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(54) **GLYCAN ARRAYS FOR HIGH THROUGHPUT SCREENING OF VIRUSES**

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(58) **Field of Classification Search**
None
See application file for complete search history.

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(57) **ABSTRACT**

Glycan arrays that can detect and distinguish between various sub-types and strains of influenza virus are provided. Methods for using the glycan arrays with assays using nanoparticle amplification technique are disclosed. Sandwich assays using gold nanoparticles conjugated to phage particles comprising influenza virus-specific antibodies for detecting multiple serotypes using a single reaction are provided. Plurality of glycans directed to specific target HA of influenza virus comprises the array. Detector molecules comprising noble metals conjugated to (a) phage display particles expressing antibodies against hemagglutinin and (b) neuraminidase binding agents are disclosed.

46 Claims, 13 Drawing Sheets
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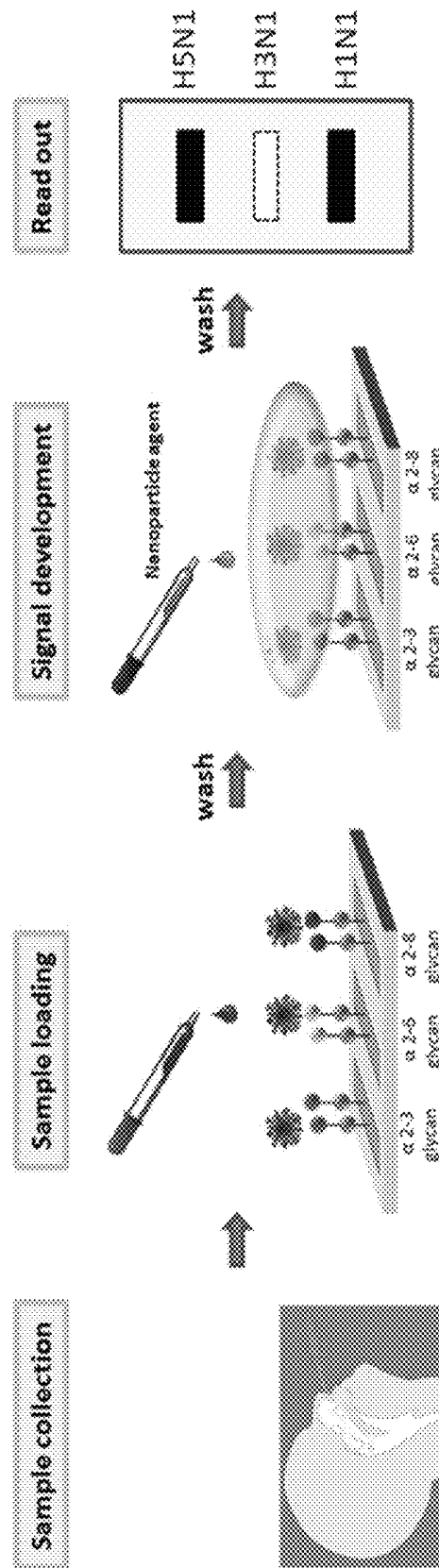
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FIG. 1



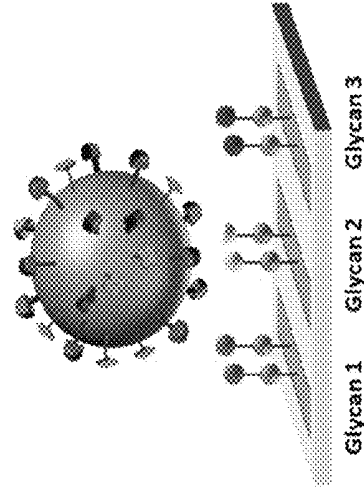
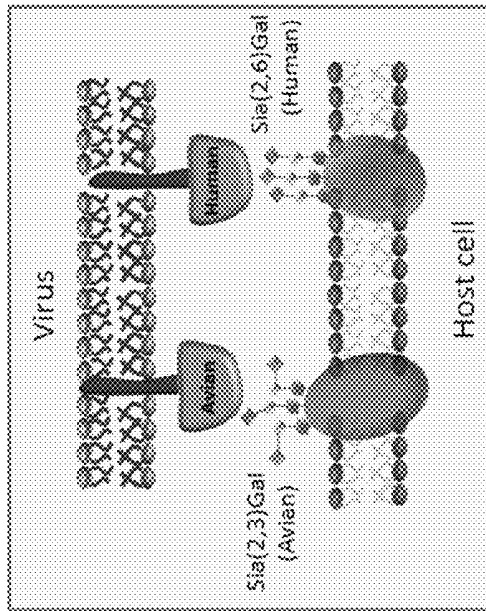


FIG. 2

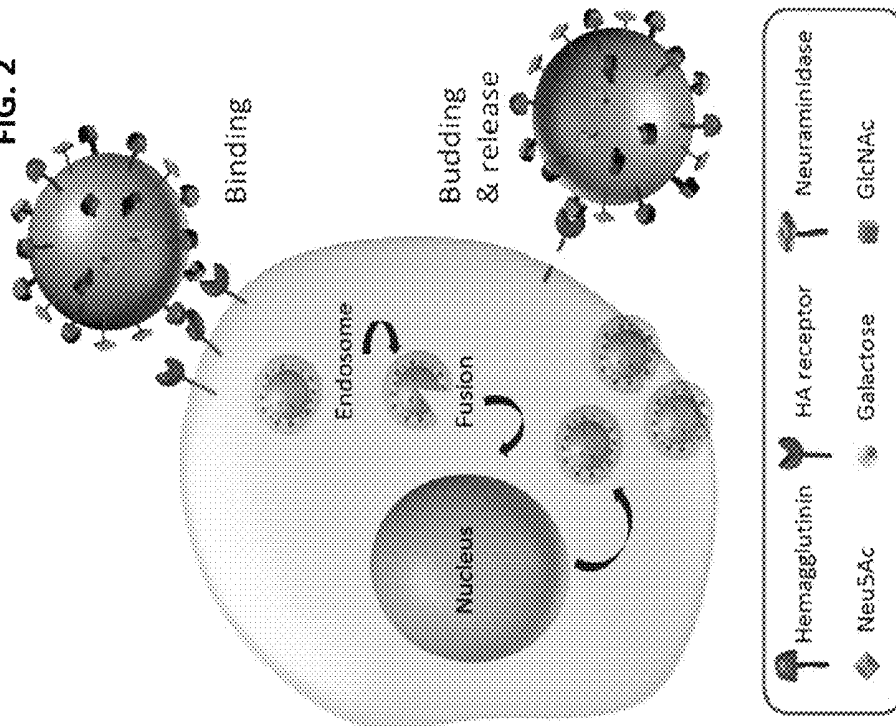


FIG. 3A

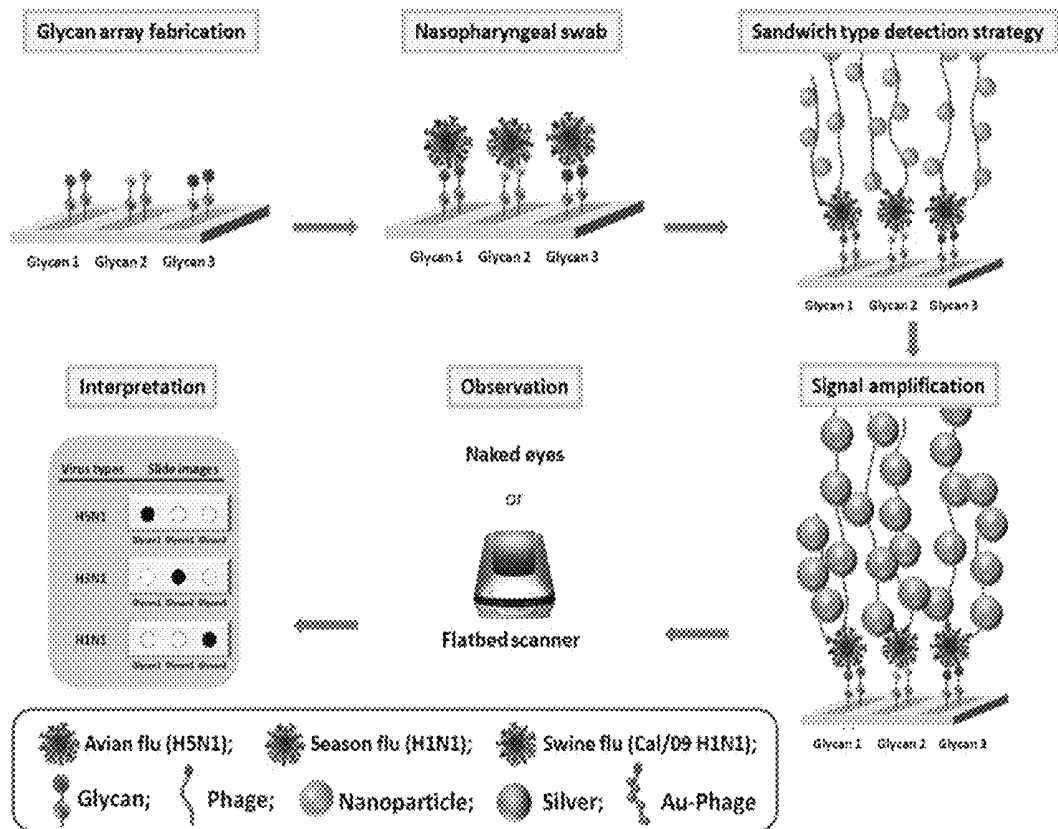


FIG. 3B

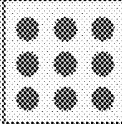


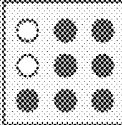


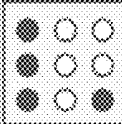
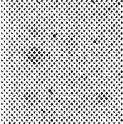

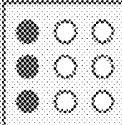


	Expected result	Phage-Au	Relenza-Au
H1N1/Cal 2009			
H1N1/Brisbane			
H3N2/Udom172			
HSN1/RG14			

