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Exploiting gender-based biomarkers and drug targets: advancing personalized therapeutic strategies in hepatocellular carcinoma

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This review systematically examines gender differences in hepatocellular carcinoma (HCC), identifying the influence of sex hormones, genetic variance, and environmental factors on the disease's epidemiology and treatment outcomes. Recognizing the liver as a sexually dimorphic organ, we highlight how gender-specific risk factors, such as alcohol consumption and obesity, contribute differently to hepatocarcinogenesis in men and women. We explore molecular mechanisms, including the differential expression of androgen and estrogen receptors, which mediate diverse pathways in tumor biology such as cell proliferation, apoptosis, and DNA repair. Our analysis underscores the critical need for gender-specific research in liver cancer, from molecular studies to clinical trials, to improve diagnostic accuracy and therapeutic effectiveness. By incorporating a gender perspective into all facets of liver cancer research, we advocate for a more precise and personalized approach to cancer treatment that acknowledges gender as a significant factor in both the progression of HCC and its response to treatment. This review aims to foster a deeper understanding of the biological and molecular bases of gender differences in HCC and to promote the development of tailored interventions that enhance outcomes for all patients.

KEYWORDS

hepatocellular carcinoma, gender heterogeneity, gender-specific therapies, cancer immunotherapy, sex hormone, molecular pathways, drug targets, treatment strategies

1 Introduction

Globally, liver cancer constitutes the third-highest cancer mortality, with approximately 90% through Hepatocellular carcinoma (HCC) (Kuwanon et al., 2022). According to the GLOBOCAN 2020 database survey, it was estimated that about 9.5 and 8.7 ratios of age-standardized new cases and deaths in the world accounted for liver cancer, respectively, which has been increasing (Wei et al., 2014). Currently, the tumor has been treated with surgical resection, liver transplantation, chemotherapy, radiotherapy, and targeted therapies such as sorafenib (Jiang et al., 2019; Qi et al., 2020; Li et al., 2023a; Su et al.,

2023a; Zhang S. et al., 2023). While surgery and transplantation can be done in the early stage of the disease, however, most of the patients are diagnosed at a later age of the tumor, where the tumor has advanced and cannot be amenable to surgery and transplantation (Pan et al., 2014; Chaoul et al., 2020; Su et al., 2022a). Chemotherapy and radiotherapy treatments are characterized by systemic toxicity and side effects, but the so-called targeted treatment is emerging and in advanced stages, it is already very promising, although it still encounters the problem of drug resistance and a high relapse rate (Kamimura et al., 2020; Su et al., 2022b; Li et al., 2023b; Su et al., 2023b; Gao et al., 2023). This really highlights the urgent need for advances in early detection and more effective systemic therapies that are individualized and take into account patient differences at all levels, including gender (Chi et al., 2023; Grani et al., 2023).

The liver is highly sexually dimorphic, and a combination of hormonal, genetic, and environmental factors greatly influence the gender differences observed in hepatocarcinogenesis, treatment, and incidence (Marker et al., 2023; Huillet et al., 2024). For instance, the liver is very sensitive to sex hormones that include androgens and estrogens, and differences in molecular pathways have been noticed during the hepatocarcinogenesis phase, such as gene expression associated with the regulation of the cell cycle, apoptosis, and DNA repair (Singhal and Schlondorff, 1987; LoMauro and Aliverti, 2021). The liver is a tissue that bears additional sex-specific risk factors, one being alcohol consumption and obesity for the development of HCC. Some sex-specific risk factors, including alcohol intake, obesity, and insulin resistance, have been implicated in hepatocarcinogenesis, likely due to sex differences in alcohol metabolism and fat distribution impacting susceptibility to HCC (D'Souza et al., 2020; Izquierdo et al., 2022; Kardashian et al., 2023). That highlights the pressing need for a transition to a gender perspective in the entire flow of liver cancer research, from epidemiological inquiry to molecular analysis.

Here, we have presented a systematic review of several dimensions of the impact of gender differences on HCC, including the genetic background of the disease, pathogenesis, treatment response, and prognosis. The aim is to promote a more precise medical approach, leading to better outcomes for all patients with liver cancer (Nan et al., 2021).

