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Glycosylation and Liver Cancer

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Abstract

Liver cancer is the 5th most common cancer, but the 2nd leading cause of cancer death, in the world, with more than 700,000 fatalities annually. The major etiology of liver cancer is infection with an hepatotropic virus such as hepatitis B virus (HBV) or hepatitis C virus infection (HCV). While chronic viral infection remains the main cause of liver disease and risk of HCC, rates of non –viral associated HCC are occurring at an alarmingly increasing rate. Like many cancers, survival rates are closely associated with time of detection. If HCC is caught early, survival rates can be as high as 50%. Regrettably, most cases of HCC are caught late where survival rates can be as low as 2–7%. Thus, there has been great interest in discovering serum biomarkers that could be used to identify those with HCC. To this end, many groups have examined the N-linked glycans to identify changes that occur with HCC. As the liver secretes the vast majority of proteins into the serum, this has often been a starting point for study. In serum, alterations in core fucosylation, outer-arm fucosylation, increased sialylation and glycan branching have been observed in patients with HCC. Similar findings have been found directly in HCC tissue suggesting that these glycan changes may play a role in tumor formation and development.

Keywords

Fucosylation; glycosylation; hepatocellular carcinoma; hepatitis B virus; hepatitis C virus; NASH; glycomics; glycoproteomics; liver cancer

Hepatocellular carcinoma

Hepatocellular carcinoma (HCC) is a malignancy of hepatocytes that arises within the liver. This cancer occurs in the background of patients with underlying liver disease such as liver fibrosis and liver cirrhosis. Approximately 80% of all liver cancers are hepatocellular carcinoma (HCC) and it is one of the most common malignancies worldwide (Block et al., 2003). The survival rate of people with primary cancers of the liver and intra-hepatic bile ducts is very low, usually less 2–7%% [7]. The low survival rates have been attributed to the late diagnosis (Di Bisceglie, 1998) and, although liver transplantation is the preferred option for surgical treatment of HCC (Kim, 1998), the paucity of organ donors means that common (worldwide) treatment is partial hepatic resection. Unfortunately, even with the advances in surgery and patient care, reported 5-year survival rates are between 40% and 50% (Poon, 2000). This low rate of survival is made even more problematic when only about 10% of HCC patients are acceptable for resection (Paterlini-Brechot, 2000). In addition, the cumulative 5-year recurrence rate is between 75% and 100% (Poon, 2000) and HCC is consequently responsible for over 700,000 deaths annually (a conservative estimate) and

ranks as the 2nd leading cause of cancer death worldwide (Bosch, 1999). Although HCC in the USA is an uncommon cancer, as figure 1 shows, the rates are increasing dramatically both in the USA (El-Serag, 1999) as well as in Japan and Europe (Deuffic, 1998; Okuda, 1987; Taylor-Robinson, 1997). In 2000, there were an estimated 10,000 cases of liver cancer in the USA. Amazingly, by 2013 that number has more than tripled with over 34,000 cases and approximately 23,000 deaths. Indeed, the occurrence of liver cancer is predicted to continue rising in the United States and is currently among the top 10 causes of cancer death (http://www.cancer.gov/cancertopics/types/liver).

HCC is characterized by its propensity for vascular invasion and microscopic venous or macroscopic portal vein invasion are recorded as being the most significant risk factors for recurrence. Indeed, both intra-hepatic metastasis and/or multi-centric occurrence contribute to recurrence in the liver remnant as does initial large tumor size (especially >5 cm). Even after liver transplantation, often viewed as a cure for HCC, intra-hepatic tumor recurrence occurs and is especially frequent in tumors >3 cm (Paterlini-Brechot, 2000). Although the cause of the tumor (viral infection, alcohol etc.) does not appear to be a significant risk factor for recurrence, there are reports of lower rates of recurrence in HBV infected individuals compared to HCV patients (Kumada, 1997; Yamanaka, 1997).