FIG. 4

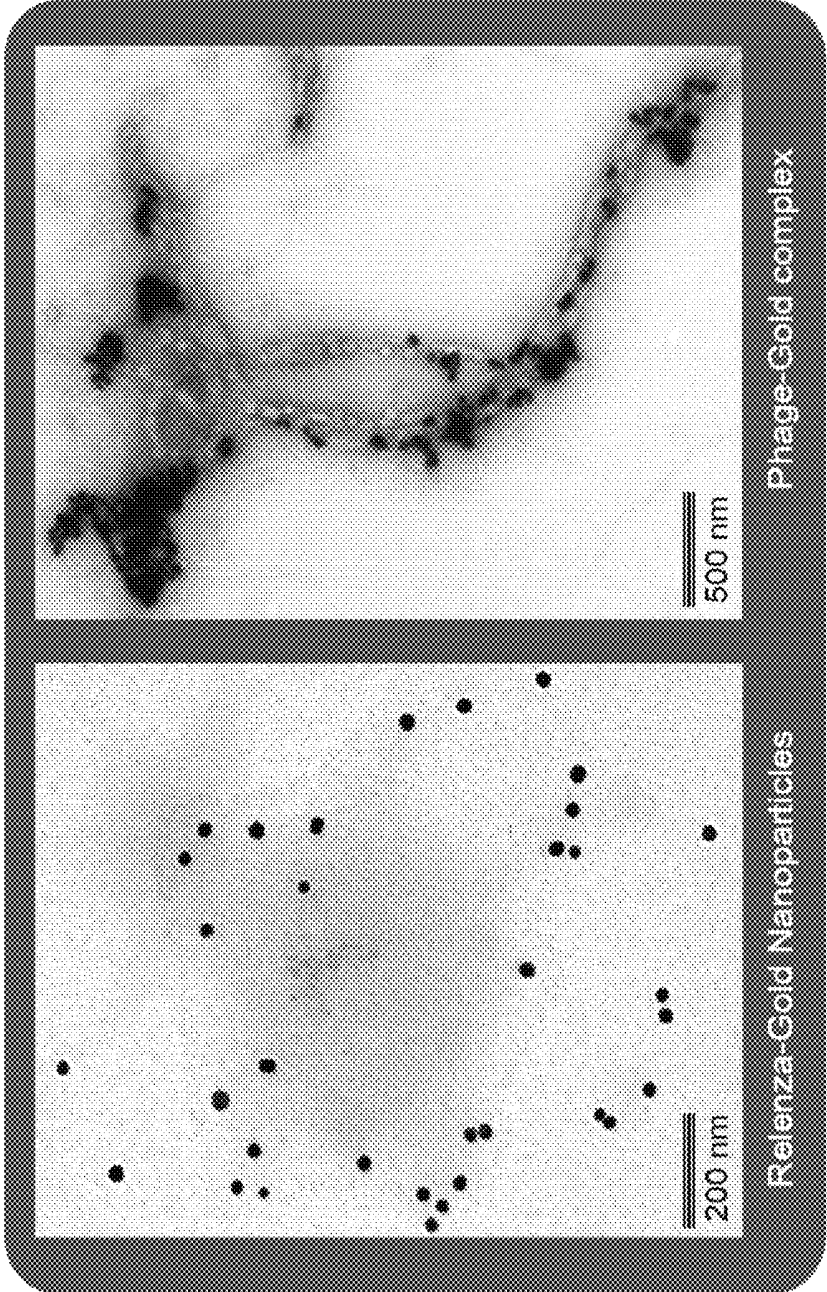


FIG. 5

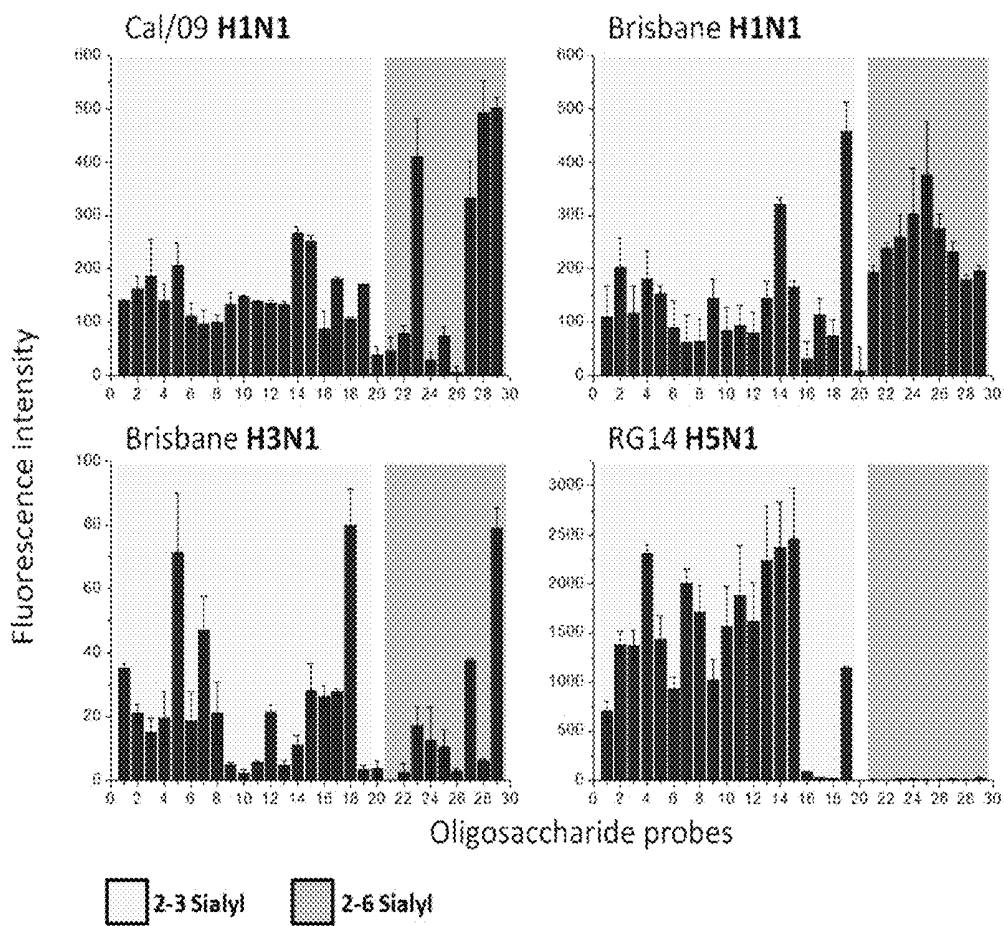


FIG. 6

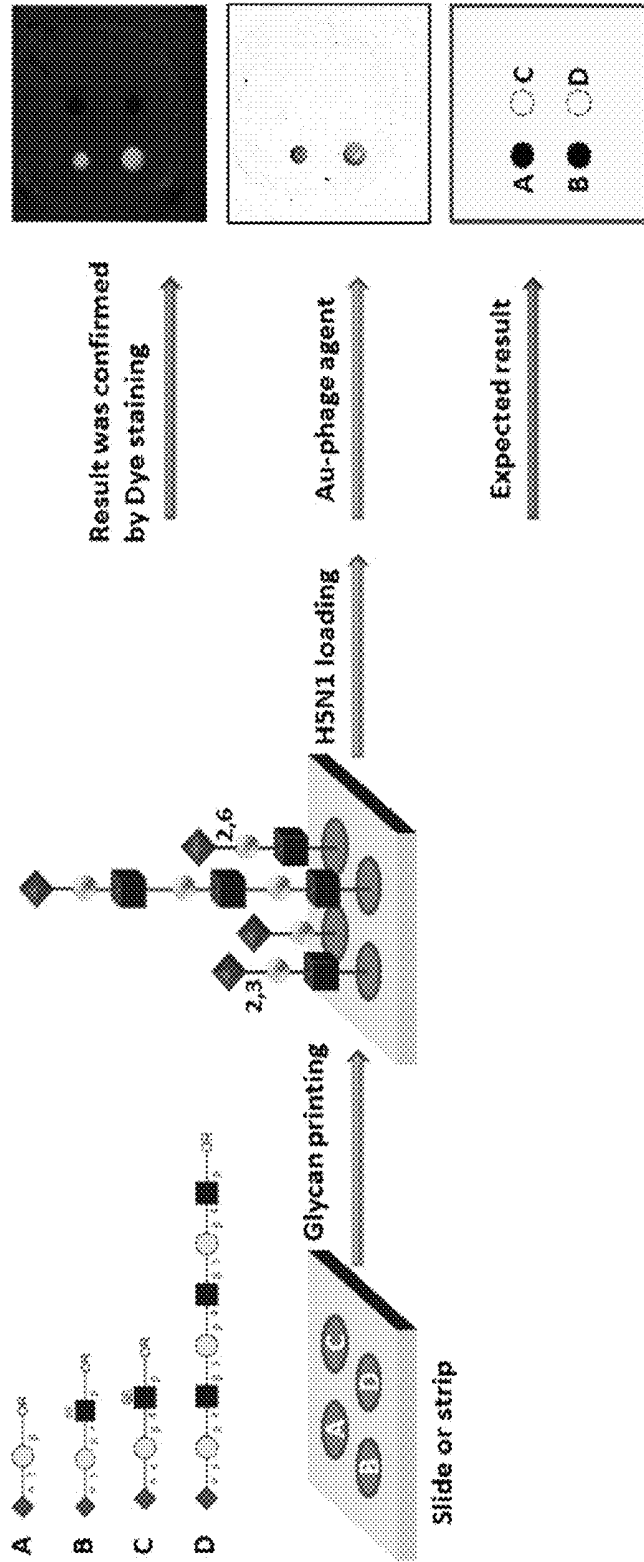


FIG. 7

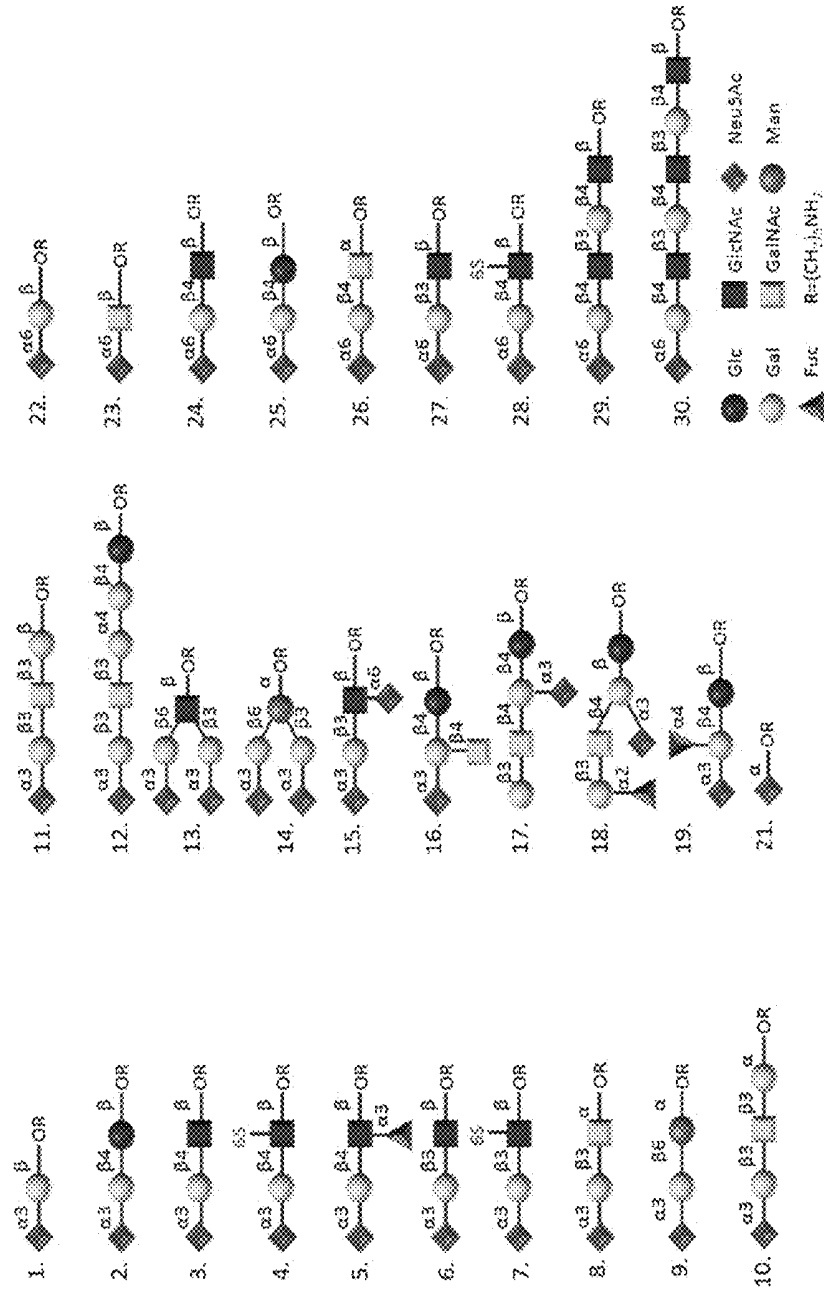
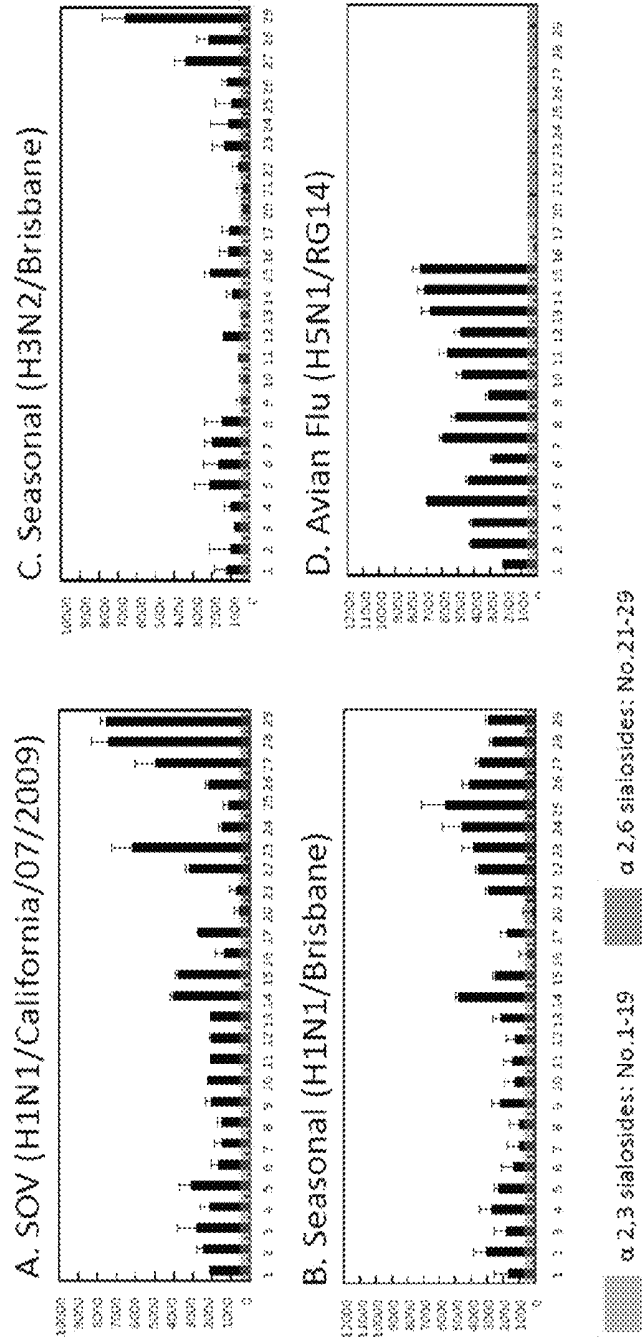


FIG. 8
Differential binding patterns of Influenza A virus subtype



The various types of terminal sialic acid linkage are indicated by the colored panels as defined at the bottom of the figure.

FIG. 9

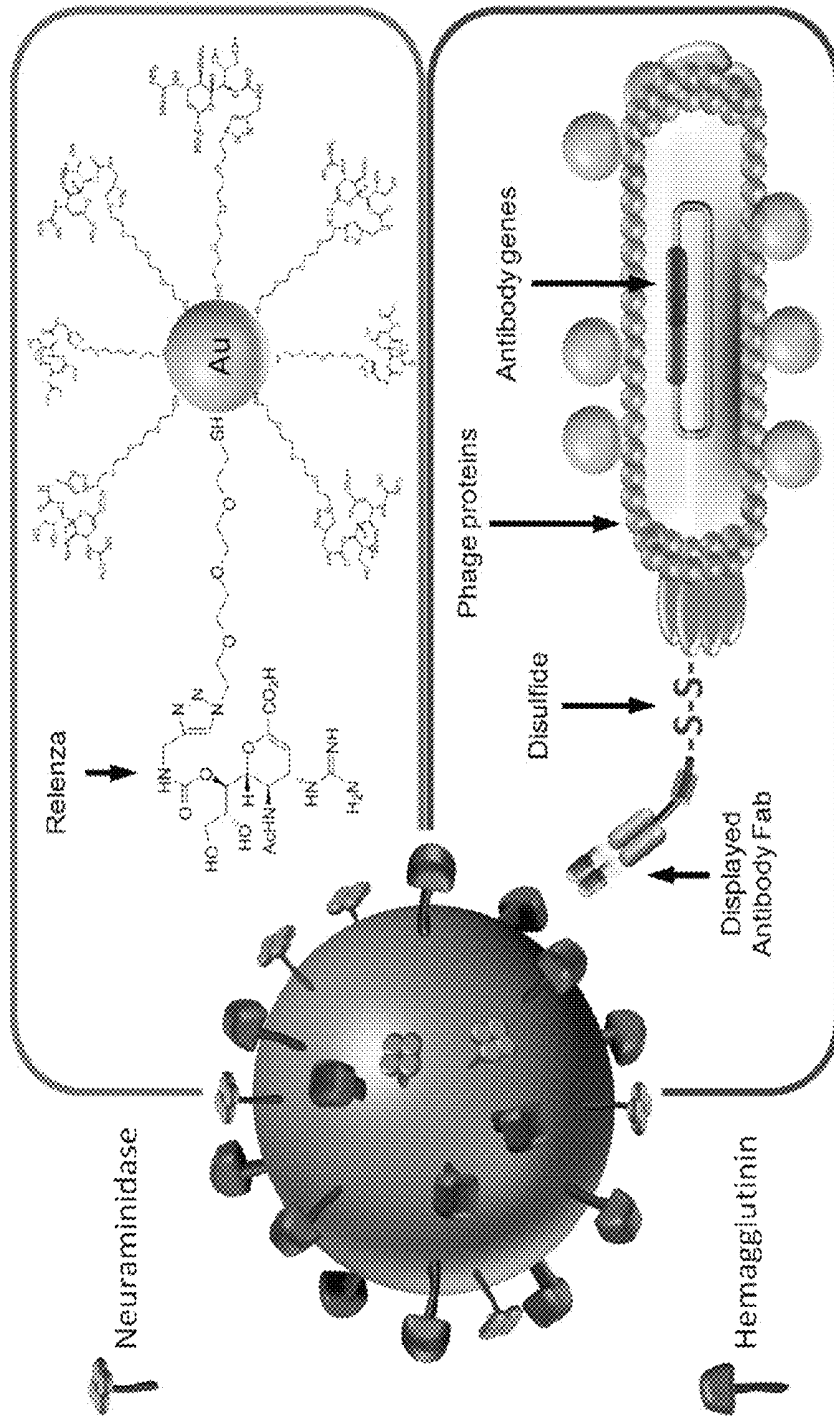


FIG. 10

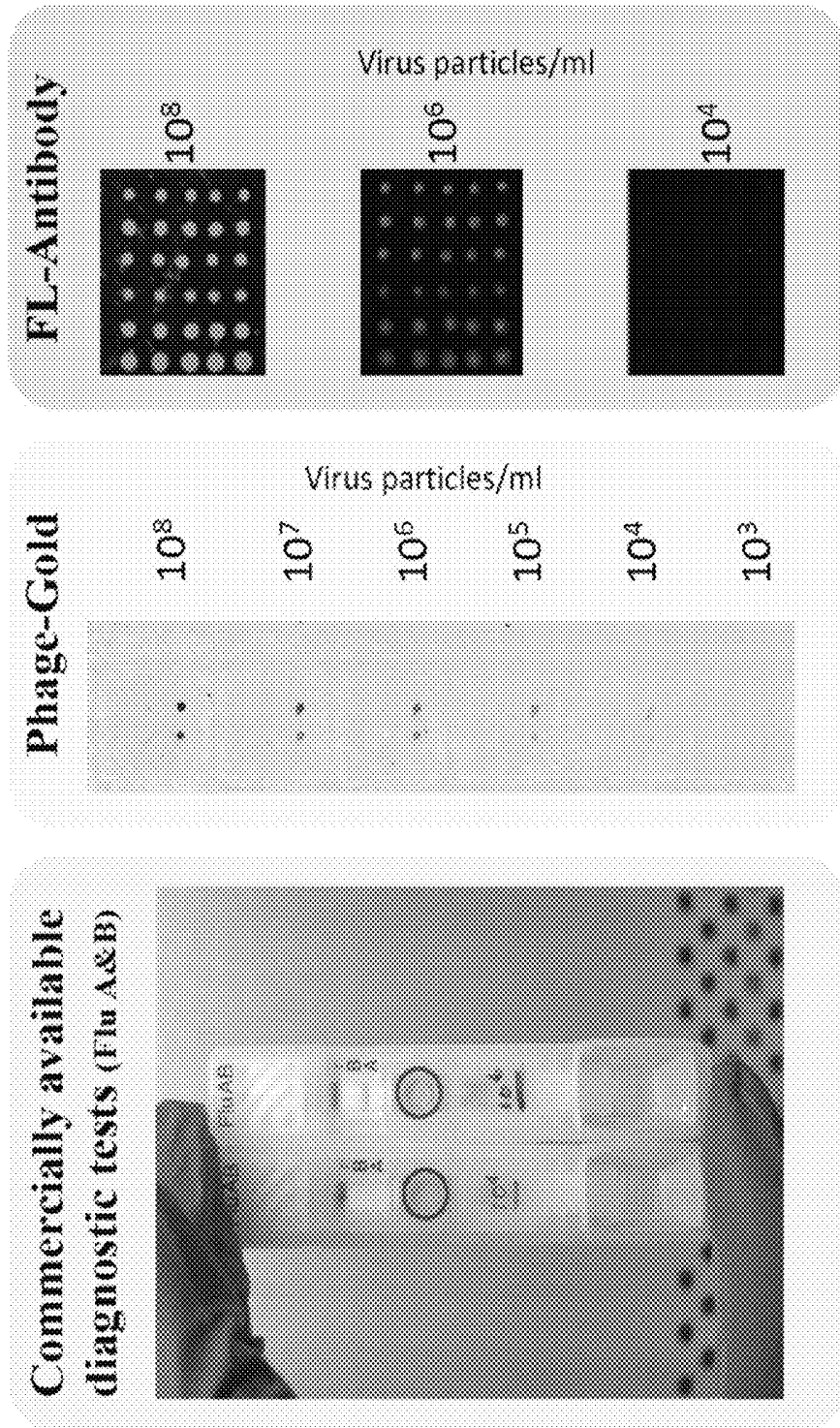
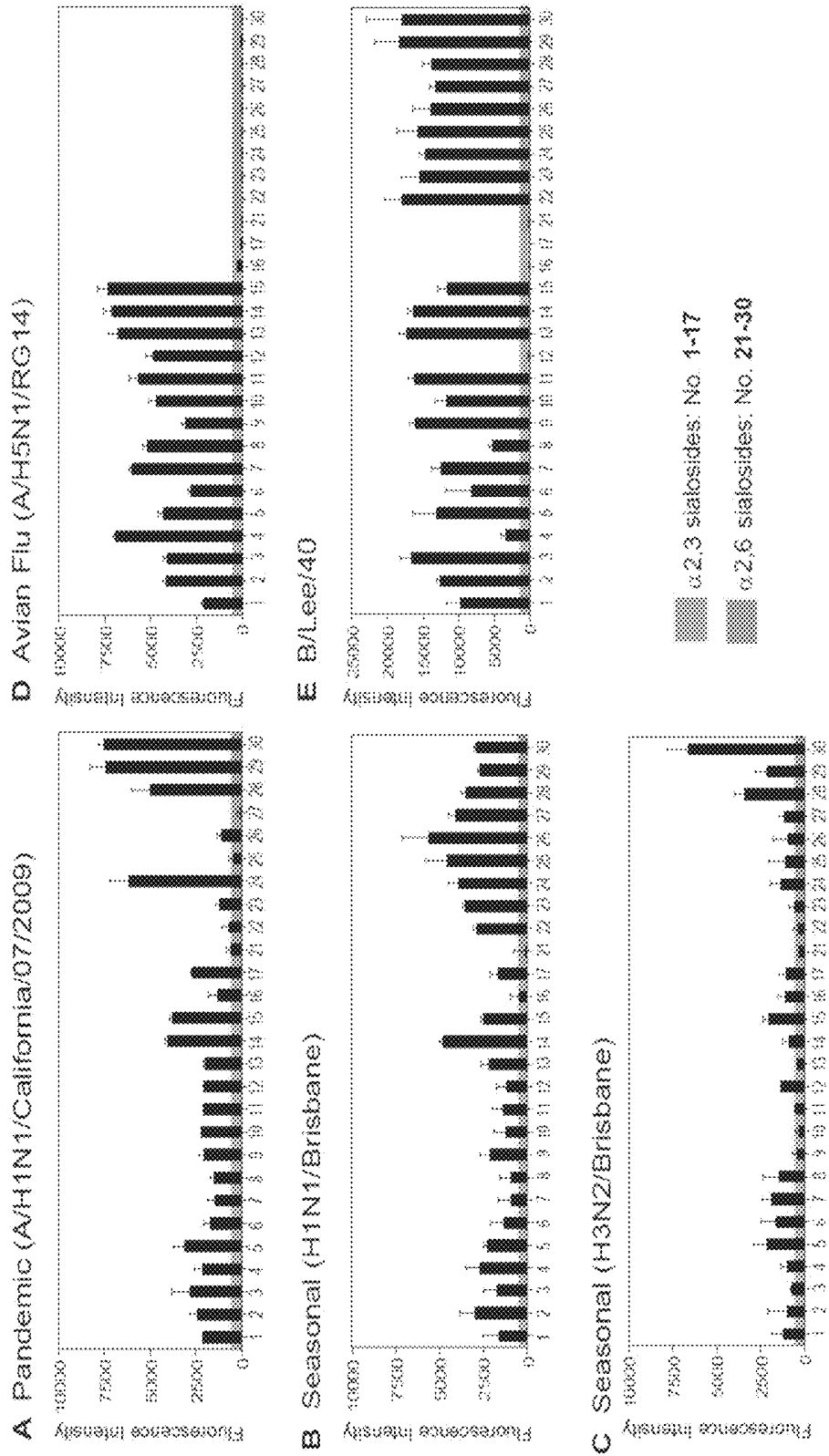


