

Hepatocellular carcinoma

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Abstract | Liver cancer is the second leading cause of cancer-related deaths globally and has an incidence of approximately 850,000 new cases per year. Hepatocellular carcinoma (HCC) represents approximately 90% of all cases of primary liver cancer. The main risk factors for developing HCC are well known and include hepatitis B and C virus infection, alcohol intake and ingestion of the fungal metabolite aflatoxin B1. Additional risk factors such as non-alcoholic steatohepatitis are also emerging. Advances in the understanding of the molecular pathogenesis of HCC have led to identification of critical driver mutations; however, the most prevalent of these are not yet druggable targets. The molecular classification of HCC is not established, and the Barcelona Clinic Liver Cancer staging classification is the main clinical algorithm for the stratification of patients according to prognosis and treatment allocation. Surveillance programmes enable the detection of early-stage tumours that are amenable to curative therapies — resection, liver transplantation or local ablation. At more developed stages, only chemoembolization (for intermediate HCC) and sorafenib (for advanced HCC) have shown survival benefits. There are major unmet needs in HCC management that might be addressed through the discovery of new therapies and their combinations for use in the adjuvant setting and for intermediate- and advanced-stage disease. Moreover, biomarkers for therapy stratification, patient-tailored strategies targeting driver mutations and/or activating signalling cascades, and validated measurements of quality of life are needed. Recent failures in the testing of systemic drugs for intermediate and advanced stages have indicated a need to refine trial designs and to define novel approaches.

Liver cancer is a major health problem, with more than 850,000 new cases annually worldwide¹. This neoplasm is currently the second leading cause of cancer-related death globally, a figure that is on the rise². Among all primary liver cancers, hepatocellular carcinoma (HCC) is the most common neoplasm, accounting for approximately 90% of cases^{1,3-12}. Various risk factors for HCC development are well defined, such as cirrhosis (chronic liver damage caused by inflammation and fibrosis), hepatitis B virus (HBV) infection, hepatitis C virus (HCV) infection, alcohol abuse and metabolic syndrome³. Other cofactors such as tobacco smoke inhalation and intake of aflatoxin B1 (a fungal carcinogen present in food supplies associated with mutations in the tumour suppressor gene *TP53*) are well-characterized contributors to HCC^{1,3-10} (FIG. 1). Recent discoveries have pointed to infection with adeno-associated virus 2 (AAV2) as a novel cause of the disease, particularly in individuals without cirrhosis¹³. Primary prevention of HCC through HBV vaccination has been demonstrated. Similarly, in patients with chronic infection, effective antiviral therapies against HBV and HCV that produce

sustained virological responses are associated with a decrease in HCC incidence. Guidelines recommend surveillance using ultrasonography every 6 months in at-risk populations.

Over the past decade, there has been an improvement in the understanding of the molecular pathogenesis of HCC¹⁴. Genomic analyses have provided a clear picture of the main drivers responsible for tumour initiation and progression. Each HCC has an average of 40 genomic aberrations, among which few are considered drivers. Common mutations affect telomere maintenance (mutations in telomere reverse transcriptase (*TERT*)), WNT pathway activation (mutations in β -catenin (encoded by *CTNNB1*)) and inactivation of cellular tumour antigen p53 (*TP53*). Common mutations also affect chromatin remodelling (mutations in AT-rich interaction domain 1A (*ARID1A*)), RAS signalling, mammalian target of rapamycin (mTOR) signalling and oxidative stress pathway activation. Only a handful of these drivers are currently druggable targets, such as amplification of fibroblast growth factor 19 (*FGF19*).

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In contrast to classification of the majority of neoplasms, classification of HCC is not based on the TNM system but on the Barcelona Clinic Liver Cancer (BCLC) staging classification, which is endorsed by European and American clinical practice guidelines^{3,15,16}. This staging system defines five prognostic subclasses and allocates specific treatments for each stage. Five treatments can extend the life expectancy of patients with HCC: surgical resection, liver transplantation, radiofrequency ablation, chemoembolization and the multikinase inhibitor sorafenib³. Approximately 40% of patients (early stages 0 and A) are eligible for potentially curative therapies: resection, transplantation or local ablation. Such treatments can provide median survival rates of 60 months and beyond, which is in contrast to a historical natural history survival of 36 months. For patients with more advanced disease, only two treatments have demonstrated survival advantages in the setting of randomized controlled trials (RCTs). Patients at intermediate stage (stage B) with preserved liver function benefit from chemoembolization^{17,18} and have an estimated median survival of 26 months. Patients at advanced stage (stage C) benefit from systemic sorafenib, which extends survival by approximately 3 months (from 8 to 11 months) and represents the standard of care in this setting¹⁹. Recently, several studies have tested therapies in the adjuvant setting, in combination or as alternatives to chemoembolization, and as alternative systemic first-line and second-line treatments.

This Primer provides an overview and updated summary of the current knowledge on the epidemiology, pathogenesis and treatment of HCC. We describe current prevention strategies, evidence-based standards of care and novel therapies emerging in light of the understanding of the pathogenesis of HCC, such as proof-of-concept studies and immunotherapy.

Epidemiology

Worldwide, liver cancer is the sixth most common cancer (approximately 850,000 new cases each year) and the second leading cause of cancer-related deaths (approximately 800,000 per year)^{1,3–10} (FIG. 1). HCC constitutes 85–90% of all primary liver cancers. In contrast to other human malignancies, the risk factors for HCC are well established. Indeed, HCC is common in patients with advanced hepatic fibrosis or cirrhosis due to chronic liver disease, and in particular with liver damage caused by HBV or HCV infection and unhealthy alcohol use.

The worldwide incidence of HCC parallels that of chronic viral hepatitis. HBV is a DNA virus that can cause insertional mutagenesis. In the context of chronic HBV infection, HCC usually occurs on a background of cirrhosis (up to 85% in selected studies)²⁰. Moreover, in patients with chronic HCV infection, which is caused by an RNA virus, HCC rarely occurs in the absence of advanced hepatic fibrosis or cirrhosis²¹. The highest incidence rates of HCC are in Asia and Sub-Saharan Africa, owing to the high prevalence of HBV infection¹ (FIG. 2). In Africa, aflatoxin B1 appears to be synergistic with HBV in causing HCC²². This synergy is a likely explanation for the earlier onset of HCC in this continent compared with the rest of the world. In North America, Europe and Japan, HCV is the leading cause of HCC. Other causes of cirrhosis associated with HCC include unhealthy alcohol use, non-alcoholic steatohepatitis (NASH), α 1-antitrypsin deficiency and haemochromatosis²³. By contrast, HCC is less common in cirrhosis that is caused by autoimmune hepatitis, Wilson disease and cholestatic liver disorders.

Together with viral hepatitis and cirrhosis, other factors can contribute to disease risk. HCC has a strong gender predilection, being threefold more common in men than women^{1,24} (FIG. 2). Most patients with HCC are \geq 45 years of age, except in Sub-Saharan Africa, given the latency between the onset of virus-mediated liver inflammation and the development of cirrhosis. Unidentified host, viral and environmental interactions are likely to be responsible for the lower age of onset in Africa. The association between tobacco use and HCC, even in the presence of HBV or HCV, has been inconsistent. An emerging cause of HCC is the metabolic syndrome due to diabetes and obesity, and the associated liver disease non-alcoholic fatty liver disease (NAFLD) and NASH²⁵. NAFLD or NASH might be — together with chronic HBV infection — the exception to the rule that HCC is always associated with advanced hepatic fibrosis or cirrhosis. A recent study that needs careful verification suggests that approximately 40% of patients with HCC and NAFLD or NASH might not have cirrhosis²⁵.

As discussed in greater detail below, HCC is one of the cancers for which prevention is possible. HBV vaccination has been shown to reduce the incidence of HCC in populations with a high prevalence of HBV²⁶. Antiviral therapy for HBV with nucleotide and nucleoside analogues reduces, but does not eliminate, the risk of HCC in treated cohorts of patients²⁷. Similarly, antiviral therapy with interferon might reduce the risk

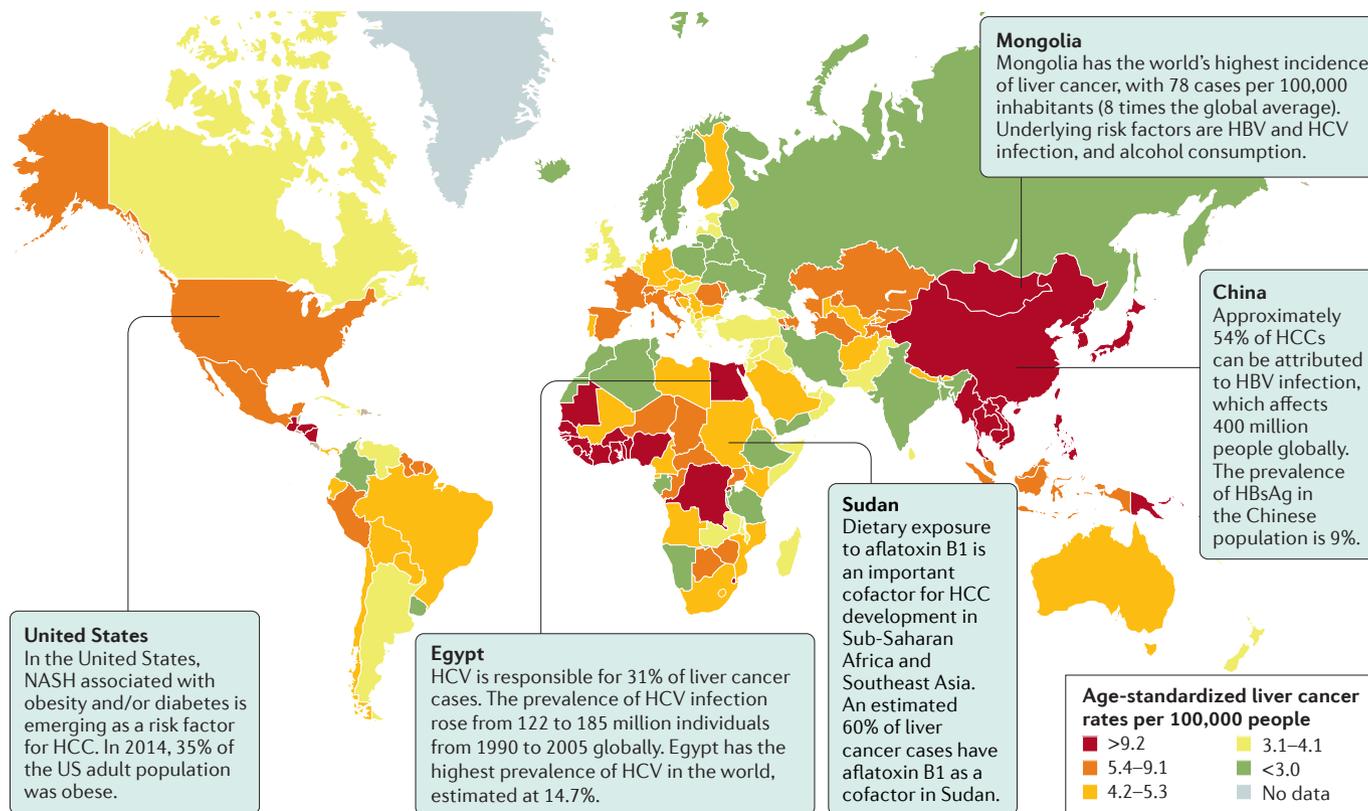


Figure 1 | **The global burden of HCC.** The incidence of hepatocellular carcinoma (HCC) is shown. The main risk factors for HCC development are hepatitis C virus (HCV) infection (for example, Egypt), hepatitis B virus (HBV) infection (China), alcohol intake, non-alcoholic steatohepatitis (NASH; United States) and aflatoxin B1 ingestion (Sudan). Mongolia has the highest incidence of HCC globally. HBsAg, hepatitis B surface antigen. Data from Globocan 2012 (REFS 1, 3–9). Adapted from REF. 10, Nature Publishing Group.

of HCC in patients with HCV infection that is associated with chronic liver disease²⁸; however, this effect will need to be reassessed with non-interferon-based direct-acting antiviral (DAA) drugs that are now approved for clinical practice. Finally, statin use and coffee consumption are associated with a reduced risk of HCC in population studies²⁹. In the future, potent liver-directed antifibrotic therapies might also reduce the risk of developing HCC.

Mechanisms/pathophysiology Molecular alterations and drivers

Early molecular alterations during hepatocarcinogenesis. HCC development is a complex multistep process that usually occurs in the context of liver cirrhosis and is related to the diversity of aetiologies of the underlying liver disease. The natural history of HCC in cirrhosis follows a sequence of events starting with the successive development of pre-cancerous cirrhotic nodules with low-grade dysplasia, called low-grade dysplastic nodules (LGDNs). LGDNs subsequently develop into high-grade dysplastic nodules (HGDNs) that can transform into early-stage HCC (stages 0 and A) and progress into more advanced HCC (stages B and C). Malignant transformation into HCC can originate from various cell types, including mature hepatocytes and stem or progenitor cells³⁰.