2 Factors affecting gender differences in HCC

The proposed mechanisms for gender differences in HCC are thought to be complex and multifactorial (Pok et al., 2016). They are currently attributed to gender differences in environmental objective factors, behavioral risk factors, immune responses, metabolic risk factors, tumor biology and hormonal factors (Bashir Hamidu et al., 2021).

2.1 Environmental and lifestyle factors

Geographical differences in HCC and its etiology are clear; in general, they are due to the distribution of risk factors and different development between regions (Mousavi et al., 2013;

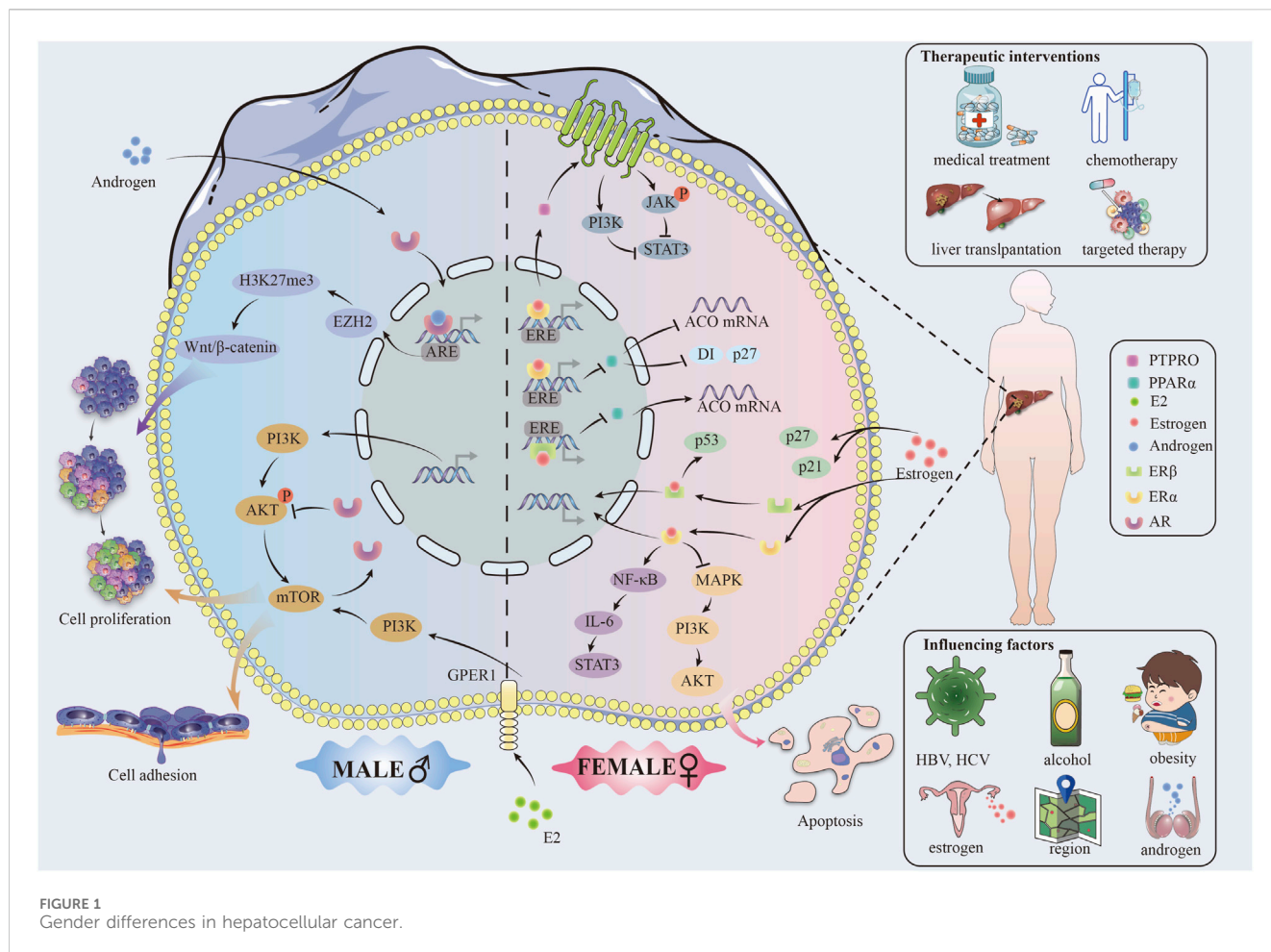
Yan et al., 2020; Enomoto et al., 2021). Indeed, the highest age-standardized incidence rates (ASRs) of HCC are estimated in East Asia, North Africa, and South-East Asia (Jiang et al., 2012; Okoronkwo et al., 2017). Sex differences are also reflected in the risk factors of HCC: Studies in recent years demonstrate that HBV and HCV are the major infectious agents associated with liver cancer (Zhang et al., 2020; Wang et al., 2021). The prevalence of HBV infection is greater among males than females (Poorolajal and Majdzadeh, 2009). However, the incidence of HCV is higher among females at 20.36 cases per 100 person-years than among males at 15.20 cases per 100 person-years (Puri et al., 2014). These days, the impact of viral hepatitis on liver cancer is waning, due to effective therapies (HBV, HCV) and vaccines (Nasr et al., 2023).