FIG. 12



GLYCAN ARRAYS FOR HIGH THROUGHPUT SCREENING OF VIRUSES

This application is a U.S. National Stage entry of International Application No. PCT/US2011/032192 filed Apr. 12, 2011 which application claims priority under the Paris Convention to U.S. Provisional Patent Application Ser. No. 61/323,300, filed Apr. 12, 2010, the contents of which are incorporated herein by reference.

TECHNICAL FIELD OF THE INVENTION

The present invention relates to classification of influenza virus subtypes. Specifically, the invention relates to glycan arrays which can detect and distinguish between influenza virus subtypes. More specifically, the invention relates to methods for detecting influenza virus subtypes using nanoparticle-based detection methods. The invention relates to detector molecules comprising noble metals conjugated to (a) phage display particles expressing antibodies against hemagglutinin and (b) neuraminidase binding agents.

BACKGROUND OF THE INVENTION

Influenza has a long history of pandemics, epidemics, resurgences and outbreaks. Avian influenza, including the H5N1 strain, is a highly contagious and potentially fatal pathogen, but it currently has only a limited ability to infect humans. However, avian flu viruses have historically observed to accumulate mutations that alter its host specificity and allow it to readily infect humans. In fact, two of the major flu pandemics of the last century originated from avian flu viruses that changed their genetic makeup to allow human infection. The emergence of new influenza A (H1N1) virus (henceforth: influenza A(H1N1)_v, virus, where v stands for variant, according to nomenclature agreed by the World Health Organization Global Influenza Surveillance Network—WHO GISON) in humans has led to the requirement for sensitive and specific assays for the differential diagnosis and confirmation of influenza A(H1N1)_v virus infections, necessary to guide public health actions.

Triple-reassortant swine influenza viruses, which contain genes from human, swine, and avian influenza A viruses, have been identified in swine in the United States since 1998. In April, 2009, the U.S. Centers for Disease Control and Prevention identified novel swine-origin influenza A virus which contains a unique combination of gene segments from both North American and Eurasian swine lineages, colloquially called swine flu. Co-circulation of current seasonal human H1N1, H3N2, and Swine-Origin Influenza (S-OIV) A (H1N1) Viruses in the upcoming flu seasons poses a challenge for sub-typing individual strains and potential reassortants. The more complicated, and perhaps dangerous, scenario is the reassortment of Swine-Origin Influenza A with highly pathogenic avian H5N1 or with other serotypes.

Traditional methods for influenza detection and subtype identification are based on virus isolation in tissue culture. Methods for subtyping of the virus require expansion of viruses in embryonated eggs, followed by subtyping with serological methods (HI tests). This procedure might take a week and considerable effort. Although virus isolation has long served as the standard for the diagnosis of influenza virus, the approach alone is inefficient when worldwide outbreaks occur as it is less sensitive, time-consuming, and requires considerable technical expertise. The rapid shell vial culture assay, although more rapid than the standard

tissue culture based method, the time to completion is still more than 24 h. Currently, more rapid methods with higher sensitivity and specificity have been developed to identify different subtypes of influenza virus for humans and for poultry; the serological method include immunodiffusion test, counter-Immune-electrophoresis, latex agglutination test and immunity fluorescence (IF) enzyme-linked immunosorbant assay (ELISA) and molecular biology methods include RT-PCR, nested RTPCR, rRT-PCR, nucleic acid sequence-based amplification, loop-mediated isothermal amplification, and DNA microarrays are not suitable for on-site use in field investigations or in clinical practice due to constraints such as test accessibility, and requirements for highly trained personnel, time-intensive procedures, appropriate containment laboratory facilities and elaborate instrumentation.

Limitations of most of the conventional diagnostic methods are lack of accuracy, sensitivity and delay in getting results. Importantly, the current standard for influenza subtype identification relies on either a polymerase chain reaction test or culture approach, neither of which is a quick (or inexpensive) test. The current crop of quick test products on the market is only capable, due to limitations in their technology platform, of providing a yes/no answer to the presence of influenza. While swine-origin influenza virus (S-OIV; National Virus Reference Laboratory, NVRL, Dublin) real time PCR detection is available, it may not be applicable for more-complex reassortant strains. Available real-time PCR assays (HPA A(H1)v, CDC A (H1)v, HPA A(N1)v and NVRL S-OIV assays are suitable as first-line tests but accurate assessment requires concurrent use of primary diagnostic and confirmatory assays (Ellis J., et al. Euro Surveill. 2009; 14(22):pii=19230). Further, these methods require relatively sophisticated laboratories, which are sometimes unavailable or inconvenient for clinical application.

Glycans are typically the first and potentially the most important interface between cells and their environment. As vital constituents of all living systems, glycans are involved in recognition, adherence, motility and signaling processes. For example, all cells in living organisms, and viruses, are coated with diverse types of glycans; glycosylation is a form of post or co-translational modification occurring in all living organisms; and altered glycosylation is an indication of an early and possibly critical point in development of human pathologies. (Hirabayashi, J. 2003, Trends in Biotechnology 21 (4): 141-143; Hakomori, S-I. Tumor-associated carbohydrate antigens defining tumor malignancy: Basis for development of and cancer vaccines; in The Molecular Immunology of Complex Carbohydrates-2 (Albert M Wu, ed., Kluwer Academic/Plenum, 2001). These cell-identifying glycosylated molecules include glycoproteins and glycolipids and are specifically recognized by various glycan-recognition proteins. Carbohydrates are involved in inflammation, cell-cell interactions, signal transduction, fertility, bacteria-host interactions, viral entry, cell differentiation, cell adhesion, immune response, trafficking, and tumor cell metastasis.

Carbohydrates can also be expressed on the outer surface of a majority of viral, bacterial, protozoan, and fungal pathogens. The structural expression of carbohydrates can be pathogen-specific, making carbohydrates an important molecular target for pathogen recognition and/or infectious diseases diagnosis. Glycans, chains of sugars that often form complex branched structures on proteins or lipids, are major components of the outermost surface of many viruses. Receptor specificity for the influenza virus is usually con-

trolled by the glycoprotein HA on the virus surface. Features of the differential binding among influenza virus suggest new flu as an intermediary genetic mixing vessel and facilitate a development of diagnostics. This pathogen specific expression of carbohydrates also can aid in vaccine development. Most interactions of virus with their hosts are influenced to an important degree by the pattern of glycans and glycan-binding receptors that each expresses. This holds true at all stages of infection, from initial colonization of host epithelial surfaces, to tissue spread, to the induction of host-cell injury are dominated by glycans (See FIG. 2). The two major surface proteins of the virus are hemagglutinin (HA) and neuraminidase (NA). The HA and NA are grouped into 16 and 9 subtypes, respectively, both have high sequence variability even within subtypes and thus provide an effective means of monitoring changes that might occur in a virus. The HA protein protrudes from the surface of the virus and allows it to attach to a cell to begin the infection cascade. The NA protein is also located on the surface of the virus and allows the release of new particles within the infected cell by cleaving the sialic acid moiety of cellular receptors.

The development of nucleotide and protein microarrays has revolutionized genomic, gene expression and proteomic research. ((Skena, M. et al. *Science*, 1995, 270:467-70; MacBeath, G. and Schreiber, S. L. 2000, *Science*, 289, 1760-1763). One feature of the post-genomic period is the exploration of biophysical, biochemical, and immunological properties of carbohydrate-carbohydrate and carbohydrate-protein interactions. Thus, a method is needed to study protein-carbohydrate interactions and to better understand these important biological processes.

Glycomics, the comprehensive study of glycomes, focuses on the interactions of carbohydrates with other biological processes. Carbohydrate microarrays are a platform for glycomic studies probing the interactions of carbohydrates with other biopolymers and biomaterials, in a versatile, rapid, and efficient manner. One particular advantage of the carbohydrate microarray is that a glycomic analysis requires only picomoles of a material and permits typically hundreds of interactions to be screened on a single microarray. The miniaturized array methodology is particularly well suited for investigations in the field of glycomics, since biological amplification strategies, such as the Polymerase Chain Reaction (PCR) or cloning, do not exist to produce usable quantities of complex oligosaccharides. Presenting carbohydrates in a microarray format can be an efficient way to monitor the multiple binding events of an analyte, such as, a protein interacting with one or more carbohydrates immobilized on a microarray surface.

The development of glycan microarrays has been very slow for a number of reasons. First, it is difficult to immobilize a library of chemically and structurally diverse glycans on arrays, beads or the like. Second, glycans are not readily amenable to analysis by many of the currently available molecular techniques (such as rapid sequencing and in vitro synthesis) that are routinely applied to nucleic acids and proteins. methods of preparing glycan arrays have been described in PCT/US2005/007370 filed Mar. 7, 2005 titled "High Throughput Glycan Microarrays" (Blixt), and U.S. Pat. App. Pub. No. 20080220988 (Zhou).

Microarray signals are detected by many technologies. Fluorescent labeling and detection is the most popular technique used to identify hybridization signals because it is sensitive and much easier and safer to handle than radioactive labeling methods (Parrish, M. L. et al. *J. Neurosci. Methods*, 2004, 132, 57-68). Sensitive fluorescence detec-

tion commonly uses a laser and a confocal microscope, e.g., DNA microarray detector made by Affymetrix Inc., which are typically very expensive and need a trained technician to operate.

The detection of protein analytes on microarrays has emerged as a powerful tool for proteomics as well as diagnostics (Macbeath, G. et al. *Science* (2000), 289, 1760-1763; Moody, M. D. et al. *Biotechniques* (2001), 31, 186-194; Nielsen, U. B. et al. *Journal Immunol. Meth.* (2004), 290, 107-120) A variety of different detection methods have been developed for labeling antibody arrays including, but not limited to, fluorescence, (Macbeath, G. et al. *Science* (2000), 289, 1760-1763; Li, Y. L. et al. (2003), 19, 1557-1566) chemiluminescence (Moody, M. D.; et al. *Biotechniques* 2001, 31, 186-194), resonance light scattering (Nielsen, U. B. et al. *Journal Immunol. Meth.* (2004), 290, 107-120), and SERS (Grubisha, D. S. et al. *Anal. Chem.* (2003), 75, 5936-5943). Signal amplification strategies such as rolling circle amplification (RCA) also have been used to increase the detection sensitivity of fluorescence-based strategies. (Schweitzer, B et al. *Nat. Biotechnol.* (2002), 20, 359-365; Wiltshire, S. et al. *Proc. Natl. Acad. Sci. U.S.A.* (2000), 97, 10113-10119) These methods have provided high sensitivity detection (<10 pg/mL) of protein analytes. However, the reproducible preparation of highly purified antibody reagents is both challenging and time consuming (Jayasena, S. D. *Clin. Chem.* (1999), 45, 1628-1650).

Rapid and simple diagnostic methods for confirming infection with influenza virus are urgently needed. Especially at the beginning of a new pandemic outbreak, an early differential diagnosis may alter clinical management, such as infection control procedures, consideration of antiviral treatment options and avoiding the inappropriate use of drugs. Thus, there is a need for novel techniques to classify subtypes of influenza viruses. There is a need for rapid and sensitive methods for detecting and classifying influenza viruses using glycan arrays.

SUMMARY OF THE INVENTION

Glycan arrays are ideal for virus-cell applications as the arrays present glycan ligands in such a way that mimics cell-cell interactions. Because each virus protein has characteristic binding patterns, a glycan array might be feasible to analyze the subtype of influenza viruses and map the evolution of new influenza subtypes based on their binding preferences. Glycan arrays also have proven to be invaluable in the early identification of epidemics caused by viruses.

The current invention provides glycan assays and arrays that can detect and distinguish between various sub-types and strains of an influenza virus using any suitable nanoparticle amplification technique on glycan assay. The assay can be performed in a single reaction slide or strip. The assay or array can use more than one probe to amplify and detect specific target HA of influenza. Using the information obtained from the assay, it is able to distinguish between various sub-types and strains of an influenza virus. Specifically, the assay can provide a positive or negative (y/n) determination of the presence or absence of influenza virus types A and B, and sub-types H1N1, H3N1, and H5N1 in a sample. Importantly, screening results can be observed directly by naked eyes in a fast manner. This technique also has great potential in detection of vaccination response in individuals.

A comprehensive and sensitive glycan array system for detection and subtype identification of influenza viruses is provided. In one embodiment, a set of nine glycans were

selected from a library of twenty nine sialosides to capture the influenza virus and form a unique scanometric fingerprint for each subtype of influenza virus on glass slides.

The sensitivity and specificity of detection by this method is higher compared with the commercially available influenza detection kits. A convenient and efficient profiling system to differentiate influenza virus subtypes is provided. Due to its sensitivity, simplicity and cost effectiveness, the nanoparticle-based glycan array has great potential for being widely adopted as a valuable diagnostic tool to facilitate recognition of influenza outbreaks, even in low resource areas.

One of the most notable aspects about this nanoparticle-based detection method is it requires nothing more than naked eye to read results that currently require chemical labeling and confocal laser scanners. This advantage enables a faster diagnostics for any possible new variant; it can also rapidly determine whether the strain has developed drug resistance.

In one embodiment, the probe targets neuraminidase (NA) using Relenza®-gold nanoparticle complex. In another embodiment, phage techniques are applied to construct phage-gold nanoparticle complex which can specifically target hemagglutinin (HA) subtypes.

The invention relates to methods for detecting at least one type of target analyte in a sample, the method comprising the steps of: a) providing a substrate having at least one type of glycan capture probe bound at a discrete location on the substrate, wherein the capture probe can bind to the target analyte; b) providing at least one type of nanoparticle probe comprising detector moieties, wherein the detector moieties on each type of probe has a configuration that can bind to the target analyte; c) contacting the substrate with the sample under conditions suitable for binding of the target analyte in the sample to the glycan capture probe; d) contacting the target analyte immobilized on the substrate with the nanoparticle probe under conditions that are effective for the binding of the detector moieties to the target analyte; and e) detecting whether the nanoparticle probe binds to the target analyte, wherein the presence or absence of the complex is indicative of the presence or absence of the specific target analyte in the sample.

The invention relates to methods for detecting at least one influenza serotype in a sample, the method comprising the steps of: a) providing a substrate having at least one type of glycan capture probe bound at a discrete location on the substrate, wherein the capture probe can bind to a specific influenza serotype target; b) providing at least one type of nanoparticle probe conjugated to a detector moiety, wherein the detector moiety binds to the specific influenza serotype; c) contacting the substrate with the sample and the nanoparticle probe under conditions suitable for the binding of the glycan capture probe to the specific influenza serotype and the binding of the nanoparticle probe to the specific influenza serotype to form a complex at the discrete location on the substrate; and d) detecting the presence or absence of the complex wherein the presence or absence of the complex is indicative of the presence or absence of the specific influenza serotype in the sample.

In some aspects, the influenza serotype is selected from the group consisting of influenza A serotypes H1N1, H2N2, H3N1, H3N2, H5N1, H7N7, H1N2, H9N2, H7N2, H7N3, and H10N7.

In some aspects, the detector moiety comprises an antibody or fragment thereof that binds to the specific influenza serotype. In some embodiments, the antibody or fragment thereof comprises a phage particle from a phage display.

In some aspects, the target analyte is an antibody, an enzyme, a viral protein, a cellular receptor, a cell type specific antigen, or a nucleic acid, a cellular component or a tissue component from a pathogen, from a prokaryote, prion, virus, bacterium or eukaryote.