Similar to other epithelial solid tumours, HCC is the result of the accumulation of somatic genomic alterations in passenger and driver cancer genes. As previously defined³¹, a cancer driver would be a cell-autonomous or non-cell-autonomous alteration that contributes to tumour evolution at any stage — including initiation, progression, metastasis and resistance to therapy — by promoting various functions, including proliferation, survival, invasion or immune evasion. In each HCC nodule, a mean number of 40 functional somatic alterations are accumulated in coding regions; consequently, each tumour is the result of a unique combination of genetic alterations mixed with epigenetic modifications^{32,33}. This general observation underlines the complexity of hepatocarcinogenesis and the huge diversity of HCC^{33–38} (FIG. 3; TABLE 1). However, genomic alterations are not randomly accumulated, suggesting that several pathways can cooperate to promote oncogenesis and that some of these pathways can be related to specific risk factors³³.

Molecular markers that were identified in order to discriminate early-stage HCC from the pre-cancerous nodules (LGDNs and HGDNs) have provided some clues about the early steps of carcinogenesis that occurs in the context of cirrhosis^{39–43}. On the basis of these markers, the mechanism of hepatocyte malignant transformation has been shown to include WNT- β -catenin

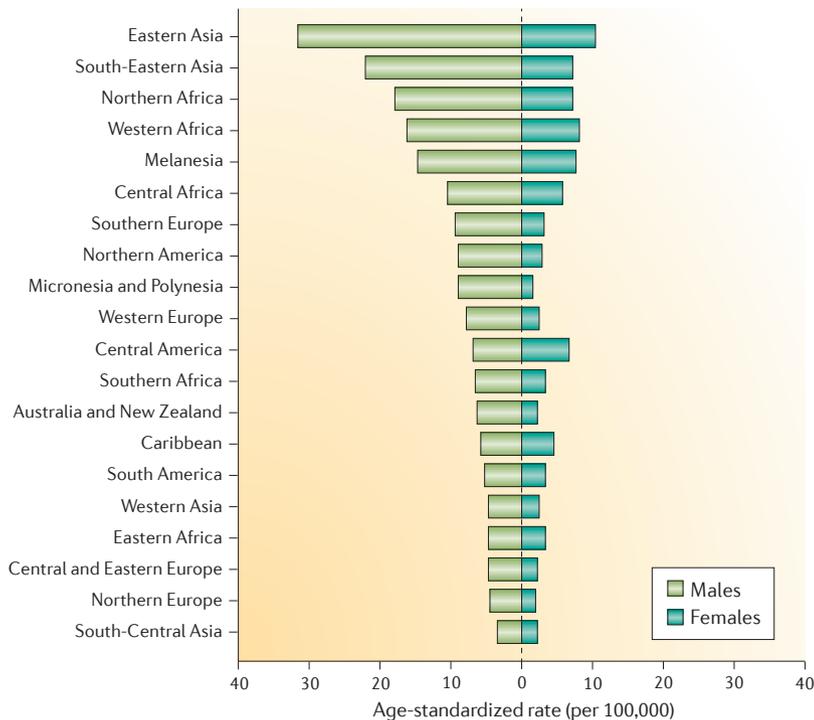


Figure 2 | **Liver cancer incidence according to region and sex.** The age-standardized incidence rate per 100,000 inhabitants is shown. Adapted with permission from REF. 1, Wiley.

pathway activation, re-expression of fetal genes, deregulation of protein-folding machinery and the response to oxidative stress. Moreover, several lines of evidence have shown that telomere maintenance and the telomerase complex that controls the nucleotide TTAGGG, a repeated sequence at the end of chromosomes, play a major part in the initiation and promotion of HCC in cirrhosis^{44,45}. First, mice deficient in telomerase RNA component (*Terc*), which encodes the catalytic unit of the telomerase complex, exhibited short telomeres and developed cirrhosis followed by HCC⁴⁶. Second, constitutive inactivating mutations in *TERT*, which encodes the telomerase reverse transcriptase, are associated with an increased risk of cirrhosis in humans^{47–49}. However, progression to HCC involves a second step, with telomerase reactivation required to promote liver carcinogenesis and to allow uncontrolled hepatocyte proliferation (the ‘telomerase switch’)^{46,50}. In humans, *TERT* is not expressed in normal hepatocytes, but becomes re-expressed early during hepatocarcinogenesis in LGDNs and particularly HGDNs^{42,51}. In these lesions, telomerase re-expression is related to the occurrence of point mutations at two hotspots in the *TERT* promoter. These alterations are the most frequently recurrent somatic mutations identified in LGDNs (6%), HGDNs (20%) and HCC (60%)^{33–38} (FIG. 3). Together, these results suggest that *TERT* promoter mutations are oncogenic and, in most cases of HCC (>90%), telomerase activation is selected during malignant transformation and tumour progression in cirrhotic and non-cirrhotic livers^{34,37}. Within this paradigm, *TERT* promoter activation is required at an early step of transformation to bypass the replicative

senescence of cirrhotic hepatocytes. By contrast, acquisition of genomic diversity appears to be a late event in liver carcinogenesis¹⁴.

HCV and HBV infections are also associated with early molecular alterations involved in malignant transformation through the induction of chronic inflammation, the expression of viral proteins and the viral life cycle^{52,53} (FIG. 3). Specific molecular alterations are frequently related to HBV infection, which can induce mutagenesis by inserting viral DNA into major driver genes of hepatocarcinogenesis⁵⁴. The most frequent insertions of HBV DNA in hepatocytes occur within the *TERT* promoter and activate telomerase and other oncogenes, including lysine (K)-specific methyltransferase 2B (*KMT2B*; also known as *MLL4*), cyclin E1 (*CCNE1*) and SUMO1/sentrin-specific peptidase 5 (*SENP5*)⁵⁵. In cooperation with HBV infection, exposure to aflatoxin B1, which is common in subtropical regions, induces DNA adducts and the occurrence of frequent mutations, in particular within *TP53*, that have a specific nucleotide signature^{22,33}. Recently, deep sequencing analysis revealed another DNA virus — AAV2 — that is related to a frequent harmless infection in the general population and causes insertional mutagenesis in rare cases of HCC¹³. AAV2 insertions were mainly identified in HCC that had developed in normal liver tissues and without other classical risk factors. Viral insertions are found randomly inserted in the genome of normal hepatocytes, whereas in cancerous cells, insertions normally occur within typical oncogenes such as *TERT*, cyclin A2 (*CCNA2*), *CCNE1*, tumour necrosis factor superfamily member 10 (*TNFSF10*) and *KMT2B*.

Cancer drivers in progressed HCC. Several pathways and processes have been implicated in HCC progression (TABLE 1). First, telomere maintenance contributes to the evasion of cellular senescence. As previously mentioned, telomerase is overexpressed in 90% of HCC and this overexpression is related to *TERT* promoter mutations in 60% of cases and to gene amplification in 5% of cases^{33,34,38}. The two hotspots of mutations are located at nucleotide positions –124 and –146 upstream of the ATG. Mutations at both sites can create a new binding site that is recognized by a transcription factor that induces *TERT* mRNA expression.

Second, the WNT- β -catenin pathway is frequently activated in HCC through *CTNNB1* mutations that activate β -catenin (11–37% of HCC cases), particularly in patients without HBV infection and with well-differentiated tumours^{56,57}. Inactivating mutations or deletions are also frequently identified in axin 1 (*AXIN1*; 10% of HCC cases) or more rarely in adenomatous polyposis coli (*APC*; 1–2% of HCC cases) and zinc finger finger 3 (*ZNRF3*; 3% of HCC cases). All of these mutations result in activation of the WNT- β -catenin pathway^{33,38}.

Third, inactivation of p53 and alterations in the cell cycle are major defects in HCC, particularly in cases related to HBV infection. In this context, patients who have been exposed to aflatoxin B1 present a specific *TP53* mutation (R249S) hotspot^{22,33,38,58}. Inactivation of

the retinoblastoma pathway is also frequently observed through retinoblastoma 1 (*RB1*) mutations (3–8% of HCC cases) or cyclin-dependent kinase inhibitor 2A (*CDKN2A*) deletions (2–12% of HCC cases). Most of these molecular defects are associated with a poor prognosis and could contribute to a more aggressive phenotype^{33,35,59}.

Fourth, chromatin remodelling complexes and epigenetic regulators are frequently altered in HCC. These alterations include mutations in the BRG1- or HRBM-associated factors (BAFs) and polybromo-associated BAF (PBAF) chromatin complex, specifically in AT-rich interaction domain 1A (*ARID1A*; 4–17% of cases) and in *ARID2* (3–18% of cases). Mutations also occur in the histone methylation writer family (KMT2 (also known as MLL) family genes mutated in 2–4% of cases), which can also be modified by HBV insertions in *KMT2B* (10% of cases)^{33,38,55}. Recently, the H3K9 modifier histone-lysine *N*-methyltransferase SETDB1 was identified as overexpressed in HCC^{60,61}. SETDB1 overexpression promotes cancer cell growth via p53 methylation and is associated with tumour aggressiveness and a poor prognosis. Interestingly, DNA methylation is globally altered in HCC, and aberrant modifications are associated with prognosis⁶² or HBV infection⁶³.

Fifth, the RAS–RAF–MAPK (MAP kinase) and the phosphoinositide 3-kinase (PI3K)–AKT–mTOR pathways are frequently activated in HCC. These changes are caused by amplification of a region that includes *FGF3*, *FGF4* and *FGF19* in approximately 5% of tumours, and can also be related to inactivating mutations in tuberous sclerosis 1 (*TSC1*) or *TSC2* (3–8% of cases), or in phosphatase and tensin homologue (*PTEN*) (1–3% of cases). Mutations in ribosomal protein S6 kinase, 90 kDa, polypeptide 3 (*RPS6KA3*) that cause inactivation of ribosomal protein S6 kinase $\alpha 3$ (also known as RSK2; 5–9% cases) lead to activation of RAS–MAPK signalling^{32,33}, whereas mutations that activate RAS proteins themselves (*KRAS*, *HRAS*, *NRAS* or *BRAF*) are rarely identified (<2% of cases). However, additional mechanisms of pathway activation remain to be identified.

Last, the oxidative stress pathway is constitutively activated in HCC owing to mutations that activate nuclear factor erythroid 2-related factor 2 (*NFE2L2*) or that inactivate Kelch-like ECH-associated protein 1 (*KEAP1*) in 5–15% of HCC cases. Interestingly, these observations suggest that *NFE2L2* can protect against HCC occurrence during the development of chronic liver disease but its constitutive activation can also contribute to late-stage tumour progression^{32,64}.

