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APPENDIX I Meetings

I-V Instructions to authors

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Evaluation of virus-specific cellular immune response in transplant patients

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Abstract

Virus-specific immune responses have a major impact on the outcome of the infection. Viral agents that are characterized by latency, such as herpesviruses and polyomaviruses, require a continuous immune control to reduce the extent of viral reactivation, as viral clearance cannot be accomplished, independently from the anti-viral treatment. In transplant patients, morbidity and mortality related to viral infections are significantly increased. In fact, the key steps of activation of T-cells are major target for anti-rejection immunosuppressive therapy and anti-viral immune response may be altered when infected cells and cellular effectors of immune response coexist in a transplanted organ. The role of cellular immune response in controlling viral replication and the main methods employed for its evaluation will be discussed. In particular, the main features, including both advantages and limitations, of available assays, including intracellular cytokine staining, major histocompatibility complex - multimer-based assays, Elispot assay, and QuantiFERON test, will be described. The potential applications of these assays in the transplant context will be discussed, particularly in relation to cytomegalovirus and polyomavirus BK infection. The relevance of introducing viro-immunological monitoring, beside virological monitoring, in order to identify the

risk profile for viral infections in the transplant patients will allow for define a patient-tailored clinical management, particular in terms of modulation of immunosuppressive therapy and anti-viral administration.

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Key words: T-cell; Immune response; Viral replication; Interferon- γ ; Transplantation

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INTRODUCTION

Virus-specific immune responses have a major impact on the outcome of the infection. Viral infections are usually followed by the complete clearance of the virus. However, in some cases, immune response is not able to eliminate completely the virus, thus the infection may become persistent. In general, cellular immune response plays a more relevant role in the viral clearance, whereas humoral immune response protects against the reinfection. Immune response may vary according to genetic substrate of the individual and the degree of immunocompetence.

In transplant patients, morbidity and mortality related to viral infections are significantly increased. In fact, anti-rejection immunosuppressive therapy weakens the im-

immune functions and anti-viral immune response may be altered when infected cells and cellular effectors of immune response coexist in a transplanted organ.

In particular, viral agents that are characterized by latency, such as herpesviruses and polyomaviruses, require a continuous immune control to reduce the extent of viral reactivation, as viral clearance cannot be accomplished, independently from the anti-viral treatment. The immunologic control of these viruses in the immunocompromised host is complex and involves both the innate and adaptive immune systems. As regards innate immune system, polymorphisms of Toll-like receptors as well as certain proteins, including complement proteins, and defects in natural killer cells are associated with an increased risk of viral reactivation. Adaptive immune responses of B and T cells are critical in controlling viral replication. In particular, while B cells may be important in the humoral response in that they produce neutralizing antibodies targeting virions, T-cell mediated responses, including both CD4+ and CD8+ T-cells, are crucial components for controlling viral replication of persistent viruses^[1]. Several phenotypic markers and functions have been investigated in order to characterize virus-specific CD4+ and CD8+ T cell responses, evidencing a great heterogeneity against different viruses, with functional signatures being probably specific for each virus and being predominantly regulated by the levels of antigen load. In this context, polyfunctional secretion and proliferation [i.e., interferon (IFN)- γ and interleukin-2] of CD4+ and CD8+ T cells play a protective role in terms of antiviral immunity in chronic viral infections^[2,3].

METHODS FOR EVALUATING VIRUS-SPECIFIC CELLULAR IMMUNE RESPONSE

Evaluation of virus-specific T-cell responses can be made by different methods (Table 1), including: intracellular cytokine staining (ICS), major histocompatibility complex (MHC)-multimer-based assay, Enzyme-linked Immunospot (ELISPOT) assay and QuantiFERON-cytomegalovirus (CMV) assay (specific for CMV)^[4-6]. Beside these virus-specific assays, it is also available a non-specific test, the ImmunKnow assay, that is used to evaluate the overall CD4+ immune response.

Most of these assays have been used in experimental settings and only for some of them commercial kit are available. The majority of the assays are based on the detection of IFN- γ after stimulation with specific viral antigens or viral lysates, the so-called IFN- γ releasing assays (IGRA). Anyway, other markers, including different cytokines (e.g., interleukin-2, tumor necrosis factor- α , *etc.*) can be used. In terms of clinical utility, an ideal test should evaluate both virus-specific CD4+ and CD8+ T-cell immune response from both quantitative (number of virus-specific T cells) and function (number of functional T cells) points of view. Moreover, for an appropriate use in the clinical setting, an assay should be easy and rapid to perform, relatively inexpensive, highly reproducible, and

applicable in different routine contexts. At the moment, all the assays present specific advantages and limitations.

Intracellular cytokine staining

Most studies have analyzed virus-specific T-cell responses using ICS for IFN- γ using flow cytometry^[4]. Moreover, ICS allows for evaluation of polyfunctionality of T cells^[2,3]. Whole blood or isolated peripheral blood mononuclear cells (PBMCs) are stimulated with virus-specific peptides or viral lysates. The assay is not restricted for human leukocyte antigen (HLA) when viral lysate is used and there is no need to know HLA type. Stimulated cells are stained with monoclonal antibodies directed against IFN- γ . The method is rapid, with a short incubation time and results being available within 24 h; can be performed starting from low blood volume (approximately 1 mL); it allows for identification of CD4+ and CD8+ T cells. The major drawbacks are the need for a flow cytometer and the lack of standardization. Among the advantages, there is the possibility to freeze the cells and send them to reference laboratory for testing.

MHC - multimer-based assays

MHC-multimer-based assays is characterized by the direct staining of peptide-specific T-cells using peptide-conjugated MHC class I tetramers or pentamers^[7]. This method evaluates CD8+ T-cell responses, however it is epitope-specific and require knowledge of the patient's HLA type. As for ICS, there is the need for access to a flow cytometer and the assay is not standardized. Among the advantages, the assay is rapid (1-2 h) and can be performed starting from low blood volume (0.5-1 mL).

Elispot

The ELISPOT assay determines the number of T-cells secreting IFN- γ in specific response to a viral agent. Following stimulation with viral peptides or viral lysates, the produced IFN- γ is captured by a specific antibody, and then quantified using a labeled antibody^[8]. The assay evaluates both CD4+ and CD8+ responses and there is no need to know HLA, as well as to use a flow cytometer. There is the possibility to freeze the cells and send them to reference laboratory for testing. Among the disadvantages, the method requires a relatively high volume of blood (approximately 7-10 mL) and cannot differentiate between CD4+ and CD8+ cells. Although some approaches to standardize the assay, it is still not standardized. Results are available within 24-30 h. A mitogen control assay can determine general T-cell responsiveness. Commercially available kits for virus-specific ELISPOT assays are available (AID, Autoimmun Diagnostika GmbH, Strassberg, Germany).

QuantiFERON-CMV

This is a CMV-specific ELISA-based IFN- γ release assay and is commercially available (Cellestis Inc., Melbourne, Australia). It can be easily performed starting from low blood volume (3 mL) and results are available after

Table 1 Methods for evaluating cellular immune response

Method	Advantages	Limitations
Intracellular cytokine staining	Low volume blood Rapid Knowledge of HLA not required Identification of CD4+ and CD8+	Flow cytometer required Not standardized
MHC multimer staining	Low volume blood Rapid	Flow cytometer required Not standardized
Elispot assay	Identification of CD4+ and CD8+	Not standardized

MHC: Major histocompatibility complex; HLA: Human leukocyte antigen.

30-40 h. It evaluates only CD8+ responses. The assay may yield nonresponse results in the presence of global immunosuppression (nonresponse to mitogen) as in transplant patients. Test sensitivity decreases in lymphopenic patients because an appropriate number of T-cells are required for the production of IFN- γ .

ImmunKnow assay

The Cylex ImmunKnow assay (Cylex Inc., Columbia, MD, US) is a specific assay, which is commercially available. It measures the overall immune response and is indicative of immunosuppression. It determines the amount of ATP produced in response to whole-blood stimulation by an aspecific mitogen (phytohemagglutinin).

ROLE OF VIRUS-SPECIFIC CELLULAR IMMUNE RESPONSE IN TRANSPLANT PATIENTS

T-cell responses, including both CD4+ and CD8+, are critically important for controlling viral replication. This has been demonstrated by the use of adoptive immunotherapy for treatment of CMV and EBV infections and by the higher frequency of viral reactivation in patients treated with anti-lymphocyte agents. Early reconstitution of cellular immune response prevents or reduces the duration of the infection, thus avoiding the onset of disease or relapses. On the other hand, a delayed or reduced response represents the pathogenic base for the occurrence of repeated episode of infection and symptomatic disease (in the absence of anti-viral treatment)^[7-11]. The role of cellular immune response in the context of organ transplantation has been studied particularly for CMV. In particular, it has been evidenced the basic role played by both CD4+ and CD8+ responses^[9]. The CD8+ response is prevalent during the acute phase of infection and it provides for an immediate control of viral replication by the killing of cells in which CMV is replicating. The CD4+ response is fundamental for the long-term maintenance of antiviral control. In a study on solid-organ transplant recipients, it has been demonstrated that stable levels of CMV-specific CD4+ cells correlates with the absence of infectious complications, whereas in patients with unstable levels of specific-CD4+ cells, several episodes of viral reactivation occurred^[10]. The median

frequency of CMV-specific CD8+ cells was significantly higher in a group of 27 heart and lung transplant patients in cases that did not developed CMV-disease^[11]. Moreover, in a study on 73 renal transplant recipients, also the median frequency of CMV-specific CD4+ cells was significantly higher in patients that did not developed CMV disease^[12,13]. Gerna and coll. proposed the classification of transplant recipients into two groups in relation to the temporal profile for CMV-specific cellular immune response^[14]. The Authors considered a group of early responders, in which reconstitution of cellular immune response occurred within 30 d posttransplantation, and a group of late responders, in which cellular immune response reconstitution occurred at > 30 d posttransplantation and/or was reduced. In these patients, the delay in CD4+ response appeared to be particularly critical^[15].

Another virus for which specific cellular response has been investigated is polyomavirus BK. It has been evidenced that healthy BKV-seropositive individuals have CD4+ and CD8+ cells specific for BKV major antigens (including large T antigen and capsid viral protein VP1)^[16]. The unbalance between viral replication and BKV-specific cellular immune response should represent the common denominator for the pathogenesis of polyomavirus-associated nephropathy, a viral-associated complication potentially leading to the lost of the transplanted organ and mainly occurring in renal transplant patients^[15,16]. It has been evidenced that cellular response to large T antigen and VP1 is significantly higher in patients with decreasing viremia in comparison to those with increasing viremia^[16]. Moreover, it seems that the level of immune response is correlated particularly to the administration of some immunosuppressive drugs. For example, in a study on kidney transplant patients *in vivo*, responses were inversely correlated with tacrolimus through levels, but not mycophenolate mofetil, prednisone or the overall immunosuppressive dosing^[17]. However, the clinical role of BKV viro-immunological monitoring in renal transplant recipient needs to be further investigated, in particular it is likely that it could represent an approach to modulate immunosuppression.

An interesting issue in the context of protective immunity is represented by the role of mucosal immunization. As mucosal surfaces represent the major entry for many human pathogens (including HSV, HIV, respiratory viruses, as well as mycobacteria), induction of mucosal

immune system, including both innate and adaptative responses (CD4+ T helper cells, Th17 cells, high avidity CD8+ cytotoxic T lymphocytes, as well as IgA and IgG1 neutralizing antibodies) seem required for an effective protection against pathogens that lead to chronic infections^[18,19].

CONCLUSION

The increase in the number of transplant patients and the use of deeply immunosuppressive drugs have lead to the emergence of viral infections that may influence the outcome of these patients. Beside the adoption of protocols for close virological monitoring, several studies have underlined the role of viro-immunological monitoring in the evaluation of patient's risk of infection and disease, decision on treatment by modulating immunosuppression and/or using antiviral, and adoption of other diagnostic strategies. There is no defined method to evaluate the cellular immune response in transplant recipients, as at the moment no assay is standardized and further studies, particularly on procedures, quality controls and references, as well as interpretation of results are required to standardize. However, ELISPOT assay is gaining increasing recognition due to the potential to evaluate both CD4+ and CD8+ responses and other favoring features. Further studies on the clinical role of cellular immune responses are required, in particular with the aim of define modes and temporal profile for viro-immunological monitoring in different transplant contexts and for different viral agents.

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Roles of the PI3K/Akt pathway in Epstein-Barr virus-induced cancers and therapeutic implications

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Abstract

Viruses have been shown to be responsible for 10%-15% of cancer cases. Epstein-Barr virus (EBV) is the first virus to be associated with human malignancies. EBV can cause many cancers, including Burkett's lymphoma, Hodgkin's lymphoma, post-transplant lymphoproliferative disorders, nasopharyngeal carcinoma and gastric cancer. Evidence shows that phosphoinositide 3-kinase/protein kinase B (PI3K/Akt) plays a key role in EBV-induced malignancies. The main EBV oncoproteins latent membrane proteins (LMP) 1 and LMP2A can activate the PI3K/Akt pathway, which, in turn, affects cell survival, apoptosis, proliferation and genomic instability *via* its downstream target proteins to cause cancer. It has also been demonstrated that the activation of the PI3K/Akt pathway can result in drug resistance to chemotherapy. Thus, the inhibition of this pathway can increase the therapeutic efficacy of EBV-associated cancers. For example, PI3K inhibitor Ly294002 has been shown to increase the effect of 5-fluorouracil in an EBV-associated gastric cancer cell line. At present, dual inhibitors of PI3K and its downstream target mammalian target of rapamycin have been used in clinical trials and may be included in treatment regimens for EBV-associated cancers.