Non-viral causes (especially heavy consumption of alcohol) appear to have partially replaced the role of diseases caused virally in the case of HCC (Lee et al., 2021; Zhang J. et al., 2023). Effects of alcohol and its metabolites vary with age, race, and gender, with gender being marked mostly by differences. In terms of alcohol metabolism and in the context of heavy drinking, the relationship with HCC in women is stronger than in men, perhaps due to higher activities of alcohol dehydrogenases in women or a more prominent link of alcohol intake with cirrhosis risk in women (Bell et al., 2004; KASL, 2012). In meta-analyses, heavy drinking (≥ 4 drinks/day) was associated with about a fourfold risk for women but only about a 59% increase for men (McGlynn et al., 2021). However, a higher intake of alcohol by men is experienced than women (Milman and Kirchoff, 1996). Although heavy alcohol drinking has been established as one of the risk factors for liver cancer, most data indicated a weak negative association with light or moderate alcohol drinking and a reduced risk of HCC (Gao et al., 2020; Liu et al., 2022; Singh et al., 2023).

2.2 Inheritance and gene expression

Males and females present an active difference in gene expression. Figure 1 For example, studies have demonstrated that in male hepatocytes derived from individuals with HCC, the androgen receptor (AR) significantly enhances the expression of Enhancer of zeste homolog 2 (EZH2) at the transcriptional level. This enhancement facilitates an increase in the trimethylation level at lysine 27 of histone H3 (H3K27me3), effectively repressing the inhibitors of Wnt signaling pathways. This event activates Wnt/ β -cyclin signaling and promotes the proliferation and transformation of liver tumor cells (Tsang et al., 2016; Baliou et al., 2020). On the other hand, estrogen in females, acting through the ER α receptor, can upregulate the protein tyrosine phosphatase receptor type O (PTPRO), which serves as a wide spectrum of cancer types (HCC, colorectal carcinoma, etc.) tumor suppressor protein (Asbagh et al., 2014; Xu et al., 2014). α binds to the estrogen response element (ERE) of the PTPRO gene promoter, inducing dephosphorylation of Janus kinase 2 (JAK2) and phosphatidylinositol 3-kinase (PI3K), which in turn causes a decrease of the activity of the transcription factor STAT3, thus leading to inhibition of the HCC cell proliferation (Wu and Lou, 2023; Su et al., 2024).

Moreover, Era binds directly to the ERE of the peroxisome proliferator-activated receptor alpha (PPAR α) gene, which is a



nuclear receptor protein with the function of a transcription factor, crucial for the oxidative processes in the hepatocytes (Memaj et al., 2023). Together, they decrease transcription of the PPARα gene and further regulate PPARα target acyl-coenzyme A oxidase (ACO), cell cycle proteins D1 and P27, blocking the proliferation of cancer cells and promoting apoptosis (Meng and Liu, 2022).

ERβ can downregulate PPARα and its downstream genes through interaction with the EREs of the PPARα gene to inhibit HCC development (Meng and Liu, 2022). In addition, it is through the action of ERβ that the translocation of PPARα from the cytoplasm to the nucleus is prevented, and the transcription activity of PPARα consequently decreases. This hormone-receptor complex subsequently induces homodimerization or heterodimerization of ER, translocation to the nucleus, binding to EREs on promoters of target genes, and induction of genomic effects of gene activation and epigenetic changes (Krolick and Shi, 2022).