In some aspects, the sample is blood, serum, anti-serum, monoclonal antibody preparation, lymph, plasma, saliva, urine, semen, breast milk, ascites fluid, tissue extract, cell lysate, cell suspension, viral suspension, nasopharyngeal aspirate, blood, saliva, or a combination thereof.

In some aspects, the captured target-nanoparticle probe complex is detected by photonic, electronic, acoustic, opto-acoustic, gravity, electro-chemical, electro-optic, mass-spectrometric, enzymatic, chemical, biochemical, or physical means.

In some aspects, the nanoparticles are made of a noble metal. In some embodiments, the nanoparticles are made of gold or silver.

In some aspects, the substrate is a magnetic bead. In some aspects, the substrate has a planar surface. In some aspects, the substrate is made of glass, quartz, ceramic, or plastic.

In some aspects, the detecting comprises contacting the substrate with silver stain.

In some aspects, the detecting comprises detecting light scattered by the nanoparticle. In some embodiments, the detecting comprises observation with an optical scanner. In some embodiments, the scanner is linked to a computer loaded with software capable of calculating grayscale measurements, and the grayscale measurements are calculated to provide a quantitative measure of the amount of target analyte or influenza serotype detected.

In some embodiments, the substrate is addressable. In some embodiments, a plurality of glycan capture probes, each of which can recognize a different target influenza serotype, are attached to the substrate in an array of discrete spots. In some embodiments, the plurality of glycan capture probes comprise glycan structures of at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more of glycans found on HA receptors in human upper respiratory tract tissues. In some embodiments, the plurality of glycan capture probes comprises a glycan structure of at least one molecule shown in FIG. 7.

In some aspects, the substrate is selected from the group consisting essentially of one of glass, semiconductor, organic polymer, membrane, quartz, silicon, mineral, metal, metal alloy, gold, silver, and mixtures and compositions thereof.

In some embodiments of the method, sample is first contacted with the nanoparticle probe such that a target influenza serotype present in the sample binds to the detector moiety on the nanoparticle probe, and the target influenza serotype bound to the nanoparticle probe is then contacted with the substrate so that the target influenza serotype binds to the glycan capture probe on the substrate.

In some embodiments of the method, sample is first contacted with the substrate so that a target influenza serotype present in the sample binds to a glycan capture probe, and the target influenza serotype bound to the glycan capture probe is then contacted with the nanoparticle probe so that the target influenza serotype binds to the detector moiety on the nanoparticle probe.

In some embodiments of the method, the sample, the nanoparticle probe and the glycan capture probe on the substrate are contacted simultaneously.

In some embodiments of the method, detecting the presence or absence of the complex indicative of the presence or

absence of the specific influenza serotype in the sample comprises evaluating a flu vaccination response in an individual from whom the sample is obtained.

These and other aspects will become apparent from the following description of the preferred embodiment taken in conjunction with the following drawings, although variations and modifications therein may be affected without departing from the spirit and scope of the novel concepts of the disclosure.

BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present disclosure, the inventions of which can be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein. The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. 1 shows a schematic of an influenza virus type test procedure using a glycan array.

FIG. 2 shows invasion and replication of the influenza virus. The steps of virus binding and releasing are shown on the right panel.

FIG. 3A shows a schematic description of a synergy of nanomaterials and glycan array showing viruses's binding preferences. First, selected glycans were immobilized on a glass slide. A nasal aspirate fluid was then incubated with slides. Glycans with different structures can target hemagglutinin specific to H5N1, H3N1, and H1N1 serotypes. Next, specific antibodies, Relenza-Au (targeting NA), or phage-Au complex (targeting HA) were introduced. Influenza A serotypes can be observed by naked eyes in the case of Relenza-Au and phage-Au and be classified by glycan patterns on glass slides. FIG. 3B shows the fingerprint patterns of glycan array for each influenza serotype tested.

FIG. 4 shows TEM image of gold nanoparticle (left panel) and Au-phage (right panel).

FIG. 5 shows glycan array analyses of the four viruses investigated. Numerical scores for the binding signals are shown as means of duplicate spots at 100 μ M per spot (with error bars). The arrays consisted of twenty eight sialylated oligosaccharide probes, printed on NHS-coated glass slides (NHS: N-Hydroxy Succinimide). These are listed in Table 2 and arranged according to sialic acid linkage, oligosaccharide backbone chain length and sequence. The various types of terminal sialic acid linkage are indicated by the colored panels as defined at the bottom of the figure.

FIG. 6 shows a procedure for H5N1 fingerprint pattern construction.

FIG. 7 shows symbolic representations of common monosaccharides and linkage. (reprinted from Consortium for Functional Glycomics: www.functionalglycomics.org)

FIG. 8 shows the receptor binding repertoire of the Cal/09 H1N1, Brisbane H1N1, Brisbane H3N2, and RG14H5N1 strains of influenza virus as tested against twenty nine sialosides including nineteen (2 \rightarrow 3 linked) and ten (2 \rightarrow 6 linked) glycans (according to FIG. 7).

FIG. 9 shows two strategies for making nanoparticle-based probes in influenza virus subtype detection: Relenza-gold nanoparticle complex target neuraminidase (NA) and phage-gold nanoparticle complex target hemagglutinin subtypes (HA).

FIG. 10 shows detection limits of the Flu A&B test, GNBSSGA and the analogous fluorophore glycan array system.

FIG. 11 shows differential binding patterns of HA from H1N1, H3N2, H5N1, H7N7, and H9N2 viruses.

FIG. 12 shows glycan array analyses of the four viruses investigated. The binding signals are shown as means of duplicate spots at 100 μ M per spot. Each experiment was repeated twice. Arrays consisted of twenty seven sialylated oligosaccharide probes, printed on NHS-coated glass slides (NHS: N-Hydroxy Succinimide). The various types of terminal sialic acid linkage are indicated by the colored panels as defined at the bottom of the figure.

DETAILED DESCRIPTION OF THE INVENTION

The terms used in this specification generally have their ordinary meanings in the art, within the context of the invention, and in the specific context where each term is used. Certain terms that are used to describe the invention are discussed below, or elsewhere in the specification, to provide additional guidance to the practitioner regarding the description of the invention. For convenience, certain terms may be highlighted, for example using italics and/or quotation marks. The use of highlighting has no influence on the scope and meaning of a term; the scope and meaning of a term is the same, in the same context, whether or not it is highlighted. It will be appreciated that same thing can be said in more than one way. Consequently, alternative language and synonyms may be used for any one or more of the terms discussed herein, nor is any special significance to be placed upon whether or not a term is elaborated or discussed herein. Synonyms for certain terms are provided. A recital of one or more synonyms does not exclude the use of other synonyms. The use of examples anywhere in this specification including examples of any terms discussed herein is illustrative only, and in no way limits the scope and meaning of the invention or of any exemplified term. Likewise, the invention is not limited to various embodiments given in this specification.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. In the case of conflict, the present document, including definitions will control.

Definitions

Affinity: As is known in the art, "affinity" is a measure of the tightness with a particular ligand (e.g., an HA polypeptide) binds to its partner (e.g., an HA receptor). Affinities can be measured in different ways.

Binding: It will be understood that the term "binding", as used herein, typically refers to a non-covalent association between or among agents. In many embodiments herein, binding is addressed with respect to particular glycans. It will be appreciated by those of ordinary skill in the art that such binding may be assessed in any of a variety of contexts. In some embodiments, binding is assessed with respect to free glycans. In some embodiments, binding is assessed with respect to glycans attached (e.g., covalently linked to) a carrier. In some embodiments, binding is assessed with respect to glycans attached to an HA receptor. In such embodiments, reference may be made to receptor binding or to glycan binding.

Binding agent: In general, the term “binding agent” is used herein to refer to any entity that binds to glycans. Binding agents may be of any chemical type. In some embodiments, binding agents are polypeptides (including, e.g., antibodies or antibody fragments); in some such embodiments, binding agents are HA polypeptides; in other embodiments, binding agents are polypeptides whose amino acid sequence does not include an HA characteristic sequence. In some embodiments, binding agents are small molecules. In some embodiments, binding agents are nucleic acids. In some embodiments, binding agents are aptamers. In some embodiments, binding agents are polymers. In some embodiments, binding agents are non-polymeric. In some embodiments, binding agents are carbohydrates. In some embodiments, binding agents are lectins. In some embodiments, binding agents compete with hemagglutinin for binding to glycans on hemagglutinin receptors.

Biologically active: As used herein, the phrase “biologically active” refers to a characteristic of any agent that has activity in a biological system, and particularly in an organism. For instance, an agent that, when administered to an organism, has a biological effect on that organism, is considered to be biologically active. In particular embodiments, where a protein or polypeptide is biologically active, a portion of that protein or polypeptide that shares at least one biological activity of the protein or polypeptide is typically referred to as a “biologically active” portion.

Hemagglutinin (HA) polypeptide: As used herein, the term “hemagglutinin polypeptide” (or “HA polypeptide”) refers to a polypeptide whose amino acid sequence includes at least one characteristic sequence of HA. A wide variety of HA sequences from influenza isolates are known in the art; indeed, the National Center for Biotechnology Information (NCBI) maintains a database (www.ncbi.nlm.nih.gov/genomes/FLU/flu.html). Those of ordinary skill in the art, referring to this database, can readily identify sequences that are characteristic of HA polypeptides generally, and/or of particular HA polypeptides (e.g., H1, H2, H3, H4, H5, H6, H7, H8, H9, H10, H11, H12, H13, H14, H15, or H16 polypeptides; or of HAs that mediate infection of particular hosts, e.g., avian, camel, canine, cat, civet, environment, equine, human, leopard, mink, mouse, seal, stone martin, swine, tiger, whale, etc. In some embodiments, an HA polypeptide has an amino acid sequence that includes residues that participate in glycan binding. In some embodiments, an HA polypeptide includes at least 2, 3, 4, or all 5 of these residues.

Pure: As used herein, an agent or entity is “pure” if it is substantially free of other components. For example, a preparation that contains more than about 90% of a particular agent or entity is typically considered to be a pure preparation. In some embodiments, an agent or entity is at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% pure.

Vaccination: As used herein, the term “vaccination” refers to the administration of a composition intended to generate an immune response, for example to a disease-causing agent. For the purposes of the present invention, vaccination can be administered before, during, and/or after exposure to a disease-causing agent, and in certain embodiments, before, during, and/or shortly after exposure to the agent. In some embodiments, vaccination includes multiple administrations, appropriately spaced in time, of a vaccinating composition.

Wild type: As is understood in the art, the phrase “wild type” generally refers to a normal form of a protein or nucleic acid, as is found in nature. For example, wild type

HA polypeptides are found in natural isolates of influenza virus. A variety of different wild type HA sequences can be found in the NCBI influenza virus sequence database, www.ncbi.nlm.nih.gov/genomes/FLU/FLU.html.

5 Influenza Virus Assays

This invention provides an influenza virus assay that can detect and distinguish between various sub-types and strains of an influenza virus using any suitable nanoparticle amplification technique on glycan array. This assay can be performed in a single reaction slide.

10 Influenza viruses are RNA viruses which are characterized by a lipid membrane envelope containing two glycoproteins, hemagglutinin (HA) and neuraminidase (NA), embedded in the membrane of the virus particular. There are 16 known HA subtypes and 9 NA subtypes, and different influenza strains are named based on the number of the strain’s HA and NA subtypes. Based on comparisons of amino acid sequence identity and of crystal structures, the HA subtypes have been divided into two main groups and four smaller clades. The different HA subtypes do not necessarily share strong amino acid sequence identity, but the overall 3D structures of the different HA subtypes are similar to one another, with several subtle differences that can be used for classification purposes. For example, the particular orientation of the membrane-distal subdomains in relation to a central α -helix is one structural characteristic commonly used to determine HA subtype (Russell et al., *Virology*, 325:287, 2004).

HA exists in the membrane as a homotrimer of one of 16 subtypes, termed H1-H16. Only three of these subtypes (H1, H2, and H3) have thus far become adapted for human infection. One reported characteristic of HAs that have adapted to infect humans (e.g., of HAs from the pandemic H1N1 (1918) and H3N2 (1967-68) influenza subtypes) is their ability to preferentially bind to α -2-6 sialylated glycans in comparison with their avian progenitors that preferentially bind to α -2-3 sialylated glycans (Skehel & Wiley, *Ann. Rev Biochem*, 69:531, 2000; Rogers, & Paulson, *Virology*, 127:361, 1983; Rogers et al., *Nature*, 304:76, 1983; Sauter et al., *Biochemistry*, 31:9609, 1992; Connor et al., *Virology*, 205:17, 1994; Tumpey et al., *Science*, 310:77, 2005).

Several crystal structures of HAs from H1 (human and swine), H3 (avian) and H5 (avian) subtypes bound to sialylated oligosaccharides (of both α -2-3 and α -2-6 linkages) are available and provide molecular insights into the specific amino acids that are involved in distinct interactions of the HAs with these glycans (Eisen et al., *Virology*, 232:19, 1997; Ha et al., *Proc Natl Acad Sci USA*, 98:11181, 2001; Ha et al., *Virology*, 309:209, 2003; Gamblin et al., *Science*, 303:1838, 2004; Stevens et al., *Science*, 303:1866, 2004; Russell et al., *Glycoconj J* 23:85, 2006; Stevens et al., *Science*, 312:404, 2006). For example, the crystal structures of H5 (A/duck/Singapore/3/97) alone or bound to an α -2-3 or an α -2-6 sialylated oligosaccharide identifies certain amino acids that interact directly with bound glycans, and also amino acids that are one or more degree of separation removed (Stevens et al., *Proc Natl Acad Sci USA* 98:11181, 2001). In some cases, conformation of these residues is different in bound versus unbound states.

The assay method according to the present invention can use more than one or more probes to amplify and detect specific target HA of influenza. Using the information obtained from an amplification reaction it is possible to distinguish between various sub-types and strains of the influenza virus. Specifically, an assay can provide a positive or negative (yes/no) determination of the likely presence or absence of influenza virus types A and B, and sub-types

H1N1, H3N2, and H5N1 in a sample. An assay also can be used to monitor for one or more mutations in an influenza virus strain. Mutations in an influenza virus, within, for example the HA and NA, can alter viral infectivity and lethality in different hosts and different tissues.

Receptor specificity for the influenza virus is usually controlled by the glycoprotein HA on the virus surface. These viral HAs bind to host cell receptors containing terminal glycan called sialic acids. With a modest change of two amino acid mutations on HA, the 1918 influenza pandemic switch its binding preference from the human α -2,6 to the avian α -2,3 sialic acid receptor. (See FIG. 2). Features of the differential binding among influenza virus suggest new flu as an intermediary genetic mixing vessel and facilitate a development of diagnostics.

Design of Glycan Arrays

The glycan arrays of the invention can detect and distinguish between various sub-types and strains of an influenza virus using any suitable nanoparticle amplification technique on glycan assay. This assay can be performed in a single reaction slide or strip. The assay or array can use more than one probe to amplify and detect specific target HA of influenza. Using the information obtained from the assay, it is able to distinguish between various sub-types and strains of an influenza virus. Importantly, screening results can be observed directly by naked eyes in a fast manner. This technique also has great potential in detection of vaccination respond to individuals.

The present invention encompasses the finding that binding of influenza virus subtypes to glycans correlates with ability to mediate infection of particular hosts, including for example, humans.

In some embodiments, influenza virus subtypes bind to array glycans (e.g., α 2-6 sialylated glycans) with high affinity. For example, in some embodiments, influenza virus subtypes bind to array glycans with an affinity comparable to that observed for wild type HA that mediates infection of a humans (e.g., H1N1 HA or H3N2 HA). In some embodiments, influenza virus subtypes bind to array glycans with an affinity that is at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% of that observed under comparable conditions for binding to a wild type HA that mediates infection of humans. In some embodiments, influenza virus subtypes bind to array glycans with an affinity that is greater than that observed under comparable conditions for binding to a wild type HA that mediates infection of humans.

In certain embodiments, binding affinity of influenza virus subtypes is assessed over a range of concentrations. Such a strategy provides significantly more information, particularly in multivalent binding assays, than do single-concentration analyses. In some embodiments, for example, binding affinities of inventive binding agents are assessed over concentrations ranging over at least 2, 3, 4, 5, 6, 7, 8, 9, 10 or more fold. In certain embodiments, influenza virus subtypes show high affinity if they show a saturating signal in a multivalent glycan array binding assay such as those described herein.

In some embodiments, influenza virus subtypes bind to α 2-6 sialylated glycans; in some embodiments, influenza virus subtypes bind preferentially to α 2-6 sialylated glycans. In certain embodiments, influenza virus subtypes bind to a plurality of different α 2-6 sialylated glycans. In some embodiments, influenza virus subtypes are not able to bind to α 2-3 sialylated glycans, and in other embodiments influenza virus subtypes are able to bind to α 2-3 sialylated glycans.

In some embodiments, influenza virus subtypes bind to glycans found on receptors on human upper respiratory epithelial cells. In certain embodiments, influenza virus subtypes bind to glycans corresponding to those on HA receptors in the bronchus and/or trachea. In some embodiments, influenza virus subtypes are not able to bind glycans corresponding to those on receptors in the deep lung, and in other embodiments, influenza virus subtypes are able to bind glycans corresponding to those on receptors in the deep lung.