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Key words: Epstein-Barr virus; Latent membrane proteins 1; Latent membrane proteins 2A; Phosphoinositide 3-kinase/protein kinase B; Carcinogenesis; Drug resistance

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INTRODUCTION

It is now evident that virus-induced cancers account for 10%-15% of all cancer cases^[1,2]. Studies of viruses as causes of cancer have played an important role in the elucidation of the mechanisms of carcinogenesis, as indicated by several Nobel Prizes being awarded to scientists in the field of oncoviruses. The initial work to demonstrate that viruses can induce cancer was done by Peyton Rous^[3,4]. He identified Rous sarcoma virus as the cause of chicken sarcoma in 1911, and the discovery earned him the 1966 Nobel Prize. The human analogue of the viral oncogene *v-Src* was found and named *c-Src*, which was the first human oncogene^[5,6]. This work led to the awarding of a Nobel Prize to John Michael Bishop and Harold E. Varmus in 1989. More recently, Harald zur Hausen identified human papillomavirus (HPV) as the cause of cervical cancer (Nobel Prize, 2008)^[7]. This discovery led to the invention of the vaccines Gardasil and Cervarix which can effectively prevent HPV-associated cervical cancer^[8,9]. The Epstein-Barr virus (EBV); [also called human herpesvirus 4 (HHV-4)] is the first virus identified (in 1964) to be associated with human cancers^[1]. It belongs to the

B-lymphotropic γ -herpesvirus family with a genome consisting of 172 kb of linear double-stranded DNA^[1,10,11]. EBV infects both epithelial and B-cells and, thus, can induce both epithelial cancers and lymphoma^[12,13]. After EBV infection, there are two viral phases: lytic and latent^[14]. In its lytic phase, the virus replicates in epithelial cells, and, in its latent phase, it transforms B-cells.

Cancer is characterized by the loss of the balance between cell proliferation and apoptosis^[15-17]. It has been demonstrated that EBV can increase cell proliferation and decrease apoptosis^[18]. EBV has been shown to cause several B-cell lymphomas, including Burkitt's lymphoma, Hodgkin's lymphoma and post-transplant lymphoproliferative disorders (PTLDs). This notion is demonstrated by the detection of EBV virus in these cancers, the replication of the virus and its ability to transform B-cells^[18,19]. EBV is also closely associated with epithelial cancers. For example, EBV can cause nasopharyngeal carcinoma (NPC), a highly metastatic cancer^[20]. The EBV latent membrane proteins (LMP) 1 and LMP2A are frequently detected in NPC^[21]. LMP1 may also lead to metastasis of the cancer, as it has been demonstrated that LMP1 can cause epithelial-mesenchymal transition (EMT) *via* transcription factor Snail^[22]. Both LMP1 and Snail are correlated with NPC metastasis^[22]. Overall, EBV has been shown to be responsible for about 10% of gastric cancers worldwide^[23-25]. However, the mechanisms for EBV-induced gastric cancer are not clear.

Many EBV proteins are expressed in the latent phases and are potentially related to carcinogenesis. These proteins include EBV nuclear antigen (EBNA)-1, -2, -3A, -3B, -3C and leader protein, and LMP-1, -2A and -2B^[14]. However, the major identified oncoproteins in EBV are LMP1 and LMP2A^[20,26]. These proteins can activate multiple signal pathways, such as the phosphoinositide 3-kinase/protein kinase B (PI3K/Akt), the mitogen-activated protein kinase (MAPK) and the signal transducer and activator of transcription 3, all of which are important for carcinogenesis^[15,27,28]. LMP1 is considered as an analog of the tumor necrosis factor receptor 1, and it can transform human B-lymphocytes and rodent fibroblasts *via* activation of multiple intracellular signal pathways through its two signaling domains, the carboxyl-terminal activating regions 1 and 2 (CTAR1 and CTAR2)^[29]. Activated pathways include the nuclear factor κ B (NF- κ B), PI3K/Akt, Notch, MAPK and Jun N-terminal protein kinase (JNK) signaling pathways^[27,30-32]. It has been demonstrated that point mutations in the C-terminal region of the LMP1 cytoplasmic domain can influence the transforming potential of the EBV by reducing the ability of LMP1 to activate PI3K/Akt, NF- κ B and AP1^[29]. LMP1 is essential for EBV-mediated B-cell transformation and is sufficient to transform several cell lines, such as rodent fibroblasts^[33]. A recent study showed that LMP1 expression is regulated by C/EBP in addition to EBNA2^[34]. This article will discuss how EBV-expressed proteins activate the PI3K/Akt pathway to cause carcinogenesis in EBV-associated cancers. Although EBV oncogenes can

affect many signal pathways, such as NF- κ B, MAPK, and JNK, it seems that the PI3K/Akt pathway is the most important. In an LMP1-mediated transformation of rodent fibroblasts, inhibition of PI3K activity by Ly294002 induced apoptosis and inhibited cell growth, however, the NF- κ B inhibitor BAY 11-7085 had no such effect^[35]. Another study also showed that the PI3K/Akt pathway, but not the MAPK or NF- κ B pathways, can account for the LMP-1-induced transformation^[36].

ROLE OF PI3K/AKT SIGNAL PATHWAY IN CARCINOGENESIS AND METASTASIS

In 1985, Lewis Cantley initially discovered that PI3K plays an important role in cancer^[37-41]. PI3K has now been extensively studied with investigation determining its role in carcinogenesis and the potential use of its inhibitors in the treatment of cancers^[42-44]. This kinase phosphorylates the 3' OH position of phosphatidylinositol 4,5-bisphosphate (PIP2) and converts it to phosphatidylinositol 3,4,5-triphosphate (PIP3), leading to activation of Akt^[45,46], which causes a cascade of cellular signal alterations *via* its downstream target proteins^[39].

Many factors, such as insulin, insulin-like growth factor-1, vascular endothelial growth factor, and cytokines interleukin (IL)-6, IL-17 can increase the activity of the PI3K/Akt pathway^[6,47-52]. Mutations of genes encoding key components in the pathway have been found to cause the pathway activation in many cancers^[38,53]. Many cancer-related viruses can also activate the PI3K/Akt pathway and rely on it for their transformations^[38,39]. Such viral oncoproteins include polyoma virus middle-T antigen, Rous sarcoma virus oncoprotein v-Src, HPV oncoproteins E6, E7 and the human T-cell leukemia virus type 1 oncoprotein Tax^[54-57]. It has also been demonstrated that the PI3K/Akt pathway plays a critical role in the carcinogenesis of EBV viral oncoproteins^[27].

Activated Akt, which is phosphorylated by PDK1, can affect many downstream targets^[38,42]. The resulting biological effects include increased genomic instability, increased proliferation, decreased apoptosis and changed cytoskeleton. (Figure 1)^[58]. Genomic instability is important for the accumulation of genetic mutations necessary for carcinogenesis^[59,60]. Recently, it was reported that constitutively active (CA) Met tyrosine kinase (hepatocyte growth factor receptor) can induce chromosomal instability (CIN), as indicated by increased centrosome counts, multinucleated cells and micronuclei formation^[61-63]. While CA-Met increased both phosphorylated Akt and phosphorylated Erk, only phosphorylated Akt is critical in CA-Met-induced CIN. The PI3K inhibitor Ly294002, PTEN (an inhibitor of PI3K), and siRNA against Akt all abolished CA-met mediated CIN^[62]. It has also been demonstrated that phosphorylation of Akt can block checkpoint kinase 1 (Chk1), which controls cell cycle progression and maintains genomic stability^[61,63,64]. The activation of Chk1 will phosphorylate cdc25A and induce the transient arrest of cells in G1 and S phase before

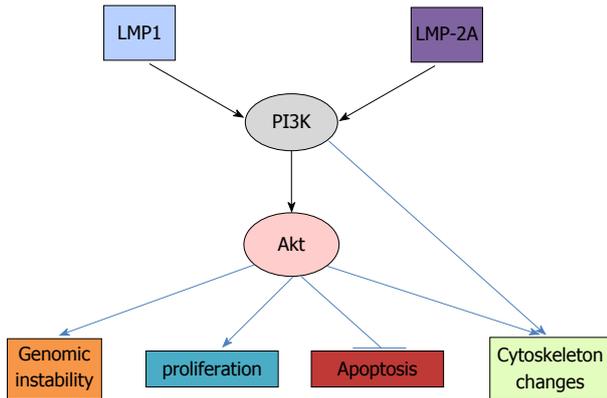


Figure 1 Epstein-Barr virus activates the phosphoinositide 3-kinase/protein kinase B pathway to transform cells. The Epstein-Barr virus latent proteins latent membrane protein (LMP)1 and LMP2A activate the phosphoinositide 3-kinase/protein kinase B (PI3K/Akt) pathway, which promotes carcinogenesis by increasing cell proliferation, genomic instability and cytoskeleton changes and by decreasing apoptosis.

the onset of mitosis^[65]. The inhibition of Chk1 has been shown to increase double-strand DNA breaks^[66].

The activation of Akt can increase cell proliferation and cell size by accelerating the cell cycle and cell metabolism. Akt can phosphorylate glycogen synthase kinase 3 β (GSK3 β) and, thus, deactivate it, leading to increased cyclin D1 and Myc^[67]. Myc is an oncoprotein that upregulates cyclin-dependent kinase 4 (CDK4)^[68]. Additionally, the Akt-mediated inhibition of the forkhead protein results in the downregulation of the cell cycle proteins p27 and p21^[69], thus promoting cell cycle progression^[70]. Both p27 and p21 are G1-checkpoint CDK inhibitors which can promote G1/S transition and thus, accelerate cell cycle^[17,71,72]. Another target activated by the activation of Akt is mTORC1, which plays an important role in the carcinogenesis of many cancers, including Burkitt's lymphoma and NPC^[73-75]. Phosphorylated Akt blocks TSC1 and 2 (tuberous sclerosis complex 1 and 2) and, thus, activates Rheb (Ras homolog enriched in brain), thereby activating the mTORC1 complex^[38]. The mTORC1 is composed of mammalian target of rapamycin (mTOR), regulatory associated protein of mTOR (Raptor), mammalian LST8/G-protein β -subunit like protein (mLST8/G β L), PRAS40 and Deptor^[73]. The activation of mTORC1 can increase protein synthesis, cell growth and cell metabolism *via* its downstream targets^[76-78]. The mTORC1 increases protein translation by activating the 70 kDa ribosomal S6 kinase (S6K), and inhibiting the elongation-initiation factor 4E binding protein^[79,80]. A recent study using phosphoproteomic technique and new inhibitor Torin1 revealed many more proteins regulated by mTORC1 including protein Grb 10 which feedback inhibits PI3K^[76]. Further study may elucidate the roles of these proteins in mTORC1 mediated carcinogenesis.

The activation of Akt can decrease apoptosis by decreasing Fas ligand transcription *via* blocking the forkhead protein and thus affecting FasL-mediated apoptosis^[58]. Akt decreases the pro-apoptotic proteins BAD and BAX

and increases anti-apoptotic Bcl-xl, Bcl-2 and Mcl1 to promote cell survival^[81]. Akt also inhibits the p53 tumor-suppressor, which can cause apoptosis under stimulation of DNA damage or environmental factors^[82,83].

Akt can also regulate cytoskeleton, which is important for cell mobility and the metastasis of cancers^[84-86]. The p70 S6K, a downstream target of mTORC1, has been demonstrated to promote actin cytoskeleton change to increase cancer cell migration^[87]. In addition, PI3K can cause the change of cytoskeleton independent of Akt. It can activate Rac1, which also causes reorganization of actin cytoskeleton^[88-90].

INCREASED PI3K/AKT PATHWAY IN EBV-INDUCED CANCERS

Examination of activated PI3K in EBV-associated cancers provides evidence for the critical role of the PI3K/Akt pathway in the carcinogenesis of EBV. Adams *et al*^[91] (2009) examined eight cases of post-transplant Hodgkin lymphoma and found that all of them expressed PI3K. Analyses of NPC biopsy samples using microarray and affymetrix assays showed PI3K mediated LMP2A-induced expression of the carcinogenic UDP-glucose dehydrogenase (*UGDH*) gene^[92,93]. The overexpression of LMP2A in HEK293 cells increased the expression of *UGDH* which was abolished by the inhibition of the PI3K/Akt pathway^[92]. Proteomic analyses of the EBV-infected gastric carcinoma cell line NU-GC-3 [EBV (+)] showed that EBV infection upregulated the phosphorylated Akt^[94]. The fact that the increased phosphorylated HSP27 was reduced by treatment with the PI3K inhibitors Ly294002 and wortmannin suggests that EBV infection can upregulate the phosphorylation of HSP27 *via* the PI3K/Akt pathway. In PTLDs, protein microarrays of samples from patients showed that PI3K, mTOR and NF- κ B were also dysregulated^[95].

The activated PI3K/Akt pathway in EBV-associated cancers have been demonstrated to be mediated by LMP1 and LMP2A. A study showed that LMP1 expression in EBV-infected B-cells induced the production of cellular IL-10, an autocrine growth factor for B cell lymphomas, in a PI3K-dependent manner^[96]. In these cell lines, PI3K/Akt pathway is activated and the LMP1-mediated IL-10 production is suppressed by mTORC1 inhibitor rapamycin. It has also been demonstrated that expression of dominant negative forms of LMP1 in EBV-immortalized monocytic and lymphocytic cell lines resulted in decreased Akt and NF- κ B activities with increased apoptosis^[97]. At present, six identified sequence variants of LMP1 including Alaskan, China 1, China 2, Med+, Med-, and NC have been shown to induce the PI3K/Akt signaling pathway to similar extents after being transformed into Rat-1 fibroblasts, HFK cells and BJAB cells^[98]. EBV LMP2A has also been shown to activate PI3K in epithelial cells and to affect differentiation^[26]. In epithelial cells, the overexpression of LMP2A of Rhesus lymphocryptovirus (LCV), which is highly homologous to EBV LMP2A activated

the PI3K/Akt pathway, indicated by Akt activation and GSK3 β inactivation^[26]. LMP2A was shown to act as a B-cell receptor (BCR) signal, which results in B cells exiting the bone marrow and decreases B cell apoptosis in the periphery *via* the activation of PI3K^[99].

EBV CAUSES CANCER VIA THE ACTIVATION OF THE PI3K/AKT PATHWAY

There are many studies demonstrating that EBV can affect the PI3K/Akt pathway to cause cancers. EBV activation of the PI3K/Akt pathway can increase carcinogenesis *via* multiple downstream targets, including increased genomic instability, cell proliferation, decreased apoptosis and increased cytoskeleton dynamics.

EBV increased genomic instability through the activation of the PI3K/Akt pathway

Genomic stability is important to avoid carcinogenesis and is maintained by the DNA repair system^[16,59,60,100-102]. It has been demonstrated that genomic instability plays an important role in EBV-induced cancers^[103-107]. In human epithelial cells, LMP1 represses DNA repair *via* the CTAR1-mediated activation of PI3K/Akt pathway^[33]. The activated PI3K/Akt pathway resulted in inactivation of FOXO3a, which plays an important role in DNA repair *via* DNA damage-binding protein 1^[33]. The critical role of FOXO3a was further demonstrated by the fact that constitutive expression of an active FOXO3a abolished LMP1-mediated repression of DNA repair^[33]. Furthermore, a recent study has shown that phosphorylated Akt can block Chk1 to affect genomic instability^[62]. This effect may be involved in LMP-1-induced genomic instability and warrants further study.