In order to gain a comprehensive understanding of the factors influencing sex differences, it is essential to consider the regulatory networks downstream of hormones, in addition to genetic factors and the direct role of sex hormones. Estrogens can indirectly bring about the expression of genes by interaction with specific transcription factors through non-genomic effects, which can influence signaling pathways for the development of HCC

(Mandalà, 2020). For example, ERα interacts with the repressor NF-κB by inhibiting the IL-6/STAT3 activation pathway (Meng and Liu, 2022).

2.3 Influence of sex hormone

Estrogen and androgen have a key role in the molecular mechanisms of HCC (Liu et al., 2020). Estrogen can block the production of IL-6, a pro-inflammatory tumor growth and metastasis-promoting factor, through the JAK/STAT signaling pathway. At the same time, estrogen decreases the expression of TNF-α, another pro-inflammatory cytokine able to activate cancer cells through the NF-κB signaling pathway (Miller, 2018). On the other side, androgens could further enhance the development of HCC through increased expression of the above pro-inflammatory cytokines, exaggerating the inflammatory response (Wu et al., 2015). Androgens also have been demonstrated to upregulate the proliferation of HCC cells by activating their receptor AR, which in turn promotes the expression of c-Myc, an important regulator of cell proliferation and survival (Bao et al., 2020; Cho et al., 2020; Cui et al., 2020; Zhu et al., 2020; Gao et al., 2021) (Supplementary Table S1).

3 Molecular mechanisms and gender differences in HCC

3.1 Mechanisms of proliferation, invasion and metastasis

In HCC, gender differences have profound effects on tumor cell proliferation, invasion, and metastasis, where mechanistic target of rapamycin (mTOR) signaling is associated with many features of cancer (Ferrín et al., 2020). (FIGURE) On the one hand, AR negatively regulates the feedback activation of AKT-mTOR signaling (Zhang et al., 2018). On the other hand, mTOR promotes the expression of nuclear AR protein by inhibiting ubiquitin-dependent AR degradation and enhancing its nuclear localization through enhancing the nuclear localization of AR, consequently mechanistically explaining AR overexpression in the nucleus of HCC cells (Zhang et al., 2018). AR overexpression was strongly associated with advanced tumor stage and low survival 29220539. Approximately a third of HCC tumors showed overexpressed nuclear AR protein in a series of 142 paired HCC tumors and their neighboring non-cancerous liver tissues (Zhang et al., 2018).

Furthermore, research has demonstrated that the estrogen receptor complex inhibits the mTOR signaling pathway, thereby impeding tumor growth (Ke et al., 2022). The activation of the PI3K-Akt (~70%) and mechanistic target of rapamycin complex 1 (mTORC1) (~45%) pathways was observed in HCC and demonstrated a positive correlation with tumor metastasis, recurrence and poor prognosis (Chaturantabut et al., 2019). A study using the HCC zebrafish model suggested that G protein-coupled estrogen receptor 1 (GPER1) could be a factor in the progress of hepatocarcinogenesis by inducing proliferation of hepatocytes and regulating organ growth via GPER1-PI3K-mTOR signaling transduction (Wojnarowski et al., 2022). E2-The pro-proliferative consequences of PI3K-mTOR signaling activation by GPER1 and the strong response to the presence of GPER1 antagonist therapy during cancer development and progression, as evidenced by *in vivo* human data (Ferrín et al., 2020; Tian et al., 2023). All these experimental results point to the fact that drugs targeted at E2-GPER1 should offer a new promising application for therapeutic use in liver cancer prevention and treatment (Chaturantabut et al., 2019).

Activation of the PI3K/AKT signaling pathway promotes hepatocyte proliferation and increases the capability of epithelial mesenchymal transition (EMT) through increasing HCC cell growth, migration, and invasion (Cantile et al., 2019). AR upregulates integrin β 1 expression through the PI3K/AKT/mTOR signal pathway, consequently, increasing in cellular adhesion, which could be a potential characteristic of advanced hepatocellular cancer with high metastasis (Carlos-Reyes et al., 2021). However, it was found that mice lacking hepatic AR developed more undifferentiated tumors and larger tumor sizes at the late metastatic stage compared to mouse models expressing AR, and these mice also died earlier due to increased lung metastasis. This suggests that hepatic AR may play a dual but opposing role in promoting HCC development and inhibiting HCC metastasis (Ma et al., 2012; Wen et al., 2014).