In some embodiments, glycans corresponding to those on bind to at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more of the glycans found on HA receptors in human upper respiratory tract tissues (e.g., epithelial cells). In some embodiments, influenza virus subtypes bind to one or more of the glycans illustrated in FIGS. 7A-7C. In some embodiments, influenza virus subtypes bind to multiple glycans illustrated in FIGS. 7A-7C. In some embodiments, influenza virus subtypes bind with high affinity and/or specificity to glycans illustrated in FIGS. 7A-7C.

In some embodiments, influenza virus subtype binding is mediated through HA polypeptides. For example, the present invention provides glycan arrays that bind to HA polypeptides with specificity. In different embodiments, HA polypeptides that bind to the glycan arrays are H1, H2, H3, H4, H5, H6, H7, H8, H9, H10, H11, H12, H13, H14, H15, or H16 polypeptides.

In certain embodiments, the HA polypeptide is a variant of a known wild type HA polypeptide in that its amino acid sequence is identical to that of a known wild type HA but for a small number of particular sequence alterations. In some embodiments, the wild type HA is an HA polypeptide found in a known natural isolate of an influenza virus. In some embodiments, HA polypeptide variants have different glycan binding characteristics than their corresponding known wild type HA polypeptides.

The invention also provides anti-idiotypic antibodies that bind to glycans wherein the anti-idiotypic antibodies are directed to antibodies that react with circulating influenza virus subtypes present in patients. The anti-idiotypic technology is used to produce monoclonal antibodies which mimic an epitope on influenza virus and/or HA polypeptide. For example, an anti-idiotypic monoclonal antibody made to a first monoclonal antibody will have a binding domain in the hypervariable region which is the "image" of the epitope bound by the first monoclonal antibody. An antibody suitable for binding to a glycan is specific for at least one portion or region of the glycan. For example, one of skill in the art can use a whole glycan or fragment of glycan to generate appropriate antibodies of the invention.

Fabrication of Glycan Arrays

The arrays of the invention employ a library of characterized and defined glycan structures. A plurality of glycan molecules carried by at least one solid support. In a related embodiment the solid support is one or more of arrays, beads, microspheres, plates, slides and probes. The array is validated with a diverse set of carbohydrate binding proteins such as Influenza Hemagglutinins and anti-carbohydrate antibodies (from crude sera, purified serum fractions and purified monoclonal antibody preparations).

The glycan libraries, arrays and methods have several advantages. One particular advantage of the invention is that the arrays and methods of the invention provide highly reproducible results.

Another advantage is that the libraries and arrays of the invention permit screening of multiple glycans in one reac-

tion. Thus, the libraries and arrays of the invention provide large numbers and varieties of glycans. For example, the libraries and arrays of the invention have at least two glycans, at least three glycans, at least ten glycans, at least 30 glycans, at least 40 glycans, at least 50 glycans, at least 100 glycans, at least 150 glycans, at least 175 glycans, at least 200 glycans, at least 250 glycans or at least 500 glycans. In some embodiments, the libraries and arrays of the invention have more than two glycans, more than three glycans, more than ten glycans, more than 40 glycans, more than 50 glycans, more than 100 glycans, more than 150 glycans, more than 175 glycans, more than 200 glycans, more than 250 glycans or more than 500 glycans. In other embodiments, the libraries and arrays of the invention have about 2 to about 100,000, or about 2 to about 10,000, or about 2 to about 7500, or about 2 to about 1,000, or about 2 to about 500, or about 2 to about 200, or about 2 to 100 different glycans per library or array. In other embodiments, the libraries and arrays of the invention have about 50 to about 100,000, or about 50 to about 10,000, or about 50 to about 7500, or about 50 to about 1,000, or about 50 to about 500, or about 50 to about 200 different glycans per library or array. Such large numbers of glycans permit simultaneous assay with a multitude of different glycans.

As described herein, the present arrays are used for screening a variety of glycan binding proteins, specifically influenza virus, HA and NA proteins. The glycan arrays of the invention are reusable after stripping with acidic, basic aqueous or organic washing steps. Experiments demonstrate that little degradation of the glycan occurs and only small amounts of glycan binding proteins are consumed during a screening assay. Hence, the arrays of the invention can be used for more than one assay.

The arrays and methods of the invention provide high signal to noise ratios. The screening methods provided by the invention are fast and easy because they involve only one or a few steps. No surface modifications or blocking procedures are typically required during the assay procedures of the invention.

The composition of glycans on the arrays of the invention can be varied as needed by one of skill in the art. Many different glycoconjugates can be incorporated into the arrays of the invention including, for example, purified glycans, naturally occurring or synthetic glycans, glycoproteins, glycopeptides, glycolipids, bacterial and plant cell wall glycans and the like. Immobilization procedures for attaching different glycans to the arrays of the invention are readily controlled to easily permit array construction.

An essential requirement for microarray analyses is that the probe spots be discreet and readily distinguishable from each other. Without this, no valid conclusions can be drawn. As a consequence, analysis of replicate array probes of the same sample is highly preferred in order to draw definitive conclusions about changes in gene expression. The quality of arrays is critically important due to a large number of genes to be probed and detected on the microarray hybridization chip.

Spacer molecules or groups can be used to link the glycans to the arrays. Such spacer molecules or groups include fairly stable (e.g. substantially chemically inert) chains or polymers. For example, the spacer molecules or groups can be alkylene groups. One example of an alkylene group is $-(CH_2)_n-$, where n is an integer of from 1 to 20. In some embodiments, n is an integer of from 1 to 10.

Unique libraries of different glycans are attached to defined regions on the solid support of the array surface by any available procedure. In general, the arrays are made by

obtaining a library of glycan molecules, attaching spacer molecules with linking moieties to the glycans in the library, obtaining a solid support that has a surface derivatized to react with the specific linking moieties present on the glycans of the library and attaching the glycan molecules to the solid support by forming a covalent linkage between the linking moieties and the derivatized surface of the solid support.

The derivatization reagent can be attached to the solid substrate via carbon-carbon bonds using, for example, substrates having (poly)trifluorochloroethylene surfaces, or more preferably, by siloxane bonds (using, for example, glass or silicon oxide as the solid substrate). Siloxane bonds with the surface of the substrate are formed in one embodiment via reactions of derivatization reagents bearing trichlorosilyl or trialkoxysilyl groups.

The glycans of the invention can have spacers, linkers, labels, linking moieties and/or other moieties attached to them. These spacers, linkers, labels, linking moieties and/or other moieties can be used to attach the glycans to a solid support, detect particular glycans in an assay, purify or otherwise manipulate the glycans. For example, a glycan library can be employed that has been modified to contain primary amino groups. Thus, in some embodiments, the glycans of the invention can have amino moieties provided by attached alkylamine groups, amino acids, peptides, or proteins. For example, the glycans can have alkylamine groups such as $-O(CH_2)_nNH_2$ attached that provide the primary amino group. The primary amino groups on the glycans can react with an N-hydroxy succinimide (NHS)-derivatized surface of the solid support. Such NHS-derivatized solid supports are commercially available. For example, NHS-activated glass slides are available from Accelr8 Technology Corporation, Denver, Colo. (now Schott Nexterion, Germany). After attachment of all the desired glycans, slides can further be incubated with ethanolamine buffer to deactivate remaining NHS functional groups on the solid support. The array can be used without any further modification of the surface. No blocking procedures to prevent unspecific binding are typically needed. FIG. 1 provides a schematic diagram of such a method for making arrays of glycan molecules.

The substrate can be any suitable solid material, including without limitation solid materials formed from or containing silicons (such as, but not limited to semi-conductors), organic polymers (e.g., cellulosic paper, polymeric membranes, and the like), inorganic polymers (e.g., membranes), micaceous minerals, quartzes, plastics, glasses, metals and metal alloys (such as, copper, platinum, palladium, nickel, cobalt, rhodium, iridium, gold, silver, titanium, and aluminum), and combinations or composites thereof. More preferred solid materials are fabricated from or comprise quartz, glass, paper, gold, silver, titanium, aluminum, copper, nickel, silicon, or organic polymer. Even more preferably, the substrate is a microscope glass slide (e.g., CorningTM, Corning, N.Y.), silicon wafer, or quartz.

The substrate can have any three-dimensional geometric shape. Preferably, the substrate is substantially a flat plane or approximates one of a sphere, cylinder, capillary, or wire. While the method is described with reference to a multiple format substrate, such as a microarray, it is to be understood that it can be applied to a single format substrate, such as a nanoparticle.

Each type of glycan is contacted or printed onto to the solid support at a defined glycan probe location. Suitable printing methods include piezo or pin printing techniques. A microarray gene printer can be used for applying the various

glycans to defined glycan probe locations. The printing process is shown diagrammatically in FIG. 3. Printing in the X direction gives rise "columns" of glycans and printing in the direction orthogonal to the X direction gives rise to "rows." During printing, the inkjet is generally stationary, and a stepping stage moves the glass slide or other solid surface over the head in the X direction. As the wafer passes over the head, it prints the appropriate glycan to each glycan probe location. Several nozzles simultaneously dispense a selected amount of glycan solution.

For example, about 0.1 nL to about 10 nL, or about 0.5 nL of glycan solution can be applied per defined glycan probe location. Various concentrations of the glycan solutions can be contacted or printed onto the solid support. For example, a glycan solution of about 0.1 to about 1000 μ M glycan or about 1.0 to about 500 μ M glycan or about 10 to about 100 μ M glycan can be employed. In general, it may be advisable to apply each concentration to a replicate of several (for example, three to six) defined glycan probe locations. Such replicates provide internal controls that confirm whether or not a binding reaction between a glycan and a test molecule is an actual binding interaction.

An "addressable substrate" used in a method of the invention can be any surface capable of having glycans bound thereto. Such surfaces include, but are not limited to, glass, metal, plastic, or materials coated with a functional group designed for binding of glycans. The coating may be thicker than a monomolecular layer; in fact, the coating could involve porous materials of sufficient thickness to generate a porous 3-dimensional structure into which the glycans can diffuse and bind to the internal surfaces.

Influenza Virus Detection

The invention provides methods of detecting viral infection, for example, influenza infection. The method involves contacting a test sample from a patient with a library or array of glycans and observing whether virus, or viral antigens present in the test sample are reactive with the array. The presence of such viral antigens and viral particles can be detected by detecting their binding to glycans that have been determined to previously bind those viral antigens and viral particles. Hence, the glycans to which the viral antigens or viruses bind indicate whether an infection is present. Such glycans can be viral-specific glycan epitopes or viral binding sites that are present on host cells. One of skill in the art can readily prepare glycan arrays for screening for viral infection using the teachings provided herein.

The affinity interaction of the glycan molecules to the influenza virus or fragments or peptides thereof can be measured by optical (UV-Vis), fluorescence, surface-enhanced fluorescence, surface plasmon resonance, surface-enhanced Raman scattering microscopy, or electrochemical and chemiluminescent techniques. Commonly, the detection method is direct immunoassay, sandwich immunoassay with a labeling or unlabeled approach. To enhance the sensitivity and specificity of the assay a sandwich assay is used.

The glycosylation of viral proteins is generally performed by host cell, rather than viral, enzymes. Given that many viral genomes are so mutable, the glycosylation of viral proteins by host enzymes likely gives rise to antigenic epitopes that are more stable than the epitopes generated by translation of easily mutated viral nucleic acids. Hence, virally-associated glycans may form the basis of improved compositions, including vaccines, for inhibiting and treating viral infection.

Influenza virus hemagglutinin binds to Neu5Aca2-3-linked to galactosides, but not to any Neu5Aca2-6- or

Neu5Aca2-8-linked sialosides. Intact influenza viruses, such as H1N1/Brisbane, H1N1/swine, H3N1/Brisbane and H5N1/Vietnam, also bind the array and show specificity for both α 2-3 and α 2-6 sialosides. (FIG. 5) Influenza viruses also bind Neu5Aca2-3- and Neu5Aca2-6-linked to galactosides as well as certain O-linked sialosides.

The term "capture probe" refers to a glycan immobilized on an addressable substrate. Target analytes such as proteins, polypeptides, fragments, variants, and derivatives of influenza virus also may be used to prepare antibodies using methods known in the art. Thus, antibodies and antibody fragments that bind to target analytes may be used in sandwich assays after the influenza virus or protein or fragment thereof is captured on a substrate. Antibodies may be polyclonal, monospecific polyclonal, monoclonal, recombinant, chimeric, humanized, fully human, single chain and/or bispecific.

Polyclonal antibodies directed toward a target analyte generally are raised in animals (e.g., rabbits or mice) by multiple subcutaneous or intraperitoneal injections of the polypeptide and an adjuvant. It may be useful to conjugate a target analyte protein, polypeptide, or a variant, fragment or derivative thereof to a carrier protein that is immunogenic in the species to be immunized, such as keyhole limpet heocyanin, serum, albumin, bovine thyroglobulin, or soybean trypsin inhibitor. Also, aggregating agents such as alum are used to enhance the immune response. The preparation of polyclonal antibodies is well-known to those skilled in the art (Green et al., *Production of Polyclonal Antisera*, in *Immunochemical Protocols* (Manson, ed.), pages 1-5 (Humana Press 1992); Coligan et al., *Production of Polyclonal Antisera in Rabbits, Rats, Mice and Hamsters*, in *Current Protocols in Immunology*, section 2.4.1 (1992), which are hereby incorporated by reference). For example, an HA or HA mixture is injected into an animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animal is bled periodically. Polyclonal antibodies specific for a glycan or glycan fragment may then be purified from such antisera by, for example, affinity chromatography using the glycan coupled to a suitable solid support.

Monoclonal antibodies directed toward target analytes are produced using any method that provides for the production of antibody molecules by continuous cell lines in culture. The preparation of monoclonal antibodies likewise is conventional (Kohler & Milstein, *Nature*, 256:495 (1975); Coligan et al., sections 2.5.1-2.6.7; and Harlow et al., *Antibodies: A Laboratory Manual*, page 726 (Cold Spring Harbor Pub. 1988)), which are hereby incorporated by reference. Briefly, monoclonal antibodies can be obtained by injecting mice with a composition comprising an antigen (HA), verifying the presence of antibody production by removing a serum sample, removing the spleen to obtain B lymphocytes, fusing the B lymphocytes with myeloma cells to produce hybridomas, cloning the hybridomas, selecting positive clones that produce antibodies to the antigen, and isolating the antibodies from the hybridoma cultures. Monoclonal antibodies can be isolated and purified from hybridoma cultures by a variety of well-established techniques. Such isolation techniques include affinity chromatography with Protein-A Sepharose, size-exclusion chromatography, and ion-exchange chromatography (Coligan et al., sections 2.7.1-2.7.12 and sections 2.9.1-2.9.3; Barnes et al., *Purification of Immunoglobulin G (IgG)*, in *Methods in Molecular Biology*, Vol. 10, pages 79-104 (Humana Press

1992)). Methods of in vitro and in vivo multiplication of monoclonal antibodies are available to those skilled in the art.

The antibodies may be employed in direct and indirect sandwich assays (Sola, *Monoclonal Antibodies: A Manual of Techniques* 147-58 (CRC Press 1987)) for detection and quantitation of the target viruses.

Sandwich assays generally involve the use of antibodies capable of binding to an immunogenic portion, or epitope, of the protein to be detected and/or quantitated. In a sandwich assay, the test sample analyte is typically bound by a glycan which is immobilized on a solid support, and thereafter an antibody binds to the analyte, thus forming an insoluble three part complex. See, e.g., U.S. Pat. No. 4,376,110. The second antibody may itself be labeled with a detectable moiety (direct sandwich assays) or may be measured using an anti-immunoglobulin antibody that is labeled with a detectable moiety (indirect sandwich assays). For example, one type of sandwich assay is an ELISA assay, in which case the detectable moiety is an enzyme.

Antibodies can also be prepared through use of phage display techniques. In one example, a subject is immunized with an antigen, such as influenza serotypes. Lymphocytes are isolated from the spleen of the immunized subject. Total RNA is isolated from the splenocytes and mRNA contained within the total RNA is reverse transcribed into complementary deoxyribonucleic acid (cDNA). The cDNA encoding the variable regions of the light and heavy chains of the immunoglobulin is amplified by polymerase chain reaction (PCR). To generate a single chain fragment variable (scFv) antibody, the light and heavy chain amplification products may be linked by splice overlap extension PCR to generate a complete sequence and ligated into a suitable vector. *E. coli* are then transformed with the vector encoding the scFv, and are infected with helper phage, to produce phage particles that display the antibody on their surface. Alternatively, to generate a complete antigen binding fragment (Fab), the heavy chain amplification product can be fused with a nucleic acid sequence encoding a phage coat protein, and the light chain amplification product can be cloned into a suitable vector. *E. coli* expressing the heavy chain fused to a phage coat protein is transformed with the vector encoding the light chain amplification product. The disulfide linkage between the light and heavy chains is established in the periplasm of *E. coli*. The result of this procedure is to produce an antibody library with up to 10^9 clones. The size of the library can be increased to 10^{18} phage by later addition of the immune responses of additional immunized organisms that may be from the same or different hosts. Antibodies that recognize a specific antigen can be selected through panning. Briefly, an entire antibody library can be exposed to an immobilized antigen against which antibodies are desired. Phage that do not express an antibody that binds to the antigen are washed away. Phage that express the desired antibodies are immobilized on the antigen. The phage are then eluted and again amplified in *E. coli*. This process can be repeated to enrich the population of phage that expresses antibodies that specifically bind to the antigen. After phage are isolated that express an antibody that binds to an antigen, a vector containing the coding sequences for the antibody can be isolated from the phage particles and the coding sequences can be recloned into a suitable vector to produce an antibody in soluble form. In another example, a human phage library can be used to select for antibodies, such as monoclonal antibodies, that bind to specific influenza serotypes. These methods may be used to obtain human monoclonal antibodies that bind to specific influenza serotypes.