EBV increased cell proliferation through the activation of the PI3K/Akt pathway

In EBV-immortalized B-cells, also known as lymphoblastoid cell lines, the activation of the PI3K/Akt pathway can promote E2F transcriptional activity to affect the cell cycle and increase proliferation^[108]. Inhibition of the PI3K by Ly294002 in these cells reduced both cyclin D2 and cyclin D3, which are two key regulators of cell cycle and increased p27, a cyclin-dependent kinase inhibitor^[108]. CTAR1 of LMP1 has been identified to mediate the activation of PI3K signaling and associated induction of cell cycle markers in G1/S transition^[30]. This PI3K activating effect was mapped to the TRAF-binding domain within CTAR1. In Rat-1 fibroblast cells, PI3K/Akt has been demonstrated to be a key factor in LMP1 mediated rodent fibroblast transformation^[35]. Inhibition of the pathway abolished LMP1-induced cell growth. CTAR1 but not CTAR2 is critical for the activation of the PI3K/Akt pathway and associated cell growth. In human fibroblasts, LMP1 also caused phosphorylation of Akt and decreased levels of p27 and thus increased cell proliferation^[35]. A

study showed that, in an EBV-positive NPC cell line, LMP1 enhanced cell growth and migration through the activation of PI3K/Akt and NF- κ B signaling which was reduced by the inhibition of PI3K, Akt, and NF- κ B^[109]. However, it has been shown that constitutive activation of Akt alone is not sufficient to promote cell growth; NF- κ B activation is also required by LMP1 for its effect. Activation of PI3K/Akt and NF- κ B has also been demonstrated to increase glucose import which is necessary for increased cell proliferation^[110].

EBV decreased apoptosis through the activation of the PI3K/Akt pathway

Several studies have shown that LMP2A can decrease apoptosis *via* the activation of the PI3K/Akt pathway. In LMP2A transgenic mice, peripheral BCR-negative B-cells have CA Ras, an upstream protein of PI3K with correlated increased expression of Bcl-xL, a downstream target protein of PI3K^[111]. The specific inhibitors of PI3K and Akt can cause apoptosis of these cells, suggesting the important role of the PI3K/Akt in LMP2A mediated B-cell survival. In an EBV-associated gastric cancer cell line, LMP2A activated PI3K/Akt pathway has been associated with the resistance to apoptosis induced by chemotherapy^[112]. In PTL-D-derived EBV+ B cell lines, LMP2A increased caspase inhibitor XIAP to block apoptosis *via* the activation of PI3K/Akt pathway^[113]. In NPC cell lines, expression of LMP1 activated the PI3K/Akt pathway and its downstream Bcl-2, which in turn suppressed the pro-apoptotic activity of prostate apoptosis response-4^[114]. These studies provide sufficient evidence that PI3K/Akt is a key pathway in LMP1 and LMP2A-mediated decreased apoptosis.

EBV increased cytoskeleton dynamics through the activation of the PI3K/Akt pathway

The cytoskeleton plays an important role in carcinogenesis through the control of cell mobility^[84-86], and several cancer therapies have been developed targeting the proteins regulating the cytoskeleton^[115,116]. The PI3K/Akt pathway has been shown to play a key role in LMP1-induced actin stress-fiber formation^[56]. This pathway may be also important in microtubule activity. A study has shown that EBV LMP1 can activate cdc2, which, in turn, phosphorylates Op18/stathmin, a regulator of microtubules^[117]. It is possible that this process is mediated by the PI3K/Akt pathway, as Akt has been shown to increase cdc2 activity^[118].

INHIBITION OF PI3K FOR THE TREATMENT OF EBV-ASSOCIATED CANCERS

The PI3K/Akt pathway is not only important in carcinogenesis and maintenance of cancer but is important in metastasis and drug resistance to chemotherapy^[119-121]. For example, insulin can increase drug resistance *via* this pathway^[47,122-124]. Many studies have been performed to

test PI3K/Akt inhibitors and their utilization in combination with chemotherapeutic agents^[125-131]. In EBV-associated cancer, the PI3K/Akt pathway is increased, as described above. Thus, the inhibition of the pathway may be effective for the treatment of these cancers. Indeed, some preliminary studies have shown that inhibiting the pathway increased the effect of chemotherapy on EBV-associated cancers.

In an EBV-positive gastric cancer cell line, SNU-719, Ly294002 was tested in combination with 5-fluorouracil (5-FU), a common chemotherapeutic agent^[112,132]. In these cells, the use of 5-FU alone increased phosphorylation levels of Akt and NF- κ B. The increased activity of the PI3K/Akt is known to cause drug resistance to chemotherapy^[120,121]. By contrast, the sequential treatment of 5-FU and Ly294002 decreased their levels, as well as bcl-2 expression, and increased the sensitivity of these cancer cells to 5-FU. The therapeutic efficacy of the mTOR inhibitor rapamycin has been demonstrated; it decreased tumor growth and metastasis in a mouse model of EBV-associated Burkitt's lymphoma established by over-expression of both LMP2A and myc^[74]. Ly294002 and Akt inhibitor II also induced the apoptosis of EBV-associated NK/T-cell lymphoma cell lines Hank-1 and NK-YS, which have high levels of activated PI3K^[133]. NPC is usually treated by radiotherapy, and studies have shown that inhibition of the PI3K/Akt/mTOR pathway can increase the sensitivity of cancer cells to radiotherapy^[131]. Thus, it may be useful to apply PI3K inhibitors in the treatment of EBV-associated NPC.

At present, dual inhibitors of PI3K and mTOR including BEZ235, PI-103, SF1126 and XL756 have been developed and some of them are in clinical trials to treat cancers with activated PI3K^[38,134,135]. These inhibitors may be ideal compounds to be added into treatment regimens for EBV-associated cancers. Compounds from traditional medicine have been studied to inhibit signaling pathways; specifically, curcumin and flavonoids can inhibit either the PI3K/Akt pathway or its downstream targets cyclooxygenase-2 and NF- κ B^[136-142]. These compounds could also be tested for their effects on EBV-associated cancers.

CONCLUSION

The PI3K/Akt pathway can be activated by the EBV virus proteins LMP1 and LMP-2A and plays an important role in the carcinogenesis of EBV-associated cancers. This pathway is also known to be involved in drug resistance to chemotherapy. Thus, the inhibition of the pathway may have therapeutic implications for EBV-associated cancers. Indeed, some inhibitors of the PI3K/Akt pathway have been tested in EBV-associated cancer cell lines. At present, dual inhibitors of PI3K and mTOR have been developed and may be useful in the treatment of EBV-associated cancers.

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Hepatitis viruses and non-Hodgkin's lymphoma: A review

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Abstract

Non-Hodgkin's lymphoma (NHL) is among the haematological malignancies with high prevalence worldwide, causing estimated 355 900 new cases and 191 400 deaths in 2008. High prevalence of NHL is documented in economically more developed areas while low prevalence is observed in less developed areas of the globe. A wide array of environmental factors have been reported to be either directly involved or in modifying the risk of NHL development. In addition to these factors, a number of infectious agents, chiefly viruses have also been implicated in the development of NHL. This article reviews the available literature to discuss the role of hepatitis viruses in NHL development, possible mechanisms of lymphomagenesis and also identify the areas in which further research is required to better understand this disease. A brief discussion on the clinical aspects such as classification, staging, treatment approaches have also been included in this article.

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INTRODUCTION

Cancer is a multifaceted disease, and arise mostly due to the changes in the somatic genetic material where, the interaction with the external factors play a very important role, apparently both modifying the effect of each other^[1,2]. The disease, according to the GLOBOCAN 2008 data published by the IARC (International Agency for Research on Cancer), is the most important cause of death in developed countries; while second most important cause of death in developing countries and is responsible for about 7.6 million deaths in 2008, worldwide^[3].

Cancer is a heterogeneous class of diseases displaying a wide range of pattern, origin site, distribution and malignancy. Of the wide range, lymphomas constitute an important group of cancers of the white blood cells that arise in lymphoid tissues and generally remain localized in lymph nodes or certain locations other than the bone marrow. Lymphomas are broadly separated into two groups, namely Hodgkin's lymphoma (HL) and non-Hodgkin's lymphoma (NHL). The characteristic presence of large, usually multinucleate cells called 'Reed-Sternberg cells' in tumour biopsy samples differentiate HL from NHL^[4]. About 80% to 90% NHLs are of B-cell origin, while rest are of T-cell origin^[5]. The staging and diagnostic approaches have been reviewed elsewhere^[6,7].

NHL is among the haematological malignancies with high prevalence worldwide. NHL ranks 8th and 11th among the most common cancers in men and women respectively, contributing 5.1% of all cancer cases and

2.7% of all cancer deaths^[8]. An estimated 355 900 new cases and 191 400 deaths have been attributed to NHL in 2008^[3,9]. NHL is more frequent in developed areas, with the highest incidence rates found in Australia/New Zealand, Western, Northern and Southern Europe, and North America, while lowest rates are found in South-Central and Eastern Asia, Eastern Europe and the Caribbean^[3,8]. The incidence of NHL is usually low in Africa, but in some sub-Saharan areas (particularly in East Africa) incidence of Burkitt's lymphoma (a subtype of NHL) caused by Epstein-Barr virus (EBV) among children is remarkably high^[9]. NHL incidence rates are also increasing in certain developing countries such as Thailand and Uganda, probably due to the acquired immunodeficiency syndrome epidemic.

Worldwide, the occurrence of NHL has been found to be higher in men with age-standardized rate per 100 000 (ASR, standardized to the World Standard Population) of 6.1 as compared to 4.2 for women^[3,8]. The ASR of NHL incidence has been found to be 10.3 and 4.2 in males from more developed and less developed areas respectively. The ASR for NHL related mortality in males has been found to be 3.6 and 3.0 in more developed areas and less developed areas respectively. On the other hand, in females, the ASR of NHL incidence and mortality has been found to be 7.0 and 2.2 respectively from more developed areas, compared to incidence and mortality to 2.8 and 1.9 respectively from less developed areas^[3,8]. Furthermore, the rise in incidences of NHL has been found to be consistent across the globe which still remains an enigma^[10]. As NHL is a group of related yet diverse cancers, originating from different and complex etiologies, the issue of increase in the incidence is poorly understood.

ETIOLOGY

It has already been recognized that the major factors for the development of NHL include genetic alterations/damage to the cells and/or factors that are associated with immunosuppression. Further, NHL tumours have a high rate of genetic alterations like translocations, detectable in up to 90% of NHL cases^[6,10,11]. Recently, Lan and colleagues have shown that polymorphisms in the Th1/Th2 cytokine genes may contribute to lymphomagenesis^[12]. In addition, compromised immune system may also increase the risk of NHL incidence by allowing cancerous cells to escape the surveillance of immune system as higher rates of NHL is observed in people with inherited or acquired immunodeficiency syndromes and in people receiving immunosuppressive therapy^[13,14]. However, genetic predisposition on the higher incidence of NHL among certain families is still a debatable issue^[15]. The common genetic changes in NHL, may occur due to varied reasons: rearrangements of Immunoglobulin heavy chain (IgH), Immunoglobulin κ light chain (Igk), T cell receptor β chain (TCRb), T cell receptor γ chain (TCRg); and translocations of BCL-6, C-MYC, *etc.*^[6].

Similar to most of the other cancers, several environmental factors have been implicated in the origin of NHL. Exposures to different agricultural chemicals like certain herbicides (phenoxy-, triazine- groups), insecticides (organo-chlorine and organophosphates), and industrial chemicals like polychlorinated biphenyls and polybrominated biphenyl, dioxins, organic solvents seems to be significant risk factors for the onset of the disease^[15-17]. It was found that exposed population (like farmers) of these chemicals have higher rates of NHL than non-exposed populace^[18,19]. Again, long term exposure of nitrate in drinking water, UV light, X-ray, radionuclides or electromagnetic fields, *etc.* have also been implicated in the development of NHL^[15,20]. Further, use of hair dyes, alcohol, tobacco, certain diets, certain immunological conditions may also facilitate in the development of NHL^[15]. However, positive correlation among the above mentioned risk factors and the incidence of NHL is still a dubious issue^[4,7,8,10,15-20].

During the last 3 decades, the role of infectious agents, mainly viruses, in oncogenesis has become increasingly significant. Approximately 15% to 20% of cancers are associated with viral infections^[21]. Apart from the above mentioned genetic and environmental etiologic factors, development of NHL has also been attributed to different viruses^[22,23]. For several years EBV has been considered as important cause of NHL. In the later years, human immunodeficiency virus (HIV), hepatitis viruses B, C and G (HBV, HCV, HGV/GBV-C), HTLV-1, HHV 8 and Simian Virus 40 (SV40) have also been implicated in the development of NHL^[7,14,15,22]. This review will mainly focus on the hepatitis viruses, HBV, HCV and HGV/GBV-C.

Both the hepatitis viruses, HBV and HCV have been strongly associated with the hepatocellular carcinoma (HCC)^[24]. Previously these two viruses were thought to be solely hepatotropic, but lately their occult lymphotropic characteristic has been proved in human subjects as well as in animal models^[25-27]. Although, the association of HBV and HCV with NHL has been established, it remains the question if these associations simply reflect causal relationships. In this context, Marcucci and Mele, have put forward 3 possibilities to explain these associations- (1) the immunosuppressive effect of the tumor increases the risk of viral infection or reactivation; (2) some previously unknown virus with a similar mode of transmission might trigger the oncogenic signal; and (3) the actual causal relationships between hepatitis viruses and NHL^[10]. The authors refuted the first two possibilities and found the third to be correlating with the available literature. The first possibility being ruled out based on the fact that NHL is observed in a number of patients in which immune deficiency is not significant, while the second possibility was refuted for lack of any evidence^[10]. Available studies apparently support the third possibility of the oncogenic role of hepatitis viruses in development of NHL^[22,23]. However the association of HCV and HBV with the development of NHL is much weaker as compared to the major risk for HCC development caused by HBV and HCV^[24,28].

