

CIRCULATING CANCER BIOMARKER AND ITS USE

Cross Reference To Related Application

[0001] This application claims the benefit of U.S. Provisional Application No. 61/892796, filed

5 October 18, 2013, the contents of which are incorporated herein by reference.

Technical Field

[0002] Aspects of the present disclosure relate generally to the field of using circulating nucleic acids in a subject as a biomarker to identify and monitor a disease development in the

10 subject.

Background

[0003] The fundamental cause of tumor/cancer has been attributed to genetic alterations caused by hereditary or environmental factors. These genetic alterations, once ir-repaired or irreparable, will accumulate and eventually cause normal cells to become malignant. As a tumor/cancer develops its own unique spectrum of genetic alterations, monitoring these alterations can provide information about the tumor/cancer.

[0004] Both normal and tumor/cancer cells undergo cycles of turnover where chromosomes of dead cells are fragmented and released into body fluids, such as blood circulation. Sequencing of these fragments indicates that these circulating cell-free DNA from the blood or serum of cancer patients carry the genetic alterations from the original tumor/cancer. This finding points to the

potential of using circulating cell-free DNA.

[0005] The conventional design of using host genome sequences containing specific genetic alterations as probes for capturing cancer/tumor-specific nucleic acid sequences from total circulating cell-free DNA works for advanced cancer, where the tumor is sufficiently large and a significant amount of tumor-specific nucleic acid sequences (more than 5% of total circulating DNAs) is released into the circulation. Given its limited amount (0.01%~1% in total blood), circulating cell-free DNA is hard to detect even in an advanced cancer. As a result, for early or intermediate stage of cancer, the proportion of circulating cancer/tumor DNA is too low to be reliably detected. Moreover, cancer/tumor-specific mutations are usually single-base mutations, small insertions or deletions which are very difficult to be separated from nucleic acid sequences without such mutations released from the non-tumor somatic cells. In other words, not all circulating DNA bears the altered genetic information; most of the circulating DNA is unaltered and from host genome.

BRIEF DESCRIPTION OF THE DRAWINGS

[0006] Many aspects of the present disclosure can be better understood with reference to the following figures. The components in the figures are not necessarily drawn to scale with the emphasis instead being placed upon clearly illustrating the principles of the present disclosure.

[0007] FIG. 1 schematically shows general progression of virus-infected cells.

[0008] FIG. 2 schematically shows an exemplary method of obtaining target circulating cell-free DNA.

[0009] FIG. 3 shows the specificity of viral-host junction.

[0010] FIG. 4 shows the changes in the amount of specific viral-host junction before and after tumor resection.

DETAILED DESCRIPTION

5 [0011] 1. Introduction

[0012] Certain human tumors/cancers, such as hepatocellular carcinoma (HCC), are caused by chronic infection of hepatitis B virus (HBV). These cancers accumulate genetic alterations in their genomes. Among such alterations, a unique one is the integration of viral genome into the host genome, usually occurring in the early stage of infections. Superimposed upon these mutations are
10 other somatic mutations that continue to occur and finally transform the cells to tumor/cancer.

[0013] As noted, when HCC cells turn over, fragmented genetic contents will be released into the body fluids. Circulating DNA which is DNA that floats freely in the circulatory system, such as blood, usually comprises DNA fragments. These fragments include those from host genome, from viral genome, and/or from the viral integration sites, such as the viral-host junction.

15 [0014] Infected cells, such as hepatocytes in a HBV-infected patient, proliferate if they become cancerous and so is the amount of the viral integrants carried by the infected cells. The amount of viral integrants thus is in proportion to the size of tumor/cancer in general. In addition, as the viral DNA integrates into the host genome at different sites, each tumor/cancer carries a unique spectrum of viral integration sites. This observation indicates that the viral integration sites, and/or the
20 viral-host junction, are cancer/tumor-specific and can be used as biomarkers for the diagnosis of cancer/tumor development.

[0015] FIG. 1 shows a cancer development process of cells. Referring to FIG. 1, hepatocytes 10 in a subject generally have the same host genome. Referring again to FIG. 1, hepatocytes 10 comprise a plurality of hepatocytes A2, B2, C2, D2 and E2. Upon HBV 11 infection, HBV 11 can integrate its viral genome 13 into the host genome of the infected hepatocytes. Parts of HBV 5 genome 13 are integrated into the host genome, generating infected hepatocytes with different viral integration sites and different integrated viral gene sequence. As show in FIG. 1, viral sequence A1 is integrated into cell A2, viral sequence B1 is integrated into cell B2, viral sequence C1 is integrated into cell C2, viral sequence D1 is integrated into cell D2 and viral sequence E1 is integrated into cell E2. The integration of HBV DNA sequences creates viral-host junctions in host 10 cell genome. Infected cells A2, B2, C2, D2 and E2 grow, develop and accumulate additional genetic alterations with time. Both host and viral sequences, altered or not, might lead to proliferation, stable stage or cell death. Referring again to FIG. 1, cell A2 carries the alterations that induce malignant transformation and lead to proliferation or clonal expansion. It is to be noted that a viral-host junction may lead to malignant transformation or may be an insignificant integration 15 that does not lead to proliferation.

