QUANTITATIVE, HIGHLY MULTIPLEXED DETECTION OF NUCLEIC ACIDS

STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

[0001] This invention was made with support of a U.S. Dept. of Homeland Security grant, Contract Number HSHQDC-10-C-00053. The government has certain rights in the invention.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0002] This application claims priority to Provisional U.S. Patent Application No. 61/463,580, filed February 18, 2011, and Provisional U.S. Patent Application No. 61/561,198, filed November 17, 2011, the full disclosures of which are hereby incorporated herein by reference in their entirety for all purposes.

FIELD OF THE INVENTION

[0003] The invention is in the field of real-time DNA amplification, detection and quantification, as well as associated consumables, devices, and systems, including arrays.

BACKGROUND OF THE INVENTION

[0004] Real time PCR is routinely used for detection of nucleic acids of interest in a biological sample. For a review of real time PCR see, e.g., M TevfikDorak (Editor) (2006) Real-time PCR (Advanced Methods) Taylor & Francis, 1st edition ISBN-10: 041537734X ISBN-13: 978-0415377348, and Logan et al. (eds.) (2009) Real-Time PCR: Current Technology and Applications,Caister Academic Press, 1st edition ISBN-10: 1904455395, ISBN-13: 978-1904455394. For additional details, see also, e.g., Gelfand et al. "Homogeneous Assay System Using The Nuclease Activity of A Nucleic Acid Polymerase" USP 5,210,015; Leone et al. (1995) "Molecular beacon probes combined with amplification by NASBA enable homogenous real-time detection of RNA." Nucleic Acids Res. 26:2150-2155; and Tyagi and Kramer (1996) "Molecular beacons: probes that fluoresce upon hybridization" Nature Biotechnology 14:303-308. Traditionally, single well multiplexing, used to detect more than one target nucleic acid per sample in a single reaction container (e.g., well of a multiwell plate),

is achieved using self-quenched PCR probes such as TAQMAN™ or Molecular Beacon probes that are specific for each amplicon. Upon binding to the amplicon in solution, or upon degradation of the probes during PCR, the probes unquench, producing a detectable signal. The probes are labeled with fluorophores of different wavelengths, permitting a multiplexing capability of up to about 5 targets in a single "one pot" reaction. More than about 5 probes per reaction is difficult to achieve, due to practical spectral range and label emission limitations. This severely limits multiplexing of a single reaction, which, in turn, significantly limits how many targets can be screened per sample and drives up reagent cost and instrument complexity in detecting multiple targets of interest.

[0005] Nucleic acid arrays represent another approach to multiplexing the detection of amplification products. Most typically, amplification reactions are performed on a sample, and amplicons are separately detected on a nucleic acid array. For example, Sorge "Methods for Detection of a Target Nucleic Acid Using A Probe Comprising Secondary Structure" US 6,350,580 propose the capture of a probe that is released upon amplification by purifying the probe out of the amplification mixture and then detecting it. This multiple-step approach to making and detecting amplicons makes real time analysis of the amplification mixture impractical.

[0006] Various approaches that amplify the reactants in the presence of the capture nucleic acids have also been proposed. For example, Kleiber et al. "Integrated Method and System for Amplifying And Detecting Nucleic Acids," US 6,270,965, propose detection of an amplicon via evanescence induced fluorescence. Similarly, Alexandre et al "Identification and Quantification of a Plurality of Biological (Micro) Organisms or Their Components," US 7,829,313, proposes detection of amplicons on arrays. In another example, target polynucleotides are detected by detecting a probe fragment that is produced as a result of amplification, e.g., by binding to an electrode, followed by electrochemical detection. See, e.g., Aivazachvilli et al. "Detection of Nucleic Acid Amplification" US 2007/0099211; Aivazachvilli et al. "Systems and Methods for Detecting Nucleic Acids US 2008/0193940, and Scaboo et al. "Methods And Systems for Detecting Nucleic Acids" US 2008/0241838.

[0007] These methods all suffer from practical limitations that limit their use for multiplex target nucleic acid detection. For example, Kleiber (US 6270,965) relies on

evanescence induced fluorescence to detect fluorescence of amplicons at the array surface, and requires complex and expensive optics and arrays. Alexandre (7,829,313) propose detection of amplicons on an array; as in Kleiber this increases array costs significantly, because each array has to be custom designed to detect each amplicon. In practice, it can be difficult to achieve similar hybridization kinetics for disparate amplicons on an array, particularly where the amplicons are relatively large, as in Alexandre. Furthermore, this art provides little guidance regarding how to detect signal on an array where there is an accompanying solution phase that also comprises high levels of signal background, or of arrays that remain stable through in situ thermal cycling.

[0008] The present invention overcomes these and other problems in the art. A more complete understanding of the invention will be obtained upon complete review of the following.

SUMMARY OF THE INVENTION

[0009] The invention provides methods and associated devices, systems and consumables that permit highly multiplexed detection of nucleic acids of interest, e.g., for the detection of viruses, bacteria, plasmodium, fungi, or other pathogens in a biological sample. The consumable comprises a signal-optimized chamber having a high-efficiency thermo-stable nucleic acid detection array on an interior surface of the chamber. The array is configured to detect up to about 100 or more different universal labeled probes. The methods generate the labeled universal probes (as "probe fragments") during amplification of a portion of a nucleic acid of interest, with the amplification reaction being performed in the chamber. The universal probes are hybridized to the array after a few amplification cycles, and subsequent to selected amplification cycles thereafter, allowing for both detection and quantification of one or more nucleic acids of interest in the sample, in real time.

[0010] Accordingly, in a first aspect, methods of detecting a target nucleic acid are provided. This includes providing a detection chamber that has at least one high efficiency nucleic acid detection array on at least one surface of the chamber. The high efficiency array typically has a non-rate limiting number of capture nucleic acids that permits an increased capture rate of detectable probe fragments produced by a reaction in the chamber, and the

capture nucleic acids are configured to capture relatively small probe nucleic acids, which also increases array efficiency. Detection of binding of the probes to the array is preferably carried out under conditions that are selected or configured to reduce background signal levels proximal to the array, e.g., resulting from unbound free probe. For example, in certain embodiments, the chamber itself is configured to reduce signal background proximal to the array, e.g., by shaping the chamber to reduce background (e.g., by making the chamber relatively thin proximal to the array, e.g., the chamber is typically about 500μm or shallower above the array). Thinner chambers also have less thermal mass, and can be temperature cycled more rapidly and more efficiently than thicker chambers. Other ways in which the system and methods are configured to reduce the level of background signal are described in greater detail, below.