HCV AND NHL

Mostly, the studies on the lymphomagenic role of hepatitis viruses have remained focused on HCV^[10]. The simple evidence of an oncogenic role of HCV in NHL came from antiviral therapy studies, which shows, *peginterferon* and *ribavirin* (standard antiviral therapy against HCV) could completely or partially restrict lymphoma in HCV positive, but not in HCV-negative NHL patients^[29,30]. More interestingly, in most patients, in a study, it was found that antiviral treatment results in disappearance of Ig heavy chain (IgH)C and t (14;18) translocation^[31], suggesting the role of HCV in causing the genetic changes that are associated with NHL.

The association between HCV and NHL is strongest in geographic areas with highest prevalence of the viral infection^[15]. In a recent meta-analysis of 15 selected studies, the pooled relative risk (RR) of all NHL among HCV-positive persons was found to be 2.5 (95% CI: 2.1-3.1) in case-control studies and 2.0 (95% CI: 1.8-2.2) in cohort studies^[32]. Interestingly, the RR was significantly elevated in geographic areas with high HCV prevalence compared to areas with low HCV prevalence, which correlate well with previous studies from countries with low HCV prevalence, that could not observed any association between HCV and NHL^[33,34]. It was suggested that undetectable association in countries with low HCV prevalence, was mainly due to relatively small sample size of HCV positive subjects^[35].

HCV is a positive, single-stranded RNA virus of the *Flaviviridae* family^[36]. During its replicative cycle it goes through a negative-stranded RNA, but replication does not include a DNA step, hence integration of HCV nucleic acid sequences into the host genome seems improbable, lacking a critical property of classical oncogenic retroviruses^[24,35]. The HCV genome produces a single polyprotein that is proteolytically processed by viral and cellular proteases to produce structural (nucleocapsid, E1, E2) and nonstructural (NS) proteins (NS2, NS3, NS4A, NS4B, NS5A, and NS5B). Studies have demonstrated that NS5A acts as a transcriptional activator, interacts with other proteins and plays a crucial role in hepatocarcinogenesis^[37]. In addition, it participates in HCV protein maturation and RNA replication, regulates gene expression in hepatocytes, stimulates cell proliferation, inhibits apoptosis and influences interferon effect^[38]. It has been proposed that the E2 protein of HCV may be accountable for chronic antigen-driven polyclonal B-cell proliferation, leading to lymphomagenesis^[39]. However, the oncogenic mechanism remains unclear.

HBV AND NHL

In comparison to HCV, the association of HBV with NHL has been studied less thoroughly, despite the fact that the first reports were published almost simultaneously on positive association between these two viruses and NHL^[40,41]. The association between HBV and NHL

was studied by several authors in both HBV endemic countries (e.g., South Korea, China) and non-endemic countries (e.g., USA, Australia)^[40,42-49]. As discussed by Nath and colleagues^[50], results of previous retrospective case-control studies have generally supported an association (odds ratios: 1.5-3.6). However, the available data may be an underestimate of the real association between HBV and NHL, because another form of silent HBV infection, known as occult hepatitis B infection has been identified and established in the recent years^[25,51].

Occult HBV infections is defined for patients who test negative for the most widely practised HBsAg detection, but carry HBV-DNA in serum or tissues or both^[25,51]. Moreover, replication-competent HBV-DNA is supposed to persists in the liver or lymphocytes or in both the compartments for many years or even life long, indicating complete HBV eradication to be an infrequent event^[25,52]. HBV DNA has been detected within lymphocytes but whether HBV could directly transform lymphocytes is uncertain, as some studies have not been able to detect HBV in NHL cells^[42,44]. In addition, the long incubation period of HBV makes it difficult to precisely estimate the significance of HBV in NHL^[10].

HBV is a small partially dsDNA prototype virus of the *Hepadnaviridae* family^[53]. During replication, it undergoes transformation into covalently closed circular dsDNA and replicate through an RNA intermediate. It can also integrate into the host genome^[54]. HBV is characterized by a genome consisting of 4 overlapping open-reading frames: the *S* gene, encoding envelope proteins; the core gene, encoding the core and "e" proteins; the *P* gene, encoding DNA polymerase; and the "x" gene, encoding a transcriptional transactivator. The HBV NS X protein, a key regulatory protein of the virus that modulates viral replication, pathogenesis, interacts with a wide range of cellular proteins including *P*⁵⁷ has largely been held responsible for the carcinogenic properties of HBV^[55].

HGV/GBV-C AND NHL

Discovered lately, HGV/GBV-C are two viral agents that have been shown to be different strains of the same virus based on sequence similarity^[56]. Overall, the worldwide prevalence of HGV/GBV-C in blood donors ranges from 0.9% to 10%. HGV/GBV-C is a parenterally transmitted virus, which in most cases occurs in the setting of co-infection of HBV and/or HCV. This coinfection has been attributed to similar modes of transmission, as HBV and HCV. The genome of HGV/GBV-C is a positive-sense RNA having sequence and organization similar to other viruses belonging to the *Flaviviridae* family. The viral genome contains a continuous open reading frame (ORF) headed by a 458 nucleotide long 5' untranslated region (UTR) followed by a 315 nucleotide long 3' UTR. The ORF encodes a polyprotein of 2873 amino acids with a helicase motif, two chymotrypsin-like protease motifs and an RNA-dependent RNA polymerase motif^[56].

Although initially associated with hepatitis, consideration of HGV/GBV-C primarily as a hepatotropic virus is still under debate^[57]. It has been demonstrated that in absence of coinfection with other hepatotropic viruses, liver injury or viral replicative forms are usually not detectable in the liver^[58,59]. Since the majority of HGV/GBV-C positive patients with HCC are also found to be coinfecting with either HBV or HCV, it is difficult to assess the true role of HGV in the etiology of HCC^[56]. Nevertheless, results from a number of studies clearly indicate a primary lymphotropic nature of GBV-C/HGV as the viral replicative forms (an indicator of active GBV-C/HGV replication) have been detected in circulating lymphocytes, bone marrow, spleen, mononuclear cells and lymph nodes in a proportion of GBV-C/HGV infected patients^[57,59-63].

Considering the similarity between HCV and HGV/GBV-C a similar relationship to the development of lymphoma has been expected^[64]. In anticipation, some recent studies have shown the positive correlation between HGV/GBV-C and NHL. Renzo and colleagues reported that, in a series of unselected and untransfused patients in Italy, the prevalence of HGV infections were significantly higher in patients suffering from lymphoproliferative disease compared to healthy subjects^[65]. Similar reports on the association of HGV and NHL can also be found from the countries like Germany, Canada, and Greece^[64,66-69]. On the contrary, a study from Turkey, suggested neither HCV nor HGV can be linked to NHL^[70]. Considering relatively late discovery studies on the exact role of HGV/GBV-C and NHL development are scarce and further studies are needed to firmly conclude about any correlation.

MECHANISM OF VIRUS INDUCED NHL

Based on the results of the association studies, Engels classified known or suspected infectious agents of NHL into three broad groups to explain the mechanism of NHL development^[23]. These three mechanisms are schematically shown in Figure 1. First comes the lymphocyte infecting and transforming viruses, which disrupt normal cell functions and promote cell division. Second are those infectious agents that lead to immune deficiency (e.g., HIV) resulting in elevated risk of NHLs. Third group includes certain yet unknown infectious agents that may increase NHL risk through continual immune stimulation and lymphocytes activation. Two other hypothesis were also proposed to explain the mechanism; the “*hit-and-run*” hypothesis, which assumes that an agent significantly initiates oncogenic stimulus in the lymphocyte and disappears till NHL develops, and other “*hygiene*” hypothesis assumes that exposure to common infectious agents in early childhood, modulates NHL risk later in life. Although previous studies seem to support the initial three mechanisms, but the last two hypotheses (*hit-and-run* and *hygiene* hypothesis) are difficult to verify or prove since the oncogenic stimulus/agent is not detectable/lost at the time of NHL diagnosis.

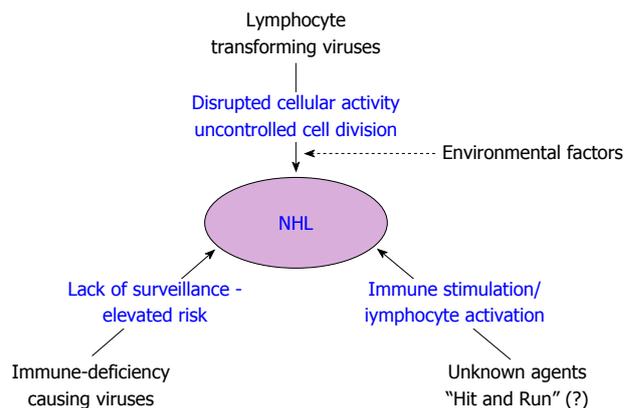


Figure 1 Schematic diagram showing mechanisms for development of non-Hodgkin's lymphoma. NHL: Non-Hodgkin's lymphoma.

Recently different workers have proposed that different individual etiological mechanisms are not mutually exclusive, but development of NHL is a multi causal event^[10,27,71,72]. Recently, Marcucci and Mele hypothesised that each of the individual etiological agents provides subliminal oncogenic signals and are thus not strong enough to cause pathogenesis by them alone^[10]. However, they suggested that integration of two or more oncogenic signals give rise to a supraliminal composite signal, necessary for lymphomagenesis. To explain the observed geographic discrepancies between incidence rates of NHL and prevalence rates of viral infections, it was suggested that geographic areas with a low prevalence of viral infection may have a high prevalence of a yet undefined environmental factor that may integrate with the viral oncogenic signal in a tissue specific manner^[10,73].

Among the three hepatitis viruses, namely HBV, HCV and HGV/GBV-C, mechanism of HCV related NHL development is most widely studied (Figure 2). HCV is considered a classical example of infectious agent causing NHL through persistent immune stimulation, associated with a range of immune-related conditions that can lead to NHL^[23,74]. However, a direct oncogenic role of HCV through B-cell infection and deregulation has been proposed since the virus is lymphotropic, but this has never been proved^[75]. The observation of HCV viral genome or proteins in only a subset of the neoplastic cells of HCV-associated NHLs, whereas frequently detection of viral genome and proteins in the stromal cells surrounding the neoplastic cells suggest that specific B-cell clones proliferate as a consequence of the chronic antigenic stimulation sustained by HCV. The immunoglobulin variable region genes expressed by B-NHL cells from HCV-positive patients show somatic mutations suggestive of an antigen selection process and the amino acid sequences of B-cell receptors in HCV-associated lymphoproliferations has been reported to have a similarity with anti-HCV antibodies^[75-78]. Moreover, the histologic presentation of many B-NHL cells from HCV positive patients are characteristic of germinal center (GC) and post-GC B-cells, suggesting the occurrence of lymphom-

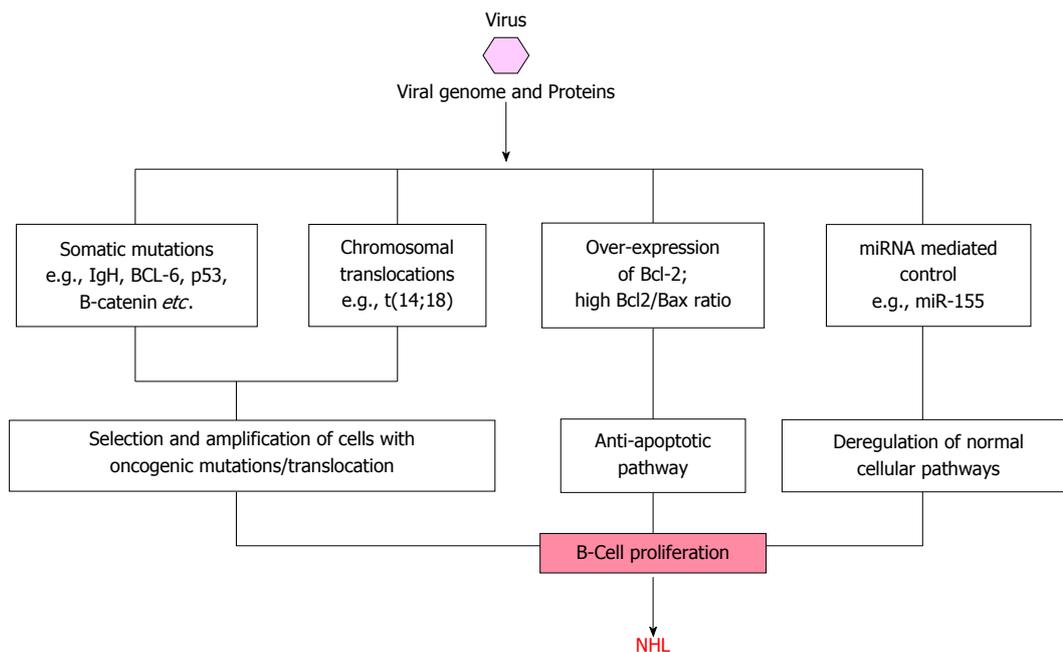


Figure 2 Schematic diagram showing possible modes of transformation of normal cells to non-Hodgkin's lymphoma by viral agents. IgH: Immunoglobulin heavy chain; miRNA: MicroRNAs; NHL: Non-Hodgkin's lymphoma.

agenesis at the time of B-cells proliferation in response to a viral antigen^[76].

Neoplastic transformation may also be the result of direct anti-apoptotic pathways activated by HCV within B-cells. In fact, HCV sequences have been detected in lymph node biopsy specimens from patients with B-NHL^[79] and the presence of HCV-associated proteins within lymphoma cells has also been demonstrated^[80]. Moreover, studies in severe combined immunodeficiency mice have provided evidence of the persistence and low-rate multiplication of HCV infection in human mononuclear cells^[81]. Finally, some HCV proteins have been shown to exert anti-apoptotic effects in infected cells in transgenic mice^[82,83].