[0016] Referring again to FIG. 1, infected cell A2 proliferates, expands in cell number and transforms into a malignant cell, which subsequently forms a cancerous or tumorous cell cluster. Cells B2, C2, D2, E2 do not go through malignant progression and remain in very small population or die out. All infected cells A2 bear the same hereditary information, including the host genome, at 20 least partial viral genome, and the viral-host junctions. If the infected cells A2 proliferate, the number of cell A2-specific viral-host junctions would increase proportionally in general. The same

viral-host junctions are present in the same cancerous cell lineage whether they trigger cancer development or not. As depicted schematically in FIG. 1, the cancerous clone goes through rapid proliferation and turnover, and some of the infected cells A2 rupture and die. DNA strands 12 of these ruptured and dead infected cells A2 are released into the circulatory system or body fluids such as blood. These DNA strands 12 become fragmented, float freely through the circulatory system and become part of circulating cell-free DNA (ctDNA) in the blood stream. As used herein, with reference to the present application, it shall be clearly understood that the terms “circulating cell-free DNA”, “circulatory cell-free DNA” and “ctDNA” refer to DNA that is obtained from the blood stream or circulatory system of a subject or patient, wherein the DNA that is obtained from the blood stream or circulatory system of the subject or patient is either substantially free of other cellular components, or is essentially entirely free of other cellular components. Some of the ctDNA is later on digested or cleaned by functional cells such as macrophages while some remain in the blood stream especially when the ctDNA is in large amount. By examining and/or detecting the ctDNA in the circulatory system or body fluids, one can obtain information about cancer/tumor development.

[0017] 2. Methods

[0018] Methods of performing the present invention are described below. It is to be noted that the methods, material and process described below are exemplary embodiments, and do not limit the scope of the invention in any way.

[0019] Referring to FIG. 2, a schematic view of isolating target ctDNA is shown. Circulating DNA from dead tumor/cancer cells is released into blood in fragments. Such ctDNA is collected

and ligated with adaptors 21 and forms ctDNA A, B, C and D. The ctDNA is amplified by using any suitable approach, for instance, using a primer complementary to the sequence of the adaptor 21 in an appropriate amount. It is to be noted that preferred amplification methods amplify all ctDNA in a similar or the same proportions so that the amplified ctDNA provides genuine information as to the amount of ctDNA existing in the blood. In FIG. 2, sequences derived from viral genome are designated in hatch area while sequences derived from host genome are designated in black. The amplified ctDNA can be categorized into ctDNA having only host genome sequences (ctDNA D), ctDNAs having only viral genome sequence (not shown), and ctDNA having both viral and host genome sequences and thus comprising viral-host junctions 22 (ctDNA A, B, and C). According to a preferred approach, all ctDNA is incubated with polynucleotide probes 23 (derived from the viral genome sequence) to allow hybridization to occur. It is to be noted that the probes 23 shown in FIG. 2 may have different sequences even though all drawn alike. Referring again to FIG. 2, only ctDNA having viral genome sequence alone and ctDNA having at least a viral-host junction (ctDNA A, B and C) would form probe-ctDNA complexes 24. These complexes are isolated from the ctDNA that does not hybridize with the probe. The target ctDNA, the ctDNA having only viral genome sequence and ctDNA having at least a viral-host junction are then obtained from the complexes and separated. The sequences of target ctDNA are obtained. Tissue origins of the target ctDNA are identified based on tissue tropism and specificity of virus infection.

[0020] 2.1 Subjects

[0021] Human subjects are employed in the tests to illustrate the present invention. Subject 1

has a 12x10x9 (cm) tumor diagnosed by computer tomography. According to the histological report when Subject 1 is employed in this test, Subject 1 is defined as a Grade III HCC patient. Subject 2 has a 18x13.5x9 (cm) tumor diagnosed by computer tomography. According to the histological report, Subject 2 is defined as a Grade III HCC patient. Subject 3 has a 8x7.5x7 (cm) tumor identified by computed tomography. According to the histological report, Subject 3 is defined as a Grade III HCC patient. Subject 4 has a 2x2x2 (cm) tumor and is at Grade II. Subject 5 has a tumor smaller than 2x2x2 (cm) and the stage of the cancer development is not determined and/or not available at the time of test enrollment.

[0022] 2.2 Obtaining ctDNA in subjects

[0023] Multiple blood samples are obtained from each subject. Each time, blood is drawn, collected in a clinically suitable container and, if needed, stored in a suitable condition for later analysis. Each blood sample is processed to obtain serum, such as by centrifugation. ctDNA is extracted by a commercial kit, for example, MagNA Pure LC Total Nucleic acid Isolation kit (Roche). The tumor tissues are obtained and genomic DNAs of tumor cells are extracted.