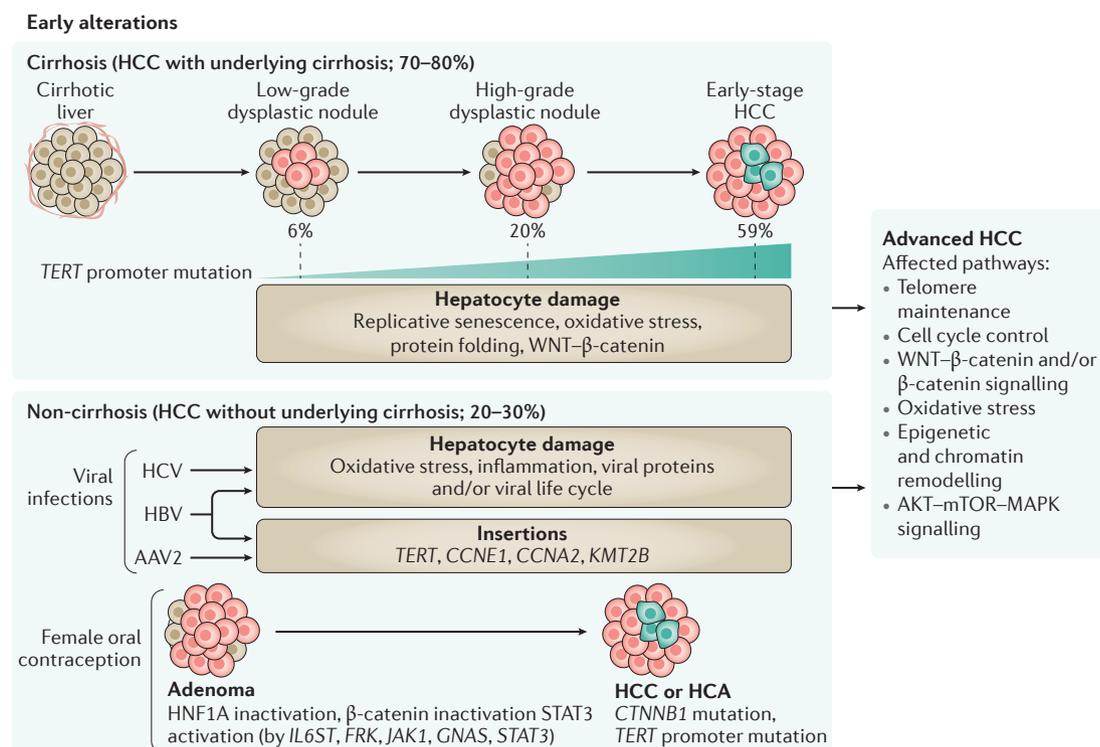


Figure 3 | Cancer progression and driver genes. Major recurrent molecular defects that are observed early in liver carcinogenesis. Telomere reverse transcriptase (*TERT*) promoter mutations are common early events that are identified in most cases of hepatocellular carcinoma (HCC) that develops in a cirrhotic liver. Other mechanisms are specifically related to risk factors; for example, hepatitis B virus (HBV) and adeno-associated virus 2 (AAV2) infections induce insertional mutagenesis that recurrently targets oncogenes. In addition, hepatocellular adenoma (HCA), a rare benign liver tumour occurring most frequently in women who take oral contraception, can transform into HCC with sequential accumulation of mutations in β -catenin (encoded by *CTNNB1*) and in the *TERT* promoter with or without signal transducer and activator of transcription 3 (STAT3) activation^{33–38}. *CCN*, cyclin; *FRK*, fyn-related Src family tyrosine kinase; *GNAS*, *GNAS* complex locus; HCV, hepatitis C virus; HNF1A, hepatocyte nuclear factor 1a; *IL6ST*, interleukin 6 signal transducer; *JAK1*, Janus kinase 1; *KMT2B*, lysine (K)-specific methyltransferase 2B; MAPK, MAP kinase; mTOR, mammalian target of rapamycin.

DNA amplifications are also associated with HCC. The most common high-level amplifications in HCC are in chromosome regions 11q13 and 6p21 (5–10% of cases)^{32,35,65,66}. Cyclin D1 (*CCND1*) and *FGF19* are bona fide oncogenes in 11q13 and represent potential therapeutic targets⁶⁶. Similarly, high-level gains of 6p21 that contain more than four copies of vascular endothelial growth factor A (*VEGFA*) have been identified in 4–8% of HCC cases⁶⁵. *VEGFA* amplification induces both neoangiogenesis and tumour proliferation through the induction of macrophage-mediated hepatocyte growth factor (HGF) secretion⁶⁷. Whether these amplifications represent targetable oncogenic addiction loops in HCC remains to be elucidated by the testing of selective molecules in clinical trials.

Modelling of HCC development in mice is a useful approach to achieve a better understanding of the mechanisms of hepatocarcinogenesis and to test for new therapies. For drug screening, HCC cell lines or primary tumours xenografted in immunodeficient mice are an easy way to test for drug response. In more sophisticated models, candidate oncogenes or tumour suppressor genes can be genetically modified in classical transgenic or knockout animal models. More recently,

siRNA⁶⁸ and CRISPR–Cas9 techniques have emerged as powerful methods to generate tumours in mice and to subsequently test for drug responses⁶⁹.

Molecular classes

Genomic studies^{65,70–73} have revealed molecular subclasses of HCC (reviewed in REF. 14). Two main molecular classes, each representing approximately 50% of patients, have been identified: proliferative and non-proliferative HCC^{65,71,73}. The proliferative class is enriched by activation of RAS, mTOR and insulin-like growth factor (IGF) signalling and by *FGF19* amplification, and is associated with HBV-related aetiologies and poor outcomes^{65,71,72,74}. Some authors have proposed that there are two subtypes of the proliferative class: the WNT–transforming growth factor- β (TGF β) group and the progenitor cell group. The progenitor cell group is enriched in progenitor cell markers, such as epithelial cell adhesion molecule, and the overexpression of α -fetoprotein (AFP)^{65,71,72,74,75}. By contrast, the non-proliferative class is more heterogeneous, but there is still a clear subtype characterized by *CTNNB1* mutations that are associated with alcohol-related and HCV-related HCCs⁷⁵. Direct translation of molecular HCC subclasses into clinical management is yet to be achieved.

Role of the microenvironment

Chronic inflammation. An altered microenvironment is now perceived to be a key enabling characteristic of cancer and is known to be involved in all stages of malignant progression, from the initial transformation phases to invasion and metastasis^{76,77}. Pathologists have long recognized that some tumours are densely infiltrated by cells of both the innate and adaptive arms of the immune system and thereby mirror inflammatory conditions arising in non-neoplastic tissues^{76,78}. HCC is a prototypical inflammation-associated cancer, with approximately 90% of the HCC burden associated with prolonged hepatitis due to viral hepatitis, excessive alcohol intake or NAFLD or NASH. This result indicates that the immune microenvironment has pivotal roles in the pathogenesis of this disease⁷⁹. Interestingly, in fully developed HCC, the presence of immune infiltrates is associated with a better prognosis, which is probably due to more effective antitumour immunity⁸⁰. Remarkably, an unbiased screen of gene expression patterns in HCC revealed that activation of the key innate inflammatory signalling mediators nuclear factor- κ B (NF- κ B), epidermal growth factor (EGF) and interleukin-6 (IL-6) in the liver parenchyma, but not in tumour cells, is associated with a poor prognosis⁸¹. Furthermore, as noted above, genomic screens of HCC also did not reveal mutations that activate inflammatory signalling pathways. Thus, it seems that the inflamed liver promotes the seminal HCC cells at early phases of development⁸².

Multiple cell types interact with hepatocytes in the chronically inflamed liver, including macrophages, stellate cells, endothelial cells and lymphocytes. All of these cell types were shown in certain mouse models to favour tumour growth. Importantly, although the liver is envisaged as a metabolic organ, it maintains a

Table 1 | Major recurrent molecular aberrations observed in advanced HCC

Pathway(s)	Gene(s)	Alteration	Frequency in HCC
Telomere maintenance	<i>TERT</i>	Promoter mutation	54–60%
		Amplification	5–6%
Cell cycle control	<i>TP53</i>	Mutation or deletion	12–48%
		<i>RB1</i>	Mutation or deletion
	<i>CCND1</i>	Amplification	7%
	<i>CDKN2A</i>	Mutation or deletion	2–12%
WNT- β -catenin signalling	<i>CTNNB1</i>	Mutation	11–37%
	<i>AXIN1</i>	Mutation or deletion	5–15%
Oxidative stress	<i>NFE2L2</i>	Mutation	3–6%
	<i>KEAP1</i>	Mutation	2–8%
Epigenetic and chromatin remodelling	<i>ARID1A</i>	Mutation or deletion	4–7%
	<i>ARID2</i>	Mutation	3–18%
	<i>KMT2A (MLL1)</i> , <i>KMT2B (MLL4)</i> , <i>KMT2C (MLL3)</i> and <i>KMT2D (MLL2)</i>	Mutation	2–6%
	<i>RPS6KA3</i>	Mutation	2–9%
AKT–mTOR–MAPK signalling	<i>TSC1</i> and <i>TSC2</i>	Mutation or deletion	3–8%
	<i>PTEN</i>	Mutation or deletion	1–3%
	<i>FGF3</i> , <i>FGF4</i> and <i>FGF19</i>	Amplification	4–6%
	<i>PI3KCA</i>	Mutation	0–2%
	<i>VEGFA</i>	Amplification	3–7%

ARID, AT-rich interaction domain; *AXIN1*, axin 1; *CCND1*, cyclin D1; *CDKN2A*, cyclin-dependent kinase inhibitor 2A; *CTNNB1*, β -catenin; *FGF*, fibroblast growth factor; HCC, hepatocellular carcinoma; *KEAP1*, kelch like ECH associated protein 1; *KMT*, lysine (K)-specific methyltransferase; *MAPK*, MAP kinase; *MLL*, myeloid/lymphoid or mixed-lineage leukaemia (trithorax homologue, *Drosophila*); *NFE2L2*, nuclear factor, erythroid 2 like 2; *PI3K*, phosphoinositide 3-kinase; *PTEN*, phosphatase and tensin homologue; *RB1*, retinoblastoma 1; *RPS6KA3*, ribosomal protein S6 kinase, 90kDa, polypeptide 3; *TERT*, telomerase reverse transcriptase; *TP53*, cellular tumour antigen p53; *TSC*, tuberous sclerosis; *VEGFA*, vascular endothelial growth factor A.

uniquely tolerant immune system, which is necessary to prevent the induction of immunity against multiple antigens and immunostimulatory molecules such as gut-derived nutrients and microbiota-derived signals that constantly flood the liver via the portal system. Understanding this unique hepatic immune system is likely to be important in the context of the complex interactions between malignant hepatocytes and the liver immune system^{83,84}.

The mechanisms through which immune cells promote growth of early-stage HCC are beginning to be elucidated. Multiple experimental models have substantiated that secretion of various cytokines by immune cells can change the function of the interacting hepatocyte, rendering it less sensitive to intracellular tumour suppressor pathways (and possibly also to extracellular ones such as antitumour adaptive immune responses). An example is the secretion of TNF by macrophages in the chronic inflammatory hepatic infiltrate, which activates the NF- κ B pathway in hepatocytes, rendering hepatocytes less sensitive to apoptosis and thus promoting carcinogenesis⁸⁵. Two important inflammatory signalling pathways that are activated by inflammatory cytokines in chronically inflamed livers and promote HCC are the NF- κ B and the Janus kinase (JAK)–signal transducer and activator of transcription (STAT) pathways⁸⁶. Similarly, multiple molecules that are secreted by microenvironmental constituents have been shown to promote hepatocyte growth; these constituents include TNF, lymphotoxin- α , lymphotoxin- β ⁸⁶, IL-6 (REF. 87) and HGF⁸⁸. The ability of inflammatory cells to produce potentially mutagenic reactive oxygen species and reactive nitrogen species is considered by many to underlie some of their pro-tumorigenic activity⁸⁹; however, this idea must still be substantiated by rigorous testing in animal models. Nevertheless, it is clear that the increased hepatocyte proliferation that occurs in chronic hepatitis can potentiate DNA damage-induced mutations⁹⁰.

Fibrosis. Hepatic stellate cells normally reside in the liver sinusoids and have multiple roles in hepatic homeostasis, including retinoid storage, immunomodulation, liver regeneration and vasoregulation. Importantly, upon liver injury they are the primary cellular mediators of hepatic fibrosis and cirrhosis, which are strongly associated with HCC⁷⁹. The presence of a stellate cell gene expression signature is a poor prognosis indicator in human HCC⁹¹, and overexpression of platelet-derived growth factor C (PDGFC) in the mouse liver induces stellate cell activation and hepatic fibrosis followed by HCC⁹². Taken together, these data indicate that hepatic fibrosis and cirrhosis have a causative role in HCC. The mechanisms through which activated stellate cells could drive HCC progression include cytokine secretion, angiogenesis promotion, pro-tumorigenic extracellular matrix components, increased tissue stiffness and immunosuppression. However, the human relevance of each of these mechanisms and its relative contribution remain to be elucidated⁹³. In summary, chronic liver inflammation generates a pathological microenvironment, infiltrated by adaptive and innate immune

cells and stellate cells, together producing a pathological milieu composed of collagen, multiple extracellular matrix proteins, growth factors and cytokines that can form a pro-tumorigenic stroma.

Targeting the microenvironment in HCC. As the tumour microenvironment has a pivotal role in the natural history of HCC, there is a strong rationale for modulating the dynamic crosstalk between hepatocytes and the stroma as treatment for this disease⁷⁹, in particular in HCC prevention. Reversal of liver fibrosis is already feasible in patients with chronic liver disease, using antifibrotic therapies⁹⁴. Conceivably, targeting of various immune cells is also achievable, as is the targeting of specific molecules that are present in the pro-tumorigenic hepatic microenvironment. Despite these possibilities, improved knowledge of the relative contribution of the different cells and molecules comprising the chronically inflamed hepatic network to HCC pathogenesis, and elucidation of the network's hierarchy, are needed for planning potent preventive or therapeutic schemes. Such developments will require a better understanding of the complex natures of the interactions that take place in chronically inflamed human livers, in concert with meticulous testing of their functional relevance in animal models that recapitulate the different aetiologies of hepatic inflammation (viral, metabolic and others). The ideal preventive treatment should convert a pro-tumorigenic microenvironment into an antitumorigenic one.

