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Review

Roles of DLK1 in Liver Development and Oncogenesis

Ahmad Azmi Nasution, Msy Rulan Adnindya, Indriyani and Isabella Kurnia Liem

1Department of Anatomy, Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia
2Master Program in Biomedical Sciences, Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia
3Department of Anatomy, Faculty of Medicine and Health Science, Universitas Bengkulu, Bengkulu, Indonesia
4Department of Anatomy, Faculty of Medicine, Sriwijaya University, Palembang, Indonesia
5Department of Anatomy, Faculty of Medicine, Universitas Muhammadiyah Palembang, Palembang, Indonesia
6Department of Anatomy, Faculty of Medicine, Universitas Indonesia, Jakarta, Indonesia

Abstract: Hepato Cellular Carcinoma (HCC) has an increased mortality rate in the last decade. Protein expression in HCC has similarities to the liver cells during the development process. One of the proteins expressions is Delta-Like 1 homolog (DLK1) that was found during liver development and oncogenesis. This permits the opportunity to study pathophysiology and signaling pathway of DLK1 and to find an early detection and therapeutic target for HCC. This review will explain the signalling mechanism and the roles of DLK1 during liver development, oncogenesis of HCC, as a tumor marker and targeting therapy.

Keywords: Hepatocellular Carcinoma, DLK1, Liver Development, HCC Oncogenesis, Tumor Marker

Introduction

Hepatocellular Carcinoma (HCC) is one of malignancies which has high mortality rate. American Cancer Society has reported an increase in the mortality rate since 2003 until 2012 as much as 2.7% due to this illness (ACS, 2016). Hepatocellular carcinoma and liver cirrhosis are the main cause of chronic hepatitis B and hepatitis C virus that made patients death. Approximately 1.45 million people are infected by these viruses (WHO, 2016). Because of the HCC incidence and high in mortality, it becomes a concern of researcher to make diagnostic and effective therapeutic strategies. It requires a comprehensive knowledge of liver development to understand the preventive measures, causes determination and pathogenesis of liver diseases (Sokol, 2002). One of the proteins target in liver oncogenesis is Delta-Like 1 homolog (DLK1).

Delta-Like 1 homolog (DLK1) is a candidate biomarker of liver stem/progenitor cells (Wang and Sul, 2006; Bujak et al., 2015; Kopan and Ilagan, 2009) and plays a significant role in HCC oncogenesis (Baladron et al., 2005; Laborda et al., 1993; Nueda et al., 2007). DLK1+ HCC cells have the same characteristics as cancer stem/progenitor cells. However, molecular mechanism of HCC is still not yet well-established (Falix et al., 2012; Xu et al., 2012). This review explains the roles of DLK1 in the process of liver development, HCC oncogenesis, as a tumor marker and targeting therapy.

Delta-Like 1 Homolog

Delta-like 1 homolog is a transmembrane protein that has three major regions, i.e., an extracellular region composed of six EGF-like (epidermal growth factor like), a juxtamembrane region with TACE cleavage site (ADAM17) and an intracellular region (Bujak et al., 2015; Wang and Sul, 2006). The repeated structure of amino acid sequences of EGF are very similar to the structure of Delta-Like canonical Ligand (DLL) (Baladron et al., 2005; Nueda et al., 2007; Bujak et al., 2015); however, DLK1 does not have N-terminal Delta-Serrate-LAG-2 (DSL)-domain (Yin et al., 2006; Kopan and Ilagan, 2009). Consequently, Delta and OSM-11-like proteins (DOS) co-ligand functioned to inhibit NOTCH signalling. DOS is a specialized tandem of EGF-repeats (Baladron et al., 2005; Kopan and Ilagan, 2009; Nueda et al., 2007; Fig. 1). DLK1 shows inhibitory activity in NOTCH signalling pathway (Kopan and Ilagan, 2009). It is expressed widely during embryonic development and controls the determination process of cell fate, proliferation and differentiation (Baladron et al., 2005; Falix et al., 2012; Nueda et al., 2007; Fig. 1).
Fig. 1. Schematic diagram of NOTCH1, NOTCH2, NOTCH3 and NOTCH4 receptors and their four ligands (JADDED1, JADDED2, DLL1 and DLK1). NOTCH receptors consist of multiple extracellular EGF-like repeats, which are different in the repeating number in each receptor. NOTCH receptors have two domains, i.e., extracellular (NECD) and transmembrane-intracellular (NTMIC). Ligand binding will release intracellular (NICD) fragment and leads to NOTCH signalling activity. Two NOTCH receptor ligands family are Jagged and DLL ligands. Those canonical ligands contain DSL, DOS and EGF motifs. DLK1 is a non-canonical ligand that lacks of its DSL domain; consequently, it will acts as DOS ligand.