[0024] 2.3 Providing probes

[0025] Polynucleotides having HBV genome sequence are used as probes here. The probes can be either synthesized or obtained from the fragmentation of viral genome. Synthesis of the probes is described. Information of whole HBV genome sequences is obtained from the National Center for Biotechnology Information. Polynucleotides are synthesized according to the HBV genome sequence and cover the whole HBV genome sequence. The polynucleotides are synthesized using commercial kit, for example, Ion TargetSeq Custom Enrichment Kit (Life Technologies). All

polynucleotides are about 50 to 200 or 50 to 120 residues in length. After the synthesis of probes, each probe is labeled, for example biotinylated, at least one end of the polynucleotide. Biotinylation of probes can be performed by using commercial kit, for example, Ion TargetSeq Custom Enrichment Kit (Life Technologies). The probes are subsequently attached or linked to a bead, for example through biotin.

[0026] 2.4 Ligating adaptors

[0027] In order to proportionally amplify the ctDNAs obtained from the subject, certain DNA with known sequences are attached or ligated to at least one end or both ends of the ctDNA. Ligating adaptors to at least one end or both ends of the ctDNA can be performed by using TruSeq DNA Sample Preparation (Illumina), IonTorrent (Life Technologies), or other equivalent reagents.

[0028] 2.5 Amplifying target ctDNAs

[0029] After the ctDNAs are ligated with adaptors, each ctDNA in the sample from the subject is amplified, for example by using TruSeq DNA Sample Preparation (Illumina) or IonTorrent (Life Technologies).

[0030] 2.6 Capturing and isolating target ctDNAs

[0031] ctDNA samples of subjects are mixed with beads coated with biotinylated probes and incubated to allow hybridization between ctDNA and the probes. The ctDNA that have at least partial viral sequences anneal to the complementary sequences on the probes and form a bead-probe-ctDNA complex. The ctDNA that does not bind to the probes float freely and does not form any complex. The bead-probe-ctDNA complexes are separated from non-binding ctDNA by, for example, centrifugation. The complexes are obtained and target ctDNA is removed from the

complexes and collected. Capturing of circulating DNA hybridized with the probes can be performed by using TargetSeq Hybridization & Wash Buffer Kit (Life Technologies), or by other equivalent reagents.

[0032] 2.7 Sequencing and identifying target ctDNA

- 5 **[0033]** Primers having complementary sequences to the adaptor sequences are used to sequence the target ctDNAs. Target ctDNA is sequenced using IonTorrent platform, HiSeq 2500 (Illumina), or some other sequencing platforms.

[0034] 3. Results

[0035] 3.1 Target ctDNA sequences

- 10 **[0036]** Subject 1

[0037] Table 1 shows top ten target sequences identified in the DNA samples obtained from Subject 1 tumor tissue. As shown, a junction sequence is inserted into the host chromosome (Host Chromosome #) at a specific integration position (Integration Position) with an accumulated read number (Accumulated Reads). Accumulated read number is obtained by sequencing result.

- 15 Sequences having the same junction are counted to give the number of the junction present in the sample. Each sequence contains at least partial viral genome sequence (underlined) and partial host genome sequence and forms a viral-host junction.

[0038] Table 1

Junction Data of Subject 1 Tumor				
#	Host Chromosome #	Integration Position	Junction Sequence	Accumulated Reads
1	17	22247083	<u>GGTCTTACATAAGAGGACTCAGAAAATACTTT</u> GTGATGAT	290

2	17	22251295	AACTCCTTTTGAGAGCGCAGT <u>GTTCGGTGCAG</u> <u>GTCCCCAG</u>	234
3	1	121360041	ATCATCACAAAGTATTTTCTGAGTCCTCTTATG <u>TAAGACC</u>	192
4	12	118876274	TGAGGTGAGAGGATCTCTTGAGCACAGATGAT <u>GGGATAGG</u>	115
5	X	58568585	AAACGTCCACTTGCAGATTTTATGTAATTGGA <u>AGTTGGGG</u>	102
6	8	56895765	<u>AGCAGGAAAATATATGCCCCACCTTCCCTTTC</u> TCTGACCC	106
7	1	121475300	<u>AGGAAGACTGCCTACTCCCA</u> CAGGCCTGAAAG CGCTCCAA	85
8	X	58563641	AGCATTCGGGCCAGGGTTC <u>ACTCAGGCTCAGG</u> <u>GCACATTG</u>	67
9	16	21525068	<u>GCATTTGGTGGTCTATAAGCACACCCGCCAC</u> ACCAATCT	38
10	18	77932557	CAAGACCAGCCTGAGGATGACTGTCTCTTAGA <u>GGTGGAGA</u>	26

[0039] Table 2 shows the target sequences identified in the ctDNA samples obtained from the blood of Subject 1. ctDNA samples are obtained from Subject 1 13 days before a tumor excision. As shown, each sequence contains at least partial viral genome sequence (underlined) and partial host genome sequence and forms a viral-host junction.