[0011] A sample that has one or more copies of the target nucleic acid to be detected is loaded into the detection chamber. An amplification primer and a labeled probe are hybridized to the one or more target nucleic acid copies. At least a portion of one or more of the target nucleic acid copies is amplified in an amplification primer dependent amplification reaction. The amplification reaction results in cleavage of the labeled probe, e.g., due to nuclease activity of an amplification enzyme. This results in release of a labeled probe fragment, which is to be detected by the array. The labeled probe fragment is hybridized to the high-efficiency array (typically after a few amplification cycles are run to amplify the amount of probe fragment released in the chamber). A label signal produced by binding the labeled probe fragment to the array is then detected, thereby detecting the target nucleic acid.

[0012] The precise configuration of the detection chamber can vary. The configuration is selected to reduce signal background in the chamber proximal to the array. Generally, at least 1%, and often, about 5% or more of the signal in the chamber is concentrated at the array (e.g., about 6%, 8%, or even 10% or more) in the region of the array. Background of 99% or less total signal can be normalized by the system, though lower levels are often desirable. In typical embodiments described herein, levels of 95% or less total background are achieved by optimizing the configuration of the chamber proximal to the array. This configuration optimization is achieved, e.g., by keeping the depth of the chamber above the array to a minimum. In typical embodiments, the chamber is less than about 1 mm in depth or other

dimension proximal to the array, more typically about 500 μm or less in at least one dimension proximal to the array, preferably less than about 250 μm or less, e.g., between about 10 μm and about 200 μm and in some embodiments the chamber is about 150μm in a dimension proximal to the array. In one example herein, the chamber is about 142 μm in depth above the array. In another example herein, the chamber is about 100 μm in depth. The relevant chamber dimension depends on the signal detection path of the detection system, for example, where the signal is generated by passing light onto the array, where some of the light escapes through the array and into the fluid above the array, the relevant dimension is the depth of the chamber above the array. In addition to reducing the level of background signal detected, reducing chamber thickness also has the benefit of reducing the contribution of background noise components, e.g., detector responses unrelated to the specific detection of array spot signal and background signal from the reaction fluid. In particular, one major noise contributor is the shot noise from the detectors used, which generally increases with the square root of the total amount of signal detected, which, in turn, scales with the thickness of the reaction chamber. Accordingly, by providing reduced thickness of the reaction chamber, one reduces the background noise, and consequently increases the signal to background noise ratio (SNR) of the overall system. Other potential noise contributors include detection of excess light, e.g., unfiltered excitation light, unintended ambient light, scattered fluorescence, autofluorescence of system components, or the like. A number of these noise contributors may be mitigated through the conventional approaches, such as through the use of appropriate optical filters, e.g., to eliminate or reduce excess excitation light, sealed optical systems that reduce or prevent ambient light at the detector, and through the configuration of array spot size and spacing to reduce or eliminate signal cross talk at the detector. In particularly preferred aspects, the SNR for the assay methods and systems of the invention will typically be 2.5 or greater, preferably greater than 3, greater than 4, greater than 5, greater than 10, and in some cases, greater than 20 or more.

[0013] Alternative or additional approaches for configuring the system and methods of the invention to reduce background signal can also be employed in conjunction with the devices and methods of the invention. For example, the devices and systems of the invention may be configured to provide excitation illumination to the capture array using a total internal

reflection fluorescence microscopy ("TIRF") configuration, where excitation light is directed into the substrate underlying the capture array such that it is entirely internally reflected (see, M. Tokunaga et al., Biochem. and Biophys. Res. Comm. 235, 47 (1997) and P. Ambrose, Cytometry, 36, 244 (1999)). Notwithstanding this, an evanescent wave is generated at the substrate-fluid interface of the array that decays exponentially away from the surface, resulting in effective illumination adjacent to the surface, e.g., to a depth of 100 nm, without exciting fluorophores in the remainder of the solution.

[0014] In still another alternative or additional approach, the reactants employed in the analytical methods of the invention are configured to reduce background signal relative to actual probe/array binding signal. For example, background signal may be reduced through the use of cooperative fluorophores on both the capture array probes and the labeled probe fragment, e.g., in a FRET construct. In particular, a donor fluorophore, having a first excitation spectrum and a first emission spectrum may be coupled to one of the capture probe or the labeled probe fragment. An acceptor fluorophore that has an excitation spectrum that overlaps the emission spectrum of the donor, and that is different from the donor's excitation spectrum, is coupled to the other probe. When the capture probe and labeled probe fragment hybridize, the donor and acceptor are brought into sufficient proximity for energy transfer, yielding a distinctive fluorescent signal corresponding to the emission spectrum of the acceptor fluorophore. By configuring the optical system to excite only within the donor's excitation spectrum, and filter the emission spectrum of the donor, one can selectively detect signal arising from the energy transfer signal from the acceptor, upon hybridization. A wide variety of FRET label pairs have been described previously (See, e.g., U.S. Patent Nos. 6,008,373, to Waggoner, and 7,449,298, to Lee et al.). As will be appreciated, a number of methods may be employed in the context of the invention for reducing the contribution of signal from unbound, intact labeled probe in the reaction solution, or background signal, relative to the signal detected from bound labeled probe fragment, including, for example, configuring the reaction chamber to concentrate signal within the focal plane of the detector, employing interactive labeling techniques that either present different emission spectra when bound to the array versus when unbound in solution, or self quenching probes that have reduced fluorescence when present in the same intact probe, versus when separated in a cleaved probe fragment.