Phage display methods to isolate antigens and antibodies are known in the art and have been described (Gram et al., *Proc. Natl. Acad. Sci.*, 89:3576 (1992); Kay et al., *Phage display of peptides and proteins: A laboratory manual*. San Diego: Academic Press (1996); Kermani et al., *Hybrid*, 14:323 (1995); Schmitz et al., *Placenta*, 21 Suppl. A:S106 (2000); Sanna et al., *Proc. Natl. Acad. Sci.*, 92:6439 (1995)). Gold Nanoparticle—Phage Conjugation & Gold Nanoparticle-Neuraminidase Inhibitor Conjugation for Designing Nanoparticles Probes

There are two strategies for making nanoparticle-based probes in influenza virus subtype detection: one is attempting to target neuraminidase (NA) using a gold nanoparticle complex comprising a neuraminidase binding agent, such as a neuraminidase inhibitor. Second is applying phage technique to construct phage-gold nanoparticle complex which can specifically target hemagglutinin subtypes (HA).

Neuraminidase inhibitors are a class of antiviral drugs targeted at the influenza virus, which work by blocking the function of the viral neuraminidase protein, thus preventing the virus from reproducing by budding from the host cell. Oseltamivir (Tamiflu®) a prodrug, Zanamivir (Relenza®), Laninamivir (Inavir®), and Peramivir belong to this class. Unlike the M2 inhibitors, which work only against the influenza A, neuraminidase inhibitors act against both influenza A and influenza B. Relenza® (or Zanamivir) is a neuraminidase inhibitor used in the treatment of influenza caused by influenza A virus and influenza B virus. Gold nanoparticles were conjugated with modified relenza service as a universal probe for influenza virus detection. The Relenza-Au probes have advantages in detecting a new strain of influenza or co-infection of two strains of influenza viruses. Another approach is fabricating a hemagglutinin probe consisting of bacteriophage (phage) assembled with gold (Au) nanoparticles. HA subtype specific binding phages were affinity selected through biopanning. Phage antibodies with higher affinity may be enriched during successive rounds of selection by decreasing the concentration of antigen. Four different high affinity HA-specific phages were named as MG4B for Cal/09 H1N1, CW2B for Brisbane H1N1, 12a for Brisbane H3N2 and 8a for RG14 H5N1, respectively. The selected phages, which carry up to 4000 analyte-binding domains on its surface, can be used to conjugate gold nanoparticles. The assembly of Au nanoparticles onto phage occurs without modification of the pVIII major capsid proteins or complex conjugation chemistry. Au nanoparticles appear as black dots connecting long, white, filamentous phage structures. Once assembled, the phage in these networks still maintained their ability to target HA. Furthermore, these phages were dramatically more effective and sensitivity for the visualization of binding to influenza virus in glycan array dot blot assays. Due to the HA specificity of phages, a sialoside-phage sandwich assay give more specificity in influenza serotype identification.

The modified nanoparticle probes for in situ virus quantification can provide rapid and inexpensive diagnostics for detection and characterization of influenza viruses. One of the most notable aspects about this nanoparticle-based detection method is that it requires nothing more than naked eye to read the results.

Nanoparticle-Based Detection

A nanoparticle-based detection for glycan arrays was developed by Liang et al. who synthesized iron oxide/gold core/shell nanoparticles conjugated with antibodies or proteins (Liang C H et al. *Anal. Chem.* 2009; 81, 7750-7756). Iron oxide/gold core/shell nanoparticles unite the ability of magnetic property for enrichment, surface modification, and

signal enhancement in a single entity. This powerful combination enables researchers to quickly concentrate viruses by an external magnetic field, easily conjugate biomolecules on gold surface, and amplify signal by depositing silver on gold surface of core/shell nanoparticles. The nanoparticle-based assay can reach sub-attomole detection level and has clear advantages in screening different types of viruses.

Nanoparticles have been recently introduced for detecting DNA microarray hybridization. DNA probes are synthesized on gold nanoparticles and hybridized with DNA on glass surface. The sensitivity of the gold labeling method is almost equal to that of fluorescent labeling (Cao, Y. C.; Jin, R.; Mirkin, C. A. *Science*, 2002, 289, 1757-60; T. A. Taton, C. A. Mirkin, R. L. Letsinger, *Science* 289 (2000) 1757-1760). Silver enhancement is usually pursued to amplify the signal.

Particles may be of any suitable size including nanoparticles and micro-sized particles, 1 μm or less in diameter, and may be made of any suitable material such as polymers (e.g., polystyrene), metals (e.g., gold or silver), ceramics, semiconductor material. Methods of making metal, semiconductor and magnetic nanoparticles are well-known in the art. See, e.g., Schmid, G. (ed.) *Clusters and Colloids* (V C H, Weinheim, 1994); Hayat, M. A. (ed.) *Colloidal Gold: Principles, Methods, and Applications* (Academic Press, San Diego, 1991); Massart, R., *IEEE Transactions On Magnetism*, 17, 1247 (1981); Ahmadi, T. S. et al., *Science*, 272, 1924 (1996); Henglein, A. et al., *J. Phys. Chem.*, 99, 14129 (1995); Curtis, A. C., et al., *Angew. Chem. Int. Ed. Engl.*, 27, 1530 (1988). Suitable gold nanoparticles are commercially available from, e.g., Ted Pella, Inc. (gold), Amersham Corporation (gold), Nanoprobes, Inc. (gold).

Sandwich assays generally involve the use of two antibodies, each capable of binding to a different immunogenic portion, or epitope, of the protein to be detected and/or quantitated. In a sandwich assay, the test sample analyte is typically bound by a first antibody which is immobilized on a solid support, and thereafter a second antibody binds to the analyte, thus forming an insoluble three part complex. See, e.g., U.S. Pat. No. 4,376,110. The second antibody may itself be labeled with a detectable moiety (direct sandwich assays) or may be measured using an anti-immunoglobulin antibody that is labeled with a detectable moiety (indirect sandwich assays). For example, one type of sandwich assay is an ELISA assay, in which case the detectable moiety is an enzyme.

The present invention provides a modified sandwich assay in which the first antibody is replaced with influenza serotype specific glycans immobilized on an array. FIG. 3 illustrates a representative sandwich assay involving a glycan array having capture glycan probes, a detection probe having a detector phage having an antibody fragment specific for an influenza serotype labeled with a detection moiety (e.g., gold), and a target analyte (influenza virus) sandwiched between the capture probe and detector probe.

Methods for preparing gold nanoparticle probes have led to the development of a colorimetric sensing scheme for oligonucleotides and non-nucleic acid targets. See, for instance, U.S. Pat. No. 6,506,564, which describes a colorimetric sensing scheme based on DNA-modified nanoparticles. This method is based on the hybridization of two gold nanoparticle probes to two distinct regions of a target of interest. The binding of the target results in the formation of target/gold nanoparticle probe aggregate when sufficient target is present. The target recognition results in a colorimetric transition due to the decrease in inter-particle distance between the particles. This colorimetric change can be monitored optically, with a UV-visible spectrophotometer,

or visually with the naked eye. In addition, the color is intensified when the solutions are concentrated onto a membrane. Therefore, a simple colorimetric transition provides evidence for the presence or absence of a specific target.

As described herein, nanoparticle probes, particularly gold nanoparticle probes comprising phage particles, are surprising and unexpectedly suited for detection of influenza serotypes on glycan arrays. A silver-based signal amplification procedure in a microarray-based assay can further provide ultra-high sensitivity enhancement. Silver staining can be employed with any type of nanoparticles that catalyze the reduction of silver. Preferred are nanoparticles made of noble metals (e.g., gold and silver). (See Bassell, et al., *J. Cell Biol.*, 126, 863-876 (1994); Braun-Howland et al., *Biotechniques*, 13, 928-931 (1992)). Silver staining can be used to produce or enhance a detectable change in any assay performed on a substrate, including those described above. In particular, silver staining has been found to provide a huge increase in sensitivity for assays employing a single type of nanoparticle so that the use of layers of nanoparticles, aggregate probes and core probes can often be eliminated.

A nanoparticle can be detected in a method of the invention, for example, using an optical or flatbed scanner. The scanner can be linked to a computer loaded with software capable of calculating grayscale measurements, and the grayscale measurements are calculated to provide a quantitative measure of the amount of analyte detected.

Suitable scanners include those used to scan documents into a computer which are capable of operating in the reflective mode (e.g., a flatbed scanner), other devices capable of performing this function or which utilize the same type of optics, any type of grayscale-sensitive measurement device, and standard scanners which have been modified to scan substrates according to the invention.

The software can also provide a color number for colored spots and can generate images (e.g., printouts) of the scans, which can be reviewed to provide a qualitative determination of the presence of an influenza virus serotype, the quantity of an influenza virus serotype, or both. In addition, it has been found that the sensitivity of assays can be increased by subtracting the color that represents a negative result from the color that represents a positive result.

The computer can be a standard personal computer, which is readily available commercially. Thus, the use of a standard scanner linked to a standard computer loaded with standard software can provide a convenient, easy, inexpensive means of detecting and quantitating an influenza virus serotypes when the assays are performed on substrates. The scans can also be stored in the computer to maintain a record of the results for further reference or use. Of course, more sophisticated instruments and software can be used, if desired.

A nanoparticle can be detected in a method of the invention, for example, using resonance light scattering, after illumination by various methods including dark-field microscopy, evanescent waveguides, or planar illumination of glass substrates. Metal particles >40 nm diameter scatter light of a specific color at the surface plasmon resonance frequency (Yguerabide, J.; Yguerabide, E. E. *Anal. Biochem.* (1998), 262, 157-176) and can be used for multicolor labeling on substrates by controlling particle size, shape, and chemical composition (Taton, T. A.; Lu, G.; Mirkin, C. A. *J. Am. Chem. Soc.* (2001), 123, 5164-5165; Jin, R. C.; Cao, Y. W.; Mirkin, C. A.; Kelly, K. L.; Schatz, G. C.; Zheng, J. G. *Science* (2001), 294, 1901-1903) In another embodiment, a nanoparticle can be detected in a method of the invention, for example, using surface enhanced raman spectroscopy

(SERS) in either a homogeneous solution based on nanoparticle aggregation (Graham and coworkers, *Angew. Chem.*, 2000, 112, 1103) or on substrates in a solid-phase assay (Porter and coworkers, *Anal. Chem.*, 1999, 71, 4903-4908), or using silver development followed by SERS (Mirkin and coworkers, *Science*, 2002, 297, 1536-1540).

In another embodiment, the nanoparticles of the invention are detected by photothermal imaging (Boyer et. al, *Science*, 2002, 297, 1160-1163). In another embodiment, the nanoparticles of the invention are detected by diffraction-based sensing technology (Bailey et. al, *J. Am Chem. Soc.*, 2003, 125, 13541). In another embodiment, the nanoparticles of the invention are detected by hyper-Rayleigh scattering (Kim et. al, *Chem Phys. Lett.*, 2002, 352, 421).

With the use of nanobiotechnology, a nanoparticle-based assay for in situ virus quantification is provided which can provide rapid diagnostics for detection and characterization of viruses. It can tell the subtypes of influenza A such as H1N1/Brisbane, H1N1/swine, H3N1/Brisbane, and H5N1/Vietnam. The method is inexpensive and easily reproducible and requires no advanced specialized training.

An exemplary sequence of steps according to the invention is shown in FIG. 1.

Step 1: sample collection. A typical animal or avian sample comprises a nasopharyngeal aspirate, blood, saliva, or any other bodily fluid to be tested. In addition, a sample can be obtained from a mammal, such as a human, or a bird. In the case of pandemic influenza A (H1N1) virus 2009 detection, a nasopharyngeal swab or saliva is the preferred specimen.

Step 2: sample loading. An assay or array is composed of naturally occurring or synthetic oligosaccharides (glycans). Glycans can be immobilized on a glass slide or other templates. A nasal aspirate fluid, pharyngeal swab fluid or saliva (collected from step 1) is incubated on the glass surface or other templates. At this step, glycans with different structures can target hemagglutinin specific to H5N1, H3N1, and H1N1 serotypes for influenza virus detection.

Step 3: signal development. The amplification and detection is based on the gold-phage technique. Gold nanoparticle-phage probe (nanoparticle agent specific for an influenza virus serotype) is introduced to incubate with virus immobilized on the glass slide surface or other assay template. The nanoparticle amplification method used in an assay can be gold nanoparticle or gold-phage complex and optionally, other types of nanoparticles, such as silver nanoparticles. Gold nanoparticles have an increased detectable signal upon hybridizing to phage. An assay for an amplification target containing variations may use one detection probe for all variations, a single Au-phage probe for one variant, or multiple Au-phages probes, one for each variant. In addition, silver reagent can be applied to further amplify the signal (optional).

Step 4: read out. Results, such as Influenza serotypes, can be observed by naked eyes, barcode scanner or laser pen on glass slides and classify by fingerprint patterns on glycan array.

A sensitive glycan array using gold nanoparticle-phage probe was developed. When coupled with a signal amplification method based on nanoparticle-promoted reduction of silver, the sensitivity of Au phage assay reached higher sensitivity in virus detection. This technique is suitable for rapid screening, is easy to operate, and signals generated can be read by naked eye. The experimental procedure is shown in FIG. 3.

First, glycans were immobilized on a glass slide. A nasal aspirate fluid or pharyngeal swab fluid was incubated on the

glass surface. Glycans with different structures can target hemagglutinin specific to H5N1, H3N1, and H1N1 serotypes. In the next step, nanoparticle-phage complex were introduced. Silver reagent was then applied to amplify the signal (this step is optional). In the last steps, Influenza A serotypes can be observed by naked eyes on glass slides and classified by patterns on glycan array.

The fingerprint read-out information from small-scale glycan assay is important to the development of a successful influenza diagnostic product. On main reason is that the time to produce a H1N1 specific diagnosis using the current serological methods or molecular biology methods is too long for effective use during this pandemic. As we known, rapid diagnosis of pandemic virus, especially at the beginning of a new community outbreak or for unusual cases, has important implications for case management. Assays described here provide a simple, rapid and cost effective method for influenza virus subtype detection and hence, ought to be implemented for large-scale detection aimed at controlling influenza virus outbreaks. This influenza diagnostic assay can also be rapidly adapted to identify a new strain of virus while still keeping the current identifications through the simple measure of establishing and validating a new read-out pattern/fingerprint for the emerging threat. In addition, this test will be in a simple slide format that can give a quick test result in order to save both time and money. Importantly, it also has great potential in evaluating the flu vaccination response to individuals.

Specificity of Gold Nanoparticle Based Small Scale Glycan Array (GNBSSGA) for Distinguishing Virus Types

The first step in proper prevention and treatment of disease is accurate diagnosis. Several rapid influenza diagnostic tests (including so-called "point-of-care" diagnostic tests) are commercially available. However, studies indicate that rapid diagnostic tests miss many infections with pandemic (H1N1) virus and therefore negative results cannot rule out disease and should not be used as grounds to withhold therapy or lift infection control measures. In addition, co-circulation of current seasonal human H1N1, H3N2, and Swine-Origin Influenza (S-OIV) A (H1N1) viruses poses a challenge for sub-typing individual strains and potential reassortants. The rapidly evolving nature of the influenza virus will continue to pose tremendous threat to public health. Since gold nanoparticle based small scale glycan array (GNBSSGA) is able to distinguish influenza serotype by their fingerprint patterns, a unique fingerprint pattern occurs when co-infection or re-assortment of two strains of influenza viruses occurs. The GNBSSGA is able to be rapidly adapted to identify co-infection or new strains of influenza.

Rapid detection and classifying of influenza virus and identification of its various strains is critical to identification and control of a potential human pandemic. The present invention provides multiple levels of identification—the first level classifies the virus and alerts the user to the presence of pandemic threat viruses and the second level precisely identifies the pathogen. The fingerprint read-out information from glycan assay is critical to the development of a successful seasonal and pandemic influenza diagnostic product for two main reasons. First, the time to produce an H1N1 specific quick test using the current technologies and methods is too long for effective use during this pandemic. Second, the next pandemic flu will almost certainly be a new or modified influenza strain (HxNy), making any of the current quick test diagnostics that might be directed to a particular flu sub-type obsolete or marginally effective, or both. The influenza triage diagnostic assay can be rapidly

adapted to identify the new strain of virus while still keeping the current identifications through the simple measure of establishing and validating a new read-out pattern/fingerprint for the emerging threat. Further, the technology and its application is not limited to the detection of the H1N1 virus or even new virus. This technology can be quickly and effectively applied to detect any pandemic virus or biological agent.

EXAMPLES

Without intent to limit the scope of the invention, exemplary instruments, apparatus, methods and their related results according to the embodiments of the present invention are given below. Note that titles or subtitles may be used in the examples for convenience of a reader, which in no way should limit the scope of the invention. Moreover, certain theories are proposed and disclosed herein; however, in no way they, whether they are right or wrong, should limit the scope of the invention so long as the invention is practiced according to the invention without regard for any particular theory or scheme of action.