HCV related lymphoproliferation is thought to be due to binding of HCV to receptors on the surface of B-lymphocytes lowering their threshold for antigen response, inducing DNA mutations, increased frequency of abnormal chromosomal translocations associated with NHL^[84,85]. The identification of the specific binding of HCV E2 protein to the ubiquitously abundant B-cell surface molecule CD81, has supported the hypothesis that a consistent polyclonal B-cell response to viral antigens favour the development of lymphoproliferative disorders^[27,84]. Although HCV can infect lymphocytes, there is lack of evidence for its direct lymphomagenic role^[75]. Different studies have showed a significant association between HCV infection and Bcl-2 rearrangement t(14;18 translocation)^[85-89]. In these patients, clonal expansion of B-cells harboring translocation t(14;18) was demonstrated, with overexpression of the anti-apoptotic Bcl-2 protein, resulting in higher Bcl-2/bax ratio^[87,90]. Fascinatingly, the observation that treatment with interferon- α of HCV positive patients with splenic marginal zone NHL,

results in HCV clearance, reduced frequency of translocation t(14;18) and regression of NHL clearly implies the causal role of HCV infection in at least certain subsets of NHLs^[29,31,90-92]. Different possible modes of NHL causation by viral infection are schematically presented in Figure 2.

Recently, Machida and colleagues have demonstrated that HCV infection resulted in a 5 to 10-fold increase in somatic gene mutation frequency in IgHC, *BCL-6*, *p53*, and β -*catenin* genes of *in vitro* HCV-infected B-cell lines and HCV-associated peripheral blood mononuclear cells, lymphomas, and HCC, and proposed that this mutator phenotype of HCV leads to selection and amplification of deleterious mutations in the protooncogenes or tumor-suppressor genes in tumors^[93]. They also suggested two different mechanisms of mutation, based on the observation that nucleotide-substitution pattern of *p53* and β -*catenin* is different from that of IgHC. Very interestingly this mutator function of HCV was found to be unique among oncogenic viruses, as similar amplification of protooncogene mutations in HCV-associated lymphomas and HCCs were not detectable in other types of tumors, lymphomas not related to HCV, HBV-associated HCCs, and HCCs of nonviral origin. Furthermore, the ability of HCV to induce high mutation frequency of cellular genes suggests that HCV may cause tumor formation by a *hit-and-run* mechanism.

Quite obviously, being of multi-factorial aetiology, there are a number of possible mechanisms through which HCV can induce lymphomagenesis, some elucidated, rest remain to be explored. Compared to HCV, HBV was discovered much earlier and its lymphotropic properties have been documented long back. Despite this fact, ironically, HBV related research has not been properly

focused on its lymphomagenic properties. In contrast, HGV/GBV-C being relatively newly discovered, studies are in progress to describe different properties and mechanisms of pathogenesis. It is assumed that being a member of the *Flaviviridae* family, as HCV does, HGV/GBV-C might utilize similar mechanisms.

MicroRNAs AND NHL

MicroRNAs (miRNA) are a group of lately discovered, highly conserved small noncoding RNAs arising from eukaryote genomes, that play an extremely important role in post-transcriptional regulation and are involved in a wide variety of biological pathways^[94-96]. They control gene expression through base-pairing with the 3'-UTRs of target mRNAs, inducing mRNA degradation or suppressing translation, depending on the perfection of base-pairing^[97-99]. One miRNA is capable of regulating the expression of multiple target genes; computational analyses have indicated that expression of more than 30% human genes is regulated by miRNAs^[100]. MiRNAs show a highly tissue specific expression pattern, having important role in organ development, cellular differentiation, homeostasis, immune response, apoptosis and carcinogenesis also^[95,101,102]. Very interestingly, apart from eukaryotes, a number of DNA viruses have also been shown to encode miRNAs, which probably help these viruses in modulating host gene expression favourable for its own replication^[96]. Among the human DNA viruses, mainly Herpesviruses (EBV; human cytomegalovirus, hCMV; herpes simplex virus, HSV; Kaposi's sarcoma-associated herpesvirus, KHSV, *etc.*), Polyomaviruses, and Adenoviruses (human adenovirus, hAV) have been reported to encode and express miRNAs^[96]. Using computational approaches, recently, Jin and colleagues found that HBV (*Hepadnavirus* family, DNA virus) could putatively encode atleast one candidate pre-miRNA, which could target one of its own viral mRNA, but could not target any of the cellular transcripts^[103]. However this data remains to be experimentally validated at the cellular level. In contrast, using standard sequencing or advanced sequencing techniques, no viral miRNAs have been identified HPV or in RNA viruses such as Lentiviruses (human T-cell leukemia virus I, HTLV-1) or Flaviviruses (HCV; dengue virus, DENV, *etc.*), which led to a general thought that RNA viruses might not encode or express similar regulatory small RNAs^[95,104-106]. Interestingly, recently, Andrew Fire's group studied infection of six different RNA viruses (including HCV, DENV, West Nile viruses, WNV, *etc.*) in 41 experimentally susceptible and resistant host systems, and reported identification of a class of RNA virus-derived small RNAs, termed as "vsRNAs", 99.97% of them showing perfect homology only with the infecting virus genomes. The authors also found that the cellular short RNA apparatus was capable to employ these vsRNAs as vsRNA-primed Ago (Argonaute) complexes, but the degree to which these complexes executed silencing of functional viral RNAs and modulation of cellular miRNAs require further investigations^[107].

Whether virus encoded regulatory small RNAs are detectable or not in the infected cells, viral infection has been shown to modulate the host cellular miRNA expression, altering the cellular environment, leading to pathogenesis^[96]. Fascinatingly, it is well established that certain viruses such as EBV, Vesicular Stomatitis virus (VSV) induces host miR-155 expression which is one of the typical multifunctional miRNAs involved in B-cell differentiation and proliferation, and has been shown to be overexpressed in Hodgkin and non-Hodgkin lymphomas, chronic lymphocytic leukaemia^[95,108-114]. MiR-155 is involved in numerous physiological and pathological processes including innate and adaptive immunity, inflammation and tumorigenesis^[115]. It has been shown to be important for immunoglobulin class switching and to prevent potentially oncogenic chromosomal aberrations through regulation of activation induced cytidine deaminase^[116,117]. In addition to miR-155, EBV also induces miR-146a expression in B-cells^[118]. MiR-146a can target TNF receptor associated factor 6 and Interleukin-1 receptor-associated kinase 1, of the Toll-like Receptor signaling pathway, suggesting a negative-feedback loop to limit innate immune responses^[119,120]. Similarly, E6 protein of HPV downregulates the expression of miR-34a (a p53-regulated miRNA) and miR-218, that leads to increase in cell growth and tumorigenicity^[121,122]. In contrast, viruses may also induce miRNAs that restrict viral replication. For example, HCV is known to upregulate IFN- β , which induces cellular miR-196, miR-296, miR-351, miR-431, and miR-448, *etc.*, which in turn attenuate viral replication and viral accumulation^[123].

Apart from modulating the cellular miRNA expression, viruses can even encode mimics of host miRNAs, the later been hypothesized to cause pathogenesis^[95,96]. Support to this thought comes from the fact that the chicken oncogenic Marek's disease virus type 1 (MDV-1), expresses a miR-155-mimic, while the non-oncogenic MDV-2 does not express miR-155. Viral mimic of cellular miR-155, known as miR-K12-11 has also been reported from KSHV^[124]. More interestingly, viruses have been recognized to utilize certain cellular miRNA for tissue specific infection also. HCV has been demonstrated to exploit a liver tissue specific miR-122 to positively regulate RNA replication^[125]. Mammalian miR-122 expression is generally confined to the liver, and it helps maintain liver tissue identity by regulating fatty acid and cholesterol biosynthesis, pathways^[95,96]. The liver-specific expression of miR-122 and its positive effect on HCV replication has been associated with hepatic tissue tropism of HCV and it has been hypothesized that tissue specific expression of certain miRNAs subject viruses to selective pressures, and viruses get optimized or evolved for replication in certain tissues (target tissue), while certain other tissues with different miRNAs might pose significant hurdles for viral replication, rendering them non-target tissues for the given virus^[95]. This hypothesis has been firmly supported by experimental findings that engineering cellular miRNA target sites in the viral genomes can alter tissue tropism^[126]. Even though further investigations are need-

ed to conclude, but this might be a consistent explanation for the compartmentalization of different variants/genotypes of the same virus in different tissues of the same subject, a phenomenon very frequently observed in a number of viral infection^[127].

Although the miRNA expression patterns have been widely studied in different human cancers, but similar studies on NHL is relatively scarce, despite its immense importance. Recently some studies have focused on the role of miRNA in development of NHL^[128-131]. Generally, up-regulation of miR-155 has been described in NHLs, as well as in several other solid and hematologic malignancies. Another miR-17-92 cluster has been found to be frequently amplified in malignant B-cell lymphomas, and is over-expressed in 65% of B-cell lymphoma patients^[132]. MiR-143 and miR-145 expression is shown to be reduced in B-cell malignancies^[133]. A recent study showed that enforced expression of the miR-17-92 cluster accelerated MYC induced lymphomagenesis^[134]. Unfortunately however, there is hardly any published data on the miRNA expression patterns among NHL patients infected with HBV/HCV or HGV/GBV-C. A recent study clearly demonstrated the existence of HBV- and HCV specific differential cellular miRNAs expression profiles in HBV and HCV infected liver samples as well in Huh 7.5 cell culture models, revealing that entirely different pathways were modulated in HBV or HCV infected liver^[135]. These results clearly depict the contribution of the hepatitis viruses (at the focus of this review mainly HBV and HCV) in cellular miRNA deregulation leading to liver pathogenesis. Similarly, it is plausible to assume that similar to hepatocytes, these hepatitis viruses may also alter the miRNA expression patterns in lymphocytes.

CLINICAL AND THERAPEUTICS FOR NHL

NHL comprises diverse subtypes of lymphoproliferative malignancies with distinct epidemiologic, etiologic, morphologic, genetic/molecular, clinical, immunologic and histological features^[136,137]. Compared to HL, different NHLs have a higher tendency for extranodal sites. Like most other cancers, prognosis of NHL largely depends on the accuracy of histological classification, stage at detection and response to treatment^[138,139]. A number of classification systems have been proposed and updated in the past decades, systems such as Rappaport and Lukes Collins classification system (developed in 1966, modified by Lukes Collins in 1974), Kiel classification system (developed in 1974), Working Formulation (developed in 1982), and the Revised European-American Lymphoid neoplasms classification (REAL, published in 1994) are the important ones. Earlier, classification was solely based on morphological characteristics, but later immunological, cytogenetic and molecular features were incorporated, that facilitate precise classification^[138]. Presently, the World Health Organization classification (based on the principles of the REAL system, published in 2001, updated in 2008) is widely accepted and practised^[138,140,141].

However, for selecting a therapeutic strategy, Ann Arbor anatomic staging system is presently in practice^[138,142,143].

Being highly heterogeneous, different NHL subtypes are associated with a variety of typical and atypical clinical manifestations. However, more than 70% of the patients do not present classic symptoms, and are incidentally diagnosed while undergoing treatment for other nonspecific complaints. Usually NHL may present atypically with fever, fatigue, loss of appetite, drenching night sweats, weight loss, red patchy skin, *etc.* These general symptoms are termed as "B symptoms" and are generally associated with increased cancer "burden" due to delayed detection and poor prognosis. In contrast to Hodgkin's disease, most patients with NHL present with advanced stage III or IV disease. The most typical clinical presentation of NHL is lymphadenopathy or extranodal mass in one or more lymph nodes. NHL involving abdominal lymphatic tissues often present with swelling of belly and lymphoma involving thymus is frequently presented with chest pain, or respiratory problems, *etc.* Sites often involved in NHL include skin thyroid, breast, gastrointestinal tract, brain, and ovaries or testes^[138]. NHL may also involve unusual sites, such as epitrochlear or popliteal nodes or Waldeyer's ring (nasopharynx).

Generally, NHLs are divided into two prognostic groups, the indolent lymphomas (mostly nodular or follicular in morphology) have a relatively good prognosis and the aggressive lymphomas have a shorter natural history. Early-stages (I and II) of indolent lymphomas are effectively treated with radiation therapy, but almost incurable in advanced stages. However, a considerable number of patients with aggressive lymphoma are curable with intensive combination chemotherapy.

Significant improvements in the field of NHL management made in the recent years have resulted in cure of 30% to 60% patients with aggressive NHL. Decision on treatment depends largely on lymphoma sub-type, stage, age and overall health condition of the patient, *etc.* often, in certain cases of indolent lymphomas, treatment delayed till the manifestation, technically known as "watchful waiting". Nevertheless, majority of the patients require treatment consisting of chemotherapy, radiation therapy, and bone marrow/stem cell transplantation, alone or in a combination.

Chemotherapy is the most imperative treatment and often includes anti-cancer drug combinations^[138,144,145]. Methotrexate, Doxorubicin Hydrochloride, Chlorambucil, Nelarabine, Tositumomab, Bleomycin, Cyclophosphamide, Liposomal Cytarabine, Pralatrexate, Romidepsin, Rituximab, Vinblastine Sulfate, Vorinostat, *etc.*, are some of the drugs used for chemotherapy. Conversely, CHOP (Cyclophosphamide, Hydroxydauno-rubicin/doxorubicin, Oncovin, Prednisone or prednisolone), rituximab with CHOP (R-CHOP), cyclophosphamide, oncovin, procarbazine and prednisone, Etoposide, doxorubicin, vincristine, prednisone, and cyclophosphamide, ifosfamide, carboplatin and etoposide are some of the recipe used for combination chemotherapy. Although chemo-

therapy alone can cure several high-grade lymphomas, but sometimes patients with recurring or drug irresponsive lymphomas are considered for higher dose of chemotherapy followed by autologous bone marrow transplant. The most widespread therapy for NHL is the R-CHOP combination therapy and consists of the CHOP chemotherapy along with Rituximab immunotherapy (a chimeric monoclonal antibody against CD20 protein, principally found on B cells surface), which distinctively targets certain lymphoma cells and selectively kills them.

Apart from chemo-immune therapy, radio-immuno conjugates (radio actives conjugated to monoclonal antibodies) are also used for selective destruction of cancerous cells. This therapy is among the best treatment for NHL, as NHL is highly radiosensitive. In this therapy, Iodine-131 (Tositumomab) or the Yttrium-90 (Ibritumomab tiuxetan) is conjugated to antibodies against CD20, increasing the specificity, while diminishing off-target damage^[145]. In addition, conjugation of immunotherapeutic monoclonal antibodies with immunomodulators (such as α -Interferon) is also under clinical trials^[145]. Other treatment approaches for NHL, drug regimen, efficacy and results of different clinical trials may be found elsewhere in more details^[138,139,144,145]. In addition, novel therapeutic approaches, target pathways and potential small molecule inhibitors for treatment of NHL resistant to conventional treatment have also been reviewed recently^[146].