5 **[0040]** Table 2

Junction Data of Subject 1 Serum				
#	Host Chromosome #	Integration Position	Junction Sequence	Accumulated Reads
11	17	22251295	CACTCCTTTTGAGAGCGCAGT <u>GTTCAGGTGCA</u> <u>GGGTCCCC</u>	94
12	1	121360041	ATCATCACAAAGTATTTTCTGAGTCCTCTTATG <u>TAAGACC</u>	82
13	1	13727	<u>AACAGAAAGATTTCGTCCCCAAATCCAATCTGT</u> CTTCCATC	68
14	8	56895765	<u>AGCAGGAAAATATATGCCCCACCTTCCCTTTC</u> TCTGCCCT	62
15	17	22247083	<u>GGTCTTACATAAGAGGACTCAGAAAATACTTT</u> GTGATGAT	42

16	16	21525068	<u>GCATTTGGTGGTCTATAAGCACACCCGCCAC</u> <u>ACCAATCT</u>	31
17	8	56895953	<u>ATCATCCTGGGCTTTCTGCACTTCCCATAGGTA</u> <u>ATCAAAG</u>	16
18	X	58563641	<u>AGCATTCGGGCCAGGGTTC</u> <u>ACTCAGGCTCAGG</u> <u>GCACATTG</u>	9

[0041] As illustrated in Tables 1 and 2, at least #3 (in tumor sample) and #12 (in serum sample), #1 and #15, and #2 and #11 each pair have the same viral-host junction sequences. Similar patterns (including the relative amount of reads) of viral-host junction sequences identified in both tumor DNA and ctDNA indicate that chimera ctDNA in serum is derived from tumor DNA. By selectively enriching the ctDNAs carrying at least a portion of the viral genome in the serum, viral-host junctions are identified to provide tumor-specific information about the subject.

[0042] Subject 2

[0043] Table 3 shows the target sequences identified in the DNA samples obtained from Subject 2 tumor tissue. As shown, each sequence contains at least partial viral genome sequence (underlined) and partial host genome sequence and forms a viral-host junction.

[0044] Table 3

Junction Data of Subject 2 Tumor				
#	Host Chromosome #	Integration Position	Junction Sequence	Accumulated Reads
1	3	111653312	ATGAAGCTATTTATAATAAAACAACTTTATTTAAATCTAGTTTAAATGCCCTTACTCTCTTTTTTGCCCTCTGACTTCTTTCCTTCTATTCGAGATCTCCT	4183
2	2	80278757	TTTCATTGTTGCTGTTTTTCAAATTGATTTTGGGATCCAGCCTGTTATTCTACTCCCTTAACTTCATGGGATATGTAATTGGAAGTTGGGGTACTTTACC	3772

3	3	111653206	TCTCCCTTTAGACTTCAAACACTTCAAAATATGACT TCACTACAAAGCTTTATAGAATGCCAGCCTTCCAC <u>AGAGTATGTAAATAATGCCTAGTTTTGAA</u>	1269
4	2	80278655	CCAGCACATTTGTCTATAAATTTACATTCTTGGATA TTAGCAAAATTGCAAACAGACCAATTTATGCCTAC <u>AGCCTCCTAGTACAAAGACCTTTAACCTA</u>	752
5	1	189879551	TCCAGTGTTTGTGGGTTGAGCAGTATTATTGCATGG CCCAGTGGTGGTGGTTGATGTTCTTGGAAGTAGAG <u>GACAAACGGGCAACATACCTTGGTAGTCC</u>	485
6	1	189879474	TGCAAGTGGTTGCAGTTCTTTTGCTTTGCCACCACC ACTGGGCCATGCAAACCTGCACGATTCTCTGCTCA <u>AGGAACCTCTATGTTTCCCTCTTGTTGCT</u>	174
7	20	60227034	CAGGAGGAGGTGATGGACCCACTGGGTGGTGAAG AACAGTTTCTCTTCCAAAATTACTTCCCACCCAGGT <u>GGCCAGATTCATCAACTACCCCAACACAG</u>	169
8	22	26941239	ATCTGTAAAATTGGGATCATCACACTTTCCTTTTAT TGGGGTTTAAATGAATACCCAAAGACAAAAGAAA <u>ATTGGTAATAGAGGTA AAAAGGGACTCAAG</u>	100
9	20	60227112	TGGCCGAGGCCATCTTCTAAATAAATGTGTGGAAG AGAAACTGTTCTTCAGTATTTGGTGTCTTTTGGAGT <u>GTGGATTTCGACTCCTCCCGCTTACAGAC</u>	93
10	5	1295309	AGGACGGGTGCCCGGGTCCCCAGTCCCTCCGCCAC GTGGGAAGCGCGGTCCAGACCAATTTATGCCTACA <u>GCCTCCTAGTACAAAGACCTTTAACCTAAT</u>	37

[0045] Table 4 shows the target sequences identified in the ctDNA samples obtained from blood of Subject 2. Serum samples are obtained from Subject 2 at tumor excision. As shown, each sequence contains at least partial viral genome sequence (underlined) and partial host genome sequence and forms a viral-host junction.