Hepatitis- A major risk factor for HCC

Infection with hepatitis B virus (HBV) and/or hepatitis C virus (HCV) is the major etiology of HCC (Benvegnu, 1994; Brechot, 1996; Hoofnagle, 1999). HBV causes both acute and chronic infections of the liver and most chronically infected individuals remain asymptomatic for many years and clinical disease (HCC) is not apparent until decades later. Nearly 25% of all chronic carriers eventually develop untreatable liver cancer and it is estimated that over one million people worldwide die due to HB- associated liver cancer (Parkin, 1999). Indeed, HBV infection is associated with over 80% of all HCC cases worldwide and can be as high as 96% in regions where HBV is endemic (Beasley, 1988). More than 350 million people worldwide are chronically infected with HBV, including 1.25 million in the USA (Hoofnagle, 1997). With 140,000–320,000 new cases of HBV reported in the USA each year the *at risk* population (for HCC) has been consistently rising. This is unfortunate since an effective vaccine has been available for nearly 20 years. Only recently have universal vaccination programs gotten under way in developed countries. However, the huge pool of infected individuals remains since no effective therapy is available.

The progression of liver disease in asymptomatic chronic carriers of HBV and HCV is monitored by serum liver function tests (LFTs) and ultra sound imaging for detection of small masses in the liver (Hepatitis B Foundation, 1994). Many of the constituents of the LFT panel vary throughout the course of chronic hepatitis and are of limited use in early detection of HCC. Ultra-sound detection requires at least a 2 cm tumor mass to be present, and often occurs at a stage at which the prognosis is very poor (Brechot, 1987; Hoofnagle, 1997). Imaging modalities such as computed axial tomography (CAT scan) or Magnetic resonance imaging (MRI) have great value and are in many ways the "gold standard". However, even these methods have limitations such as poor sensitivity of a per lesion basis and excessive cost. Thus, as early surgical and chemotherapeutic intervention is the best

hope for patient survival (Brechot, 1987; Di Bisceglie, 1998), early detection of HCC though the use of a biomarker is necessary to identify the need for intervention.

Proteomic identification of biomarkers of liver cancer

Over the last 15 years various proteomic methodologies have been proposed to identify proteins that are altered in the serum of those with HCC. Most methods have involved the comparative analysis of several patients groups, most notably, healthy subjects, those infected with a hepatitis virus such as HBV or HCV, those with liver cirrhosis and those with liver cirrhosis and HCC. Early proteomic efforts utilized simple two-dimensional gel electrophoresis (2DE) and looked for spot alterations in the serum proteome(Chignard and Beretta, 2004; Feng et al., 2005; Park et al., 2002a; Poon and Johnson, 2001; Shalhoub et al., 2001; Steel et al., 2001; Takashima et al., 2003). Proteins identified using this approach identified limited changes in the serum proteome with the development of HCC, as compared to those with just cirrhosis. Additionally, 2DE was combined with several groups to identify auto-antibodies as potential biomarkers of liver cancer(Le Naour et al., 2002).

2DE was also used initially to examine proteomic differences between HCC tissue and adjacent tissue in an effort to identify those proteins that are specifically altered in HCC. These studies have identified alterations in several tumor pathways that have previously been identified in other cancers(Chignard and Beretta, 2004; Ding et al., 2004; Higai et al., 2003; Melle et al., 2004; Park et al., 2002b; Yokoo et al., 2004; Zeindl-Eberhart et al., 2004).

Recently, more intensive proteomic methods utilizing more complex analysis of been utilized to identify potential biomarkers of HCC. Most of these methods forgo the use of gel based imaging and use mechanisms to deplete serum samples of the major acute phase proteins. By utilizing more sensitive machines and methods, low abundance proteins that change with cancer development can be found and may be more directly related to the cancer. Using such methods, proteins such as peroxiredoxin 3 (Ai et al., 2006; Chen et al., 2010b; Guo et al., 2007; Li et al., 2008; Lu et al., 2010; Qiao et al., 2012; Song et al., 2009; Wang, 2007; Yue et al., 2007) and osteopontin have been identified as potential markers of HCC (Abu El Makarem et al., 2011; Chen et al., 2010a; Chen et al., 2011; Kim et al., 2006; Lin et al., 2011; Phillips et al., 2012; Qin and Tang, 2004; Shang et al., 2012; Tang et al., 2004; Ye et al., 2003; Zekri et al., 2011). While these markers have been shown to be elevated in other cancers, they may still have great value in the early detection of liver cancer (Chahed et al., 2008; Lehtonen et al., 2004; McAllister et al., 2008; Mirza et al., 2008; Park et al., 2008; Park et al., 2007; Reiniger et al., 2007; Schremmer et al., 2007; Tigrani and Weydert, 2007; Tuck et al., 2007; Whiteaker et al., 2007). However, large multicenter studies using peroxiredoxin 3 and osteopontin have either not been done or have not been successful enough at detecting HCC in the background of cirrhosis to alter clinical care. Thus, in many ways, proteomics has failed to discover changes in the serum proteome that could be used to detect cancer in the background of liver cirrhosis.