CONCLUSION

The available literature clearly signifies that hepatitis viruses (HBV, HCV and HGV/GBV-C) have strong lymphotropic properties and most of the published data corroborate a causal association between these viruses and NHL. Additionally, prevailing data showing rapid increase in incidences and deaths due to NHL highlight the magnitude of disease burden in developed as well as less developed areas. Despite its significance, hepatitis virus associated NHL remains poorly understood. Although, mechanism of HCV related NHL has been studied in some details, but the other two viruses have remained poorly studied from the perspective of their involvement in NHL development. It is also evident that there is scarcity of data related to miRNA regulation patterns in HBV, HCV and HGV/GBV-C related NHL. The availability of miRNA regulation data might help reveal important facets of lymphomagenic mechanisms. Therefore research efforts focused on hepatitis virus induced NHL is essential to properly understand the virus induced lymphomagenic mechanisms, in order to develop effective intervention strategies and to reduce the disease burden.

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Antiviral treatment to prevent chronic hepatitis B or C-related hepatocellular carcinoma

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Abstract

Antiviral treatment is the only option to prevent or defer the occurrence of hepatocellular carcinoma (HCC) in patients chronically infected with hepatitis B virus (HBV) or hepatitis C virus (HCV). The approved medication for the treatment of chronic HBV infection is interferon- α (IFN α) and nucleos(t)ide analogues (NAs), including lamivudine, adefovir dipivoxil, telbivudine, entecavir and tenofovir disoproxil fumarate. IFN α is the most suitable for young patients with less advanced liver diseases and those infected with HBV genotype A. IFN α treatment significantly decreases the overall incidence of HBV-related HCC in sustained responders. However, side effects may limit its long-term clinical application. Orally administered NAs are typically implemented for patients with more advanced liver diseases. NA treatment significantly reduces disease progression of cir-

rhosis and therefore HCC incidence, especially in HBV e antigen-positive patients. NA-resistance due to the mutations in HBV polymerase is a major limiting factor. Of the NA resistance-associated mutants, A181T mutant significantly increases the risk of HCC development during the subsequent course of NA therapy. It is important to initiate treatment with NAs that have a high genetic barrier to resistance, to counsel patients on medication adherence and to monitor virological breakthroughs. The recommended treatment for patients with chronic HCV infection is peg-IFN plus ribavirin that can decrease the occurrence of HCC in those who achieve a sustained virological response and have not yet progressed to cirrhosis. IFN-based treatment is reserved for patients with decompensated cirrhosis who are under evaluation of liver transplantation to reduce post-transplant recurrence of HCV. More effective therapeutic options such as direct acting antiviral agents will hopefully increase the response rate in difficult-to-treat patients with HCV genotype 1. However, the risk of HCC remains in cirrhotic patients (both chronic HBV and HCV infection) if treatment is initiated after cirrhosis is established. Future research should focus on investigating new agents, especially for those patients with hepatic decompensation or post-transplantation.

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Key words: Hepatitis B virus; Hepatitis C virus; Hepatocellular carcinoma; Antiviral therapy; Interferon; Nucleos(t)ide analogues; Virological response

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INTRODUCTION

Hepatocellular carcinoma (HCC), one of the most common and aggressive malignancies, is the third leading cause of cancer-related deaths worldwide^[1]. Chronic infection with hepatitis B virus (HBV) and hepatitis C virus (HCV) affect over 400 million and 170 million individuals respectively, together contributing to 75%-80% of global HCC^[2]. The incidence of HCC has a wide geographical variation due to the heterogeneous penetration of the main causal factors within a given population^[3]. In HCC-endemic areas, such as Asia and Africa, chronic HBV infection is the principal etiological factor. While in the West and Japan, chronic HCV infection plays a predominant role. Chronic HBV and HCV are progressive diseases; the dynamic process involving the interplay between the hepatitis viruses and host inflammatory factors contributes to the development of advanced liver diseases such as HCC. The most effective measure to avert HCC is to prevent HBV and HCV infection. Hepatitis B vaccination for newborns has led to a substantial reduction in the incidence of HCC in HBV endemic regions, while no vaccine is currently available for HCV. For individuals who are chronically infected with HBV or HCV, antiviral therapy is the only option for the prevention of HCC. In chronic hepatitis B or C patients without cirrhosis, antiviral therapy may prevent the occurrence of HCC by slowing the progression of liver diseases and possibly reversing liver damage^[4]. In patients with advanced fibrosis or cirrhosis, eradication or oppression of HBV or HCV does not remove this risk, but can control the complications and gain the time to prepare for liver transplantation^[5]. Postoperative antiviral therapy also improves the prognosis of HBV/HCV-related HCC^[6,7]. Therefore, the treatment might be of greater benefit if patients are treated earlier and adhere to medications during the course of chronic HBV or HCV infection^[8]. Several safe and effective medications have been approved. Decision to start or defer treatment should take into consideration the stage of liver disease, initial virus replication status, adverse effects, drug resistance and costs of the treatment. Moreover, the response should be closely monitored so that the treatment can be modified in a timely fashion.

ANTIVIRAL THERAPY AND PREVENTION OF HBV-RELATED HCC

The natural course of chronic HBV infection consists of 4 phases, namely immune tolerant, immune clearance, inactive (carrier) and reactivation phases. The immune tolerance phase [or hepatitis B e antigen (HBeAg)-positive chronic hepatitis B] is characterized by the presence of HBeAg, normal serum alanine aminotransferase (ALT) and high HBV DNA levels. Most patients in this phase have minimal liver injury and little or no fibrosis^[9]. The immune clearance phase is characterized by the presence of HBeAg, high serum HBV DNA levels, persistent or intermittent elevation of ALT and active inflammation

in the liver. During this phase, some patients undergo spontaneous HBeAg seroconversion which occurs at a rate of 10%-20% per year and others may experience recurrent hepatitis flares and even progress to cirrhosis or hepatic decompensation. The inactive (carrier) phase is characterized by the absence of HBeAg, presence of HBe antibody (anti-HBe), persistently normal ALT levels and low or undetectable levels of serum HBV DNA. Patients in this phase have a favorable prognosis^[10]. The reactivation phase (or HBeAg-negative chronic hepatitis B) is characterized by the absence of HBeAg, presence of anti-HBe, intermittently or persistently elevated serum HBV DNA and ALT levels, and active inflammation in the liver. Patients in this phase are usually older and have more advanced liver disease than those in other phases^[11]. However, patients vary regarding which phases they go through. This is largely influenced by the HBV genotype and host immune status. Previous studies have demonstrated that the presence of HBeAg and persistently high serum HBV DNA levels are risk factors for the occurrence of cirrhosis and HCC^[12-14].

Moreover, chronic infection with HBV genotype C is more likely to cause liver cirrhosis than genotype B^[15]. Chronic infection with genotype C (C2) is related to HBV-associated HCC, especially in cirrhotic patients aged > 50 years, whereas HBV B2 infection is related to high prevalence of HCC in non-cirrhotic young patients and HCC recurrence after resection^[16]. In addition, precore or core promoter HBV variants that occur in most patients can prevent or decrease the production of HBeAg^[11]. Different HBV subgenotypes have distinct patterns of mutations. We and others have found that serum HBV load (> 10⁴ copies/mL) and viral mutations in the enhancer II/basal core promoter (Enh II/BCP) regions (such as C1653T, T1753V, A1762T/G1764A, T1674C/G and C1766T/T1768A) and in the precore/core gene (such as G1899A, C2002T, A2159G, A2189C and G2203A/T), as well as in the preS region (such as T53C, preS2 start codon mutation, preS1 deletion, C2964A, A2962G, C3116T and C7A) are significantly associated with the occurrence of HCC^[17-22]. Reduction of CD8⁺ T cell epitopes in HBV to evade immune clearance is one of the most common ways of these mutations. It remains to be evaluated if the HCC-associated HBV mutants are still sensitive to the antiviral treatment.

Clinical assessment of the treatment response relies on intermediate outcomes, including a decrease in levels of serum HBV DNA, HBeAg seroconversion, loss of HBsAg, normalization of ALT levels and a decrease in hepatic inflammation. The ultimate goal of the antiviral therapy is to obtain clinical benefits by reducing complications, including HCC. However, treatment choices mainly depend on the degree of viral replication and disease progression. Other factors, such as the patient's age, HBeAg status, family history of HCC, occupational requirement and need for immunosuppressive or cancer chemotherapy, could also influence the decision to start or defer antiviral treatment. In patients with life-threaten-

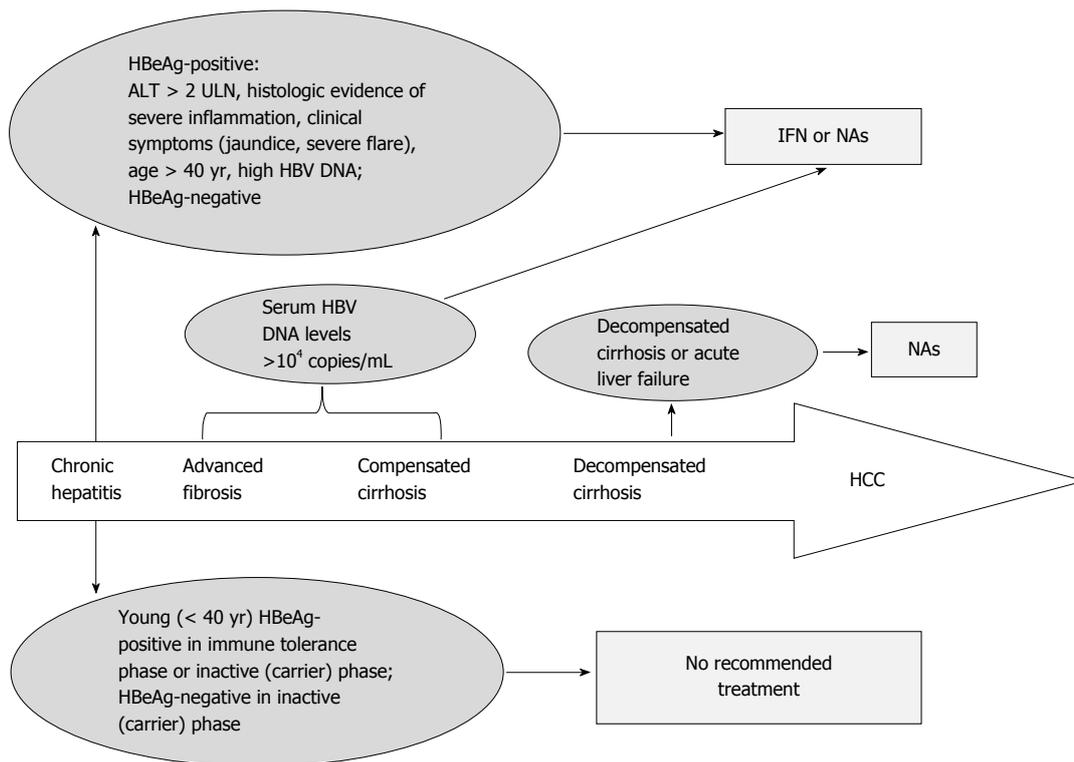


Figure 1 Flowchart of therapy choice for patients with chronic hepatitis B virus infection. ALT: Alanine aminotransferase; HBeAg: Hepatitis B e antigen; HCC: Hepatocellular carcinoma; HBV: Hepatitis B virus; IFN: Interferon; NAs: Nucleos(t)ide analogues; ULN: Upper limit of normal.

ing liver diseases, such as acute liver failure, decompensated cirrhosis or severe exacerbation of chronic hepatitis B, antiviral treatment should be initiated as soon as possible in order to stabilize liver function and prepare for liver transplantation^[23]. In patients with advanced fibrosis or compensated cirrhosis (those whose laboratory tests indicate normal hepatic function and no evidence of portal hypertension), antiviral treatment should be initiated when serum HBV DNA levels > 10⁴ copies/mL because the risks of cirrhosis and HCC increase when serum HBV DNA reaches or exceeds this level^[13,24]. HBeAg-positive chronic hepatitis patients who have ALT levels persistently twice the normal upper limit or with clinical and/or histological evidence of severe inflammation should be considered for treatment. Patients older than 40 years should be treated if HBeAg remains positive and the serum HBV DNA level is still high, regardless of ALT levels. Given that sustained spontaneous remission is rare, patients who have HBeAg-negative chronic hepatitis should also be considered for treatment. However, it is not recommended to initiate antiviral therapy for young HBeAg-positive patients (< 40 years) in the immune tolerance phase because most have little or no fibrosis and a favorable prognosis during follow-up of up to 10 years^[25]. Another reason for deferring treatment is that antiviral treatment is less efficacious during this phase due to the low likelihood of treatment-related HBeAg seroconversion. Continued monitoring is necessary for timely initiation of treatment if patients fail to undergo spontaneous HBeAg seroconversion. Treatment may also be deferred

in the inactive (carrier) phase because no evidence supports the hypothesis that antiviral therapy will alter the outcome of patients who are truly in this phase. However, the decision should only be made on the premise that patients have been observed for at least one year of HBV DNA and ALT levels tested on three or four occasions (Figure 1).

Currently, interferon- α (IFN α) and nucleos(t)ide analogues (NAs) are the two main categories of medications approved for the treatment of chronic hepatitis B. IFN α has an immunomodulatory activity that can lead to a higher rate of HBeAg seroconversion and HBsAg loss^[12,13]. Treatment with IFN α may significantly decrease overall HCC incidence in sustained responders, especially in Asians^[26-28]. IFN α may be used in carefully selected patients with compensated cirrhosis. It is most appropriate for young patients, particularly among HBeAg-positive patients who have a genotype A infection. However, it is contraindicated in patients with decompensated cirrhosis to avoid sepsis and liver failure. It is also not used in patients with severe exacerbations of chronic hepatitis B or acute liver failure, and in those undergoing immunosuppressive or cancer chemotherapy. The major advantages of IFN α -based treatment include short treatment duration and a sustained off-treatment response once achieved. However, low probability of achieving a response and high costs as well as side-effects may limit its long-time clinical use.

Treatment with NAs can also result in a significantly lower incidence of HCC compared to untreated patients

but it does not completely eliminate the risk of HCC, particularly in patients with pre-existing cirrhosis. Hence, patients with chronic hepatitis B require careful surveillance for HCC, even when they are undergoing antiviral therapy^[29,30]. Another disadvantage of NA treatment is the long-term continuous treatment course, resulting in antiviral drug resistance^[31]. The choice of treatment should consider the initial HBV-DNA levels, HBV genotype/subgenotype, age of the patient and any contraindication to NA treatment. NAs are most appropriate for patients who have decompensated liver diseases or contraindications to IFN, and those who are willing to commit to a long duration of treatment. The treatment should be initiated with NAs with a high genetic barrier to resistance (that is, a low potential for drug resistance).

