detection efficiency and sensitivity. Given its frequent expression in CSCs and CTCs, EpCAM remains a promising therapeutic target for HCC (Fig. 2). While preclinical studies highlight its potential, clinical application faces challenges due to tumor heterogeneity. Further research and development are needed to realize the full therapeutic potential of EpCAM-targeted strategies.

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Data availability No datasets were generated or analysed during the current study.

Declarations

Consent for publication Not applicable.

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