Glycomic methodologies for the identification of biomarkers of liver cancer

Glycomics is the analysis of sugars or glycans, either free or attached to larger molecules such as proteins or lipids. In regards to liver cancer, glycomic methodologies have long been used to either improve or discover biomarkers of liver cancer. Initial work showed that AFP with an attached α -1,6 core fucosylated monosaccharide was a better marker of HCC than AFP alone(Aoyagi, 1994; Aoyagi et al., 1998; Aoyagi et al., 2002; Aoyagi et al., 1993a; Aoyagi et al., 1993b; Aoyagi et al., 1988; Buamah et al., 1986; Yamashita et al., 1993). Subsequently, other highly abundant serum proteins such as transferrin and alpha-1-antitrypsin (A1AT) were found to contain increased levels of fucosylation with HCC(Aoyagi et al., 1993a; Callewaert et al., 2003; Comunale et al., 2006; Goodarzi and Turner, 1995; Miyoshi et al., 1999; Morelle et al., 2006; Naitoh et al., 1999b; Noda et al., 1998; Nuck et al., 1992; Ryden et al., 1999; Thompson et al., 1988; Turner, 1995). Core fucosylated AFP is the success story in the field of glycomics as it has shown great clinical value and is currently the only test approved by the United States Food and Drug Administration (USFDA) for the detection of HCC. This test, known as AFP-L3 has shown much greater specificity in HCC detection as compared to AFP alone. In a recent, well-controlled study of over 800 patients, the core fucosylated form of AFP had a specificity of 94% (92–97 95% CL) while AFP alone had a specificity of only 82% (76–94 95% CL)(Marrero et al., 2009). Unfortunately, the complexity of the assay for the detection of fucosylated forms of AFP lead to a reduction in sensitivity from 70% (56-77 95% CL) to 50% (44-55 95% CL). This result highlights several key points with glycomics markers for HCC. The first is that they can be used to significantly increase the specificity of detection. This implies that the alterations in glycosylation are directly associated with the tumor. The other fact is that the protein to which they are attached limits the information they can provide. For example, total AFP has a sensitivity of ~70%, a value which can not be really improved upon by the examination of the fucosylated glycoforms. That is, the fucosylated glycoform is just a subset of the total AFP protein level, thus the sensitivity will not necessarily be improved. However, as the results with AFP-L3 indicate that fucosylation is a highly specific HCC modification, groups have combined this glycomic information with proteomics to identify other more abundant proteins with glycan changes that could be used as biomarkers of liver cancer(Block et al., 2005a; Comunale, 2006; Comunale et al., 2010; Comunale et al., 2009a; Comunale et al., 2011; Drake et al., 2006; Marrero et al., 2005; Morota et al., 2011b; Wang et al., 2009a; White et al., 2009).

Glycomic analysis of total serum, with limited protein information has been, utilized by several groups to detect HCC. Glycans identified include increases in core α -1,6 linked and α -1,3 linked outer-arm fucosylation as well as increases in branching and sialylation (Block et al., 2005a; Comunale, 2006; Goldman et al., 2009; Liu et al., 2007; Mehta et al., 2012). However, while many of these groups have identified changes in glycosylation, the ability to translate these changes to valid biomarkers of liver cancer has proved challenging.