IFN α

Two forms of IFN α are currently available: conventional IFN α and the pegylated, long-acting formulation (PEG-IFN). The introduction of PEG-IFN mainly impacts tolerability. It allows for weekly injections compared to the daily or three times/week schedules of conventional IFN α administration, while maintaining similar antiviral efficacy. Long-term follow-up of patients treated with conventional IFN α therapy shows that responders have a decreased incidence of decompensated cirrhosis or HCC and improved overall survival compared with non-responders^[32]. A retrospective analysis of PEG-IFN in patients with HBeAg-positive hepatitis showed that factors associated with response to treatment included high ALT, low HBV DNA, female sex, older age and the absence of previous IFN therapy. Patients with the best outcomes were those with genotype A and high ALT or low HBV DNA, and those with genotypes B or C and both high ALT and low HBV DNA^[33]. A recent meta-analysis of 14 trials suggested that PEG-IFN facilitated HBsAg clearance or seroconversion in chronic hepatitis B patients. According to an assessment conducted in 24 wk after completion of a 1 year course of PEG-IFN, approximately 30% of HBeAg-positive patients achieved HBeAg seroconversion and undetectable serum HBV DNA, and 15% of HBeAg-negative patients had normalized ALT levels^[34]. Compared with the placebo, a 1 year course of PEG-IFN therapy resulted in a greater HBV DNA decline in HBeAg-seropositive patients (32% *vs* 11%)^[35]. A large study evaluated long-term outcomes of IFN α therapy in HBeAg seropositive patients by comparing 233 IFN α -treated patients with 233 well-matched untreated controls and the cumulative incidences at the end of 15 years of follow-up (median 6.8 years, range 1.1-16.5 years) in the IFN α -treated patients *vs* the controls were: HBeAg seroconversion 74.6% *vs* 51.7% ($P = 0.031$); HBsAg seroclearance 3% *vs* 0.4% ($P = 0.03$); cirrhosis 17.8% *vs* 33.7% ($P = 0.041$); and HCC 2.7% *vs* 12.5% ($P = 0.011$)^[26]. Another meta-analysis with a total of 2742 subjects pooled from 12 studies has shown that the risk of HCC in patients treated by IFN α is reduced by 34% (RR = 0.66, 95%CI: 0.48-0.89) and the benefit is more significant

among patients with early cirrhosis than among those without cirrhosis^[23]. These data indicated that the main advantages of IFN are durable administration course and a high rate of HBsAg loss and HBeAg seroconversion, particularly among HBeAg-positive patients who have a genotype A infection compared with patients who are infected with other HBV genotypes. However, the adverse effects of IFN α , including initial flu-like illness, fatigue, bone marrow suppression and exacerbation of autoimmune illnesses, should be closely monitored.

NAs

There are five NAs approved for the treatment of chronic hepatitis B: lamivudine, adefovir dipivoxil, telbivudine, entecavir and tenofovir disoproxil. We have summarized the pros and cons of each NA for the treatment of chronic HBV infection in Table 1.

In patients who do not respond to IFN α , an oral sequential therapy with NAs is preferable because of its predictable efficacy and minimal side-effects. It has been demonstrated that a 1 year course of NA treatment results in high rates of undetectable serum HBV DNA, normalization of ALT levels and increase in liver function, but low rates of HBsAg loss in chronic hepatitis B patients with either positive or negative HBeAg^[36,37]. Extending the duration of NA treatment to more than 1 year can increase rates of HBeAg seroconversion to 40%-50%, but rates of HBsAg loss remain below 10% in patients with HBeAg-positive chronic hepatitis B patients after 5 years of treatment^[38,39]. In a randomized controlled trial, 651 HBsAg-positive patients with compensated liver diseases were allocated into two groups: receiving 100 mg/d lamivudine ($n = 436$) or receiving placebo ($n = 215$). HCC occurred in 3.9% of those in the lamivudine group and 7.4% of those in the placebo group (HR = 0.49, 95%CI: 0.25-0.99, $P = 0.047$) after a median treatment duration of 32.4 mo (ranging from 0 to 42 mo)^[40]. A meta-analysis pooling 5 studies ($n = 2289$) compared the incidence of HCC in patients with and without NA treatment. It found that the incidence of HCC was reduced by 78% (RR = 0.22, 95%CI: 0.10-0.50) in the treatment arm, especially in HBeAg-positive patients^[27]. Similarly, a recent meta analysis pooling 3881 patients with NA treatment and 534 untreated controls from 21 studies has concluded that NA treatment is associated with a lower incidence of HCC (2.8% *vs* 6.4%, $P = 0.003$)^[29].

Current approved NAs act primarily by inhibiting the reverse transcription of the pregenomic HBV RNA to the first strand of HBV DNA rather than directly inhibiting cccDNA. Therefore, viral relapse is common after treatment. In addition, inadequate or slow decline in serum HBV DNA levels during the first 12-24 wk of NA treatment is associated with an increased risk of antiviral drug resistance during continued therapy. Patients receiving NAs with a low genetic barrier to resistance, such as lamivudine and telbivudine, should receive additional therapy if initial viral decline is inadequate, while patients

Table 1 Pros and cons of each nucleos(t)ide analogue therapy for the treatment of chronic hepatitis B infection

Nucleos(t)ide analogue	Regimen	Pros	Cons
Lamivudine	100 mg daily	First licensed agent Well established safety and efficacy record Lowest cost	Highest incidence of resistant mutations of M204V/I substitution (20% at year 1, 70% at year 5) Adverse effects including hepatitis flare ups, hepatic decompensation and even death
Adefovir dipivoxil	10 mg daily	Low drug resistance rate, and no cross resistance with other nucleos(t)ide analogs	Incidence of resistant mutations of N236T and/or A181V substitution (29% at year 5) Adverse effects including renal tubular acidosis with hypophosphataemia when treatment is prolonged
Telbivudine	600 mg daily	Higher seroconversion rate	Incidence of resistant mutations of M204I mutation (5% at year 1) Adverse effects including myopathy and neuropathy
Entecavir	1.0 mg daily	Anti-HBV effect Lowest rate of resistance	Incidence of resistant mutations of T184G or M250V (1.2% at year 5) (I169T and M250V, or T184G and S202I if also lamivudine-resistant) Most expensive
Tenofovir disoproxil	300 mg daily	More potent in reducing HBV load in patients with prior failure or resistance to lamivudine and/or adefovir	No resistant mutations reported at year 3

HBV: Hepatitis B virus.

who receive NAs that have a high genetic barrier to resistance, including entecavir and tenofovir disoproxil, may remain on the same drug if serum HBV DNA levels continue to decline^[41,42].

Lamivudine 100 mg/d is the first approved NA to treat chronic hepatitis B and has been extensively used for more than a decade with an excellent safety record. Lamivudine treatment can reduce disease progression of HBV-related cirrhosis, resulting in approximately a 50% decrease in HCC incidence. Such efficacy is achieved despite emergence of drug resistance in approximately 50% of cases^[28]. Long-term therapy with lamivudine leads to viral breakthrough in some patients, owing to the emergence of viral mutation harboring a M204V or I substitution in the YMDD motif^[10]. M204V/I is the most frequently encountered lamivudine-resistant mutant. L180M mutation usually concurrently occurs with M204V mutation. Another mutation, A181T, exists in a substantial proportion of lamivudine-resistant patients. More importantly, the emergence of A181T mutant significantly increases the risk of HCC development in lamivudine-resistant patients during the subsequent course of antiviral therapy^[43,44]. The rate of lamivudine resistance is 24% after 1 year and approximately 70% after 5 years^[45]. Furthermore, lamivudine-resistance causes the attenuation of HBV suppression, hepatitis flare ups, hepatic decompensation and even death, thereby posing a serious clinical challenge^[46]. Because of the overlap between the S and polymerase genes of HBV, a great proportion of patients carrying A181T mutation also possess sW172* nonsense mutation, resulting in truncation of the pre-S/S reading frames. This partially explains why chronic hepatitis B patients who fail to NA treatment at the late stage are more likely to develop HCC compared to those who respond to the treatment. Despite this, lamivudine is still widely used in several countries, mostly because of its low cost. Treatment of patients with lamivudine-

resistance includes the addition of adefovir dipivoxil or tenofovir disoproxil and entecavir rescue treatment. A daily dose of 10 mg of adefovir dipivoxil is not an ideal first-line NA therapy because of its low potency. A proportion (20%-50%) of patients fails to achieve even a 10²-fold reduction in serum HBV DNA. Although adefovir dipivoxil has been widely used in lamivudine-resistant HBV infection, up to 25% of patients fail to achieve a satisfactory response and 30% of naïve patients develop adefovir dipivoxil resistance in 5 years^[47]. Furthermore, adefovir mutations harboring a N236T and/or A181V substitution emerge more frequently in lamivudine-resistant patients than in treatment-naïve patients^[48-50]. Entecavir rescue monotherapy can be adopted as a treatment option for patients with resistance to both lamivudine and adefovir dipivoxil^[51,52]. A clinical trial studying the long-term efficacy of entecavir therapy with 146 patients has shown that among patients with up to 5 years of continuous entecavir 0.5 or 1.0 mg therapy, 94% resulted in HBV DNA reduction to < 300 copies/mL and 80% achieve normalization of ALT levels, while the HBeAg seroconversion and decrease in HBsAg rates are only 23% and 1.4%, respectively^[39]. Entecavir monotherapy may be efficacious in adefovir dipivoxil-refractory chronic hepatitis B patients with prior lamivudine-resistance if these patients have an early virological response to the monotherapy at 12 wk. Entecavir-resistance is rare in treatment-naïve patients, even with long-term therapy, but the cumulative probability of genotypic entecavir resistance with a combination of substitutions I169T and M250V, or T184G and S202I, in lamivudine-resistant patients increases up to 51% after 5 years of treatment^[41,53]. A recent meta-analysis has demonstrated that a combination therapy with lamivudine and adefovir dipivoxil is more effective and produces long-lasting effects than switching to entecavir monotherapy in treating chronic hepatitis B patients with lamivudine resistance. However, taking into account the

practical benefits and the limitations of adefovir dipivoxil, individualized therapy will be needed in patients with a prior history of lamivudine-resistant infections^[54]. Entecavir rescue therapy for 96 wk is less efficacious in patients with lamivudine/adefovur dipivoxil-refractory HBV, particularly in those who have an initial HBV DNA of $> 10^7$ copies/mL. Patients who achieve a HBV DNA level of $< 10^4$ copies/mL and a normalized ALT level should continue, rather than stop, entecavir therapy^[55]. Telbivudine is as potent as entecavir. The therapeutic response to telbivudine is superior to that of lamivudine in HBeAg-positive and HBeAg-negative patients. In HBeAg-positive patients, telbivudine has better outcomes compared to lamivudine in terms of nondetectable viremia, HBeAg loss and viral resistance^[56]. Resistance to telbivudine is associated with a signature M204I mutation in viral polymerase^[37,57]. Tenofovir disoproxil appears to be safe and effective in patients with prior resistance to lamivudine and adefovir dipivoxil and becomes the optimal choice of antiviral treatment^[58,59]. The cost-effectiveness of switching to tenofovir disoproxil or adding tenofovir disoproxil to ongoing lamivudine in lamivudine-resistance patients is still debatable. Adefovir dipivoxil-resistant mutants are usually susceptible to lamivudine, telbivudine or entecavir and they may also be sensitive to tenofovir disoproxil, depending on the mutation pattern, while telbivudine or the rare entecavir resistance strains are usually sensitive to adefovir dipivoxil and tenofovir disoproxil^[43,60]. Despite their high initial potency, 1 year of therapy with NAs does not usually lead to sustained off-therapy responses and therefore treatments usually last for several years or even longer. Nowadays, entecavir and tenofovir disoproxil are recommended as first-line treatments because of their higher potency and lower risk of resistance compared to lamivudine, adefovir or telbivudine^[43,44]. Although it is difficult to compare entecavir and tenofovir disoproxil since no comparison studies have been conducted, tenofovir disoproxil monotherapy appears to be superior to entecavir monotherapy in multidrug-resistant HBV.

ANTIVIRAL THERAPY AND PREVENTION OF HCV-RELATED HCC

Cirrhosis is the strongest risk factor for HCC among patients with chronic HCV infection. Antiviral therapy to inhibit and even eradicate HCV can result in decreasing hepatic necroinflammation and, over time, causes reversal of fibrosis and eventually decreases the risk of HCC^[61]. The standard of care in patients with chronic hepatitis C consists of a 24 to 48 wk course of PEG-IFN α 2a or PEG-IFN α 2b in combination with the guanosin analog ribavirin. This therapy leads to a sustained virological response (SVR) of 42%-52%, 65%-85% and 76%-82% of those infected with HCV genotype 1, HCV genotypes 4, 5 or 6, and HCV genotypes 2 or 3, respectively^[62,63]. A clinical trial following-up 150 patients for 5 years has shown that the clinical, virological, biochemical and histological outcomes of patients with SVR are favorable and

recovery of normal or nearly normal liver architecture is possible^[64]. The standard of care can decrease the risk of HCC, although the effect is predominantly evident in patients who achieve SVR and in those who have not yet progressed to cirrhosis^[65,66]. However, several studies have demonstrated that, for patients with advanced fibrosis or cirrhosis, the risk of developing HCC remains even if a SVR is achieved, highlighting the importance of continued surveillance in these patients^[67,68]. A recent meta-analysis pooled data from 20 studies (4700 patients with HCV-related cirrhosis) and compared untreated patients with those given IFN α alone or combined with ribavirin treatment and it showed a reduced risk of HCC in the treatment group (RR = 0.43, 95%CI: 0.33-0.56). Another meta-analysis using data from 14 studies (n = 3310) indicated that patients achieving a SVR had a lower incidence of HCC (RR = 0.35, 95%CI: 0.26-0.46) compared with nonresponders and the maximum benefits were observed in those treated with ribavirin-based regimens (RR=0.25, 95%CI: 0.14-0.46)^[65]. Due to the potential anti-tumoral, anti-angiogenic and anti-fibrotic roles of IFN α , maintaining IFN α therapy might decrease the risk of HCC in patients who fail to achieve SVR. However, several large-scale randomized controlled trials with long (3-4 years) and extended (up to 5 years) follow-up time have shown that low-dose PEG-IFN in patients with advanced fibrosis or cirrhosis have minimal or even no benefit on overall clinical outcomes^[69-71]. Although the treatment of HCV chronic infection with the standard of care therapy can eradicate HCV in 40%-90% of patients, approximately 10%-15% of patients have to discontinue the treatment due to adverse effects. The adverse effects, ranging from mild to moderate in severity, impact most organ systems and can cause serious and even life-threatening toxicity, such as psychological disturbances, poor appetite, skin rash, infection, anemia and leukopenia^[72]. Accordingly, patients should be closely monitored for adverse effects during treatment.