[0015] As noted, the array typically includes a non-rate limiting number of capture nucleic acids that hybridize to the labeled probe fragment. This means that the amplification reaction produces a number of probe fragments during amplification that results in a probe fragment concentration in the reaction mixture that is not saturating for the number of sites on the array (e.g., accessible complimentary capture nucleic acids) available to bind the probe fragments. Restated, the number of binding sites on the array is maintained in excess, and preferably well in excess, of what would be saturated at the concentration of probe fragments produced in an amplification reaction. Because the number of sites on the array is not rate limiting, the ratio of probe fragments on the array to background probe fragments in solution is optimized. Typical array densities are between about 350 fmol/cm^2 or greater, e.g., about 2,000 fmol/cm^2 or greater, 2,500 fmol/cm^2 or greater, 3,000 fmol/cm^2 or greater, 4,000 fmol/cm^2 or greater, 4,500 fmol/cm^2 or greater, or 5,000 fmol/cm^2 or greater. In some embodiments, the number of sites that bind probe on the array is at least 1X the number of sites that would be saturated by the concentration of probe fragments produced during amplification, and is optionally 5X, 10X, 50X or more. The ratio will vary with the number of amplification cycles and the amount of probe produced. The efficiency of the array is also a function of the length of the probe fragment to be captured. Shorter fragments typically display more efficient hybridization, although the probes do have to be long enough to bind at a given T_m during hybridization. Typical probe fragments to be captured by the array are about 50 nucleotides in length or less; the arrays comprise sites that have corresponding complimentary capture nucleic acid sequences (the capture nucleic acids can optionally also include additional sequences, e.g., to space the complimentary site above the surface, e.g., to reduce surface effects). More typically, the probes and capture sequences are about 40 nucleotides or less in length, e.g., about 30, about 20, or about 15 nucleotides or shorter in length.

[0016] In some cases, the capture array probes, and complementary labeled probe fragments used in a given analysis are selected such that they provide a narrow range of Tm over all members of the array. In particular, to ensure optimal and consistent hybridization to the capture array, the capture probes in a given array will each have a Tm within about 10° C of every other member of the array, and preferably, within about 7° C, 5° C, or 3° C of every

other probe in the array. Such a narrow T_m range allows for consistent hybridization and resulting signal generation across all members of the array.

[0017] In typical embodiments, the hybridization temperature is less than the temperature of the amplification reaction, so the T_m of the probe fragment for the capture nucleic acid can be less than an intra-molecular T_m of the probe (e.g., where the probe comprises a quencher to reduce background), and/or lower than the T_m of the probe for the target nucleic acid. That is, in typical thermocycling embodiments, amplification reactions are performed at higher temperatures than hybridization steps; accordingly, the probe will typically have a higher T_m for the target nucleic acid than the probe fragment has for the array. The labeled probe typically comprises a first orthogonal flap that is not complimentary to the target nucleic acid; this flap is cleaved from the labeled probe to produce the labeled probe fragment. The labeled probe optionally comprises a second orthogonal flap, e.g., coupled to a quencher moiety, which is at least partially complimentary to the first flap (e.g., to provide proximity-based quenching of a label on the first flap). Background is reduced where the second flap has a higher T_m for binding to the first flap than the first flap has for binding to the array. In such a configuration, the extension reaction occurs at a first temperature, i.e., below the T_m of the intact probe for the target nucleic acid, but above both the intra-molecular T_m of the intact probe, and the T_m of the probe fragment for the capture probe on the array). Following extension, as the reaction temperature is lowered, it crosses below the intra-molecular T_m of the probe, allowing for the formation of the secondary structure of the probe, and resultant quenching of the fluorophore. Further cooling to below the T_m of the probe fragment to the capture probe allows hybridization of the probe fragment to the array and detection of its associated fluorophore. Because the intact probe has previously formed into its secondary structure, it is both less likely to bind to the capture probe, and is quenched, thus reducing both unintended capture of intact probe, and background signal from the fluorophores present on the intact probe in solution (or that may have bound to the capture probe array. Although in certain aspects, quenchers are employed on the intact probes of the invention, in certain embodiments it has been surprisingly determined that, quenchers are not required on the probe, because the optimized chamber design and high efficiency array achieve discrimination of array signal from background, even where background is increased by omitting a quencher from the probe.

[0018] In other embodiments, the labeled probe fragment and its complementary capture nucleic acid is designed or selected to have a T_m that is higher than the extension reaction temperature, e.g., 10 or more degrees higher. Thus, where the extension reaction is carried out, for example, at between 55° and 60° C, the T_m of the labeled probe fragment and capture nucleic acid will typically be, e.g., 71°C. In such cases, hybridization of the labeled probe fragment to the capture nucleic acid on the array occurs at the same temperature as the extension reaction, obviating the need to further reduce the temperature in order to hybridize to the array and detect the resulting signal. As a result, a two-step temperature profile may be used rather than a three step profile.

[0019] In the context of the intact labeled probe, the orientation of the orthogonal labeled probe fragment relative to the probe portion that binds to the target sequence, may be varied. In particular, a release labeled probe fragment may hybridize to a capture probe on the array in an orientation where the end cleaved from the target specific portion of the probe is either proximal or distal to the point at which the capture probe is coupled to the array surface. In some cases, for example, by ensuring that any intact probe would only bind to the capture probe in an orientation that projected the target specific portion of the probe toward the surface of the array, one could then take advantage of potential surface interference with that binding, to further reduce the potential for undesired capture of intact probe by the array. Such methods are particularly useful in the case of solid surfaces on the arrays, e.g., silica substrates and the like.

[0020] Sample can be loaded into the chamber by any of a variety of mechanisms, depending on the precise configuration of the consumable. In one convenient application, the sample is loaded through at least one port or fluidic channel in operable communication with the chamber. For example, ports can be fabricated in a top surface of the consumable, with the ports leading into the chamber. This provides for simplified loading, e.g., via a pipette or other fluid delivery device. Alternatively, fluidic or microfluidic channels, capillaries, or the like, can be used for sample delivery.

[0021] The methods can be used for detection of a nucleic acid of interest in a sample and/or quantification of the nucleic acid, e.g., in real time. Thus, in one aspect, the target nucleic acid is optionally amplified in a plurality of amplification cycles prior to detecting

signal, with the target nucleic acid portion additionally being amplified after signal detection, i.e., in the presence of additional copies of the labeled probe. Resulting released labeled probe fragments are subsequently hybridized to the array and detected, with detected signal intensity being correlated to presence and/or quantity of the target nucleic acid present in the sample. Typically, the sample is amplified for more than 1 cycle before initial detection, to increase the level of signal by increasing the number of probe fragments released by the amplification. For example, the target nucleic acid can optionally be amplified for at least, e.g., 2, 3, 4, 5 or more amplification cycles prior to detecting signal from the array.