Diagnosis, screening and prevention

Prevention

Vaccination. The most effective approach for preventing HCC is prevention of the underlying liver disease, the best example of which is hepatitis B vaccination. Universal vaccination against hepatitis B would be expected to reduce HCC incidence, and this has indeed been demonstrated^{26,95}. The first evidence of the ability of the HBV vaccine to reduce the incidence of HCC came from Taiwan after the introduction of universal neonatal vaccination in 1984. This programme was associated with a reduction in the incidence of childhood HCC from 0.7 per 100,000 individuals to 0.36 per 100,000 individuals between 1981 and 1994 ($P < 0.01$)⁹⁵. As the vaccinated cohort aged, the decrease in HCC incidence was carried through to adolescents and is now being detected in young adults²⁶.

However, there are currently approximately 400 million adults who are infected with HBV. Not all of those with hepatitis B are at equal risk of developing HCC. Various risk factors are well known, including hepatitis B viral load and genotype, male sex, older age and active liver disease^{96–103}. For those who have active disease and who receive treatment for hepatitis B, the risk of HCC is reduced, although not eliminated¹⁰⁴. This effect has been demonstrated in a single RCT using the antiviral medication lamivudine¹⁰⁵, a study that unfortunately did not have HCC incidence as an end point. However, similar results have now been obtained in cohort studies using various methods to match treated and untreated populations, including historical controls¹⁰⁶.

Table 2 | Risk factors and recommended surveillance for HCC according to aetiology

Aetiology	Risk	Criteria to begin surveillance
Cirrhosis	<ul style="list-style-type: none"> Approximately one-third of patients will develop HCC in their lifetime The 5-year cumulative risk of HCC is 5–30% 	<ul style="list-style-type: none"> EASL and AASLD: cirrhosis owing to any cause APASL: only cirrhosis owing to viral origin
Hepatitis B virus (HBV) infection	<ul style="list-style-type: none"> The risk of developing HCC in cirrhosis is 2% per year The risk of developing HCC in chronic hepatitis is 0.2% per year Factors that increase HCC risk include male sex, family history of HCC, cofactors (aflatoxin intake, alcohol abuse, tobacco use and HCV infection), high levels of HBV viral load and infection with HBV genotype C 	<ul style="list-style-type: none"> EASL: HBV infection associated with cirrhosis, chronic active hepatitis or family history of HCC AASLD: HBV infection associated with cirrhosis, or HBV carriers without cirrhosis if Asian and aged >40 years (men) or aged >50 years (women), a family history of HCC, black patient aged >20 years or a REACH-B score of >8 (REF. 101)
Hepatitis C virus (HCV) infection	<ul style="list-style-type: none"> The risk of developing HCC in cirrhosis is 3–7% per year The risk of developing HCC in chronic hepatitis is 0.3% per year Factors that increase HCC risk include male sex, alcohol abuse, HBV co-infection, diabetes and obesity 	<ul style="list-style-type: none"> EASL: HCV infection associated with cirrhosis or bridging liver fibrosis (METAVIR score of F3 (REF. 3)) AASLD: HCV infection associated with cirrhosis
Alcoholic fatty liver disease (AFLD)	<ul style="list-style-type: none"> The risk of developing HCC in alcohol-induced cirrhosis is 1% per year Factors that increase HCC risk include infection with HCV or HBV 	<ul style="list-style-type: none"> EASL and AASLD: AFLD associated with cirrhosis
Non-alcoholic fatty liver disease (NAFLD)	<ul style="list-style-type: none"> Ninety per cent of patients with obesity and 70% of patients with diabetes mellitus have NAFLD Patients with obesity and diabetes have a 1.5–2-fold greater risk of HCC than the general population 	<ul style="list-style-type: none"> EASL and AASLD: NAFLD or NASH associated with cirrhosis

AASLD, American Association for the Study of Liver Diseases; APASL, Asian Pacific Association for the Study of the Liver; EASL, European Association for the Study of Liver Disease; HCC, hepatocellular carcinoma; NAFLD, non-alcoholic fatty liver disease; NASH, Non-alcoholic steatohepatitis; REACH-B, risk estimation for hepatocellular carcinoma in chronic hepatitis B.

Similarly, treatment and eradication of hepatitis C results in a decreased HCC incidence²¹. This effect has only been documented in cohort studies. There are no RCTs comparing HCC incidence in treated patients to that in untreated patients. Such a study would not be ethical. However, cohort studies have documented that the HCC incidence in those successfully treated for hepatitis C is lower than in historical untreated controls^{107–110}. Until recently, standard treatment of hepatitis C was based on interferon, and sustained virological responses in patients with hepatitis C cirrhosis have been associated with a substantial reduced risk in HCC development (hazard ratio, 0.23; confidence interval, 0.16–0.35)¹¹¹. It is too early to ascertain the effect of new DAA drugs for HCV, which achieve sustained virological responses in 90% of cases, on the occurrence of HCC¹¹². If one extrapolates from the interferon era to the current DAA therapy setting, as a greater proportion of individuals who are infected with HCV are treated, the overall hepatitis burden, and the absolute number of patients with hepatitis who become at risk for HCC, will decrease. However, the overall effect of DAA therapy will be modest because most individuals with HCV remain undiagnosed, and treatment penetrance is limited owing to socioeconomic factors. Assuming that one-third of patients with HCV come to medical attention and achieve 90% sustained virological responses with DAA agents, the burden of HCC in the United States might be reduced by 10–15% over the next decade^{113,114}.

Chemoprevention. There are several putative chemopreventive agents that have been proposed to reduce HCC incidence in at-risk populations, including statins and metformin¹¹⁵. The data on metformin are becoming more robust, as demonstrated by a meta-analysis that suggested that metformin decreases the risk of HCC in people with diabetes¹¹⁶. Moreover, a study has shown

that metformin may be safely continued in people with diabetes who also have cirrhosis¹¹⁷. Nevertheless, the evidence for the ability of metformin to reduce HCC risk is not sufficiently strong to recommend using it in at-risk patients, and prospective studies testing this agent are required.

Lifestyle modification. Whether abstinence from alcohol in those with alcoholic liver disease decreases the incidence of HCC is not yet known. Of course, primary prevention by counselling against unhealthy use would reduce the incidence of alcohol-associated cirrhosis and the attendant risk of HCC. Similarly, for those with NAFLD who successfully lose weight or otherwise control their disease, there is no information as to whether HCC incidence is reduced¹¹³. Thus, in summary, prevention of HCC largely depends on prevention or treatment of the underlying liver disease.

Surveillance of HCC

When HCC causes symptoms, the disease is most often at an advanced stage and therefore not amenable to potentially curative treatment. Death usually ensues within a few months. However, HCC has a prolonged subclinical course that provides the opportunity for early detection. Early-stage HCC lesions are small and frequently curable, often by minimally invasive methods. These considerations have led to the development of protocols for the surveillance of HCC in patients at risk for this cancer (TABLE 2). Surveillance, however, remains controversial because the only RCT that demonstrated decreased mortality was probably statistically incorrectly analysed¹¹⁸. Nevertheless, there is a wealth of evidence of lesser quality, including cohort studies with comparisons between screened and unscreened populations, and demonstration that cure is more likely with HCC that is detected by surveillance

compared with cases that are diagnosed once symptoms have become apparent^{119–124}. Several cost–efficacy analyses have also demonstrated benefits of surveillance^{125–137}. Furthermore, in considering the potential benefits of surveillance in relation to the potential harms, it is clear that benefits outweigh harms. Benefits include early detection and potential cure of HCC, whereas harms include some additional investigations and potentially some unnecessary interventions. However, as discussed below, a diagnostic algorithm has been developed that was designed to minimize false-positives, thereby reducing the likelihood of harm. More recently, there have been several risk scores developed to improve identification of the at-risk population. None has yet achieved widespread application.

The techniques for surveillance are also controversial. There is no question that ultrasound should be part of the algorithm, but the use of biomarkers remains controversial. There is some suggestion that biomarkers improve early detection^{138–144}, but there is currently no evidence that this leads to improved cure rates compared with ultrasound alone. Most importantly, the usual serum biomarkers that are used — AFP, des- γ carboxyprothrombin (DCP) and the L3 fraction of AFP (AFP-L3) — are all more frequently associated with advanced-stage disease than early-stage disease and would therefore be theoretically unsuitable for the detection of early disease^{138–144}. Among these, AFP is the most widely used, but its use remains an area of controversy.

The ideal surveillance interval for at-risk patients (TABLE 2) according to guidelines is 6 months^{3,23,145–148}. Studies have demonstrated that a 3-month interval does not enhance outcomes¹⁴⁶, and survival is lower with 12-month than with 6-month intervals¹⁴⁵.

Diagnosis

Patients who are enrolled in a surveillance programme are diagnosed by identification of a new liver nodule on abdominal ultrasound, and diagnostic confirmation using either non-invasive criteria or biopsy. These patients are generally asymptomatic and have early-stage HCC. Conversely, patients diagnosed outside surveillance usually present at advanced stages with large symptomatic tumours and/or portal vein invasion. Symptoms include malaise, weight loss, anorexia, abdominal discomfort or signs related to advanced liver dysfunction. A diagnosis can be made by non-invasive (radiological) or invasive (biopsy) approaches. Radiological diagnosis is achieved with a high degree of confidence if the lesion is found in a patient with cirrhosis. Using contrast imaging, the lesion shows the radiological hallmarks of HCC, which are hypervascularity in the arterial phase of a contrast study (using CT or MRI) and a decreased signal compared with the rest of the liver in the portal venous and/or delayed phases of the study¹⁴⁹. When these typical features are observed, the diagnosis is confirmed and a biopsy is not necessary^{3,15,150,151}. Latest generation CT and/or MRI scans following reported protocols are recommended¹⁵². MRI with liver-specific contrast agents might help in the diagnosis of HCC, but the specificity of these agents remains suboptimal.

The caveat of non-invasive radiological criteria is that this algorithm only applies to those who have an elevated risk of HCC. A biopsy is required for patients who do not have any particular risks for HCC, for the most part patients without cirrhosis. The recommended algorithm for investigation of lesions in at-risk patients is as follows^{3,15}: for nodules <1 cm in size, ultrasound follow-up at 3 months is recommended; for lesions >1 cm, the radiological hallmarks of HCC define diagnosis; if the radiology is not typical in at least one of two imaging techniques (CT and MRI), a liver biopsy is recommended^{3,15}. Notably, this accepted practice puts the assessment of HCC at a disadvantage compared with most cancers because tumour tissue for molecular studies would not be routinely obtained in clinical practice. Recent guidelines recommend obtaining tissue samples in the setting of all research studies in HCC³.

Diagnostic difficulty occurs mainly with early-stage HCC lesions, in which the radiological appearance might be atypical, necessitating a biopsy. However, biopsy is not an ideal gold standard because of variation introduced by sampling and complications. The risk of complications, such as tumour seeding and bleeding, after liver biopsy is less than 3%¹⁵³. Although the sensitivity of liver biopsies ranges between 70 and 90% for all tumour sizes³, small lesions might be missed, giving a false-negative result. In addition, in early-stage HCC, morphological changes may be minimal compared with dysplastic hepatocytes, making the diagnosis uncertain¹⁵⁴. In this setting, the use of special stains may help to resolve diagnostic uncertainties. For example, HCC cells express glypican 3, glutamine synthetase, heat shock protein 70 and clathrin heavy chain^{155–157}. Positive staining for two of these four markers is highly specific for HCC. In addition, comparison of a biopsied specimen from the tumour and the surrounding non-tumorous liver may be helpful in highlighting the early features of malignancy. Patients with suspicious lesions for whom a diagnosis cannot be confirmed by a biopsy should be closely monitored, and may even require a second biopsy.