**DLK1-NOTCH Relationship**

In determining the fate of hepatoblast cells and HCC pathogenesis, NOTCH signalling has a significant role (Lu et al., 2016). NOTCH signalling is also required for cell commitment, cell specification and maintenance process of progenitor cells during prenatal development (Chen et al., 2011; Dill et al., 2013; Lu et al., 2016; Loomes et al., 2002). NOTCH has four receptor types, i.e., NOTCH1-4 and two families ligands (Jagged and Delta-like) (Falix et al., 2012).

NOTCH receptors consist of two domains, i.e. NOTCH Extracellular Domain (NECD) and NOTCH Transmembrane-Intracellular domain (NTMIC) (Kopan and Ilagan, 2009; Falix et al., 2012). NOTCH extracellular domain is composed of varian EGF like repeats (29-36 EGF-like repeats), a region that mediates interaction between the receptor and its ligand, especially at EGF-like repeats 11-12 and 24-29 (Kopan and Ilagan, 2009). Epidermal growth factor repeats are followed by negative regulatory region or NRR that contains three cysteine-rich Lin12-Notch Repeats (LNR) and a heterodimerization domain or HD. In the absence of ligand, NRR has a special function to prevent receptor activation (Kopan and Ilagan, 2009; Falix et al., 2012; Teodorczyk and Schmidt, 2014).

NOTCH Transmembrane and Intracellular domain (NTMIC) are composed of transmembrane domain or TMD, a RBP-Jκ association module-domain for binding with DNA binding protein CSL (CBF1/RBP-Jκ/Su(H)/Lag-1) (Kopan and Ilagan, 2009), nuclear localization sequences or NLSs, a seven ankyrin reputation-domain that functions to take the coactivator Mastermind/Lag-3 and a Transactivation Domain (TAD) that habor a conserved proline/glutamicacid/serine/threonine-rich (PEST) motifs (Teodorczyk and Schmidt, 2014; Kopan and Ilagan, 2009; Geisler et al., 2008). Glutamine-rich repeat (OPA) in Drosophila has a function as transactivation domain (Kopan and Ilagan, 2009).

Two families of ligand have three structural motifs, i.e. an N-terminal DSL motif, a specialized tandem EGF repeats, i.e. DOS-domain and variable EGF-like repeats (Falix et al., 2012; D’Souza et al., 2010; Teodorczyk and Schmidt, 2014). The difference between Jagged/Serrate ligand and Delta-like ligand are based on the existence of a cysteine-rich domain. Jagged/Serrate ligand has cysteine-rich domain and Delta-like ligand do not have it (Fig. 1). N-terminal DSL and DOS region will bind with NOTCH receptor (Kopan and Ilagan, 2009; Falix et al., 2012).

NOTCH signalling pathway begins with the binding of ligand-receptor that induces the receptor. With the aid of proteolytic enzyme, NOTCH receptor releases NICD. In further, NICD enters nucleus to bind with CBF1/RBP-Jκ. It will activate target genes, such as Hes (hairy and enhancer of split homologs; Fig. 2) that has functions in the regulation of proliferation, differentiation and apoptosis of epithelial cells and carcinogenesis (Falix et al., 2012; Hansson et al., 2004; Lu et al., 2016). NOTCH signaling also controls Sox9, HNF1, TGF-β and Homeobox B expressions in the liver, which play a role in determining liver cells commitment (Dill et al., 2013; Zong et al., 2009; Zong and Stanger, 2011; Figure 2). The absence of RBP-Jκ indicates blocking of NOTCH signalling pathway (Morell et al., 2013).
In mammals, four NOTCH receptors have their own roles. NOTCH1 has a role in the normal prenatal development; nevertheless, it also involved in the regulation of oncogenesis process in adult (Falix et al., 2012). NOTCH2 is responsible for the cholangiocytes differentiation, aggressive behavior and immature morphology of HCC (Falix et al., 2012; Hayashi et al., 2015). NOTCH3 and NOTCH4 have functions in vascular development (Falix et al., 2012). DLK1 role as non-canonical ligand is as inhibitors of NOTCH signaling (Figure 2). It can be seen from the fact that increased DLK1 expression is associated with the decreased of NOTCH and Hes1 expressions (Chen et al., 2011; Tanimizu and Mitaka, 2004). While DLK1 is down regulated, NOTCH expression is increased and at the same time hepatoblasts differentiates into cholangiocytes (Baladron et al., 2005; Gordillo et al., 2015; Loomes et al., 2002; Yin et al., 2006).