[0022] The labeled probe typically comprises a fluorescent or luminescent label, although other labels such as quantum dots can also be used. In one preferred embodiment, the label is a fluorescent dye. The signal produced by the probe fragment is typically an optical signal. The labeled probe optionally comprises a label and a label quencher; cleavage of the labeled probe results in separation of the label and the quencher, thereby unquenching the label. However, as noted above, quenchers are not required in the practice of the invention.

[0023] Signal is typically detected by detecting one or more optical signal wavelengths corresponding to optical labels on the probes or probe fragments. Because binding position of probe fragments on the array can be used to discriminate between different probes, it is not necessary to use different labels on the different probes to distinguish the probes in a multiplexed amplification reaction (an amplification reaction designed to amplify multiple target nucleic acids, if more than one of the targets is present in the sample). However, multiple probes labels can be used to enhance multiplexing capabilities. Where multiple probes are used, detecting the signal can include detecting a plurality of optical signal wavelengths from a plurality of signals generated by a plurality of different labels (e.g., different fluorescent dye moieties on different probes).

[0024] Although generally described in terms of label groups that are attached to the probe fragment that binds to the array, e.g., the labeled probe fragment, it will be appreciated that other detection schemes may be employed that do not require the use of pre-labeled probes. For example, in some embodiments, intercalating dyes may be used. Intercalating dyes typically provide a detectable signal event upon incorporation, or intercalation, into double stranded nucleic acids. In the context of the invention, the hybridization of the cleaved probe

fragment to the complementary probe on the array creates a double stranded duplex at the array surface which could incorporate an intercalating dye, and provide a unique signal indiciative of that hybridization. Intercalating dyes are well known in the art and include those described in, e.g., Gudnason et al., Nucleic Acids Research, (2007) Vol. 35, No. 19, e127, which is incorporated herein by reference for all purposes. Similarly, although optical signal detection methods are particularly preferred, the probe configurations and assay methods may also generally be practiced using non-optical labeling and/or detection methods, e.g., using electrochemical detection methods, e.g., ChemFETS, ISFETS, etc., optionally in conjunction which electrochemical labeling groups, e.g., possessing large charged groups to amplify detection of hybridization of the probe fragment to an array probe at or near a detector surface.

[0025] Local background can be detected for one or more regions of the array, with signal intensity measurements being normalized by correcting for said background. Typically, the normalized signal intensity is less than about 10% of total signal, e.g., between about 1 and about 10% of the total signal. In one example class of embodiments, the normalized signal intensity is between about 4 and about 7% of total signal. Typically, where approximately 1% or more of the signal is localized to the array, e.g., where about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10% or more of the signal is localized to the array for a region of the chamber, it is possible to discriminate the array signal from background. It is possible to discriminate even lower levels of signal to background, but this is not generally preferred. The methods can also include normalizing signal intensity by correcting for variability in array capture nucleic acid spotting (e.g., by correcting for spot size, spot density, or both), or by correcting for uneven field of view of different regions of the array.

[0026] The ability to simultaneously detect multiple target nucleic acids in a sample represents a preferred aspect of the invention. The sample may have one or a plurality of target nucleic acids, with the array comprising a plurality of capture nucleic acid types that are capable of detecting more than one target per sample. The capture nucleic acid types are spatially separated on the array, eliminating the need for the use of multiple labels (although, as noted, multiple labels can be used). In multiplex approaches, a plurality of amplification probes, each specific for a different nucleic acid target, is incubated with the sample, which can include one or more target nucleic acids. For example, there can be between about 5 and about

100 or more capture nucleic acid types. Each potential target to be detected will utilize a different probe as well, e.g., there are optionally between about 5 and about 100 or more labeled probe types in the amplification reaction, each specific for a potential target of interest. The array includes corresponding capture nucleic acids, e.g., between about 5 and about 100 or more capture nucleic acid types. This permits a corresponding number of signals to be detected and processed by the array. For example, between about 5 and about 100 or more different signals can be detected based upon positioning of the signals on the array after hybridization of the probe fragments to the array. As will be appreciated, the number of capture probe types on an array will generally be dictated by the number of distinct amplification reactions that can be multiplexed within a single reaction volume. However, capture arrays having larger numbers of different capture probes, e.g., greater than 100, greater than 1000, 10,000 or more capture probe types, may also be employed in some circumstances, e.g., where amplification reactions are pooled for interrogation by the array, or the like.

[0027] An advantage of the present invention is that one capture array configuration may be used for multiple different target nucleic acid sequence panels. In particular, a probe set for a first panel will include probes that have first target specific portions specific for the targets in the panel, and second capture portions complementary to individual probes on the capture array. A probe set for a second different panel (whether partially overlapping, or completely different) will include target specific portions for that panel, while the capture portions will be the same as for the first panel's probe set. Restated, for any panel of targets, the probe set will include a semi-fixed portion of the probes used for that panel, which will always be complementary to a member of the capture array. The probes will also include variable portions that are selected for the specific panel of target nucleic acids. For example, in an analytical process, a first set of probes is employed where each probe in the first set has a first fixed portion that corresponds to a different capture probe on the capture probe array. Each probe also includes a target specific portion that is complementary to a given target sequence in the first panel. For a second panel, a second set of probes is employed where each probe in the set includes the same first fixed portion, but has a second target specific portion that is specific for the targets in that panel.

[0028] With reference to Figure 1A, portion A of the labeled probe corresponds to the variable portion, while portion B would correspond to the fixed portion that would be complementary to the probes on the array. The use of a universal or common capture array and capture probe set allows for more efficient and lower cost manufacturing of the consumables used in the invention.