Management

Evidence-based management and staging systems

The BCLC staging system provides an easy-to-use algorithm that links tumour stages with treatment allocation policies based on evidence^{3,158,159} (FIG. 4). Treatments are classified as radical therapies with potential to cure HCC or palliative therapies, which are aimed at improving survival. Radical therapies include surgical resection, liver transplantation or percutaneous ablation, whereas palliative therapies include chemoembolization and sorafenib³. Treatment allocation for standard of care follows the levels of evidence defined by the US National Cancer Institute, which rely on the strengths of the study design and end points³ (TABLE 3). Controversy regarding HCC staging systems remains. In fact, alternative staging or scoring systems have been proposed, such as the Hong Kong classification¹⁶⁰, the Cancer of the Liver Italian Program (CLIP) score¹⁶¹, the TNM system¹⁶² and the Japan Integrated Staging (JIS) score¹⁶³. None of these systems has acquired global

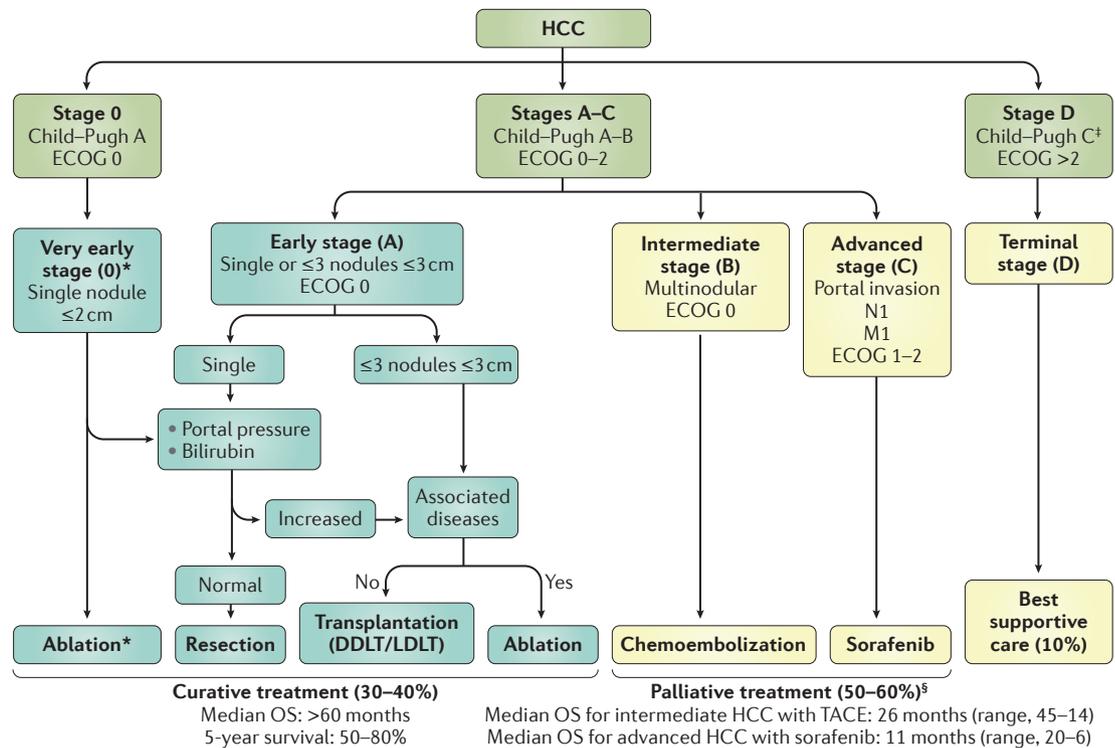


Figure 4 | BCLC staging system and therapeutic strategy. The Barcelona Clinic Liver Cancer (BCLC) classification consists of five stages to select the best candidates for the best therapies currently available. Patients with asymptomatic early tumours (stages 0–A) are candidates for radical therapies (resection, transplantation or local ablation). Asymptomatic patients with multinodular hepatocellular carcinoma (HCC; stage B) are suitable for transcatheter arterial chemoembolization (TACE), whereas patients with advanced symptomatic tumours and/or an invasive tumoral pattern (stage C) are candidates to receive sorafenib. End-stage disease (stage D) includes patients with poor prognoses who should be given the best supportive care possible. DDLT, deceased donor liver transplantation; ECOG, Eastern Cooperative Oncology Group; LDLT, living donor liver transplantation; M1, M1 metastasis; N1, N1 lymph node; OS, overall survival. *Patients at very early stages (stage 0) can be considered first for ablation in case they have contraindications for liver transplantation. †Patients in Child–Pugh class C should be first considered for liver transplantation. ‡Treatment stage migration (consider the next efficacious treatment in the algorithm when previous therapies fail). Adapted with permission from REFS 3, 159, Elsevier.

consensus. Scoring systems, such as the CLIP, are not widely used because they do not incorporate treatment allocation to distinct prognostic stages, whereas others are specifically applied in Asia (the Hong Kong system and the JIS score).

Early-stage disease. Surgical resection is the first-line option for patients with early-stage HCC (BCLC 0 or A) with solitary tumours, and confers 5-year survival rates of 70%^{3,15,164–166}. The introduction of restrictive selection of candidates for resection (patients with single nodules, absence of portal hypertension and well-preserved liver function) along with anatomical resection (in which tissue removal is performed in line with the location of functional segments of the liver) has minimized complications and reduced recurrence^{3,15,164,166}. Metastases and *de novo* HCC account for 70% of 5-year recurrence after resection¹⁶⁷, and no adjuvant therapies are able to prevent this complication¹⁶⁸. Adoptive immunotherapy¹⁶⁹ and the vitamin A derivatives acyclic retinoids¹⁷⁰ were reported as effective treatments in this setting; however, these trials were conducted in small study populations and the results have not been reproduced.

Liver transplantation is the best first-line option for patients with BCLC A tumours within Milan criteria (defined as a single tumour of ≤ 5 cm in size or up to three nodules of ≤ 3 cm in size without vascular invasion) that are unsuitable for resection^{3,171}. These criteria have been independently validated internationally and have been adopted by guidelines^{3,15,165} and liver transplant units. Nevertheless, some studies have noted that a moderate expansion of the Milan criteria might lead to acceptable and competitive long-term outcomes^{172–174}. Local ablation using radiofrequency has been proposed as an optimal alternative to resection in patients with a single tumour < 2 cm in size who are unsuitable for transplantation^{16,175}, but no RCTs specifically addressing this issue have been reported. Nevertheless, in patients with early-stage tumours (BCLC 0 or A) who are not suitable for surgery, local ablation is the standard of care with 5-year survival rates of 50–70%³.

Intermediate-stage disease. Patients with intermediate-stage HCC (BCLC B) are characterized by multinodular disease, preserved liver function, and the absence of tumour-related symptoms, vascular invasion and

Table 3 | Guideline recommendations for treatment according to levels of evidence and strength of recommendation

Category	Treatment	Eligibility criteria or alternative approaches	Evidence level	Recommendation strength
<i>Treatments accepted in EASL and AASLD guidelines, and level of evidence</i>				
Surgical treatment	Resection	Patients with solitary tumours and well-preserved liver function (normal bilirubin with either hepatic venous pressure gradient of ≤ 10 mm Hg or platelet count of $\geq 100,000$)	2A	1B
	Liver transplantation	Patients with single tumours of ≤ 5 cm or ≤ 3 nodules of ≤ 3 cm (Milan criteria) that are not suitable for resection	2A	1A
Loco-regional treatment	Local ablation	Radiofrequency or percutaneous ethanol injection for patients with BCLC 0–A tumours that are not suitable for surgery	2A	1A
	Chemoembolization	BCLC B (multinodular asymptomatic tumours without vascular invasion or extrahepatic spread)	1A	1A
Systemic treatment	Sorafenib	Patients with well-preserved liver function (Child–Pugh A) with advanced HCC tumours (BCLC C) or those with tumour progression following loco-regional therapies	1A	1A
Palliative care	Palliative support	Patients with BCLC D tumours should receive management of pain, nutrition and psychological support	N/A	2B
<i>Treatments under investigation or that require further evidence before adoption into guidelines</i>				
Surgical treatment	Resection	Patients with multifocal tumours (≤ 3 nodules of ≤ 3 cm) or with mild portal hypertension who are not suitable for liver transplantation	3A	2C
		Adjuvant treatments after resection or ablation	1D	2B
	Liver transplantation	Up-to-seven criteria in patients without microvascular invasion	2B	2B
		Neo-adjuvant loco-regional therapies if the waiting list exceeds 6 months	2D	2B
		Down-staging for HCCs exceeding conventional criteria	2D	2C
Living donor liver transplantation in patients with a waiting list exceeding 6 or 7 months	2A	2B		
Loco-regional treatment	Other ablative therapies, such as microwave, cryoablation, laser, irreversible electroporation or high-intensity focused ultrasound	Patients with BCLC 0–A tumours that are not suitable for surgery	N/A	N/A
	Chemoembolization	Use of drug-eluting beads, which has shown similar response rates to gelfoam-Lipiodol particles associated with fewer systemic adverse events	1D	2B
	Yttrium-90 (Y90) radioembolization	In BCLC B and in patients with portal vein thrombosis	1D	2B
	External 3D conformal radiotherapy	Single tumours at early stages (BCLC A)	3A	2C
Systemic treatment	Chemotherapy and hormonal compounds	<ul style="list-style-type: none"> • First line: patients with BCLC B tumours progressing to TACE or with BCLC C, Child–Pugh A, ECOG 0–1 performance status • Second line: patients progressing to sorafenib, with Child–Pugh A, ECOG 0–1 performance status 	1A	2B
	Other molecular targeted therapies	<ul style="list-style-type: none"> • First line: patients with BCLC B tumours progressing to TACE or with BCLC C, Child–Pugh A, ECOG 0–1 performance status • Second line: patients progressing to sorafenib, with Child–Pugh A, ECOG 0–1 performance status 	N/A	N/A
Palliative care	Radiotherapy to alleviate pain	Patients with bone metastasis	3A	2C

The table is based on information from European Association for the Study of the Liver (EASL) and European Organisation for Research and Treatment of Cancer (EORTC) guidelines (see REF. 3 for details of the guidelines). Strength of evidence and strength of end point are based on the US National Cancer Institute classification. Strength of evidence falls into the following categories: level 1, randomized controlled trial or meta-analysis; level 2, non-randomized controlled studies; level 3, case series. Strength of end point falls into the following categories: A, survival; B, cancer-specific survival; C, quality of life; D, others. Strength of recommendation is according to the GRADE system. The grading recommendations are: 1, strong; 2, weak. Furthermore, the quality of evidence is categorized into the following: A, high quality; B, moderate quality; C, low quality. AASLD, American Association for the Study of Liver Diseases (see REF. 15 for details of the guidelines); BCLC, Barcelona Clinic Liver Cancer; HCC, hepatocellular carcinoma.

extrahepatic spread. Chemoembolization in the form of transcatheter arterial chemoembolization (TACE) — a minimally invasive technique that combines local delivery of beads to restrict tumour blood supply with local administration of chemotherapy — is recommended based on results from RCTs and one meta-analysis of pooled data^{17,18,176}. Improvements in the selection of candidates, supra-selective embolization — the selective blockade of the artery feeding the tumour that minimizes collateral hepatic toxicity — and improvements in embolization devices (drug-eluting beads) have led to current median survival times of 26 months¹⁷⁷ and beyond 40 months in referral centres¹⁷⁸. Alternative embolization strategies, such as radioembolization using beads coated with yttrium-90 (Y90) — an isotope that emits short-range β -radiation — are effective and have a favourable safety profile¹⁷⁹, but only well-designed, properly powered RCTs will determine the therapeutic niche of this intervention.

Advanced and end-stage disease. The Sorafenib HCC Assessment Randomized Protocol (SHARP) trial demonstrated that sorafenib, a multiple tyrosine kinase inhibitor, was able to substantially increase survival in patients with advanced-stage HCC (BCLC C) from 7.9 months to 10.7 months (hazard ratio, 0.69)¹⁹. The beneficial effects of sorafenib occur regardless of HCC aetiology, as was validated in Asian patients with HBV infection¹⁸⁰. On the basis of these data, sorafenib became the standard of care in this setting. Eight RCTs of alternative systemic molecular treatments that have been reported since the SHARP trial have not shown survival benefits in HCC. These findings can be partially explained by the specific toxicity of some agents owing to the underlying liver cirrhosis, the high molecular heterogeneity of HCC, the lack of stratification of patients according to biomarkers and a relative resistance to conventional chemotherapy¹⁸¹. Patients with end-stage disease (BCLC D) should be considered for nutritional and psychological support and proper management of pain, but are not candidates for clinical trials.

Surgical therapies

Surgery is the treatment of choice for most patients with early-stage HCC, with 5-year survival in appropriately selected cases exceeding 70%; its role in more advanced HCC is more controversial^{3,165}. The large majority of patients with HCC have underlying liver disease, and the location and extent of the tumour, and the status of the non-malignant tumour liver tissue, must be considered in the choice of surgical procedure. The prognosis of chronic liver disease is commonly assessed using the Child–Pugh score, which uses five clinical measures — total bilirubin, serum albumin, prothrombin time, ascites severity and hepatic encephalopathy grade — to classify patients into one of three groups (A, B or C) of predicted survival rates. In brief, a Child–Pugh score of A reflects well-preserved liver function, a score of B indicates moderate liver dysfunction with a median life expectancy of approximately 3 years and a score of C reflects severe liver dysfunction with life expectancy of approximately 1 year¹⁸².