**DLK1-NOTCH in Liver Development**

DLK1 has dynamic expression during liver development. DLK1 expression begins since ED10.5 and increases significantly at ED14.5–ED16.5. DLK1 expression is downregulated concomitantly with the formation of cholangiocytes and the remodelling of ductal plate into intrahepatic ducts. Eventually, DLK1 expression is no longer found after neonate period (Falix et al., 2013; Tanimizu et al., 2003; Tanaka et al., 2009).

DLK1 is a marker for hepatoblast that has high proliferation and bipotentiality. DLK1 is also considered as a marker for immature hepatocytes because DLK1 cells express HNF1β, HNF3β, HNF4 and HNF6, but do not express CK19 that is expressed by cholangiocytes (Tanimizu et al., 2003; 2004). While DLK1 is down regulated, NOTCH expression is increased and at the same time hepatoblasts differentiates into cholangiocytes (Baladron et al., 2005; Gordillo et al., 2015; Loomes et al., 2002; Yin et al., 2006).

NOTCH signalling is responsible for activation of target genes, i.e., Hes, Sox9, HNF1β, that are important for cholangiocytes differentiation (Gordillo et al., 2015; Tanimizu and Mitaka, 2014; Shin et al., 2015; Jörs et al., 2015; Morell et al., 2013; Fig. 2). In addition, DLK1 also has a role for progenitor/stem cells’ maintenance and differentiation during development (Begum et al., 2014). DLK1-Wnt10b-βCatenin pathway contributes in hepatocytes proliferation during liver regeneration. DLK1+ hepatocyte cells are induced by hepatic stellate cells through paracrine effects and self-inductive (Zhu et al., 2012).

**DLK1-NOTCH Role in Hepatocellular Carcinoma Oncogenesis**

Some spectrum of tumors, such as breast cancer, small-cell lung carcinoma, leukemia, neuroblastoma,
gliomas, pancreatic cancer, colon cancer, have high DLK1 expression (Begum et al., 2014; Bujak et al., 2015). In the pathogenesis of liver diseases, NOTCH signaling has a significant role. Increased expression of NOTCH3 and NOTCH4 are found in cancer tissues. Observation of HCC HepG2 cell lines showed a relatively high NOTCH3 expression and a little expression of NOTCH4 (Geisler et al., 2008). In the pathogenesis of HCC, there is a mechanism involving DLK1 and NOTCH signaling pathway. Regulation of HCC is through multiple signaling pathways including NOTCH, RAF/MEK/ERK, Wnt/β-catenin, AKT/mTOR, EGFR, HGF/cMET and (Coral et al., 2012; Woo et al., 2009; Zhao et al., 2016; Fig. 3).

DLK1 expression can be induced by hypoxia; therefore, it is possible that oncogenesis process involving DLK1 were affected by hypoxic conditions in the microenvironment (Kim et al., 2009). DLK1 is also secreted in hepatic stellate cells selectively and will induce the activation of hepatic stellate cells in vivo and in vitro (Zhu et al., 2012). DLK1 will upregulate WNT pathway. Knockdown of DLK1 will lead to the reduction of Wnt10b, Wnt3a, necdin and Shh expression (Zhu et al., 2012). In vitro, DLK1 inhibit Mesenchymal Stem Cells (MSC) differentiation (Chen et al., 2011). In vivo, overexpression of DLK1 will increase the stemness of the tumor cell and tumor growth (Begum et al., 2014; Kim et al., 2009). DLK+ HCC showed to form a colony, spheroid colony and higher chemoresistance compared to DLK1 knockdown on HCC cells (Xu et al., 2012).

Another oncogenesis process of HCC is by activation of NOTCH signaling pathway that will lead an epithelial tranformation into mesenchymal (Fig. 3). This change will also result in the disappearance of main characteristic of epithel cells and play a role in embryonic development, liver fibrosis and cancer (Zhao et al., 2016).

NOTCH2 signalling can lead and acceleratfed HCC formation that has the same characteristics and expression pattern as hepatoblast (Hayashi et al., 2015; Dill et al., 2013), but with great migration and invasion capability (Gordillo et al., 2015).