[0029] Thus, in one embodiment in which the sample comprises multiple target nucleic acids, the method includes incubating a plurality of labeled probes, each specific for a different target nucleic acid, with the target nucleic acids. Amplifying at least a portion of the target nucleic acids in the amplification primer dependent amplification reaction results in cleavage of a plurality of labeled probe types and resulting release of a plurality of labeled probe fragment types. The plurality of probe fragment types are hybridized to the array. Each of the different probe fragment types hybridizes to a spatially discrete capture nucleic acid type. Detecting the label signal includes detecting a plurality of label signals from a plurality of spatially discrete regions corresponding to the spatially discrete capture nucleic acids on the array. Optionally, and in several preferred embodiments, the labeled probe types comprise the same label moiety, but additional multiplexing and/or use of differentially controls or registration probes can include using a plurality of different label moieties. Typically, the labeled probe types can include one or more different label moieties, with the number of different moieties being less than the number of labeled probe types.

[0030] Devices and systems for performing the methods are a feature of the invention. The devices or systems can include a detection chamber that comprises at least one high efficiency nucleic acid detection array on at least one surface of the chamber. As noted with reference to the methods, the chamber is configured to reduce signal background for signals detected from the array. The device or system typically includes a thermo-regulatory module operably coupled to the detection chamber, which regulates temperature within the chamber during operation of the device. An optical train detects signal(s) produced at the array during operation of the device.

[0031] All of the dimensional features of the chamber to reduce background noted with reference to the methods optionally apply to the device. For example, the device can be less than about 500μm in depth in at least one dimension proximal to the array, e.g., between about

10μm and about 200μm in depth in at least one dimension proximal to the array. The chamber surface on which the array is formed can be composed of any suitable material, e.g., a ceramic, glass, quartz, or a polymer. In several embodiments, e.g., those utilizing epi-fluorescence, the surface will be at least partially transparent.

[0032] As noted with reference to the methods, the capture nucleic acids on the array are typically present at a non-rate limiting density during operation of the device. The array optionally includes a plurality of capture nucleic acid types, e.g., localized to spatially distinct regions of the array. For example, 5 or more different capture nucleic acid types can be present on the array, e.g., up to about 100 or more different types. The capture nucleic acids are optionally coupled to a thermostable coating on the surface of the chamber, facilitating thermocycling of the array. Example coating can optionally include: a chemically reactive group, an electrophilic group, an NHS ester, a tetra- or pentafluorophenyl ester, a mono- or dinitrophenyl ester, a thioester, an isocyanate, an isothiocyanate, an acyl azide, an epoxide, an aziridine, an aldehyde, an α,β-unsaturated ketone or amide comprising a vinyl ketone or a maleimide, an acyl halide, a sulfonyl halide, an imidate, a cyclic acid anhydride, a group active in a cycloaddition reaction, an alkene, a diene, an alkyne, an azide, or a combination thereof.

[0033] The thermo-regulatory module optionally includes features that facilitate thermocycling, such as a thermoelectric module, a Peltier device, a cooling fan, a heat sink, a metal plate configured to mate with a portion of an outer surface of the chamber, etc. Typically, the thermo regulatory module has a feedback enabled control system operably coupled to a computer which controls or is part of the module.

[0034] The optical train can include or be operably coupled to an epifluorescent detection system. Typical optical train components include any of: an excitation light source, an arc lamp, a mercury arc lamp, an LED, a lens, an optical filter, a prism, a camera, a photodetector, a CMOS camera, and/or a CCD array. The device can also include or be coupled to an array reader module, which correlates a position of the signal in the array to a nucleic acid to be detected.

[0035] The device or system can include or be operably coupled to system instructions, e.g., embodied in a computer or computer readable medium. The instructions can control any aspect of the device or system, e.g., to correlate one or more measurements of signal intensity

and a number of amplification cycles performed by the thermo-regulatory module to determine a concentration of a target nucleic acid detected by the device.

[0036] A system can include the device, e.g., operably coupled to a computer. The computer can include, e.g., instructions that control thermocycling by the thermo-regulatory module, and/or that specify when images are taken or viewed by the optical train, and/or can convert image information into signal intensity curves as a function of time, determine concentration of a target nucleic acid analyzed by the device, and/or the like. The computer can include instructions for normalizing signal intensity to account for background, e.g., for detecting local background for one or more regions of the array, and for normalizing array signal intensity measurements by correcting for said background. Similarly, the computer can include instructions for normalizing signal intensity by correcting for variability in array capture nucleic acid spotting, uneven field of view of different regions of the array, or the like.

[0037] The invention includes, in one aspect, a nucleic acid detection consumable, e.g., for use with the devices and systems of the invention, e.g., to practice the methods of the invention. The consumable can include, e.g., a thin chamber less than about 500μm in depth, where the chamber includes an optically transparent window that has a high efficiency capture nucleic acid array disposed on an inner surface of the window. The consumable can also include at least one reagent delivery port, e.g., fluidly coupled to the chamber. Typically, the consumable is configured to permit thermocycling of fluid within the chamber.

[0038] All of the features noted above with reference to the array and chamber in the context of the devices, systems and methods of the invention apply to the consumable as well (and vice-versa). For example, the nucleic acid array can include a plurality of different capture nucleic acid types, which types are located in spatially distinct regions of the array. The density of the capture nucleic acids can be about, e.g., 2,000 fmol/cm^2 or greater, 2,500 fmol/cm^2 or greater, 3,000 fmol/cm^2 or greater, 4,000 fmol/cm^2 or greater, 4,500 fmol/cm^2 or greater, or 5,000 fmol/cm^2 or greater.

[0039] Similarly, the chamber can include a first upper surface comprising the reagent delivery port, and a bottom transparent surface comprising the window, e.g., where the top and bottom surface are joined by sidewalls formed of a pressure-sensitive adhesive material. Other structures for joining the top and bottom surface to form the chamber can also be used. For

example, the top and bottom surface can be joined together by a gasket or shaped feature on the upper or lower surface, or both. The gasket or feature is optionally fused or adhered to a corresponding region of the upper or lower surface, or both. In some embodiments, the gasket or feature directs flow of a UV curable adhesive, which adhesive is flowed between the upper and lower surfaces and exposed to UV light, thereby joining the upper and lower surfaces. In other embodiments, the upper and lower surfaces can be ultrasonically fused together, with the gasket or feature delimiting regions that are fused. In another example, the feature is a transparent region on either the upper or lower surface and a corresponding shaded region on a cognate upper or lower surface. In this embodiment, the upper and lower surfaces can be laser welded together by directing laser light through the transparent region and onto the shaded region.