Example 1: Glycan Synthesis

All oligosaccharides were prepared using synthetic procedures as described (Hsu, C.-H. et al. Chem. Eur. J. 2010, 16, 1754-1760; Hasegawa A, et al. Carbohydr. Res. 1995, 274, 165-181; Komba S, et al. Bioorg. Med. Chem. 1996, 4, 1833-1847; Otsubo N, et al. Carbohydr. Res. 1998, 306, 517-530; Yoshida M, et al. Glycoconjugate J. 1993, 10, 324). The synthetic oligosaccharides were further modified to cross-link to glass surface for the preparation of "glycan arrays" as described below.

Example 2: Virus Preparation

Samples of various viruses are collected from the Center for Disease Control and Prevention in TAIWAN, and provided by Dr. Jia-Tsong Jan (Genomic Research Center, Academia Sinica, Taiwan). All viruses were propagated in 10-day-old embryonated specific-pathogen free chicken eggs. Purified viruses were done by centrifugation at 100,000 g for 30 min and resuspended in PBS. Differences in the degree of virus purity did not influence significantly the pattern of receptor binding. Virus were inactivated by treatment with β -propiolactone (BPL; 0.05% v/v) for 60 minutes at 33° C., and resuspended in 0.01 M phosphate buffered saline pH 7.4 (PBS) and stored at -80° C. Comparison of samples of live and inactivated virus showed that BPL inactivation did not alter receptor binding specificity (Matrosovich M, et al. J. Virol. 1999, 73, 1146-1155.)

Example 3: Glycan Array Fabrication

Amino-reactive N-hydroxysuccinimide (NHS)-activated glass microscope slides were used to fabricate glycan arrays by the standard protocol of Protein Application Nexterion Slide H. The NHS groups on the glass surface react readily with the primary amines of the amino modified glycans to form an amide linkage. Amine-modified glycans with desired concentration were dissolved in printing buffer (pH 8.5, 300 mM phosphate buffer with 0.005% (v/v) Tween 20) and were spotted on the glass microscope slides by robotic pin (BioDot, Cartesian Technologies; SMP3, Telechem International) deposition. Print slides were incubated under 80% humidity at 37° C. for 2 h followed by desiccation

overnight. Before the binding assay, print slides were immersed with blocking buffer (50 mM ethanolamine in 50 mM borate buffer, pH 9.2) at room temperature for 1 h to remove remaining free NHS groups and then washed with washing buffer (PBST; 50 mM PBS buffer with 0.05% (v/v) Tween 20, pH 7.4) and DI water several times. These slides were dried by argon flow and stored at room temperature in a vacuum desiccator until use (Liang C H, et al. Anal. Chem. 2009; 81, 7750-7756).

Example 4: Phage Display

Phage display is a well-known technique utilized for the selection of antibodies that bind to a desired target. Phage-displayed antibody fragments can offer an advantage over the solubly expressed fragments for use as reporter elements in immunoassays. Herein, samples of phages were home-made by Dr. An-Suei Yang (Genomic Research Center, Academia Sinica, Taiwan). Specific Influenza serotype antibodies are displayed on the surface of phage. This was achieved by fusing the coding sequence of the antibody variable (V) regions encoding a single-chain Fv (scFv) or single domain antibodies to the N-terminus of the phage coat protein pIII using a phage vector based on the genome of fd-tet. The scFv sequence was cloned in frame with gene III and downstream of the gene III signal sequence, which normally directs export of the adsorption protein. For display of the Ab-pIII product, limited expression must be triggered, and the fusion must be incorporated into phage carrying the phagemid sequence. The former can be achieved by relieving catabolite repression (including glucose in the culture medium by addition of an extra transcriptional terminator or use of the phage shock promoter), the latter by using the phage packaging signal also carried on the phagemid and a helper phage, such as VCSM13, which supplies all structural proteins. Since the helper phage genome encodes wild-type pIII, typically over 90% of rescued phage displays have no Ab at all, and the vast majority of the rescued phage particles that do display the fusion product will only contain a single copy. This monovalent display is essential when selecting Abs of higher affinity.

Example 5: Gold Nanoparticle-Phage Conjugation

Gold-conjugated phages, obtained by coupling of gold particles to the proteins of the phage wall are used. Insertless phage (fd-tet) and phage displaying the targeting peptide on the surface of its pIII protein were amplified in host bacteria and purified. The Au nanoparticle solution was prepared following the citrate reduction procedure (Frens G. Nature Phys. Sci. 1973, 241, 20-22). Assembly of Au-phage complexes began with 10^7 transducing units (TU) of phage. 25 μ L HS-CH₂-COOH and 1 μ L HS-C₂H₄-COOH and 1 μ L HS-(CH₂)₁₀-COOH were added into the solution with slight shaking overnight. The deepened color of the solution was indicative of the modification of the nanoparticle's surface. The result solution was added to phage and allowed to stand for 1 h at room temperature. Finally, the Au-phage complex was purified by centrifugation and ready to use (FIG. 4). The gold-phage probes preserve the virus surface receptor binding and can effectively integrate the unique signal reporting properties of Au nanoparticles. The use of gold-phage-displayed signal domain antibody gives more sensitive detection.

Example 6: Glycan Array Prescreening—Binding Profiles of Influenza Viruses

Before conducting the design of naked-eye detection of influenza virus subtypes by monitoring the scanometric fingerprints on glycan array, the sialoside receptor-binding characteristics of four isolates of the influenza virus, including Cal/09 H1N1, Brisbane H1N1, Brisbane H3N2, and RG14 H5N1 were compared. Twenty nine sialosides including nineteen (2→3 linked) and ten (2→6 linked) glyicans, have been synthesized to construe a sialoside microarray on glass slides (FIG. 7) and used to profile the binding specificity of different influenza hemagglutinins. The structures of these sialosides are sialyl-terminating oligosaccharides with differing backbone types, chain lengths and branching patterns, also various sialylation, fucosylation and sulfation patterns.

A clear distinction among the receptor binding repertoire of the Cal/09 H1N1, Brisbane H1N1, Brisbane H3N2, and RG14 H5N1 was observed (FIG. 8). The Cal/09 H1N1 and Brisbane H1N1 viruses bound not only to the majority of α 2,6 linked sialyl sequences but also to a considerable range of α 2,3 linked sialyl sequences. They share similar binding profiles yet differential binding affinities towards α 2,6 sialosides bearing various lengths of sugars. The broader specificity, namely, the ability to bind to α 2,3 in addition to α 2,6 linked receptors was also pertinent to the greater virulence of the pandemic virus, and its capacity to cause severe and fatal disease in humans. In contrast, RG14 H5N1 bound exclusively to α 2,3 linked sialyl sequences. The Brisbane H3N2 influenza viruses showed a preferential binding to α 2,6 linked and α 2,3 linked sialyl sequences with strongest binding toward glycan no. 28 and glycan no. 30. Binding to α 2,3 linked receptors is thought to be associated with the ability of influenza viruses to infect the lower respiratory tract where there is a greater proportion of α 2,3 vs α 2,6 linked sialyl glyicans. After comparing to the binding profiles of testing the four influenza viruses (Cal/09 H1N1, Brisbane H1N1, Brisbane H3N2, and RG14 H5N1), a minimum set of nine sialosides containing 8, 9, 19, 22, 23, 24, 25, 27, 30 was suggested to be useful for classifying the serotype of influenza viruses.

Example 7: Fingerprints of Each Influenza Virus Subtype—Differential Receptor Binding of Influenza Viruses

Minimum numbers of glyicans needed to provide a convenient and efficient profiling system to differentiate influenza virus subtypes were determined. According to the previous screening results obtained from glycan array, we constructed a small-scale glycan array in α 3×3 matrix format. A set of nine sialosides: 8, 9, 19, 22, 23, 24, 25, 27 and 30 were immobilized on the glass slide and used to capture virus particles. Glycans with different structures can target HA specific to Cal/09 H1N1, Brisbane H1N1, Brisbane H3N2 and RG14 H5N1. After influenza virus incubation, anti-HA antibodies, Relenza-Au (targeting NA), or phage-Au complex (targeting HA) were subsequently added to glass slide for virus stain (FIG. 3A). The patterns of glycan array for each influenza serotype were predicted as their characteristic fingerprint shown in FIG. 3B. Results of small-scale glycan array show that influenza A serotypes can be observed by naked eyes in the case of Relenza-Au and phage-Au and distinguishable by their fingerprint patterns.

Identical experiments were further confirmed by fluorophore assay using anti-HA antibody.

Example 8: Screening Result for Single Virus

To demonstrate the feasibility of the method, a glycan array in α 2×2 matrix format was constructed. A and B spots were immobilized with α 2-3 glyicans as positive signal for H5N1 screening (FIG. 6). C and D spots were immobilized with α 2-6 glyicans as negative control. After H5N1 virus incubation, gold-phage agent was added to slide for virus stain. A dark-round signal was shown up within a min and observed by naked eye. An identical experiment was further confirmed by fluorophore assay.

Example 9: Specificity of Gold Nanoparticle Based Small Scale Glycan Array (GNBSSGA) for Distinguishing Virus Types

To assess the accuracy of visual inspection provided by GNBSSGA, RG14 H5N1 and HK/415742 were mixed as a co-infection sample. The effectiveness of GNBSSGA & Fluorophore A&B tests as influenza serotype indicators were compared and to see if they readily distinguished between seasonal influenza virus. Experimental results demonstrated that we were able to identify co-infection viruses with fingerprint patterns through the nanoparticle-based analysis on the glycan array. (FIG. 10) On the contrary, Flu A&B tests detect influenza type A viruses but do not discriminate between virus subtypes. Therefore, a positive result in any of these Flu A&B tests in a patient suspected of type A flu must be further subtyped.

Determination of GNBSSGA Detection Limit:

The pandemic outbreak has highlighted the need for a rapid influenza diagnostic test to facilitate early treatment of infected individuals because treatment has been beneficial only when antiviral drugs are administered within 48 hours of the appearance of symptoms. Rapid and sensitivity influenza diagnostic tests can provide results in a clinically relevant time frame to assist clinical judgment. We therefore sought to compare the analytical sensitivity of GNBSSGA and commercially available influenza rapid tests for the detection of H5N1.

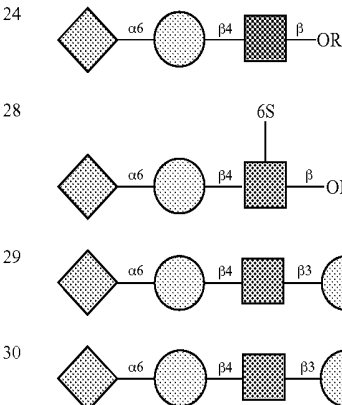
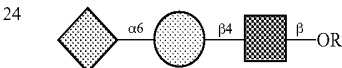
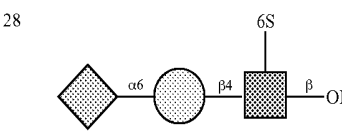
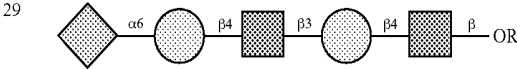
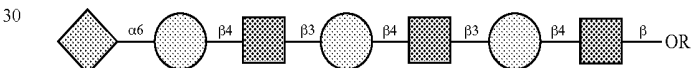
The evaluation of the detection limits of the GNBSSGA & commercial available QuickVue Influenza A+B test established with serial dilution of H5N1 indicated that the lowest detectable viral load of the H5N1 by the GNBSSGA, QuickVue test, and the analogous fluorophore system of small scale glycan array was 1E3, 1E6, and 1E5 particles/ml, respectively. Therefore, the GNBSSGA test was the most sensitive test in the present study for the detection of influenza virus. Since the GNBSSGA test can be completed rapidly and does not require extensive laboratory facilities, it may be helpful in the timely detection of influenza A virus infections. This suggests that the GNBSSGA test could be used to aid clinical decision making in primary health care settings during outbreaks of influenza.

Example 10: Differential Receptor Binding of HAs from Seasonal and Pandemic Influenza Viruses

Our ultimate goal is to differentiate influenza virus subtypes by only a specific set of glyicans. In this respect, recombinant HAs from the seasonal and pandemic viruses were examined with respect to their receptor binding specificity. The results of binding profiles for HAs from both pandemic H1N1 (California/07/2009) (FIG. 11A) and sea-

sonal H1N1 Brisbane/59/2007 (Br/59/07) (FIG. 11B) displayed similar pattern, with both higher binding activities toward longer α 2,6 sialosides. It was noticed that the maximum binding affinity of the 2009 pandemic H1 reached with α 2,6 sialoside containing 5 or 7 sugar units. Yet the H1 from Brisbane strains showed the highest binding affinity towards the α 2,6 sialoside containing 7 sugar units. The surface dissociation constant values (K_D , surf) were further determined using glycan microarray based on the Langmuir isotherms. (Liang, P. H. et al. *J. Amer. Chem. Sci.* 2007, 129, 11177-11184). The monovalent HA-sialoside binding is weak, exhibiting solution dissociation constants in the millimolar range ($K_D=2.5 \times 10^{-3}$ M) if competition based experiments were conducted. (Sauter, N. K. et al. *Biochemistry* 1989, 28, 8388-8396.) HA, however, is involved in multivalent interactions with sialosides on the host cell surface, which can be seen in the quantitative array profiling. (Wang, C. C. et al. *Proc. Natl. Acad. Sci. USA* 2009, 106, 18137-18142; Liang, P. H. et al. *J. Amer. Chem. Sci.* 2007, 129, 11177-11184). By the analysis of K_D , surf (Table 1) of both strains, the result revealed stronger binding capability of H1 from Br/59/07 than the H1 from 2009 pandemic strain toward α 2,6 sialosides, and this observation was also supported by the phenomena that Br/59/07 H1 showed a high binding affinity even when the protein was used as low as nM concentrations for sugars 29 and 30, making it difficult for the K_D determination.

TABLE 1

Sugar		K_D , surf of Hemagglutinin (nM)		
		Cal07(H1N1)	Br59 (H1N1)	Br10 (H3N2)
24		376 ± 40	233 ± 23	6350 ± 110
28		1307 ± 533	443 ± 156	2011 ± 746
29		383 ± 9	N.D.*	>10 ⁵
30		686 ± 230	N.D.*	836 ± 96

*High binding activities but no concentration-dependence was observed.

Compared to the earlier circulating strain H1N1/New Caledonia/1999 (NC/99) (FIG. 11C), it was shown that recent H1N1 strains showed strong binding affinities towards specific long α 2,6 sialosides such as 29 and 30, implying possibility that broader receptor specificity necessitate efficient transmission of influenza virus. On the other hand, the H3 from Brisbane/10/2007 (Br/10/07) showed a narrower binding profile towards only two α 2,6 sialosides, 28 and 30. The binding can be observed with sialoside 30, the glycan contains three repeats of LacNAc, but not 29 with two LacNAc repeats (FIG. 11D).

The same array was also used to profile the binding pattern of avian flu H5 (H5N1/Vietnam/1194/2004) (FIG. 11E), avian flu H7 (A/H7N7/Netherlands/219/03) (FIG. 11F), and human flu H9 (A/H9N2/Hong Kong/1073/99)

(FIG. 11G). As expected, the HAs from human and avian viruses showed respective binding profiles. The results also suggested that binding to 28 and 30 is unique to human viruses, but not avian viruses. Furthermore, H1 binds glycan 24 (FIGS. 11A-C) while H3 shows no binding (FIG. 11D), thereby providing diagnostic potential for the differentiation of H1 from H3. In addition, binding to the disaccharides 22 and 23 may imply strong foothold among human populations. These sugars, together with α 2,3-trisaccharides, can be used to differentiate HA subtypes and thus have the potential to provide a method of quick test upon emergence of an influenza outbreak.

Example 11: Binding Profiles of Real Viruses

In order to understand the relationship of real viruses and HA proteins toward sialosides binding, receptor-binding profiles of four isolates of the influenza virus by glycan array analysis were compared directly by using the same sialosides array. A clear distinction among the receptor-binding repertoire of the Cal/09 H1N1, Brisbane H1N1, Brisbane H3N1, and RG14 H5N1 was observed (FIG. 12). The Cal/09 H1N1 (FIG. 12A) and Brisbane H1N1 viruses (FIG. 12B) bound not only to the majority of α 2,6 linked sialyl sequences, but also to a considerable range of α 2,3 linked sialyl sequences. In contrast, H5N1 (FIG. 12D) bound exclusively to α 2,3 linked sialyl sequences. Similar to

recombinant H3 proteins, the H3N2 influenza viruses showed a preferential binding to α 2,6 linked and α 2,3 linked sialyl sequences with strongest binding towards 28 and 30 (FIG. 12C). Interestingly, influenza B showed a similar binding profile to both α 2,3 and α 2,6 sialosides (FIG. 12E). The broader specificity, namely, the ability to bind to α 2,3 in addition to α 2,6 linked receptors was also pertinent to the greater virulence of the pandemic virus, and its capacity to cause severe and fatal disease in humans. Binding to α 2,3 linked receptors is thought to be associated with the ability of influenza viruses to infect the lower respiratory tract where there is a greater proportion of α 2,3 vs α 2,6 linked sialyl glycans. Differences in receptor binding among the viruses may therefore formulate a good candidate for classifying the serotype of influenza viruses.

The binding preference of RG14 was the same as that of recombinant H5. In the case of H1N1 virus, the binding profile using the whole virus is slightly different from the profile obtained with recombinant proteins. Like recombinant HAs, viruses showed the strongest binding toward long α 2,6 sialosides. However, the viruses also showed significant binding to α 2,3 sialosides, which was unusual for recombinant HAs. The intrinsic binding affinity of sialosides for the hemagglutinin is dominated by polyvalent interactions at the cell surface. Therefore, weak monovalent binding may become significant in multivalent interactions, and protein presentation, such as HA orientation and density, on cell surface may have a major impact in receptor recognition. Furthermore, the tip of the globular region harbors the receptor-binding pocket, which is known to be crucial for the process of virus binding to its receptor. The orientation, quantity, and structure of N-glycans neighboring the receptor-binding pocket appear to be important regulators of receptor specificity, which may also cause the differences in binding preferences between recombinant HA and whole virus.