NOTCH2 signalling is one of key regulators in HCC. NOTCH2 signalling will increase Hes1 and Sox9 mRNA expression related to HCC formation (Tanimizu et al., 2003; Dill et al., 2013). Increased proliferation on DEN-N2ICD mice correlated to the increased of NOTCH2 expression. The increased of Hes1 mRNA will eventually form a colony in HCC formation. In addition, NOTCH2 signalling will accelerate the HCC growth (Dill et al., 2013).

In the last 5 years, researches have demonstrated the role of hepatic stellate cells and some morphogensin oncogenesis process of HCC (Zhu et al., 2012; Funk et al., 2016). Activated hepatic stellate cells will express some morphogen such as Wnt, Necdin, DLK1, Shh and NOTCH. Wnt pathway, Necdin and DLK1 have a function in HCC through the regulatory role of PPARγ. PPARγ plays a role in inhibiting tumor growth and invasion of cells to the surrounding tissues. Another function of PPARγ is to inhibit EMT process which plays a role in HCC (Fung et al., 2016; Hsu and Chi 2014; Kimura et al., 2012; Shen et al., 2012; Zhu et al., 2012). Studies that have been conducted gave indirect evidence to the relation of Wnt, Necdin, DLK1 and PPARγ in HCC. Necdin has a role in activation of Wnt pathway by binding with GN boxes on the proximal promoter of Wnt10b resulting in the repression of PPARγ. This proves that there is an opposite role of Necdin and Wnt with PPARγ (Ross et al., 2000; Zhu et al., 2012). In studies of DLK1 knockdown, induction of PPARγ was occured. It was almost identical with Necdin and Wnt mechanism in regulation of PPARγ (Zhu et al., 2012; Funk et al., 2016). Therefore, the increase of Wnt, Necdin and DLK1 expression will lead to PPARγ suppression resulting in increased expression of HGF, which has a role in EMT that will eventually develop into HCC (Fung et al., 2016; Maulik et al., 2002; Ding et al., 2010; Mizuno et al., 2005; Ozaki et al., 2003). Additionally, proliferation and invasion of HCC will be increased due to HGF stimulation of Matrix metallopeptidase 9 (MMP9) and Matrix metallopeptidase 3 (MMP3) (Wang et al., 2007; Ozaki et al., 2003; Mizuno et al., 2005; Mohammed et al., 2005; Lee et al., 2010).

**DLK1 as Hepatocellular Carcinoma Marker**

Delta-like 1 homolog is expressed in malignancy and promotes cancer cell stemness and tumorigenicity so it can be used as therapeutic target and tumor marker for cancer stem/progenitor cells. Li et al. (2015) revealed that tumor size of HCC was positively correlated to DLK1 in serum. DLK1 can be a complement to Alpha Feto Protein (AFP) in the diagnosis of HCC (Li et al., 2015; Chauhan and LahirI 2016; Shen et al., 2016).

It is possible to use DLK1 as a prognostic factor since there is an evidence that it correlates to survival rate in HCC. HCC patients with DLK1+ cells have shorter survival rate compared to HCC patients without DLK1- cells (Jin et al., 2008; Li et al., 2015).

The relationship between expression of DLK1, PPARγ and HGF needs to be studied in further, especially as marker of invasion and metastases level of HCC. HCC anti-metastatic proteins, such as E-cadherin, spleen tyrosine kinase or SYK and ECM regulator metallopeptidase inhibitor 3 (TIMP3), act as anti-metastatic in HCC (Hsu and Chi 2014; Shen et al., 2012).
Conclusion

HCC and progenitor/stem cell have similar expression pattern. A protein that is found in both condition is DLK1 that can affect cell proliferation and differentiation. Some signaling pathways, such as Wnt and NOTCH pathway, are indirectly affected by DLK1; even though, the signaling pathways are not clearly understood (Fung et al., 2016). The role of DLK1 in Wnt pathway are in non-canonical or β-catenin-independent mechanism (Vilchez et al., 2016; Fung et al., 2016) and also through PPARγ suppression mechanism. In addition, paracrine and self-inductive effect of hepatic stellate cells were able to activate DLK1 to play a role in the process of liver development, regeneration, fibrosis and malignancy (Zhu et al., 2012; Fung et al., 2016). Further researches are expected to reveal the biological role of DLK1 in the signaling pathway. This knowledge will provide solutions for HCC therapy in the future. Another research opportunity that can be further explored is the relationship between DLK1, Wnt and PPARγ in oncogenesis of HCC.

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Ahmad Azmi Nasution