[0040] The capture nucleic acid array is typically coupled to a thermally stable coating on the window. For example, the coating can include a chemically reactive group, an electrophilic group, an NHS ester, a tetra- or pentafluorophenyl ester, a mono- or dinitrophenyl ester, a thioester, an isocyanate, an isothiocyanate, an acyl azide, an epoxide, an aziridine, an aldehyde, an α,β-unsaturated ketone or amide comprising a vinyl ketone or a maleimide, an acyl halide, a sulfonyl halide, an imidate, a cyclic acid anhydride, a group active in a cycloaddition reaction, an alkene, a diene, an alkyne, an azide, or a combination thereof. The window itself can include, e.g., glass, quartz, a ceramic, a polymer or other transparent material.

[0041] All of the features noted above with respect to the methods, systems and devices apply with respect to the configuration of the chamber in the consumable. For example, the chamber can be between about 10μm and about 200μm in depth, e.g., about 140 μm in depth. The chamber can be significantly wider in other dimensions, e.g., between about 1 mm and about 50 mm in average diameter. In one specific embodiment, the chamber is between about 10 mm and about 20 mm in average diameter.

[0042] The invention includes kits, e.g., comprising the consumable of the invention. The kits can also include packaging materials, instructions for practicing the methods, control reagents (e.g., control templates, probes, or primers, e.g., which bind to control sites on an array of the consumable).

[0043] The methods, systems, devices, consumables and kits can be used in combination, e.g., with the kit providing the consumable for use in a system or device of the invention, e.g., to practice the methods of the invention. Unless stated otherwise, steps of the methods optionally have corresponding structural features in the systems, devices, consumables or kits, and vice-versa.

BRIEF DESCRIPTION OF THE FIGURES

[0044] Figure 1A and 1B are schematic illustrations of PCR probes of the invention.

[0045] Figure 2 is a schematic of a PCR chamber of the invention.

[0046] Figure 3 is a graph showing array based real time PCR curves for copy number titration for a three step amplification reaction.

[0047] Figure 4 is a graph showing solution based real time PCR curves generated from aliquots of solutions.

[0048] Figure 5 is a graph showing an array based real time PCR curve generated with an unquenched probe.

[0049] Figure 6 is a graph showing real time PCR curves for a multiplexed amplification.

[0050] Figure 7 is a graph showing array-based real time PCR curves for a 10-plex reaction with no target added.

[0051] Figure 8 is a graph showing array-based real time PCR curves with a 10-plex panel and 3 targets present at 10^4 copies each.

[0052] Figure 9 is a graph showing real-time kinetics of hybridization of a 5' flap mimic.

[0053] Figure 10 is a methods schematic.

[0054] Figure 11 is a schematic system illustration.

[0055] Figure 12 is a graph showing array based real time PCR curves for copy number titration for a two step amplification reaction.

[0056] Figure 13 is a plot showing the relation of reaction chamber thickness to the signal to background ratio.

[0057] Figure 14 is a schematic illustration of an overall detection system for mobile substrate embodiments of the invention.

DETAILED DESCRIPTION

[0058] Methods of performing target nucleic acid amplification, detection and real-time quantification are a feature of the invention. In the methods, amplification of the target nucleic acid releases a target-specific labeled probe fragment that hybridizes to an array; the array is distributed in the chamber where the amplification takes place. Signal is detected from the array, providing both detection and real-time quantification of the target nucleic acid.

[0059] The invention also provides reaction chambers, typically formatted as consumables that comprise nucleic acid detection arrays within the chamber, as well as devices and systems that interact with the consumables.

METHODS

[0060] The invention provides methods of detecting and quantifying one or more target nucleic acids in a sample, in real time. The methods are highly amenable to multiplexing, enabling specific detection and quantification of a larger number of different target nucleic acids using one chamber reaction and detection than can be achieved using available solution-based real-time nucleic acid detection methods. This is because the invention utilizes array-based detection of analytes (with the array being in contact with the analytes), rather than solution-phase spectral detection. A nucleic acid detection array has significantly greater ability to resolve analytes via array position discrimination as compared to discrimination of, e.g., different dye labels in solution. By way of comparison, it is possible to construct arrays that simultaneously detect thousands of different analytes, while it is typically not possible to detect more than about 5 differently labeled fluorophores in solution.

[0061] **Figure 10** provides a partial overview of the method. As shown, a primer is hybridized to a template along with a labeled probe. The probe comprises an orthogonal sequence that is not complimentary to the template (a "flap"), coupled to a label moiety. The probe is cleaved during an amplification reaction (e.g., a PCR amplification cycle). In one convenient approach, the natural nuclease activity of a polymerase is used to cleave the flap—in this approach, primer extension by the polymerase results in cleavage of the flap by nuclease action of the polymerase as it encounters the junction between the flap and the template. This releases the flap as a labeled probe fragment, which is then hybridized to the array, e.g., by

adjusting the temperature to conditions that permit specific hybridization. Detection of the label on the array provides for detection and quantification of the template, in real time.

[0062] In general, a sample that is to be tested for the presence (or absence) of one or more target nucleic acid(s) is subjected to an amplification reaction. The reaction can easily be multiplexed to amplify, detect and quantify between about 10 and about 100 or more different nucleic acids, in a single reaction chamber. For example, about 10, about 20, about 30, about 40, about 50, about 60, about 70, about 80, about 90, or about 100 or more nucleic acids can be detected in a single amplification/ detection chamber. A working example herein demonstrating simultaneous amplification, detection and quantification of 10 different target nucleic acids in a reaction/ detection chamber is shown below. This example, and the capabilities of the method herein, exceeds the capabilities of typical spectrally-limited, solution-based multiplex detection.

[0063] In the methods, each target nucleic acid to be detected is specifically amplified using at least one, and generally two amplification primers (the use of two primers adds specificity to the reaction, and speeds the rate of product formation, as compared to a single primer). The primers are typically specifically hybridized to the target nucleic acid(s) in the sample, and extended using a polymerase, e.g., in a standard polymerase chain reaction (PCR). The design and construction of amplification primers that can be used to amplify a target nucleic acid of interest follows known methods. For details regarding PCR primer design, see e.g., Anton Yuryev (Editor) (2007) PCR Primer Design (Methods in Molecular Biology) [Hardcover] Humana Press; 1st edition ISBN-10: 158829725X, ISBN-13: 978-1588297259, as well as the references noted below.