Resection. Patients with a single technically resectable HCC without macrovascular invasion, with preserved liver function (Child–Pugh class A with bilirubin of <1 mg per dl) and no portal hypertension are optimal candidates for partial hepatectomy, and experience low (<2%) perioperative mortality^{3,15,158,159,164–166} (FIG. 4; TABLE 3). Limited, yet anatomical, resection is preferred when possible to spare uninvolved liver parenchyma and to remove satellite tumours that result from local vascular invasion¹⁸³. When major (≥ 3 segment) resection is required, preliminary portal embolization¹⁸⁴ or lobar radioembolization¹⁸⁵ might be performed in some centres to induce growth of the future liver remnant. Over a period of 4–6 weeks following portal embolization, the volume of the contralateral liver lobe typically increases by 20–25%, thereby decreasing the risk of postoperative hepatic insufficiency. The efficacy of these practical approaches have not yet been confirmed in RCTs or adopted by guidelines. With improving technology and experience, laparoscopic resection is increasingly being used with improved early outcomes¹⁸⁶, and percutaneous thermal ablation has become an acceptable alternative for accessible tumours of <2 cm¹⁷⁵. Resection is often applied outside guidelines for patients with multifocal HCC or portal hypertension, particularly in Asia where availability of transplantation is limited, albeit with decreased 5-year survival (50–60% compared with >70% in optimal candidates)¹⁸⁷.

Recurrence of HCC in the liver is common after resection (up to 70% at 5 years)^{165,188} because the remaining liver is both the most common site of metastasis of the primary HCC and is at risk for developing *de novo* HCC. With careful follow-up, recurrence can often be treated effectively by repeat resection¹⁸⁹, thermal ablation or liver transplantation¹⁹⁰, with resultant long-term survival. There is no proven adjuvant therapy for HCC resection; small trials have produced positive results for retinoids¹⁷⁰, immunotherapy¹⁶⁹ and I-131 Lipiodol¹⁹¹, but these have not been confirmed in larger studies, and a large RCT involving approximately 1,100 patients that tested sorafenib in this setting showed no benefit¹⁶⁸.

Transplantation. Liver transplantation is indicated for patients with early-stage HCC who fall within the Milan criteria and who are not candidates for partial hepatectomy^{3,15,171}. For these patients, transplantation yields a 5-year survival rate of 70% with a recurrence rate of approximately 10%, and 10-year survival rates >50%^{3,158,159,192} (FIG. 4; TABLE 3). Transplantation has the appeal of removing unrecognized intrahepatic metastases and essentially eliminating the risk of *de novo* tumour development, but this benefit is offset by higher perioperative and late non-tumour-related mortality such that post-transplant survival, at least up to 5 years, is not substantially better than after resection¹⁸⁸. Donor organ scarcity varies geographically. To the extent that patients must wait for organs, dropout from the waiting list owing to tumour progression reduces transplant survival on an intention-to-treat basis¹⁶⁶, and loco-regional treatment to prevent progression while waiting is an integral part of the process¹⁹³. Living donor transplantation is a

way for patients with suitable donors to avoid the risk of waiting-list dropout; results are comparable with those achieved with deceased donors¹⁹⁴. The mTOR inhibitors sirolimus or everolimus are often added to the immunosuppressive regimen¹⁹⁵; however, they were not effective as antitumour therapies to prevent recurrence in a recent RCT^{196,197}.

The Milan criteria are widely used as the basis for transplant eligibility, and adherence to them yields good post-transplant survival. Increasingly, however, the benefit provided by transplant compared to the alternatives (for example, resection and loco-regional therapies), as opposed to the absolute survival rate, is being considered in discussions about donor organ allocation. Basing allocation on benefit of transplant rather than on absolute survival could lead to different choices of transplant candidates. For example, the benefit of transplant for a patient with a single HCC within Milan criteria compared with resection may be considerably less than the benefit of transplant for multinodular HCC beyond the Milan criteria compared to chemoembolization, even though the absolute survival after transplantation in the second scenario is lower¹⁹⁸. Several cohorts have explored the implication of extending the Milan criteria for transplantation in HCC¹⁹⁹. Extended criteria such as the University of California San Francisco²⁰⁰ and Up-to-seven¹⁷² proposals have been reported to yield survival rates similar to the Milan criteria, as has down-staging of HCC beyond the Milan criteria by loco-regional treatment²⁰¹. Selection criteria for extended indications based on genomic information have reported good outcomes¹⁷⁴. The reproducibility of these proposals on a large scale awaits confirmation.

Postsurgical outcomes depend on the nature of the underlying liver disease. Historically, results have been better in HBV-related HCC compared with HCV-related HCC¹⁸⁸ because viral control has been possible for HBV, leading some authors to propose more liberal surgical guidelines for patients with HBV-related HCC¹⁶⁰. There is good reason to expect that with the recent development of effective HCV treatments²⁰², improved results of both resection and transplant might lead to a broadening of the accepted indications for surgical treatment in patients with hepatitis C.

Loco-regional therapies

Percutaneous ablation. Percutaneous and intra-arterial therapies are usually performed by interventional radiologists and are the mainstay of the treatment of patients with early-stage or intermediate-stage HCC (BCLC 0–B) who are not candidates for surgery (TABLE 3). Percutaneous tumour ablation involves the insertion of a needle through the skin to access the inside of a tumour. This approach can be used to inject agents that induce tumour cell killing (usually absolute ethanol) or to insert a probe that delivers energy that induces a deleterious increase in temperature (radiofrequency, microwave or laser)²⁰³. Tumour size (3–4 cm), number (≤ 3 tumours) and location (accessible with ultrasound guidance) limit the applicability of percutaneous ablation²⁰⁴.

Several RCTs have demonstrated a significant benefit of radiofrequency ablation compared to percutaneous ethanol injection in terms of complete response rate (absence of contrast uptake within the treated lesion in the arterial phase of CT or MRI) and time to recurrence^{205,206}. As a result, radiofrequency is the standard ablative therapy at early stages of the disease as it provides better results than ethanol^{3,158,159,205} (FIG. 4). Ethanol injection is nevertheless a valuable option for tumours located near the large hepatic vessels and bile ducts, or in treatment centres with limited access to technology. Five-year survival rates after radiofrequency ablation average at 60%²⁰⁷. Although local tumour progression or relapse is higher after percutaneous ablation than after liver resection, the long-term outcomes are similar and ablation has been proposed as first-line therapy for tumours that are ≤ 2 cm in size¹⁶.

Intra-arterial therapy. The most commonly used intra-arterial therapy is TACE. This involves the sequential injection, into one or more branches of the hepatic artery, of chemotherapeutic drugs (doxorubicin, mitomycin C, cisplatin or their combinations) loaded into particles or emulsified in Lipiodol (an oily contrast agent that is selectively retained in the HCC nodules), and embolizing particles that interrupt blood flow^{208,209}. The result is the induction of acute ischaemic necrosis and eventually a prolonged exposure of tumour cells to the drugs. At present, TACE is usually performed 'on demand', with patients evaluated every 6–8 weeks with contrast-enhanced CT or MRI and additional selective TACE sessions performed only if active tumour areas are found²¹⁰. The use of the more costly drug-eluting particles results in a simpler and more standardized procedure that increases tumour response rates but does not improve survival²¹¹.

Strong scientific evidence makes TACE the standard of care for patients with large or multiple tumours (BCLC B) or with small tumours that cannot be resected or percutaneously ablated (BCLC A unsuitable for surgery or local ablation), if the patient has a preserved liver function, no cancer-related symptoms and no vascular invasion or extrahepatic spread³. Two RCTs^{17,176} and one meta-analysis of pooled data established a significant benefit of TACE versus supportive care or suboptimal therapies (tamoxifen and oral 5-fluorouracil (5-FU)) in this patient population^{3,18,158,159} (FIG. 4). Median survival after TACE ranges from 16 to 45 months in the early stage (BCLC 0–A) of disease, 15.6 to 26.3 months in the intermediate stage (BCLC B) and 6.8 to 13.6 in the advanced stage (BCLC C)^{177,212}. The largest RCT ever reported for TACE describes a median survival duration of 26 months for patients with intermediate-stage HCC¹⁷⁷. Combination strategies of TACE and systemic therapies (brivanib or sorafenib) have not resulted in clinical benefit^{177,213}. A different meta-analysis that included the combination of different loco-regional therapies (TACE and radiofrequency ablation in the active treatment groups) has questioned the benefits of TACE²¹⁴. The use of TACE alone or in combination with sorafenib for patients with advanced-stage HCC is not supported by scientific evidence or recommended by guidelines^{3,23}.

Alternatives to TACE include Y90 radioembolization, which uses much smaller embolizing particles that are injected into the hepatic arteries to provide selective internal irradiation of the tumours^{179,215}. Evidence of survival benefit for radioembolization has not yet been proven in the setting of RCTs compared to the standard of care, which is TACE in intermediate-stage HCC and sorafenib in advanced-stage HCC. Y90 radioembolization is usually offered in some centres to those patients who are suboptimal candidates for TACE because of large tumour burdens, vascular invasion or disease progression prior to TACE²¹⁶. A second alternative to TACE is bland transarterial embolization, which involves occluding the tumour blood supply using microbeads without simultaneous administration of chemotherapeutic agents. Transarterial embolization has provided lower response rates compared with TACE in RCTs²¹⁷, and a meta-analysis showed that it provides suboptimal survival rates compared with TACE¹⁸. Finally, hepatic arterial infusion chemotherapy — a catheter-based procedure for the long-term administration of agents directly into the liver — is frequently used in Japan to treat patients who are poor candidates for TACE; however, there is no scientific evidence to support this approach.

Systemic therapies and future treatment approaches

More than 100 RCTs have been reported that have tested chemotherapy or other types of systemic therapies in HCC, but only one drug, sorafenib, has demonstrated survival advantages^{19,180,218}. Treatment with systemic chemotherapy and anti-oestrogen therapies has been shown to be ineffective in HCC¹⁸. Systemic chemotherapy with doxorubicin, the PIAF (platinum, interferon, doxorubicin and 5-FU) regimen¹⁸¹ and the FOLFOX (folinic acid, 5-FU and oxaliplatin) regimen²¹⁹ lacked survival advantages and was accompanied in some instances with significant toxicity. Treatment with sorafenib is associated with manageable adverse events (diarrhoea and skin reactions on the hands and feet) and an absolute increase in median survival of 3 months¹⁹. Subsequent studies revealed a stable benefit of this drug in all regions of the world and in all HCC aetiologies²²⁰, and in recent trials, sorafenib consistently showed a median survival of approximately 10 months. Unfortunately, no predictive biomarkers of responsiveness to sorafenib have been identified²²¹. Although sorafenib is in a unique position of primacy in the management of HCC, it has some restrictions in the target population (not indicated in patients with poor liver function or in the adjuvant setting) and in the understanding of the mechanism of action. The efficacy of sorafenib is probably due to a balance between targeting of cancer cells and targeting of the microenvironment through the blockade of multiple kinases (up to 40, including vascular endothelial growth factor receptor (VEGFR), platelet-derived growth factor receptor (PDGFR), mast/stem cell growth factor receptor (KIT) and/or BRAF²²²). Interestingly, this wide blockade does not induce liver failure or other life-threatening complications.

The main characteristics of the SHARP trial have been adopted by guidelines of trial design²²³ and replicated by almost all subsequent studies testing molecular therapies in HCC²¹⁸. This seminal study enrolled patients with well-preserved liver function (as indicated by Child–Pugh A class), with advanced-stage disease (BCLC C) or those with intermediate-stage disease (BCLC B) that progressed following TACE, and defined overall survival as the primary end point (TABLE 4). Nonetheless, none of the therapies tested after the SHARP trial have demonstrated survival benefits in patients with HCC. Some of the therapies tested in the first-line setting include brivanib (a fibroblast growth factor receptor (FGFR) and VEGFR inhibitor)²²⁴, sunitinib (a KIT, VEGFR and PDGFR inhibitor)²²⁵, linifanib (a VEGFR and PDGFR inhibitor)²²⁶ and erlotinib (an EGF receptor (EGFR) inhibitor)²²⁷. Therapies tested in the second-line setting include brivanib²²⁸, everolimus (an mTOR inhibitor)²²⁹ and ramucirumab (a VEGFR2 inhibitor)²³⁰. The reasons for the disappointing Phase III clinical trial results are reviewed elsewhere²³¹ and include a marginal antitumour potency, liver toxicity, flaws in trial design and lack of biomarker-based enrichment. Randomized Phase II studies are recommended before conducting pivotal Phase III trials. Phase II studies are essential for identifying signals of efficacy, futility or toxicity, and might prevent the devotion of resources to Phase III trials that test therapies with marginal chances of success. Overall survival is the mainstay end point for Phase III studies. Although time-to-progression remains relevant in Phase II studies²²³, recent results pointing to a lack of correlation between time-to-progression and overall survival^{225,226,228} suggest that simultaneous assessment of other end points, such as objective response using the modified Response Evaluation Criteria In Solid Tumours (mRECIST)^{231,232}, is necessary. In terms of biomarkers, none of the Phase III studies were enriched by biomarker analysis, which could have indicated effectiveness of the drug in selected subpopulations.