Studies have indicated that there should be gender specificity of p53 gene mutations in the development process of HCC (Shi et al., 1995). In addition, mutations in p53, a key oncogene for cell cycle regulation and apoptosis, were seen to hasten tumor progression (Chuery et al., 2017). Men suffering from liver cancer were more

associated with the frequency of p53 mutations than women (Finch and Tower, 2014). Besides, p53 is a vital regulator for the cellular response to DNA damage (Li and Wong, 2018). The ER β complex in estrogen (ER β) partially contributes to the stabilization and activation of p53 in HCC cells, thus prohibiting the delivery of damaged DNA through aberrant cell cycle arrest and apoptosis.

3.2 Cell cycle regulation and apoptosis

Sex differences exert their influence on cell cycle regulation through the alteration of key regulatory proteins such as cyclins, cyclin-dependent kinases (CDKs), and CDK inhibitors, including p21 and p27 (Lim and Kaldis, 2013). (FIGURE) Estrogens can upregulate the expression of p21 and p27, which will lead to cell arrest in phase G1 by stopping the activity of CDK, blocking the tumor cell cycle (Eto, 2010; Madhu Krishna et al., 2018). On the other hand, androgens downregulate the expression of these inhibitory proteins, thereby bringing the cell cycle on and causing tumor proliferation (Yu et al., 2017).

Apoptosis is programmed cell death, a process that assumes huge importance as a self-regulatory mechanism in the organism (Li et al., 2019). The identified Bcl-2 family proteins to date have an anti-apoptotic function, for example, Bcl-2, and pro-apoptotic action, for example, Bax (Chen et al., 2016). Estrogens will increase the expression of pro-apoptotic proteins, including Bax, to promote programmed cell death in damaged cells, whereas androgens may support the intensification of survival signaling, for example, by increasing the expression of Bcl-2 proteins that inhibit apoptosis (Arunkumar et al., 2012; Herson et al., 2013; Sanaei et al., 2022).

4 Medical treatment in HCC

Studies carried out in the tumor microenvironment (TME), immune response, Liver Transplant (LT) acceptance rate, and hormone therapy have alluded to a significant effect of gender differences on the outcomes of cancer treatment and survival. This fact propounds that future treatment strategies can incorporate gender-specific immune response and hormone modulation for more precise and effective anti-cancer strategies.

Sexual dimorphism exists in the immune response (Rehman and Masson, 2005; Wu et al., 2009; Mitchell et al., 2020). Women generate both adaptive and innate immunity responses much stronger than men, but at the same time, they suffer from systemic autoimmune diseases much more highly than men (Murgia et al., 2022; Zhang et al., 2022). In the case of non-small cell lung cancer (NSCLC) at an early stage, males present with a cold TME in which there is a defect in T-cell rejection. Contrary to that, female patients have a hotter TME, greater infiltration of dendritic cells (DCs), CD8 T cells and CD4 T cells, and greater upregulation of immune checkpoint molecules in T cells (Conforti et al., 2021).

In advanced HCC, liver transplantation is the standard treatment for end-stage liver disease (ESLD) (Hill et al., 2023). Studies have shown that women are less likely than men to receive LT because the hypothesis responsible for the gender-based variation in radical treatment is limited by the ability of Model for End-Stage Liver Disease (MELD) scores based on cr measurements in females (Mindikoglu et al., 2013; Karnam et al., 2021). In one study, females

received 1–2.4 fewer cr-derived MELD scores compared to males with similar renal function (Allen et al., 2018). However, researchers came up with a new multivariate model, MELD 3.0, meant to account for the factor of gender difference on waiting lists (Kim et al., 2021).