Although the standard of care therapy will probably continue for some years, more effective therapeutic options with shorter treatment durations are being introduced to increase the response rate in difficult-to-treat patients (mainly infected with genotype 1) and reduce the impact of HCV infection and related complications. So far, intensive efforts have been made to develop different compounds that specifically target the replication cycle of the virus. These direct-acting antiviral agents (DAAs) act by directly inhibiting the NS3/4A serine protease (which processes the HCV polyprotein to generate mature viral proteins), the NS5B polymerase (which replicates the viral RNA genome) and the NS5A phosphoprotein (which functions as a part of the replicase complex)^[73-76]. The new standard of care for patients with chronic hepatitis C is to add nonstructural (NS) 3/4A protease inhibitors boceprevir or telaprevir to the Peg-IFN α plus ribavirin regimen. The recent sixty-first annual meeting of the American Association for the Study of Liver Diseases (AASLD) provided an overview of the pipeline of these

novel drugs. Numerous other protease inhibitors, as well as nucleoside and non-nucleoside inhibitors of the RNA-dependent RNA NS5B polymerase and inhibitors of the NS5A protein, are also under evaluation currently. These can achieve higher SVR rates in previously untreated patients infected with HCV genotype 1 and provide successful medical care for those who have failed treatment under current standard of care^[77]. In a recent phase II study, 465 chronic hepatitis C patients with poor response to PEG-IFN α plus ribavirin therapy were allocated to the triple therapy group and the control group. It was found that the triple therapy significantly increased SVR rates in these difficult-to-treat patients compared with the controls (53% *vs* 14%)^[78]. Remarkably, in a group of HCV patients treated for 24 wk with this triple therapy followed by another 24 wk of PEG-IFN α 2b plus ribavirin, the SVR rates for patients who had previously relapsed was 76% and up to 39% for those who did not respond to the standard therapy. Another report of a phase II study indicated that adding boceprevir to the standard treatment leads to a notably increased SVR (75% *vs* 38%) in treatment-naïve patients who were infected with HCV genotype 1^[79]. The combination of three agents, PEG-IFN α , ribavirin and HCV protease inhibitor, is able to increase SVR rates substantially. The potency and safety of the two first generation HCV protease inhibitors are also confirmed in large phase III studies. In the treatment-naïve patients infected with HCV genotype 1, the SVR rates are 75% with the addition of telaprevir *vs* 44% with the standard therapy and 68% with the addition of boceprevir *vs* 40% with the standard therapy. Although the upcoming triple therapy regimens including telaprevir or boceprevir may be different, this strategy means that in treatment-naïve patients, treatment duration will be reduced to 24 or 28 wk for the patients with a rapid viral response, those with a negative result of serum HCV RNA after 4 wk of exposure to an HCV protease inhibitor. In addition, the single nucleotide polymorphisms around the gene encoding interleukin 28B (*IL28B*) have been identified as key predictive factors^[80]. In treatment-naïve HCV-1 patients treated with PEG-IFN and ribavirin, among host and viral factors associated with SVR, combination of *IL28B* genotypes and rapid viral response monitoring seems to provide a high predictive value of treatment outcome, particularly in the context of emerging therapies and DDAs^[81]. Furthermore, a study combining a nucleoside polymerase inhibitor (RG7128) and danoprevir led to an average of 5.1 log reduction of plasma HCV RNA levels within 14 d^[82]. Overall, this treatment is not only an important step towards an IFN-free regimen, but also reflects the high genetic barrier to resistance associated with nucleoside polymerase inhibitors. Co-administration of different classes of DAAs, combined with or without PEG-IFN α and/or ribavirin, might make HCV RNA suppression possible in most individuals who are infected with HCV genotype 1, including those who are not responsive to PEG-IFN α ^[73]. However, it is still unclear whether the novel agents will

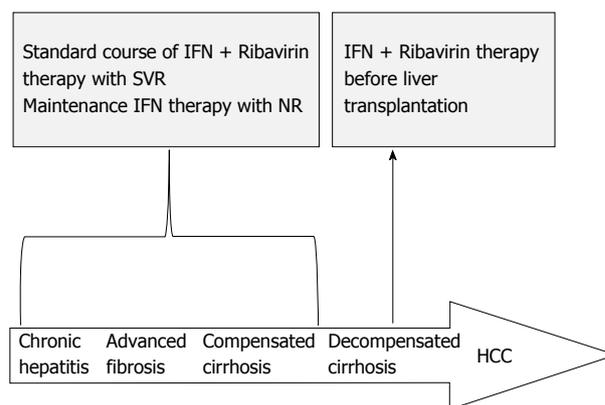


Figure 2 Flowchart of therapy choice for patients with chronic hepatitis C virus infection. HCC: Hepatocellular carcinoma; IFN: Interferon; NR: No response; SVR: Sustained virological response.

be useful in the most difficult-to-treat patients, such as those with advanced or decompensated liver diseases or after liver transplantation. Furthermore, DAAs also need to be developed for other HCV genotypes. Therefore, characterizing resistance to DAAs and the combination of antiviral agents with different resistance profiles in clinical trials are the best strategies to prevent the emergence of drug-resistant mutants and thereby maximize SVR rate.

However, given the adverse effects, it remains uncertain whether patients with decompensated cirrhosis could tolerate HCV eradication treatment and therefore should be treated to prevent progression of decompensation. The AASLD recommends those patients to be referred for consideration of liver transplantation^[83]. Eradication of HCV before liver transplantation could reduce post-transplant recurrence of HCV, especially in patients infected with HCV genotypes other than genotype 1^[84]. Thus, treatment should be reserved for those patients awaiting liver transplantation. It is recommended that patients with decompensated cirrhosis initiate treatment at a low dose of IFN-based therapy. However, the treatment should be administered with caution since it is still unclear whether the novel agents will be effective in those most difficult-to-treat patients^[79,85]. In addition, use of hematological growth factors can improve the life quality of treated patients and manage treatment-induced cytopenias (Figure 2).

CONCLUSION

In summary, antiviral treatment of chronic hepatitis B or chronic hepatitis C is so far the only option to prevent HCC. Treatment of chronic hepatitis B with IFN α may significantly decrease overall incidence of HCC in sustained responders, while the adverse effects may limit its long-term application. Orally administered NAs significantly reduce disease progression of liver cirrhosis, resulting in up to a 78% decrease in HCC incidence, especially in HBeAg-positive patients. In patients with life-threatening liver diseases, antiviral treatment should be initiated

as soon as possible in order to stabilize liver function and prepare for liver transplantation. Long-term continuous treatment with NAs results in antiviral drug resistance due to the mutations in HBV polymerase. Of the NA resistance-associated mutants, A181T mutant significantly increases the risk of HCC in lamivudine-resistant patients during the subsequent courses of antiviral therapy. In addition, it remains to be explored if the HCC-associated HBV mutants, whose emergence is likely to be selected by virus-host interaction during carcinogenesis, are sensitive to the antiviral therapy.

The recommended treatment for patients with chronic HCV infection is PEG-IFN plus ribavirin which can decrease HCC incidence in those who achieve SVR and have not yet progressed to cirrhosis. Patients with decompensated cirrhosis are under evaluation of liver transplantation, because achievement of a SVR is possible in these patients but does not forestall the disease progression. IFN and ribavirin therapy, therefore, should be reserved in these patients to prevent post-transplant recurrence of HCV. More effective therapeutic options such as DDAs are promising in increasing the response rate of difficult-to-treat patients with HCV genotype 1.

There is a great need to develop safer, more effective and affordable antiviral therapies. To optimize treatment responses, appropriate therapy should be initiated at the proper time. Patients must be educated about the importance of treatment compliance. The response to antiviral treatment should be closely monitored so that the therapy can be modified when the initial one fails. HCC risk remains in cirrhotic patients (both HBV and HCV infection) if treatment is initiated after cirrhosis is established and close monitoring is needed. Future research should focus on investigating the use of new agents, especially for patients with hepatic decompensation or after transplantation.

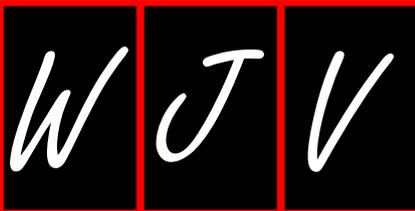
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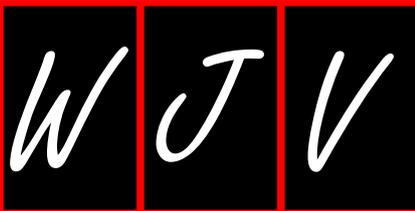
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March 11-15, 2012

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March 14-17, 2012

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Essen, Germany

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2012 HIV Vaccines
Keystone, CO, United States

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Cell Biology of Virus Entry, Replication and Pathogenesis
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Frontiers in HIV Pathogenesis, Therapy and Eradication
Whistler, BC, Canada

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2012 Molecular Virology Workshop
Daytona Beach, FL, United States

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European Molecular Biology Organization Workshop - Antigen presentation and processing
Amsterdam, Netherlands

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European Molecular Biology Organization and European Molecular Biology Laboratory Symposium - New perspectives on immunity to infection
Heidelberg, Germany

June 11-16, 2012

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Pultusk, Poland

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7th International Workshop on Hepatitis C - Resistance and New

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Cambridge, MA, United States

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European Molecular Biology Organization Conference Series - Viruses of microbes: From exploration to applications in the -omics era
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2nd World Congress on Virology
Las Vegas, NV, United States

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Viral Hepatitis Congress 2012
The Johann Wolfgang Goethe University, Frankfurt, Germany

October 18-20, 2012

2nd World Congress on Controversies in the Management of Viral Hepatitis (C-Hep)
Berlin, Germany

November 28 -December 1, 2012

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English journal article (list all authors and include the PMID where applicable)

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- 2 **Lin GZ**, Wang XZ, Wang P, Lin J, Yang FD. Immunologic effect of Jianpi Yishen decoction in treatment of Pixu-diarhoea. *Shijie Huaren Xiaobua Zazhi* 1999; **7**: 285-287

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- 3 **Tian D**, Araki H, Stahl E, Bergelson J, Kreitman M. Signature of balancing selection in Arabidopsis. *Proc Natl Acad Sci USA* 2006; In press

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- 5 **Vallancien G**, Emberton M, Harving N, van Moorselaar RJ; Alf-One Study Group. Sexual dysfunction in 1, 274 European men suffering from lower urinary tract symptoms. *J Urol* 2003; **169**: 2257-2261 [PMID: 12771764 DOI:10.1097/01.ju.0000067940.76090.73]

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- 6 21st century heart solution may have a sting in the tail. *BMJ* 2002; **325**: 184 [PMID: 12142303 DOI:10.1136/bmj.325.7357.184]

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- 7 **Geraud G**, Spierings EL, Keywood C. Tolerability and safety of frovatriptan with short- and long-term use for treatment of migraine and in comparison with sumatriptan. *Headache* 2002; **42** Suppl 2: S93-99 [PMID: 12028325 DOI:10.1046/j.1526-4610.42.s2.7.x]

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- 9 Outreach: Bringing HIV-positive individuals into care. *HRS-A Careaction* 2002; 1-6 [PMID: 12154804]

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- 10 **Sherlock S**, Dooley J. Diseases of the liver and biliary system. 9th ed. Oxford: Blackwell Sci Pub, 1993: 258-296

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- 12 **Breedlove GK**, Schorfheide AM. Adolescent pregnancy. 2nd ed. Wiczorek RR, editor. White Plains (NY): March of Dimes Education Services, 2001: 20-34

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- 13 **Harnden P**, Joffe JK, Jones WG, editors. Germ cell tumours V. Proceedings of the 5th Germ cell tumours Conference; 2001 Sep 13-15; Leeds, UK. New York: Springer, 2002: 30-56

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- 14 **Christensen S**, Oppacher F. An analysis of Koza's computational effort statistic for genetic programming. In: Foster JA, Lutton E, Miller J, Ryan C, Tettamanzi AG, editors. Genetic programming. EuroGP 2002: Proceedings of the 5th European Conference on Genetic Programming; 2002 Apr 3-5; Kinsdale, Ireland. Berlin: Springer, 2002: 182-191

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- 15 Morse SS. Factors in the emergence of infectious diseases. *Emerg Infect Dis* serial online, 1995-01-03, cited 1996-06-05; 1(1): 24 screens. Available from: URL: <http://www.cdc.gov/ncidod/eid/index.htm>

Patent (list all authors)

- 16 **Pagedas AC**, inventor; Ancel Surgical R&D Inc., assignee. Flexible endoscopic grasping and cutting device and positioning tool assembly. United States patent US 20020103498. 2002 Aug 1

Statistical data

Write as mean \pm SD or mean \pm SE.

Statistical expression

Express *t* test as *t* (in italics), *F* test as *F* (in italics), chi square test as χ^2 (in Greek), related coefficient as *r* (in italics), degree of freedom as *v* (in Greek), sample number as *n* (in italics), and probability as *P* (in italics).

Units

Use SI units. For example: body mass, m (B) = 78 kg; blood pres-

sure, p (B) = 16.2/12.3 kPa; incubation time, t (incubation) = 96 h, blood glucose concentration, c (glucose) 6.4 ± 2.1 mmol/L; blood CEA mass concentration, p (CEA) = 8.6 24.5 $\mu\text{g/L}$; CO_2 volume fraction, 50 mL/L CO_2 , not 5% CO_2 ; likewise for 40 g/L formaldehyde, not 10% formalin; and mass fraction, 8 ng/g, *etc.* Arabic numerals such as 23, 243, 641 should be read 23 243 641.

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