Most of the drugs currently being tested in Phase III trials are anti-angiogenic agents, cell cycle inhibitors, receptor tyrosine kinase inhibitors and checkpoint inhibitors (FIG. 5; TABLE 5). These broad-spectrum compounds are tested in HCC in ‘all comers’, such as levatinib (a VEGFR2 and VEGFR3 inhibitor) for first-line treatment, and regorafenib (a multikinase inhibitor, including VEGFR2 and angiopoietin 1 receptor (TIE2)) or cabozantinib (a VEGFR and hepatocyte growth factor receptor (MET) inhibitor). However, because many agents in Phase III trials failed with non-biomarker-enriched populations, current trials now tend to use more precise approaches. Primarily, Phase II proof-of-concept studies that test drugs that block potential oncogenic addiction loops, and Phase II and III studies using biomarker-based trial enrichment strategies to define activation of signalling pathways in HCC subgroups, are currently ongoing. For instance, genomic studies defined a human HCC subclass characterized by TGF β signalling activation²³³ that is associated with an aggressive phenotype⁷⁴. The small-molecule galunisertib blocks TGF β signalling and has been tested in Phase II as a single agent

Table 4 | Main recommendations in the design of Phase II and Phase III trials for patients with HCC

Aim	Factor	Considerations and recommendations
To select the target population	BCLC stage	Include patients according to the specific BCLC stage (A–C)
	Child–Pugh classification	Include patients in Child–Pugh A to minimize deaths unrelated to HCC
	Biomarker-based enrichment	Include subpopulations with specific activation of the signalling pathway or oncogenic drivers
To choose the appropriate primary end points	Overall survival	In Phase III studies assessing primary treatments
	Time to recurrence	In Phase II/III studies assessing adjuvant treatments
	Time to progression or overall response rate	In Phase II studies assessing primary treatments
	Surrogate end points	Time to recurrence, time to progression and overall response have to be assessed according to the modified RECIST criteria ²³²
	Composite end points	Progression-free survival is a vulnerable end point in HCC
To decide the adequate control treatment group	Adjuvant therapy after resection or local ablation	Placebo for control treatment group
	Intermediate-stage disease test group	Transcatheter arterial chemoembolization for the control treatment group
	First-line treatment for advanced-stage disease test group	Sorafenib plus supportive care for the control treatment group
	Second-line treatment for advanced-stage disease test group	Placebo plus supportive care for the control treatment group
To stratify factors before randomization	Adjuvant	High risk (size >3 cm, MVI and satellites) and geographical region
	Intermediate stage	Child–Pugh class, AFP and geographical region
	First-line advanced stage	ECOG scale, MVI, EHS and geographical region
	Second-line advanced stage	ECOG scale, MVI, EHS, geographical region, AFP of >400 ng per ml and type of progression

AFP, α -fetoprotein; BCLC, Barcelona Clinic Liver Cancer; ECOG, Eastern Cooperative Oncology Group; EHS, extrahepatic spread; HCC, hepatocellular carcinoma; MVI, microvascular invasion; RECIST, response evaluation criteria in solid tumours.

or in combination with sorafenib²³⁴. Similarly, over-expression and/or amplification of *FGF19* is characteristic of 10–20% of cases of HCC^{65,66}. New-generation FGFR-specific kinase inhibitors tested in preclinical models have demonstrated that *FGF19* amplification is a predictive biomarker of response²³⁵. More recently, BLU9931, a highly specific FGFR4 inhibitor, demonstrated preclinical activity in patient-derived xenografts, providing the rationale for exploring this compound in Phase I or II clinical trials²³⁶. Finally, universal activation of the RAS–MAPK axis is common in patients with advanced HCC²³⁷. First attempts to block this pathway with MEK inhibitors (for example, selumetinib) have failed to detect significant objective radiological tumour responses²³⁸. The Assessing BAY86-9766 Plus Sorafenib for the Treatment of Liver Cancer (BASIL) trial tested refametinib (a MEK1 and MEK2 inhibitor) in advanced HCC, and results indicated that *RAS* mutations could be a potential biomarker of treatment response²³⁹.

Alternatively, recent data have emerged pointing towards biomarker-driven selection of candidates in testing drugs in Phase III trials. For example, ramucirumab is currently in Phase III trials for second-line treatment of patients with advanced HCC and an AFP of >400 ng per ml on the basis of subgroup analysis data²³⁰. Similarly, tivantinib, a tubulin and MET inhibitor²⁴⁰, is currently being tested in Phase III trials

only in MET-positive patients in a second-line setting. Activation of MET is estimated to occur in approximately 50% of these patients. A similar drug, cabozantinib, is being tested as a second-line therapy in an all-comers trial after preliminary positive effects in clinical studies²⁴¹.

Immune checkpoint inhibitors have been approved by regulatory agencies owing to their considerable activity in patients with advanced-stage melanoma and lung cancer²⁴². The rationale for an immunological approach to treat HCC has been proposed for years. Indirect evidence includes the pivotal role that the immune system has in the development of chronic liver disease and HCC, dendritic cell-based approaches showing certain antitumour activity^{243,244} and occasional reports of spontaneous remission. Although pilot studies with the cytotoxic T lymphocyte protein 4 (CTLA4)-blocking antibody tremelimumab did not produce signals of efficacy²⁴⁵, a recent Phase I/II trial with the programmed cell death protein 1 (PD1) inhibitor nivolumab showed a manageable adverse event profile and produced durable responses in patients with HCC who had tumours that were resistant to sorafenib²⁴⁶. Phase III trials have been designed to test this drug. Finally, two alternative types of molecular-based therapies are currently being explored in early clinical research studies: epigenetic modifying therapies^{247,248} and microRNAs²⁴⁹.

Molecular targeted therapies are associated with acquired drug resistance. The most common traits of acquired resistance mechanisms are the persistent activation of the oncogenic target itself owing to secondary mutations — for example, mutation of *EGFR* (T790M) in gefitinib- or erlotinib-resistant patients with non-small-cell lung cancer²⁵⁰ — or acquired mutations in alternative drivers of the pathway — such as mutations in genes encoding MAPKs in vemurafenib-resistant BRAF melanoma²⁵¹. Acquired resistance to sorafenib in HCC has mostly been explored in experimental models. Several mechanisms have been implicated, including activation of MAPK14 signalling⁶⁸,

enrichment of tumour-initiating cells and reactivation of IGF-FGF signalling²⁵².

Quality of life

Unsurprisingly, as liver disease and HCC tumours progress, quality of life (QOL) suffers. The purpose of measuring QOL should be to compare outcomes between treatment groups, even if one is a placebo. There is little agreement as to the best method of measuring QOL in HCC research. Although general instruments are in use, there are two that are specific to HCC. These are the European Organization for Research and Treatment of Cancer Quality of Life Questionnaire (EORTC QLQ) 18

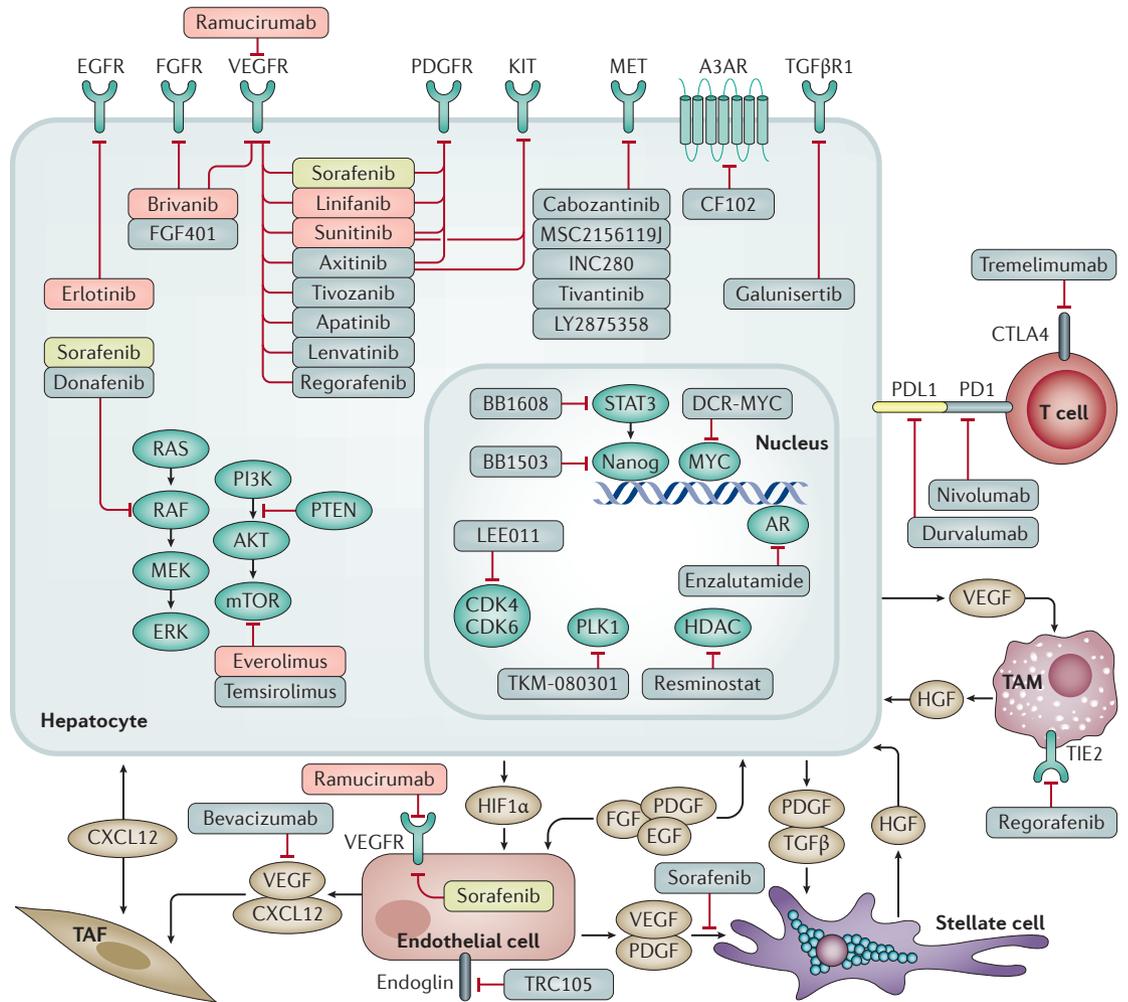


Figure 5 | Molecular targeted therapies for HCC and their target signalling pathways. Summary of treatments tested in Phase II–III clinical trials. Transforming growth factor- β (TGF β) receptor type 1 (TGF β R1) has serine/threonine kinase activity, whereas epidermal growth factor (EGF) receptor (EGFR), fibroblast growth factor (FGF) receptor (FGFR), vascular endothelial growth factor (VEGF) receptor (VEGFR), platelet-derived growth factor (PDGF) receptor (PDGFR), mast/stem cell growth factor receptor (KIT) and angiotensin 1 receptor (TIE2) have tyrosine kinase activity. Green boxes indicate drugs with positive Phase III studies, red boxes indicate drugs with negative results from Phase III trials and drugs in grey boxes have been tested in Phase II studies. A3AR, adenosine A₃ receptor; AR, androgen receptor; CDK, cyclin-dependent kinase; CTLA4, cytotoxic T lymphocyte protein 4; CXCL12, C-X-C motif chemokine 12 (also known as stromal cell-derived factor 1); HDAC, histone deacetylase; HGF, hepatocyte growth factor; HIF1 α , hypoxia-inducible factor 1 α ; MET, also known as hepatocyte growth factor receptor; mTOR, mammalian target of rapamycin; PD1, programmed cell death protein 1; PDL1, programmed cell death protein 1 ligand 1; PI3K, phosphoinositide 3-kinase; PLK1, polo-like kinase 1; PTEN, phosphatase and tensin homologue; STAT3, signal transducer and activator of transcription 3; TAF, tumour-associated fibroblast; TAM, tumour-associated macrophage.