5 **[0046]** Table 4

Junction Data of Subject 2 Serum

#	Host Chromosome #	Integration Position	Junction Sequence	Accumulated Reads
11	3	111653312	ATGAAGCTATTTATAATAAAACAAACTTTATTAAATC TAGTTTAAATGCCTTACTCTCTTTTTTGCCTTCTGACT <u>TCTTTCCTTCTATTTCGAGATCTCCT</u>	3277
12	20	60227034	CAGGAGGAGGTGATGGACCCACTGGGTGGTGAAGA ACAGTTTCTCTTCCAAAATTACTTCCCACCCAGGTGG <u>CCAGATTCATCAACTCACCCCAACACAG</u>	642
13	1	189879551	TCCAGTGTTTGTGGGTTGAGCAGTATTATTGCATGGC CCAGTGGTGGTGGTTGATGTTCCCTGGAAGTAGAGGA <u>CAAACGGGCAACATACCTTGGTAGTCC</u>	373
14	2	50012582	GTCCGTTGGTGGTGAACCTGGGCAAGATAATTGCATG GCCCAGTGGTGGTGGTTGATGTTCCCTGGAAGTAGAG <u>GACAAACGGGCAACATACCTTGGTAGTC</u>	372
15	15	48344568	AGATTGGTCTATAAATTTCTTTTACTATCTTCAGTATT TGGTATCTTTGGGAGTGTGGATTTCGCACTCCTCCCCG <u>TTACAGACCACCAAATGCCCCCTATC</u>	237
16	2	80278757	TTTCATTGTTGCTGTTTTTCAAATTGATTTTGGGATCC AGCCTGTTATTCTACTCCCTTAACTTCATGGGATATG <u>TAATTGGAAGTTGGGGTACTTTACC</u>	230
17	20	60227112	TGGCCGAGGCCATCTTCTAAATAAATGTGTGGAAGA GAAACTGTTCTTCAGTATTTGGTGTCTTTTGGAGTGT <u>GGATTTCGCACTCCTCCCGCTTACAGAC</u>	209
18	1	189879474	TGCAAGTGGTTGCAGTTCTTTTGCTTTGCCACCACCA CTGGGCCATGCAAAACCTGCACGATTCCTGCTCAAG <u>GAACCTCTATGTTTCCCTCTTGTTGCT</u>	205
19	2	50012660	GTAAGCCATTGTGGCTTTCCTGACCAGCCCACCACCA CTGGGCCATGCAAAACCTGCACGATTCCTGCTCAAG <u>GAACCTCTATGTTTCCCTCTTGTTGCT</u>	205
20	2	80278655	CCAGCACATTTGTCTATAAATTTACATTCTTGGATAT TAGCAAAATTGCAAACAGACCAATTTATGCCTACAG <u>CCTCCTAGTACAAAGACCTTTAACCTA</u>	64

[0047] As illustrated in Tables 3 and 4, at least #1 (in tumor sample) and #11 (in serum sample), #7 and #12, #5 and #3 both have the same viral-host junction sequences. Similar patterns of viral-host junction sequences identified in both tumor DNA and ctDNA show that chimera ctDNA in serum is derived from tumor DNA. By selectively enriching the target ctDNA in the serum, viral-host junctions are identified to provide tumor-specific information about the subject.

[0048] Subject 3

[0049] Table 5 shows the target sequences identified in the DNA samples obtained from Subject 3 tumor tissue. As shown, each sequence contains at least partial viral genome sequence (underlined) and partial host genome sequence and forms a viral-host junction.