Example 12: Microarray Analysis of Sugar Binding Activities of Hemagglutinin

Microarrays were prepared by printing (AD3200, BioDot) the glycan with an amide tail to the NHS-activated glass slide (Nexterion H) by robotic pin (SMP2B, TeleChem International Inc.). Nexterion H slides were spotted with solutions of sugar 1-17 and 21-30 at 100 μ M from bottom to top with 12 replicates horizontally in each grid and dried under vacuum. The spotted slides were blocked with ethanolamine in sodium borate for 1 hour just before use followed with three washes of 0.05% Tween 20 in PBS buffer (pH 7.4) (PBST). A solution of hemagglutinin at 50 μ g/mL in PBST was pre-mixed with Cy3-labeled streptavidin in 1:1 molar ratio for 1 h prior to incubation of the preformed complexes with the slides for another hour. After six washes with PBST, one wash with PBS, and three washes with distilled water, the slides were air-dried and scanned with α 532 laser using a microarray fluorescence scanner (GenePix 4000B, Molecular Devices). The PMT gain was set to 600. The resulting images were analyzed with GenePix Pro 6.0 (Molecular Devices) to locate and quantify the fluorescence intensity of all of the spots on the grid. The median of fluorescence intensity of each spot was taken to calculate the median value of binding activities towards each sugar (12 replicates for each sugar). The medians from at least three independent experiments were averaged for the figures. For KD determination, the preformed complexes were serially diluted for binding reaction, (Srinivasan A., et al. *Proc. Natl. Acad. Sci. USA* 2008, 105, 2800-2805) and the binding intensities were quantified at various concentrations of complexes and fitted to the Langmuir isotherms using the Prism (GraphPad, San Diego, Calif.). (Liang, P. H. et al. *J. Am. Chem. Soc.* 2008, 130, 12348-12354).

Example 13: Virus Binding Assay Procedure

Influenza virus A/Vietnam/1194/2004 RG14 (H5N1), A/California/7/2009 (H1N1), A/Brisbane/10/2007 (H1N1) and A/Brisbane/10/2007 (H3N2) were from Taiwan CDC. Influenza virus B/Lee/40 was obtained from ATCC (Manassas, Va., USA) and propagated. Printed slides were analyzed without any further modification. Inactivated whole virus was applied at a concentration of about 10^7 virus/mL in PBS

buffer containing the neuraminidase inhibitor Oseltamivir carboxylate (10 μ M). Suspensions of the inactivated viruses with Oseltamivir carboxylate were overlaid onto the arrays and incubated at room temperature for 1 h. Slides were subsequently washed by successive rinses in PBS-0.05% Tween, PBS, and deionized water three times. Bound viruses were detected using the following antibodies: homemade rabbit anti-H1 antibody both for SOV California/07/2009 and H1N1 Brisbane; anti-H3 antibody for H3N2 Brisbane (NR3118, Biodefence and Emerging Infections Research Resources Repository, National Institute of Allergy and Infectious Diseases, MD, USA); anti-H5 (α -293s) (Sino Biological Inc. Beijing, CH) antibody for H5N1 (RG14), and anti-flu B (Abcam, Mass., USA) for B/Lee/40. The slides were gently rocked at room temperature for 60 min. After the repeating washing steps, binding was detected by overlay with labeled secondary antibodies.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claim.

What is claimed is:

1. A method for detecting at least one influenza serotype in a sample suspected of or comprising one or more viruses, the method comprising the steps of:

- a) providing a substrate having at least one type of glycan capture probe bound at a discrete location on the substrate, wherein the capture probes can bind to a specific influenza serotype target;
 - b) providing at least one type of nanoparticle probe conjugated to a detector moiety, wherein the detector moiety binds to the specific influenza serotype;
 - c) contacting the substrate with the sample suspected of comprising one or more viruses and the nanoparticle probe under conditions suitable for the binding of the glycan capture probes to the specific influenza serotype and the binding of the nanoparticle probe to the specific influenza serotype to form a complex at the discrete location on the substrate; and
 - d) detecting the presence or absence of the complex wherein the presence or absence of the complex is indicative of the presence or absence of the specific influenza serotype in the sample;
- wherein the nanoparticle consists essentially of a noble metal, and
- wherein the limit of detection of at least one influenza serotype in said sample suspected of or comprising one or more viruses is less than 10^4 viral particles.

2. The method of claim 1, wherein the influenza serotype is selected from the group consisting of influenza A, influenza B, influenza A serotypes H1N1, H2N2, H3N1, H3N2, H5N1, H7N7, H1N2, H9N2, H7N2, H7N3, and H10N7.

3. The method of claim 1, wherein the substrate comprises an array of a plurality of glycan capture probes that bind specifically to a plurality of different influenza serotypes.

4. The method of claim 3, wherein the plurality of capture probes comprises one or more of sialosides which is selected from the group consisting of: Neu5Ac(α 2-3)Gal(β 1-3)GalNAc α , Neu5Ac(α 2-3)Gal(β 1-6)Man α , Neu5Ac(α 2-3)Fuc(α 1-4)Gal(β 1-4)Glc β , Neu5Ac(α 2-6)Gal β , Neu5Ac

(α -2)GalNAc β , Neu5Ac(α -2-6)Gal(β -1-4)GlcNAc β , Neu5Ac(α -2-6)Gal(β -1-4)Glc β , Neu5Ac(α -2-6)Gal(β -1-4)GlcNAc β , and Neu5Ac(α -2-6)Gal(β -1-4)GlcNAc(β -1-3)Gal(β -1-4)GlcNAc(β -1-3)Gal(β -1-4)GlcNAc β .

5. The method of claim 4, wherein the capture probes are able to differentially bind to influenza subtypes Cal/09 H1N1, Brisbane H1N1, Brisbane H3N2, and RG14 H5N1.

6. The method of claim 1, wherein the detector moiety comprises an antibody fragment that binds to the specific influenza serotype.

7. The method of claim 6, wherein the antibody fragment comprises a phage particle from a phage display, and the phage particle comprises a plurality of nanoparticles.

8. The method of claim 7, wherein the antibody fragment recognizes a hemagglutinin (HA) characteristic of an influenza subtype.

9. The method of claim 1, wherein the detector moiety comprises a molecule that binds specifically to one or more influenza serotypes.

10. The method of claim 6, wherein the antibody fragment recognizes a neuraminidase (NA) characteristic of an influenza subtype.

11. The method of claim 9, wherein the molecule is a neuraminidase binding agent.

12. The method of claim 11, wherein the molecule is selected from Oseltamivir (Tamiflu), Zanamivir (Relenza), Laninamivir (Inavir), or Peramivir.

13. The method of claim 11, wherein the neuraminidase binding agent detects co-infection by at least two different strains of influenza viruses.

14. A method for distinguishing between a first influenza virus serotype and a second influenza virus serotype in a sample comprising a first influenza virus serotype and a second influenza virus serotype, the method comprising the steps of:

- a) providing a substrate having at least two different types of glycan capture probes bound at discrete locations on the substrate, wherein a first capture probe can bind to the first influenza virus serotype but not the second influenza virus serotype, and a second capture probe can bind to the second influenza virus serotype but not the first influenza virus serotype;
- b) providing at least one type of nanoparticle probe comprising detector moieties, wherein the detector moieties on each type of nanoparticle probe has a configuration that can bind to both the first influenza virus serotype and the second influenza serotype;
- c) contacting the substrate with the sample under conditions suitable for binding of the first influenza virus serotype and the second influenza virus serotype in the sample to the glycan capture probes, and under suitable conditions for the binding of the nanoparticle probe to the first influenza serotype or second influenza serotype;
- d) contacting the first influenza virus serotype and the second influenza virus serotype immobilized on the substrate with the nanoparticle probe under conditions that are effective for the binding of the detector moieties to the first influenza virus serotype and the second influenza virus serotype; and
- e) detecting whether the nanoparticle probe binds to the first influenza virus serotype and/or the second influenza virus serotype at the discrete locations on the substrate where the first capture probe is located and where the second capture probe is located, wherein the presence or absence of the nanoparticle-first influenza virus serotype complex at the discrete location on the

substrate where the first capture probe is located is indicative of the presence or absence of the specific first influenza virus serotype in the sample, and the presence or absence of the nanoparticle-second influenza virus serotype complex at the discrete location on the substrate where the second capture probe is located is indicative of the presence or absence of the specific second influenza virus serotype in the sample; wherein the nanoparticle consists essentially of a noble metal.

15. The method of claim 1 or 14, wherein the sample is blood, serum, anti-serum, monoclonal antibody preparation, lymph, plasma, saliva, urine, semen, breast milk, ascites fluid, tissue extract, cell lysate, cell suspension, viral suspension, nasopharyngeal aspirate, or a combination thereof.

16. The method of claim 14, wherein the detector moiety comprises an antibody fragment that binds to the first influenza serotype or the second influenza serotype.

17. The method of claim 16, wherein the antibody fragment thereof comprises a phage particle from a phage display, and the phage particle comprises a plurality of nanoparticles.

18. The method of claim 14, wherein the captured nanoparticle-first influenza virus serotype or nanoparticle-second influenza virus serotype complex is detected by photonic, electronic, acoustic, opto-acoustic, gravity, electro-chemical, electro-optic, mass-spectrometric, enzymatic, chemical, biochemical, or physical means.

19. The method of claim 1 or 14, wherein the nanoparticles are made of gold or silver.

20. The method of claim 19, wherein the nanoparticles are made of gold.

21. The method of claim 1 or 14, wherein the substrate is a magnetic bead.

22. The method of claim 1 or 14, wherein the substrate has a planar surface.

23. The method of claim 1 or 14, wherein the substrate is made of glass, quartz, ceramic, or plastic.

24. The method of claim 1 or 14, wherein the detecting comprises contacting the substrate with specific metal stain.

25. The method of claim 1 or 14, wherein the detecting comprises detecting light scattered by the nanoparticle.

26. The method of claim 1 or 14, wherein the detecting comprises observation with an optical scanner.

27. The method of claim 26, wherein the scanner is linked to a computer loaded with software capable of calculating grayscale measurements, and the grayscale measurements are calculated to provide a quantitative measure of the amount of target analyte or influenza serotype detected.

28. The method of claim 1 or 14, wherein the substrate is addressable.

29. The method of claim 1 or 14, wherein a plurality of glycan capture probes, each of which can recognize a different target influenza serotype, are attached to the substrate in an array of discrete spots.

30. The method of claim 29, wherein the plurality of glycan capture probes comprise glycan structures of at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more of glycans found on HA receptors in human upper respiratory tract tissues.

31. The method of claim 29, wherein the plurality of glycan capture probes comprises a glycan structure of at least one molecule selected from:

Neu5Ac(α -2-3)Gal β , Neu5Ac(α -2-3)Gal(β -1-4)Glc β , Neu5Ac(α -2-3)Gal(β -1-4)GlcNAc β , Neu5Ac(α -2-3)Gal(β -1-4)(6S)GlcNAc β , Neu5Ac(α -2-3)Gal(β -1-4)[Fuc

(α 1-3)]GlcNAc β , Neu5Ac(α 2-3)Gal(β 1-3)GlcNAc β , Neu5Ac(α 2-3)Gal(β 1-3)(6S)GlcNAc β , Neu5Ac(α 2-3)Gal(β 1-3)GalNAc α , Neu5Ac(α 2-3)Gal(β 1-6)Man α , Neu5Ac(α 2-3)Gal(β 1-3)GalNAc(β 1-3)Gal α , Neu5Ac(α 2-3)Gal(β 1-3)GalNAc(β 1-3)Gal β , Neu5Ac(α 2-3)Gal(β 1-3)GalNAc(β 1-3)Gal(α 1-4)Gal(β 1-4)Glc β , Neu5Ac(α 2-3)Gal(β 1-6)[Neu5Ac(α 2-3)Gal(β 1-3)]GlcNAc β , Neu5Ac(α 2-3)Gal(β 1-6)[Neu5Ac(α 2-3)Gal(β 1-3)]Man α , Neu5Ac(α 2-3)Gal(β 1-3)[Neu5Ac(α 1-6)]GlcNAc β , Neu5Ac(α 2-3)[GalNAc(β 1-4)]Gal(β 1-4)Glc β , Gal(β 1-3)GalNAc(β 1-4)[Neu5Ac(α 1-3)]Gal(β 1-4)Glc β , Fuc(α 1-2)Gal(β 1-3)GalNAc(β 1-4)[Neu5Ac(α 1-3)]Gal(β 1-4)Glc β , Neu5Ac(α 2-3)Fuc(α 1-4)Gal(β 1-4)Glc β , Neu5Ac α , Neu5Ac(α 2-6)Gal β , Neu5Ac(α 2-6)GalNAc β , Neu5Ac(α 2-6)Gal(β 1-4)GlcNAc β , Neu5Ac(α 2-6)Gal(β 1-4)Glc β , Neu5Ac(α 2-6)Gal(β 1-4)GalNAc α , Neu5Ac(α 2-6)Gal(β 1-3)GlcNAc β , Neu5Ac(α 2-6)Gal(β 1-4)(6S)GlcNAc β , Neu5Ac(α 2-6)Gal(β 1-4)GlcNAc(β 1-3)Gal(β 1-4)GlcNAc β , and Neu5Ac(α 2-6)Gal(β 1-4)GlcNAc(β 1-3)Gal(β 1-4)GlcNAc(β 1-3)Gal(β 1-4)GlcNAc β .

32. The method of claim **29**, wherein the plurality of capture probes comprises one or more of sialosides which is selected from the group consisting of:

Neu5Ac(α 2-3)Gal(β 1-3)GalNAc α , Neu5Ac(α 2-3)Gal(β 1-6)Man α , Neu5Ac(α 2-3)Fuc(α 1-4)Gal(β 1-4)Glc β , Neu5Ac(α 2-6)Gal β , Neu5Ac(α 2-6)GalNAc β , Neu5Ac(α 2-6)Gal(β 1-4)GlcNAc β , Neu5Ac(α 2-6)Gal(β 1-4)Glc β , Neu5Ac(α 2-6)Gal(β 1-4)GlcNAc β , and Neu5Ac(α 2-6)Gal(β 1-4)GlcNAc(β 1-3)Gal(β 1-4)GlcNAc(β 1-3)Gal(β 1-4)GlcNAc β .

33. The method of claim **32**, wherein the capture probes are able to differentially bind to influenza subtypes Cal/09 H1N1, Brisbane H1N1, Brisbane H3N2, and RG14 H5N1.

34. The method of claim **14**, wherein the detector moiety comprises an antibody fragment that binds to the specific influenza serotype.

35. The method of claim **34**, wherein the antibody fragment comprises a phage particle from a phage display.

36. The method of claim **35**, wherein the antibody fragment recognizes a hemagglutinin (HA) characteristic of an influenza subtype.

37. The method of claim **14**, wherein the detector moiety comprises a molecule that binds specifically to one or more influenza serotypes.

38. The method of claim **34**, wherein the antibody fragment recognizes a neuraminidase (NA) characteristic of an influenza subtype.

39. The method of claim **37**, wherein the molecule is a neuraminidase binding agent.

40. The method of claim **39**, wherein the molecule is selected from Oseltamivir (Tamiflu), Zanamivir (Relenza), Laninamivir (Inavir), or Peramivir.

41. The method of claim **39**, wherein the neuraminidase binding agent detects co-infection by at least two different types of influenza viruses.

42. The method of claim **14**, wherein the substrate is selected from the group consisting essentially of one of glass, semiconductor, organic polymer, membrane, quartz, silicon, mineral, metal, metal alloy, gold, silver, and mixtures and compositions thereof.

43. The method of claim **1** or **14**, wherein sample is first contacted with the nanoparticle probe so that a influenza virus serotype present in the sample binds to the detector moiety on the nanoparticle probe, and the influenza virus serotype bound to the nanoparticle probe is then contacted with the substrate so that the influenza virus serotype binds to the glycan capture probe on the substrate.

44. The method of claim **1** or **14**, wherein sample is first contacted with the substrate so that a influenza virus serotype present in the sample binds to a glycan capture probe, and the influenza virus serotype bound to the glycan capture probe is then contacted with the nanoparticle probe so that the influenza virus serotype binds to the detector moiety on the nanoparticle probe.

45. The method of claim **1** or **14**, wherein the sample, the nanoparticle probe and the glycan capture probe on the substrate are contacted simultaneously.

46. The method of claim **1**, wherein detecting the presence or absence of the complex indicative of the presence or absence of the specific influenza serotype in the sample comprises evaluating a flu vaccination response in an individual from whom the sample is obtained.

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摘要(译)

提供了可以检测和区分各种亚型和流感病毒株的聚糖阵列。公开了使用纳米颗粒扩增技术的分析使用聚糖阵列的方法。使用与包含流感病毒特异性抗体的噬菌体颗粒缀合的金纳米颗粒进行夹心测定，以使用单一反应检测多种血清型。针对流感病毒的特定靶HA的多个聚糖包含该阵列。公开了包含与 (a) 噬菌体展示颗粒缀合的贵金属的检测分子，所述噬菌体展示表达抗血凝素的抗体和 (b) 神经氨酸酶结合剂。