Some of the initial methods to combine glycomics and proteomics were proposed by Jun Hirabayashi who had developed lectin based systems to analyze specific sets of glycoproteins(Hirabayashi, 2004; Hirabayashi et al., 2002; Hirabayashi and Kasai, 2003). Subsequently, several groups employed these techniques towards the discovery of

biomarkers of liver cancer(Block et al., 2005a; Comunale, 2006). Initial work in the woodchuck model of liver cancer identified a number of proteins as being hyperfucosylated with the development of HCC(Block et al., 2005b). One of the proteins identified in the serum of woodchucks with cancer and subsequently in the serum of people with HCC was golgi-proteins 73 (GP73). This protein has subsequently been analyzed in over 10,000 individuals with liver disease(Block et al., 2005b; Gu et al., 2009; Hann et al., 2010; Hu et al., 2010; Iftikhar et al., 2004; Jiang and Zhou, 2012; Liu et al., 2011; Maitra and Thuluvath, 2004; Malaguarnera et al., 2010; Mao et al., 2010; Mao et al., 2008; Marrero et al., 2005; Morota et al., 2011a; Ozkan et al., 2011; Riener, 2011; Riener et al., 2009; Schwegler et al., 2005; Shi et al., 2011; Sun et al., 2011; Tan, 2007; Tan et al., 2009; Tian et al., 2011; Wang et al., 2011a; Wang et al., 2011b; Xu et al., 2011; Yamamoto et al., 2010; Zhao et al., 2010; Zhou et al., 2012) and for the most part, shown improved performance in the detection of HCC as compared to AFP. However, in several studies, GP73 either was either not elevated in HCC versus cirrhosis (Morota et al., 2011a; Riener et al., 2009) or was no better than AFP at differentiating HCC from cirrhosis.

Increased levels of fucosylated proteins such as hemopexin(Comunale et al., 2009a; Debruyne et al., 2010; Kobayashi et al., 2012; Matsumoto et al., 1994; Morota et al., 2011a), fetuin A (Ahn et al., 2012b; Comunale et al., 2009b; Matsumoto et al., 1994), A1AT (Ahn et al., 2012a; Ahn et al., 2012b; Block et al., 2005b; Chen et al., 2012; Comunale et al., 2006; Comunale et al., 2010; Naitoh et al., 1999a), ceruloplasmin(Block et al., 2005b; Comunale, 2006; Liu et al., 2010), haptoglobin(Ahn et al., 2012a; Chandler et al., 2013; Pompach et al., 2013; Sanda et al., 2013; Zhu et al., 2014), serum paraoxonase 1 (Ahn et al., 2014; Sun et al., 2012), and histidine-rich glycoprotein (Comunale et al., 2009b; Liu et al., 2010) to name but just a few have been observed in the serum of those with HCC, either by direct glycan sequencing or by lectin based methods. These results strongly suggest that increased fucosylation, both core and outer arm, is observed in liver disease and importantly, occurs on large number of proteins.

Fucosylation is not universally increased in HCC tissue as compared to adjacent or control tissue

As discussed, increased levels of core and outer-arm fucosylation have been observed in the serum of patients with HCC(Block et al., 2005a; Comunale et al., 2006; Comunale et al., 2009a; Goldman et al., 2009; Miyoshi, 1999; Noda et al., 2003; Noda et al., 2002; Ohno, 1992). The exact reason for this change is not fully understood. The simplest explanation is that there is an increase in the enzymes that are involved in fucosylation that results in increased levels of fucosylated proteins being produced in the liver. This is the case in non-small cell lung carcinoma, where increases in FUT-8 is associated with activation of the β -catenin/Wnt signaling pathway(Chen et al., 2013). Indeed, in liver cancer, in some case of HCC, dramatic increases in fucosylation can be observed in HCC tissue through lectin staining with core fucose binding lectins (Figure 2). In this figure, we stained either HCC tissue or adjacent non malignant tissue with a recombinant *Aleuria aurantia lectin* that has greater affinity to core fucosylated structures(Romano et al., 2011). As Figure 2 shows, liver tissue from non malignant regions do have areas that stain with fucose binding lectins. These

are mostly the liver sinusoid which contain liver endothelial cells that contain large amounts of core fucosylated glycan. This is also observed in the malignant tissue (see figures 2C–D) with additional staining seen on the surface of the hepatocytes. However, such staining is present only on a small proportion of HCC tissue examined (20%) and thus it does not appear that these increases are the result of a universal increase in the level of the enzyme. Indeed, there have been numerous attempts to explain why increased levels of fucosylation are associated with HCC, such as increased levels of enzyme (FUT8) and substrate (UDP-L-fucose) however, none of these have provided a simple answer(Ito et al., 2001; Miyoshi, 1999; Moriwaki et al., 2007; Noda et al., 2003; Noda et al., 2002).