10 [0050] Table 5

Junction Data of Subject 3 Tumor				
#	Host Chromosome #	Integration Position	Junction Sequence	Accumulated Reads
1	5	1295930	GGAAATGGAGCCAGGCGCTCCTGCTGGCCGCGCAC CGGGCGCCTCACACCAGAACATCGCATCAGGACTC <u>CTAGGACCCCTGCTCGTGTTACAGGCGGGG</u>	3024
2	8	111636420	TCAAGCAGAAAAACCATGAAGATTTAAAAACTTGT AAATATTTGAATGTGGGCTCCACCCCAACAGTCCC <u>CCGTGGGGAGGGGTGAACCCTGGCCCGAAT</u>	635
3	14	52591737	CTAAGGGACACTACAGGAAACCAGCCCCGAAGTG ATTTCTTTTGAAATTCCAAATCTTTCTGTCCCCAAT <u>CCCCTGGGATTCTTCCCCGATCATCAGTTG</u>	354
4	9	138857330	CCTCGAAGCCTGTGCCAACCTAGCCCATTCTCAG GCTCAGGGCCTCCTCACATCTGTGCCAGCAGCTCCT <u>CCTCCTGCCTCCACCAATCGGCAGTCAGG</u>	190

5	1	68549419	CATTGTTACTGTGATATGCTATAATTATTCTCACCT TATGTGTCCAAGGAATACTAACATTGAGATTCCCG <u>AGATTGAGATCTTCTGCGACGCGGCGATT</u>	188
6	9	31455679	ATGGAGAATACAGCACATTATTAGGAGTAAGTTTC CTTAAACACATTTTGTATTTTGTACAATATGTTCC <u>TGTGGCAATGTGCCCCAACTCCCAATTAC</u>	172
7	17	71434403	TTTGCCACCTTCCTGCCACTTTGTAGATGCAAGATC TTGGGCAAGTTCCCGTGGGCGTTCACGGTGGTTTCC <u>ATGCGACGTGCAGAGGTGAAGCGAAGTG</u>	138
8	12	126230889	CAGTGGAAACAAAGCCACTGGGAAGTTCAAACCTG AGAGAAGCCCACCACAAGTCTAGACTCTGTGGTAT <u>TGTGAGGATTTTGTCAACAAGAAAAACCCC</u>	135
9	X	35911295	AGTATATCATCAGTTATTTTCAAGGTTTCTAAGT AAACAGTTTCTCAACCTTTACCCCGTTGCTCGGCAA <u>CGGCCTGGTCTGTGCCAAGTGTTTGCTG</u>	124
10	10	75397400	TCAGGGAGGGGATGTTGACTGCATTTTGGAGGTTC AGGGCCTACTAACAACCTGTGCCAGCAGCTCCTCCT <u>CCTGCCTCCACCAATCGGCAGTCAGGAAGG</u>	58

[0051] Table 6 shows the target sequences identified in the ctDNA samples obtained from blood of Subject 3. Serum samples are obtained from Subject 3 at tumor excision. As shown, each sequence contains at least partial viral genome sequence (underlined) and partial host genome sequence and forms a viral-host junction.

5 **[0052]** Table 6

Junction Data of Subject 3 Serum				
#	Host Chromosome #	Integration Position	Junction Sequence	Accumulated Reads
11	5	1295930	GGAAATGGAGCCAGGCGCTCCTGCTGGCCGCGCAC CGGGCGCCTCACACCAGAACATCGCATCAGGACTC <u>CTAGGACCCCTGCTCGTGTTACAGGCGGGG</u>	153

12	8	111636420	TCAAGCAGAAAAACCATGAAGATTTAAAAACTTGT AAATATTTGAATGTGGGCTCCACCCCAACAGTCCC CCGTGGGGAGGGGTGAACCCTGGCCCCGAAT	52
13	21	47565536	CCCGGGACCGACCCAGGAAGAGCCAGGGGCCCCG GGTGATCCCTGCGGGGGTCTGGCTTTCAGTTATATG GATGATGTGGTATTGGGGGCCAAGTCTGTA	27
14	21	28573066	AATGAAAATCTCATTGATTTTTCACTTATAGGTTTT ACCTTAGAGCTCCTCCTCTGCCTAATCATCTCATGT TCATGTCCTACTGTTCAAGCCTCCAAGC	25
15	7	87842849	AGAATTGATACCTAAGCTGAGCAGAAATGAGGCCG ACCATGAAGTGAGTGCCTAATCATCTCATGTTTCAT GTCCTACTGTTCAAGCCTCCAAGCTGTGCC	24
16	7	148503201	CGTAGGAAAGACAAGGTGGCATTGATGGAAAGCA GTAGTTTTTGAGCCCTTCGCAGACGAAGGTCTCAA TCGCCGCGTCGCAGAAGATCTCAATCTCGGG	19
17	1	162277132	TTAAAAAGGAGTTTTGTTTGTTAGTCTATTCACTCA TTTCAAGGAACATAGAAGAAGAAGTCCCTCGCCTC GCAGACGAAGGTCTCAATCGCCGCGTCGC	16
18	12	125048731	CAGTTCCTGGCTCCAAGCTCCCTCAAAAGATGCC CAGCTGGCCTTTCCCAAAGGCCTTGTAAGTTGGCG AGAAAGTAAAAGCCTGTTTTGCTTGTATAC	15
19	7	30412226	ACATGCCCTTCACTTCAGCCTGATGCTCCTGGCATA AGCTCAGCAATTTTGAGGTGCGAATCCACACTCCA AAAGACACCAAATATTCAAGAACAGTTTC	13
20	13	84505952	AATTTCCCCTGAATAGCTGCAGTACTCACAGACAC ACTGGATGCTACTCACCTCTGCCTAATCATCTCATG TTCATGTCCTACTGTTCAAGCCTCCAAGC	13

[0053] As illustrated in Tables 5 and 6, similar patterns of viral-host junction sequences identified in both tumor DNA and ctDNA show that ctDNA in serum is derived from tumor DNA. By selectively enriching the target ctDNA in the serum, viral-host junctions are identified to provide tumor-specific information about the subject.