[0064] PCR amplification using the primers on the target template nucleic acids can be performed using appropriate reaction conditions, including use of standard amplification buffers, enzymes, temperatures, and cycle times. For a review of PCR techniques, including hybridization conditions, buffers, reagents, reaction cycle times, and the like, see, e.g., Yuryev (*above*), van Pelt-Verkuil et al. (2010) Principles and Technical Aspects of PCR Amplification Springer; 1st Edition ISBN-10: 9048175798, ISBN-13: 978-9048175796; Bustin (Ed) (2009) The PCR Revolution: Basic Technologies and Applications Cambridge University Press; 1st edition ISBN-10: 0521882311, ISBN-13: 978-0521882316; Viljoen et al. (2005) Molecular

Diagnostic PCR Handbook Springer, ISBN 1402034032; Kaufman et al. (2003) Handbook of Molecular and Cellular Methods in Biology and Medicine Second Edition Ceske (ed) CRC Press (Kaufman); The Nucleic Acid Protocols Handbook Ralph Rapley (ed) (2000) Cold Spring Harbor, Humana Press Inc (Rapley); Chen et al. (ed) PCR Cloning Protocols, Second Edition (Methods in Molecular Biology, volume 192) Humana Press; PCR Protocols A Guide to Methods and Applications (Innis *et al.* eds) Academic Press Inc. San Diego, CA (1990) (Innis). Amplification conditions, primer design, and other details applicable to real-time based PCR methods are described, e.g., in Logan et al. (eds.) (2009) Real-Time PCR: Current Technology and Applications, Caister Academic Press, 1st edition ISBN-10: 1904455395, ISBN-13: 978-1904455394, and M Tevfik Dorak (Editor) (2006) Real-time PCR (Advanced Methods) Taylor & Francis, 1st edition ISBN-10: 041537734X ISBN-13: 978-0415377348.

[0065] A labeled probe specific for each target nucleic acid in the sample is hybridized along with the amplification primer(s) to the target nucleic acid(s). The amplification reaction cleaves the template-hybridized labeled probe to release a labeled probe fragment. This labeled fragment then hybridizes to the array in the reaction chamber, as shown in **Figure 10**.

[0066] **Figure 1A** schematically shows a probe useful in the methods of the invention. The probe comprises region A that is complimentary to a target nucleic acid. The probe also comprises "flap" B, which is not complimentary to the target nucleic acid. Label E is attached to flap B. Label E is shown in the terminal position, but the label can, in fact, be formatted at any point along Flap B. For example, any of a variety of nucleotides can be labeled, and used in standard or slightly modified nucleic acid synthesis protocols to provide a label at any desired position on the probe.

[0067] In **Figure 1A**, Optional region C, comprising label quencher D, is complimentary to a portion of flap B. Under appropriate solution conditions, region C base-pairs with flap B, bringing label E and quencher D into proximity, thereby quenching label E. This reduces signal background of the solution phase in the reaction/ detection chamber, but probe quenching is not required for practice of the invention. One surprising aspect of the invention is that it is possible to specifically detect probe fragments bound to the array, even where there is unquenched probe in solution proximal to the array. A working example of this embodiment is described herein. In general, the use of high efficiency arrays in reaction/

detection chambers that are configured to reduce solution-phase background permits discrimination of signal at the array from signal background in solution in the methods, consumables, devices and systems of the invention.

[0068] Depending upon the assay configuration, a wide variety of different label groups may be employed for labeling the labeled probe. As noted, such labels typically include fluorescent labeling groups, which may include individual fluorophores or interactive dye pairs or groups, e.g., FRET pairs, as well as donor/quencher pairs. A range of different fluorescent labeling groups suitable for labeling nucleic acid probes are described in, e.g., the Molecular Probes Handbook, 11th Edition (Life Technologies, Inc.).

[0069] While much of the discussion herein is directed to PCR based amplification, other amplification reactions can be substituted. For example, multienzyme systems involving cleavage reactions coupled to amplification reactions, such as those including the cleavage of scissile bonds (see, e.g., US 5,011,769; US 5,660,988; US 5,403,711; US 6,251,600) and forked nucleic acid structures (US 7,361,467; US 5,422,253; US 7,122,364; US 6,692,917) can be used. Helicase dependent amplification coupled to TaqMan like cleavage (Tong, Y et > al 2008 BioTechniques 45:543-557) can also be used. Nucleic acid sequence based amplification (NASBA), or the ligase chain reaction (LCR) can be used. In NASBA-based approaches, the probe can be hybridized to a template along with amplification primer(s), as in PCR. The probe can be cleaved by the nuclease action of reverse transcriptase, or an added endonuclease, releasing the probe fragment in a manner similar to the release by a polymerase in PCR. One potential advantage of NASBA is that no thermocycling is required. This simplifies overall device and system requirements. For a description of NASBA, see, e.g., Compton (1991), "Nucleic acid sequence-based amplification," Nature 350 (6313): 91–2. For the use of NASBA to detect, e.g., pathogenic nucleic acids, see, e.g., Keightley et al. (2005) "Real-time NASBA detection of SARS-associated coronavirus and comparison with real-time reverse transcription-PCR," Journal of Medical Virology 77 (4): 602–8. When an LCR-style reaction is used, the probe can be cleaved using an endonuclease, rather than relying on nuclease activity of the amplification enzyme.

[0070] In the methods herein, a detection chamber that has at least one high efficiency nucleic acid detection array on at least one inner surface of the chamber is provided. The high

efficiency array typically has a non-rate limiting number of capture nucleic acids that permits an efficient capture of probe fragments produced by the amplification reaction in the chamber. The capture nucleic acids are configured to capture relatively small probe nucleic acids, which also increases array efficiency. The chamber is configured to reduce signal background proximal to the array, e.g., by shaping the chamber to reduce background. For example, background is reduced by making the chamber thin (shallow) proximal to (e.g., above or below) the array; e.g., the chamber is typically about 500μm or shallower above or below the array, although detection in chambers as deep as 1mm or larger can work. Further details regarding the reaction chamber and array is described below with reference to the consumable useful in the methods.