Recently, evidence has been presented that in hepatocytes, fucosylation acts as a sorting signal to secrete proteins into the bile. That is, hepatocytes within the liver are normally organized to be polar, with the basolateral side facing the circulation and the apical side forming the bile canalicular network (Tuma and Hubbard, 2001). This polarity is centrally related to the complementary hepatocyte functions of protein secretion and clearance. There is evidence that N-glycosylation in general (Helenius and Aebi, 2001; Scheiffele et al., 1995), and fucosylation in particular (Nakagawa et al., 2006) plays a role in mediating the sorting and polar secretion of glycoproteins. That is, core fucosylated glycoproteins produced by hepatocytes in the liver are preferentially sorted such that they are directed apically and secreted into the bile. Non-fucosylated glycoforms of the same protein are proposed to be secreted into the circulation. The hypothesis that core fucosylation is related to sorting for apical secretion is supported by evidence from our collaborator, Dr. Miyoshi (Nakagawa et al., 2006).

One explanation that expands on the work of Miyoshi and colleagues as to why liverderived fucosylated proteins are elevated in the circulation in HCC patients is that cancer cells often loose their polarity and exhibit altered adhesive properties, and hepatocytes are no exception (Cao et al., 2007; Stamataglou and Hughes, 1994). It is further reasoned that if, as the theory suggests, fucosylated proteins are normally not secreted basolaterally into the sinusoids, loss of polarity and/or adhesion will result in their presence in the circulation. It is important to note that the explanation of why increases in fucosylation are observed may not be equal in all cancers. That is, it is understood that HCC, like most cancers, has great heterogeneity in the genetic lesions leading to malignancy.

Increased branching is observed in HCC tissue

One specific change that has been associated directly with HCC tissue is the increased presence of tetra-antennary linked glycan. Tetra-antennary N-linked glycans arise from the action of the enzyme UDP-*N*-acetylglucosamine: α mannoside β 1,6 *N*-acetylglucosaminyltransferase (MGAT-5) (Srivastava et al., 1988), which catalyzes the addition of β -1,6-GlcNAc to the growing N-linked glycan to form tri- and tetra-antenna-like oligosaccharides. This change has been observed both by N-linked glycan sequencing of excised HCC tissue (Mehta et al., 2012) and through direct N-linked glycan analysis of cancer tissue microarrays(Powers and 2014). In addition, increased levels of MGAT-V have also been observed through immunohistochemical analysis of HCC tissue (Ito et al., 2001). It is noted that MGAT-V has long been associated with cancer development and metastatic

potential(Guo et al., 2010; Miyoshi et al., 1993; Srivastava et al., 1988; Yoshimura et al., 1995) and is directly related to alterations in the hexosamine cycle and activation of the AKT pathway (Dennis, 1999; Dennis et al., 1987; Guo et al., 2010; Lau et al., 2007; Mendelsohn et al., 2007). Importantly, increased levels of tetra-antennary glycan have recently also been shown to be found in the circulation through direct glycomics(Kamiyama et al., 2013; Mehta et al., 2012), indicating that this glycan alteration could also be useful in the detection of cancer development.

Effect of glycosylation on hepatocyte growth

What role the specific changes in glycosylation play in either the development or progression of cancer is unknown. Of the major changes observed, increased outer-arm fucosylation has not been shown to be associated with HCC tissue directly, suggesting that this modification may be coming from non cancer tissue, most likely from inflammation. In contrast, increased core fucosylation has been observed in some cases of HCC (see figure 2 and (Mehta et al., 2012)) and in many other cancers as well(Chen et al., 2013; Hu et al., 2008; Ito et al., 2003; Saldova et al., 2011b; Wen et al., 2012). In work involving non small cell carcinoma, it has been shown that regulation of the FUT-8 gene is directly related to the activation of the canonical β -catenin signaling pathway(Chen et al., 2013), suggesting a direct relationship between the alteration in glycosylation with activation of known cancer pathways. Indeed, it has also been shown that alterations in epigenetic control of gene expression can have dramatic impacts upon glycosylation(Saldova et al., 2011a).