Table 5 | Molecular targeted therapies under evaluation in Phase II or III randomized controlled trials in HCC

Drug	Phase	Target(s)	Trial enrichment	Primary end point	ClinicalTrials.gov registry number
Anti-angiogenic agents					
Lenvatinib	III	VEGFR2 and VEGFR3	No	Overall survival	NCT01761266
Ramucirumab	III	VEGFR2	AFP >400 ng per ml	Overall survival	NCT02435433
Regorafenib	III	VEGFR2 and TIE2	No	Overall survival	NCT01774344
Apatinib	III	VEGFR2	No	Overall survival	NCT02329860
Axitinib	II	VEGFR, KIT and PDGFR	No	Disease control rate	NCT01273662
Tivozanib	I/II	VEGFR	No	Progression-free survival	NCT01835223
TRC105 + sorafenib	I/II	Endoglin	No	Maximum tolerated dose or time to progression	NCT01306058
Cell cycle inhibitors and antiproliferative agents					
Tivantinib	III	Tubulin and MET	MET expression	Overall survival	NCT01755767
Cabozantinib	III	MET and VEGFR	No	Overall survival	NCT01908426
INC280	II	MET	MET pathway deregulation	Time to progression	NCT01737827
MSC2156119J	I/II	MET	MET expression	Dose-limiting toxicity or time to progression	NCT01988493
LY2875358 + ramucirumab	I/II	MET and VEGFR2	No	Dose-limiting toxicity or overall response rate	NCT02082210
Galunisertib ± sorafenib	II	TGFβR1	No	Overall survival	NCT02178358
Galunisertib + nivolumab	I/II	TGFβR1 and PD1	No	Maximum tolerated dose	NCT02423343
Temsirolimus + sorafenib	II	mTOR	No	Time to progression	NCT01687673
Donafenib	I/II	RAF	No	Dose-limiting toxicity	NCT02229071
FGF401	I/II	FGFR4	FGFR4 and KLB expression	Dose-limiting toxicity, time to progression or overall response rate	NCT02325739
TKM-080301	I/II	PLK1	No	Maximum tolerated dose	NCT02191878
BLU-554	I/II	FGFR4	FGF19 amplification or overexpression	Maximum tolerated dose	NCT02508467
Immune modulators					
Nivolumab	II and III	PD1	No	Overall response rate and overall survival	NCT02576509 NCT01658878
MEDI4736 + tremelimumab	I/II	PDL1 and CTLA4	No	Dose-limiting toxicity	NCT02519348
Miscellaneous					
CF102	II	A3AR	No	Overall survival	NCT02128958
Enzalutamide	II	Androgen receptor	No	Overall survival	NCT02528643
LEE011	II	CDK4 and CDK6	No	Progression-free survival	NCT02524119
BBI503	II	Nanog	No	Disease control rate	NCT02232633
BBI608/503 + sorafenib	I/II	STAT3 and nanog	No	Dose-limiting toxicity	NCT02279719
DCR-MYC	I/II	MYC	No	Disease control rate	NCT02314052
Resminostat	I/II	HDAC	No	Dose-limiting toxicity	NCT02400788

A3AR, adenosine A₃ receptor; AFP, α-fetoprotein; CDK, cyclin-dependent kinase; CTLA4, cytotoxic T lymphocyte protein 4; FGF, fibroblast growth factor; FGFR, FGF receptor; HDAC, histone deacetylase; KIT, mast/stem cell growth factor receptor; KLB, β-klotho; MET, hepatocyte growth factor receptor; mTOR, mammalian target of rapamycin; PD1, programmed cell death protein 1; PDGFR, platelet-derived growth factor receptor; PDL1, programmed cell death protein 1 ligand 1; PLK1, polo-like kinase 1; STAT3, signal transducer and activator of transcription 3; TGFβR1, transforming growth factor-β receptor type 1; TIE2, angiopoietin 1 receptor; VEGFR, vascular endothelial growth factor receptor.

Box 1 | Unmet medical needs in HCC research**Epidemiology**

- Assess the effect of novel antiviral therapies in hepatocellular carcinoma (HCC) occurrence and prevention

Molecular pathogenesis

- Integrate molecular subclasses into the clinical staging system to better guide treatment allocation
- Improve our understanding of tumour heterogeneity
- Elucidate the roles of different microenvironment constituents in HCC pathogenesis and progression

Development of drugs

- Target oncogene addiction loops that result from DNA amplifications and gene mutations or overexpression
- Develop drugs that block β -catenin and transforming growth factor- β activity
- Improve models for the preclinical testing of novel drugs

Clinical trials

- Randomized controlled trials to test new treatments in the adjuvant setting, to prevent dropout on the waiting lists for transplantation, to test combination therapies in intermediate and advanced HCC and to test second-line therapies and radioembolization
- Pivotal proof-of-concept Phase II trials and trial enrichment for oncogenic drivers or signalling pathways
- Systematic inclusion of cost–benefit analyses

Identification and validation of biomarkers

- Identify biomarkers predicting treatment response
- Develop biomarkers for early detection in surveillance programmes

Quality of life

- Identify the best tool for measuring quality of life and integrate the tool into clinical trial design as an end point

and the Functional Assessment of Cancer Therapy–Hepatobiliary (FACT–Hep) questionnaire^{253–255}. Both of these tools are derivatives of more general QOL questionnaires for cancer and have been validated externally, but there is little indication that they are measuring the same thing or that they are comparable.

There is very little literature on QOL in HCC. Most studies report changes in QOL in studies with single treatment groups, and very few studies have been designed primarily to compare two different treatments in patients with similar stage disease. For example, one study compared QOL after resection with QOL following radiofrequency ablation²⁵⁵. As expected, QOL was much better after radiofrequency ablation than after resection, and remained superior up to 36 months post treatment. In addition, QOL following radioembolization has been compared with TACE²⁵⁶. In this study, there was no overall difference in QOL between the two groups, but the sample size was small. Despite the lack of statistically significant differences, QOL was decreased at 2 and 4 weeks in the TACE group, whereas in the radioembolization group some aspects of QOL actually improved. However,

in this study, the patients who underwent radioembolization had more advanced disease than those who underwent TACE, so the results are not directly comparable. Finally, the SHARP trial that demonstrated the survival benefits of sorafenib compared to a placebo also tested time-to-symptomatic progression — as measured by the Functional Assessment of Cancer Therapy–Hepatobiliary Symptom Index 8 (FHSI8) — as a co-primary end point. The negative results of this end point contrasted with the survival benefits obtained by sorafenib, thus challenging the accuracy of the tool used¹⁹.

Outlook**Global disease burden**

The global burden of HCC is increasing and considerable challenges are ahead for improving the understanding and treatment of this complex disease. The main unmet medical needs for HCC are summarized in BOX 1. Considering that HBV and HCV infection are the main risk factors for HCC development, it can be presumed that the implementation of new, more effective antiviral therapies might decrease the incidence of HCC on a global scale in the following decade. Antiviral therapies approved for HCV infection achieve sustained viral clearance in more than 90% of cases^{202,257}, and well-established anti-HBV therapies lead to undetectable viral titres (circulating HBV DNA) in most patients. Nevertheless, although risk factors can be eliminated (efficacy), such elimination does not always translate into global improvements (effectiveness) owing to suboptimal implementation of treatments in underdeveloped areas and for other complex reasons. Similarly, even though surveillance is cost-effective in HCC, the global implementation of such programmes remains suboptimal and is estimated to engage <50% of the target population in western countries (Europe and North America). Public health policies encouraging the implementation of such programmes in well-defined populations should lead to an increase in early tumour detection and hence survival benefits. Finally, in parallel with advances in the treatment of viral hepatitis, other aetiologies of HCC are emerging, particularly NASH-related HCC, which is associated with obesity and diabetes. The effect of these unfolding risk factors on HCC burden remains to be elucidated, but might counterbalance the decreases expected with HCV control.

Drug and biomarker discovery

High-throughput genomic studies reporting gene sequencing of large cohorts have already established the main oncogenic drivers of HCC. However, most of these drivers, such as the *TERT* promoter, *TP53* and *CTNNB1*, have not proven to be targetable and, as such, understanding of their role in HCC has not translated into improving the management of the disease²¹⁸. Drug discovery targeting these complex proteins and regulatory mechanisms should represent a major breakthrough in HCC research^{218,258}. By contrast, the identification of driver mutations or amplifications in relevant genes — such as *FGF19*, *CCND1* and *VEGF* — has not yet translated into proof-of-concept early clinical trials based on biomarkers. To understand the targets of the microenvironment

in tumour progression and the responses to therapies clearly requires further exploration^{79,231}, considering the clinical relevance of these areas in the risk of tumour development, prognosis and immunomodulation^{76–79}. In addition, despite results reporting preclinical testing of drugs in genetically modified models or patient-derived xenografts, clinically relevant models recapitulating the spectrum of human disease are still suboptimal.

Disease management

Standard therapy. Only five treatments are recommended by the European Association for the Study of the Liver (EASL) and the American Association for the Study of Liver Diseases (AASLD) guidelines for HCC management^{3,158,159} (FIG. 4; TABLE 3). Several other treatments have been tested in RCTs since the last successful therapy (sorafenib) was approved, and all of these studies produced negative or inconclusive results. In early HCC, no adjuvant therapy has shown efficacy¹⁶⁸ and this represents an important unmet medical need. In addition, since the advent of radiofrequency as the mainstay of local ablation, no other proposed approach, such as microwave, has led to major control of the disease. Chemoembolization remains the sole proven effective therapy in intermediate HCC. None of the combination therapies with chemoembolization has shown additive outcome advantages. Phase III trials testing alternative therapies, such as radioembolization, are awaited. Indications beyond guidelines for resection²⁵⁹ and TACE are widely applied in clinical practice, particularly in Asia²⁶⁰, and this represents an important challenge that needs to be addressed with robust and well-designed studies.

Progress in treating advanced disease. Management of advanced HCC has attracted substantial attention during the past decade. Trials testing systemic chemotherapy have been almost abandoned and the few that were conducted showed disappointing results²¹⁹. The regulatory approval of sorafenib represented a breakthrough and challenged the concept of advanced HCC as a cancer that is not druggable¹⁹, paving the way for testing novel drugs. What has been unexpected is the failure of all molecular agents tested after sorafenib^{224–230}. Consequently, this major cause of cancer-related death remains one of the few solid tumours with only one systemic therapy available. New avenues are being explored to overcome this situation. Among the drugs currently being tested in Phase II and III trials, some are exploring areas that led to major advancements in the management of other cancers, such as immune checkpoint inhibition^{246,261} (FIG. 5; TABLE 5). Others are targeting specific subpopulations of patients with HCC based on biomarkers identified in Phase I/II studies, such as tivantinib for patients who are MET-positive²⁴⁰ or ramucirumab for patients with tumour progression on sorafenib with an AFP of >400 ng per ml²³⁰. Finally, some studies are exploring targeting of specific tumour-driver genes that are responsible for ‘oncogenic addiction’. Oncogene addiction is defined as the state of dependency of tumour cells on a given driver. As solid tumours are expected to share four to eight drivers per tumour, the addiction to one

specific oncogene confers status of primacy to this target²⁶². Thus, clinically relevant antitumour responses are achieved when targeting those drivers, as is the case for inhibiting the effects of anaplastic lymphoma receptor tyrosine kinase (*ALK*) fusion rearrangement with crizotinib in patients with non-small-cell lung cancer²⁶³. Trial design in HCC should follow specific recommendations that are provided in TABLE 4.

The future of precision medicine for HCC. HCC is one of the few cancers for which non-invasive radiological criteria suffice for the diagnosis of the disease in patients with an underlying risk factor (cirrhosis)^{3,15}. This clinical approach conflicts with the concept of precision medicine, which is based on the administration of selective therapies targeting molecular alterations relevant to tumour progression in a given individual. To implement precision medicine in HCC, a tumour biopsy is required and, as such, routine biopsy has now been adopted in guidelines for clinical trials in HCC research³. The reliability of this strategy is based on the assumption that one tumour biopsy is sufficient to recapitulate the molecular information found in the entire neoplasm. This concept is currently debatable in oncology owing to evidence of inter-tumoral and intra-tumoral heterogeneity in all malignancies, including in HCC^{31,264}. This observation prompts an important question: can we rely on a single biopsy for decision making or should we obtain multiple biopsies, even though this more thorough approach appears clinically impractical?

To explore heterogeneity we need to understand the concept of trunk, branch and passenger mutations^{31,265}. Trunk mutations occur at the onset of the disease and are potent transforming drivers present in all cells of a given tumour at early stages³¹. Conversely, branch mutations develop late in the natural history of the tumours or as a result of acquired resistance under the pressure of therapies, and thus are only present in a subgroup of tumour cells. Finally, passenger mutations, the most common type of mutation, are of marginal relevance in terms of cell transformation, progression or dissemination, but they may be helpful in defining the clonality of tumours or their immunogenicity. Therefore, as reported in solid cancers such as non-small-cell cancer²⁶⁶, breast cancer and melanoma, molecular therapies that achieve good tumour response and survival benefits can do so by targeting trunk mutations that have been identified with a single biopsy. Conversely, heterogeneity might be cumbersome when branch mutations have a more dominant role (for instance, at very advanced stages²⁶⁶ or in the setting of acquired resistance²⁶⁵). In these instances, liquid biopsy — measuring tumour DNA and mRNA in cell-free plasma or circulating tumour cells — emerges as the most promising alternative for the molecular monitoring of tumour progression and relapse^{267,268}. Recent reports point to the benefits of liquid biopsy in recapitulating tissue trunk-driver mutations²⁶⁹ and in capturing unique branch subclonal mutations acquired under treatment pressure²⁷⁰. Finally, tumour heterogeneity has more important therapeutic implications for molecular targeted agents than for immune checkpoint inhibitors.

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Author contributions

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Competing interests

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