Sex differences in treatments that antagonize sex hormones and sex hormone receptors. Anti-ER therapy was found to promote tumor development in a mouse model, however, several studies have demonstrated that anti-AR therapy inhibits liver tumorigenesis (Ahotupa et al., 1994; Williams et al., 1997; Ma et al., 2012; Tang et al., 2021). Anti-hormonal therapy primarily disrupts the interaction between hormones and hormone receptors, thereby modulating downstream targets. However, the effect of anti-hormone therapy on HCC has been controversial. Very few clinical studies or randomized control trials demonstrate increased survival or survival in patients with advanced HCC. Most of the studies concluded that patients with HCC do not benefit from antihormonal drug therapy, mainly from side effects from the drugs and variability of the estrogen receptor. Survival outcomes in patients with HCC are affected by gender differences (Farinati et al., 1990; Martínez Cerezo et al., 1994; Grimaldi et al., 1998; Li Z. et al., 2023).

Gender differences affect survival outcomes in patients with HCC. HBV-infected male patients have an increased incidence of HCC compared to women, while men have higher serum HBV DNA titres. These data suggest that the overall survival among men is significantly shortened in comparison to women among patients with HCC (Chen et al., 2009; Sayaf et al., 2022). Female HBV patients have a decreased risk for HCC and improved survival with hormone replacement therapy (HRT) (Hassan et al., 2017; Wang et al., 2022). Ten thousand four hundred seventy-four women in the cohort study were postmenopausal and infected with HBV. Incidence rate in the HRT group of HCC and all-cause mortality of the HRT group decreased, compared with those in the no HRT group. Indeed, parallel research has concluded that an association exists between HRT and reduced HCC risk and better survival outcomes (Wang et al., 2022).

5 Discussion

The liver is a highly sexually dimorphic organ, possessing at least 72% of sexually differentiated genes (Yang et al., 2006). Sex hormones play a central role in gender preference in HCC, and thus multiple anti-sex hormone therapies or anti-sex hormone receptor therapies have been tried. Tamoxifen (TMX) therapy and hormone replacement therapy (HRT) are the two core regimens for hormone therapy in HCC (Meng and Liu, 2022). Although the efficacy of TMX in HCC remains controversial, there are still relevant studies reporting a positive relationship between the cancer inhibitory effect of TMX and ER α expression levels. In the work of Villa et al., 50 HCC patients were differentiated by wild-type ER α and ER α mRNA variant lacking exon 5 (ER Δ 5) phenotypes and the therapeutic efficacy of TMX was confirmed in patients with wild-type phenotype (Villa et al., 1996). Thereby the use of hormone therapy may largely dependent on the classification of ER α and screen or amplification of HCC patients with higher ER α expression may be beneficial to improve the sensitivity of hormone therapy. The effectiveness of estrogen replacement therapy in HCC has been demonstrated to some extent, however, estrogen may increase the risk of breast, ovarian and endometrial cancer in female patients and may have an unfavorable effects (American Medical Association, 2002; Meng and Liu, 2022; Wang et al., 2022). Exploring HCC hormone

therapy in combination with first-line drugs may be an option to improve efficacy.

AR is a crucial player in male dominant hepatocarcinogenesis. On one hand, abundant evidence shows that androgens exert tumor-promoting effects. On the other hand, AR blockade has been proved to do little benefit for HCC patients. It may be a fact that differences in sex hormone profiles are important not only in the initiation but also at the different stages of hepatocarcinogenesis, for example, the anti-tumor functions of AR in metastatic HCC (Ma et al., 2012). In addition, AR overexpression might also be used as an independent factor to predict the prognosis of patients with HCC. However, a portion of HCC was detected with the expression of C-terminal truncated AR-SVs. AR-SVs have been identified to play an important role in the acquired resistance to AR inhibitors (Dauki et al., 2020; Qiao et al., 2021; Katleba et al., 2023). Therefore, we imply that AR-SVs might also be involved in the occurrence of acquired resistance to AR inhibitors in HCC.

Author contributions

LS: Data curation, Writing–original draft. HL: Conceptualization, Data curation, Writing–original draft. YY: Writing–original draft. ZY: Writing–original draft. JLu: Writing–original draft. DX: Writing–original draft. LD: Writing–original draft. JLi: Writing–original draft, Writing–review and editing. GY: Writing–original draft, Writing–review and editing. HC: Conceptualization, Writing–original draft, Writing–review and editing.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fphar.2024.1433540/full#supplementary-material>

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