Functionally, core fucosylation has shown to increase the activity of the epidermal growth factor receptor (EGF-R). Indeed, core fucosylation of the N-glycans on EGRF may be required for the binding of EGF to the receptor and subsequent signaling(Wang et al., 2006). Thus, as EGFR is often up-regulated in cancer, it is possible that increases in core fucosylation could act as drivers to increase EGR signaling and provide a growth advantage to the transformed cell.

Conclusion

Alterations in glycosylation have long been associated with cancer. In the case of HCC, the first major changes identified included the core fucosylation of AFP, the primary serum biomarker of HCC. Recently, with the advent of modern proteomic and glycomic methodologies, several other alterations have been identified, most notably outer-arm fucosylation, increased branching and increased sialylation. What advantage these changes impart to transformed hepatocyte remains under investigation.

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Figure 1.

Rates of liver and intrahepatic bile duct cancer in the United States in from 1990 to 2014. Data is based upon the SEER Cancer Statistics Review (CSR) 1975–2011 and the NCI website on liver cancer (http://www.cancer.gov/cancertopics/types/liver).



Figure 2.

Lectin staining of HCC or adjacent normal tissue with a recombinant Aleuria aurantia lectin (AAL) that has greater affinity for core fucosylated glycan. Panels A (4X) and B (20x) are from tissue adjacent to the HCC. Areas of staining indicated with the asterisks are the liver sinusoids, which stain with the core fucose binding lectin. Panels C (4X) and D (20x) are from the HCC tissue. In addition to the liver sinusoids, which stain with the core fucose binding lectin as in panels A and B, defined staining of hepatocytes, as indicted by the arrows, can also be seen.

Table 1

Most commonly identify changes in N-linked glycosylation in HCC.

Glycan alteration ¹	Protein(s) Known? ²	Reference: ³
Core fucosylation	Yes. AFP, A1AT, hemopexin, Fetuin A	(Ahn et al., 2014; Ahn et al., 2012b; Aoyagi, 1994; Aoyagi et al., 1998; Aoyagi et al., 2002; Aoyagi et al., 1993a; Aoyagi et al., 1993b; Aoyagi et al., 1988; Block et al., 2005a; Buamah et al., 1986; Chen et al., 2012; Comunale, 2006; Comunale et al., 2010; Comunale et al., 2009a; Debruyne et al., 2010; Dennis, 1999; Goodarzi and Turner, 1995; Kamiyama et al., 2013; Kobayashi et al., 2012; Liu et al., 2010; Marrero et al., 2009; Matsumoto et al., 1994; Miyoshi, 1999; Morota et al., 2011b; Naitoh et al., 1999b; Noda et al., 1998; Ohno, 1992; Sanda et al., 2013; Turner, 1995; Wang et al., 2009a; Yamashita et al., 1993)
Outer-arm fucosylation	Yes, A1AT, hemopexin, haptogloblin, total serum glycan analysis	(Asazawa et al., 2014; Block et al., 2005a; Chen et al., 2010b; Comunale et al., 2010; Debruyne et al., 2010; Goldman et al., 2009; Kamada et al., 2013; Kamiyama et al., 2013; Liu et al., 2007; Liu et al., 2010; Matsumoto et al., 2010; Morota et al., 2011a; Pompach et al., 2013; Takeda et al., 2012; Zhu et al., 2014)
Increased branching- tetra- antennary or higher	No. Glycan analysis of serum and HCC tissue.	(Mehta et al., 2012; Powers and 2014; Wei et al., 2012), (Kamiyama et al., 2013)
Increased Sialic acid	Serum paraoxonase 1; AFP	(Mondal et al., 2011; Sun et al., 2012)

¹ The identified change in glycosylation.

²Protein(s) that have been identified to contain the altered glycan. In some cases, no protein containing the indicated glycan chain have been identified.

 3 References for the indicated glycan change.