[0054] 3.2 Tumor-specific viral-host junctions

[0055] In FIG. 3, genomic DNA of Subject 1, Subject 4 and Subject 5 are processed and analyzed by polymerase chain reaction (PCR) and quantitative PCR. Genomic DNA (gDNA) from tumor tissues and non-tumor tissues is obtained. One chimera DNA sequence in tumor gDNA is identified and selected in each subject to serve as a marker to conduct the tests. Specifically, the chimera DNA sequence of Subject 1 used in this analysis is GGTCTTACATAAGAGGACTCAGAAAATACTTTGTGATGAT (viral genome sequence underlined), Subject 4 ACTTCAAAGACTGTGTGTTTCTAATTATTTGGGGGACAT, and Subject 5 GTAGGCATAAATTGGTCTGTACCTCACTTCCCTGCTTTCC. The presence of the three specific viral-host junctions is determined in the tumor gDNA (T) and non-tumor gDNA (N). Porphobilinogen deaminase (PBGD) and miR-122 are used as internal control. No-template control (NTC) is also included. As illustrated in FIG. 3, the specific viral-host junction of Subject 1 is only present in tumor gDNA (T) but not in non-tumor gDNA (N). Same patterns are observed in Subject 4 and Subject 5, indicating that the identified viral-host junctions are tumor-specific and can be used as tumor-specific biomarkers.

[0056] 3.3 Tumor development and viral-host junction amount

[0057] FIG. 4 shows the relationships between tumor size and the amount of specific viral-host junction sequence. Junction sequences used in FIG. 4 for each subject are the same as in FIG. 3. Serial blood samples of each subject are obtained at least at pre-operation and post-operation stages. Referring to FIG. 4, gDNA refers to genomic DNA, NTC refers to no-template control, NT refers to gDNA from non-tumor tissue, T refers to gDNA from tumor tissue, Serum NA refers to DNA

obtained from serum, Pre-OP refers to serum DNA obtained at pre-operation stage, Post-OP refers to serum DNA obtained at post-operation stage, Subject 1* refers to serum DNA obtained from Subject 1 and is used in Subject 5 experiment, Subject 4* refers to serum DNA obtained from Subject 4 and is used in Subject 1 experiment, Subject 5* refers to serum DNA obtained from Subject 5 and is used in Subject 4 experiment and Normal refers to serum DNA obtained from a non-patient subject. Serum samples of Subject 1 are obtained at two time points, 13 days before tumor resection (operation) and 19 days after operation. Serum samples of Subject 4 are obtained 33 days before operation and 30 days after operation. Serum samples of Subject 5 are obtained 24 days before operation and 26 days after operation. Serum samples of non-patient subject (Normal) are also included as a control in FIG. 4. As shown in FIG. 4 left panel, the specific viral-host junction of each subject is only present in tumor gDNA and Pre-OP. In addition, the specific viral-host junction of Subject 1 is only present in Subject 1 DNA samples but not in Subject 4 DNA samples, suggesting that the viral-host junction identified is subject-specific. Referring now to the right panel of FIG. 4, the specific viral-host junction in the serum of Subject 1 is detected with relatively large amount in Pre-OP serum while the amount decreases sharply in Post-OP serum. The amount of the specific viral-host junction in Pre-OP serum and Post-OP serum is determined by qPCR and presented in the right panel of FIG. 4. In Subject 1, the amount of specific viral-host junction in Post-OP serum decreases by about 32-fold compared to in Pre-OP serum. Same patterns are observed in Subject 4 and Subject 5, showing that the viral-host junctions or the amount of junctions are tumor-specific, subject-specific, detectable in serum, reflective of tumor, and corresponsive to the tumor size changes, such as a decrease in size after an operation.

[0058] It is to be noted that by using the approach described in the present invention, mutated p53 or beta-catenin genes cannot be detected in the ctDNAs despite the mutations are identified in the tumor tissues (data not shown). The result shows that by using the method of present invention, tumor specific viral-host junctions (viral genome sequence insertion into host genome), and not
5 conventional somatic mutations, are selectively enriched and obtained to provide cancer/tumor information.

[0059] The embodiments shown and described above are only examples. Even though numerous characteristics and advantages of the present technology have been set forth in the foregoing description, together with details of the structure and function of the present disclosure,
10 the disclosure is illustrative only, and changes may be made in the detail, including in matters of shape, size and arrangement of the parts within the principles of the present disclosure up to, and including, the full extent established by the broad general meaning of the terms used in the claims.

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WHAT IS CLAIMED IS:

1. A method of identifying an amount of viral-host junctions in ctDNAs from a subject infected with hepatitis B virus comprising:

obtaining the ctDNAs in a serum of the subject;

ligating each ctDNA with at least one adaptor;

amplifying all the ctDNAs ligating the at least one adaptor in a similar proportion by using a plurality of primers, wherein each of the primers is complementary to a sequence of the corresponding adaptor;

hybridizing polynucleotide probes with the ctDNAs ligated with the adaptors;

capturing and isolating target ctDNAs hybridized with the polynucleotide probes;

sequencing the target ctDNAs, wherein the target ctDNAs having one or more viral-host junction sequences, wherein each viral-host junction sequence comprises a viral genome sequence and a host genome sequence; and

accumulating a read number related to the viral-host junctions in the target ctDNAs to identify the amount of the viral-host junctions, wherein the amount of the viral-host junctions are defines as the accumulated read number, the read number is defined as the times the viral-host junction sequence appearing in the target ctDNAs, wherein the detected viral-host junctions sequences comprises same sequences, different sequences, or a combination thereof,

and each viral-host junction sequence is counted to give the read number; and wherein the amount of the viral-host junctions are configured to indicate the hepatitis B virus-related tumor status.

2. The method of claim 1, further comprising comparing the detected amount of the viral-host junctions of the subject at the different time points, to identify changes in size of the tumor.

3. The method of claim 1, wherein the target ctDNAs are enriched by the polynucleotide probes complementary to at least one sequence derived from hepatitis B viral genome.

4. The method of claim 1, wherein the polynucleotide probes cover the whole hepatitis B viral genome sequence.

5. The method of claim 1, wherein the ctDNAs ligating with the corresponding adaptor comprise one end of each ctDNA ligates with the corresponding adaptor, both ends of each ctDNA ligates with the corresponding adaptor, and a combination thereof.

6. A method of monitoring tumor status in a subject caused by infection of hepatitis B virus, comprising:

obtaining the ctDNAs in a serum of the subject;

ligating each ctDNA with at least one adaptor;

amplifying all the ctDNAs ligating the at least one adaptor in a similar proportion by using a plurality of primers, wherein each of the primers is complementary to a sequence of the corresponding adaptor;

hybridizing polynucleotide probes with the ctDNAs ligated with the adaptors;

capturing and isolating target ctDNAs hybridized with the polynucleotide probes;

sequencing the target ctDNAs, wherein the target ctDNAs having one or more viral-host junction sequences, wherein each viral-host junction sequence comprises a viral genome sequence and a host genome sequence;

accumulating a read number related to the viral-host junctions in the target ctDNAs to identify the amount of the viral-host junctions, wherein the amount of the viral-host junctions are defines as the accumulated read number, the read number is defined as the times the viral-host junction sequence appearing in the target ctDNAs, and wherein the detected viral-host junctions sequences comprises same sequences, different sequences, or a combination thereof, and each viral-host junction sequence is counted to give the read number; and

monitoring the tumor status based on the amount of the viral-host junctions in the target ctDNAs.

7. The method of claim 6, wherein the polynucleotide probes cover the whole hepatitis B viral genome sequence.

8. The method of claim 6, wherein the ctDNAs ligating with the corresponding adaptor comprise one end of each ctDNA ligates with the corresponding adaptor, both ends of each ctDNA ligates with the corresponding adaptor, and a combination thereof.

9. The method of claim 6, wherein the tumor is a hepatocellular carcinoma induced by hepatitis B virus.

10. The method of claim 6, wherein the ctDNAs obtained at different time points, and wherein the different time points are selected from a cancerous condition, a pre-treatment condition, a post-treatment condition, a recurrence condition of the subject, and any combination thereof.

11. The method of claim 10, further comprising monitoring the tumor development of the subject by comparing the detected the amount of the viral-host junctions of the subject at the different time points.

12. The method of claim 10, wherein increases in the amount of the at least one viral-host junction in the ctDNAs of the subject are indicative of the tumor development from the post-treatment condition to a recurrence condition and decreases in the amount of the at least one viral-host junction in the circulating cell-free DNA of the subject are indicative of the tumor development from the pre-treatment condition to a post-treatment condition of the subject.

13. The method of claim 10, wherein increases in the amount of the at least one viral-host junction in the ctDNAs of the subject in the cancerous condition are indicative of growth of

a tumor and decreases in the amount of the at least one viral-host junction in the circulating ctDNAs of the subject in the cancerous condition are indicative of shrinkage of the tumor.