[0071] Signals captured by the array are detected and signal intensity is measured. Signal intensity is correlated to the presence and/or quantity of the target nucleic acid present in the sample. Typically, the sample is amplified for more than 1 cycle before initial detection, to increase the level of signal by increasing the number of probe fragments released by the amplification. For example, the target nucleic acid can optionally be amplified for at least, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10 or more amplification cycles prior to detecting signal from the array.

[0072] In one typical embodiment, fluorescent or other optical images are captured from the array at selected times, temperatures, and amplification cycle intervals, during the amplification reactions. These images are analyzed to determine whether the target nucleic acid(s) are present in the sample, and to provide quantification of starting target nucleic acid concentrations in the sample. The images are analyzed using a combination of mean gray intensity measurements, background correction and baseline adjustments. The background can be measured locally for each spot in the array. The background is computed by measuring the image intensity of a concentric annulus of the solution surrounding the array region (e.g., array spot) of interest. The signal from each region is then corrected to account for local background in the region. The corrected signal from each region can be further normalized to account for variability in spotting, as well as uneven illumination in the field of view. The average of the corrected intensity measurements obtained from the first few cycles, typically between cycle 5 and 15, are used to adjust the baseline and normalize measurements from each region.

[0073] Further details regarding methods of quantifying nucleic acids based upon signal intensity measurements following amplification can be found, e.g., in the references noted in above this section and in Jang B. Rampal (Editor) (2010) Microarrays: Volume 2, Applications and Data Analysis (Methods in Molecular Biology) Humana Press; 2nd Edition ISBN-10: 1617378526, ISBN-13: 978-1617378522; Stephen A. Bustin (Editor) (2004) A-Z of Quantitative PCR (IUL Biotechnology, No. 5) (IUL Biotechnology Series) International University Line; 1st edition ISBN-10: 0963681788, ISBN-13: 978-0963681782; and in Kamberova and Shah (2002) DNA Array Image Analysis: Nuts & Bolts (Nuts & Bolts series) DNA Press; 2nd edition ISBN-10: 0966402758, ISBN-13: 978-0966402759.

[0074] In an alternate configuration, the capture probes may optionally be coupled to a mobile substrate, such as beads, resins, particles or the like (generally referred to interchangeably herein as "beads"), rather than a static substrate. For example, as noted elsewhere herein, a planar substrate may be used to provide arrayed capture probes that will hybridize with the cleaved probe fragments produced during the amplification of the target nucleic acid sequence or sequences within the sample material. The presence of a given target nucleic acid sequence is detected by detecting which capture probe position on the array the probe fragments hybridize. Because each probe fragment is specific to a particular target sequence, if that probe fragment is present, it is indicative that the target was present and amplified. In a mobile phase substrate, each different type of capture probe in a given analysis is coupled to a different mobile substrate that also bears a unique label. The mobile substrates are then passed through a detection channel in order to identify both the bead, and by implication, the capture probe, and whether the labeled probe fragment is present. If the labeled probe is detected on a given bead that corresponds to a particular capture probe, it is indicative that the target sequence associated with that probe fragment (and complementary capture probe) was present in the sample and amplified. This aspect of the invention may be employed in endpoint detection, e.g., after completion of the overall amplification reaction, but may also be employed in quantitative analysis, e.g., siphoning a fraction of beads from the amplification mixture after one or more amplification cycles, and measuring the labeled probe fragment signal intensity from the beads.

[0075] The concentration of captured labeled probe fragments on a given bead will provide a sufficiently high signal to background ratio in the detection channel such that separation of the beads from the reaction mixture is not necessary. In addition, as with the array based substrates, the inclusion of a secondary structure in the intact probe and/or optional quenching group permits greater ability to distinguish between probe fragment and intact probe background signal, whether in solution or from unintended binding to the mobile substrate. In some cases, the nature of the intact probe's secondary structure would also be expected to give rise to steric hindrance in binding with the capture probes on the mobile substrate, resulting in some cases in a reduced likelihood that the intact probe would bind to the beads.

[0076] A variety of different bead types may be used in conjunction with this aspect of the invention. For example, polystyrene, cellulosic, acrylic, vinyl, silica, paramagnetic or other inorganic particles, or any of a variety of other bead types may be employed. As noted, the beads with typically be differentially labeled with a unique label signature. Again, a variety of different label types may be used, including organic fluorescent labels, inorganic fluorescent labels (e.g., quantum dots), luminescent labels, electrochemical labels, or the like. Such labels are widely commercially available and configured to be readily coupled to appropriately activated beads. In the case of fluorescent labeling groups, a large number of label signatures may be provided by providing different combinations of 2, 3, 4 or more spectrally distinct fluorescent labeling groups and different levels of each label, so as to provide a broad range of unique label signatures without having to use a broad spectrum of excitation radiation, e.g., multiple lasers.

[0077] The method is typically performed using the devices, systems, consumables and kits herein. All features of the devices, systems and consumables can be provided to practice the methods herein, and the methods herein can be practiced in combination with the devices, systems, consumables and kits.

CONSUMABLES

[0078] The one-pot reaction chambers of the invention are configured to reduce signal background. High-efficiency arrays are formed on at least one inner surface of the chambers. The arrays typically are in contact with amplification reactants and products during both

amplification and array hybridization steps of the methods. This allows a user to run one or more amplification reaction cycles, detect the results by monitoring signal from the array in real time, and to then run one or more additional amplification cycles, again followed by detection. Thus, signal intensity from the array can be used to both detect and quantify a nucleic acid of interest, in real time.

[0079] The consumables of the invention include a chamber and a high efficiency array on an inner surface of the chamber. The chamber is typically thin (shallow), e.g., less than about 1 mm in depth. In general, the thinner the chamber, the less solution above the array, which reduces signal background from labeled probes or probe fragments in the solution. Typical desirable chamber depths are in the range of about 1μm to about 500μm. For ease of fabrication of the consumable, the chamber is often in the range of about 10μm to about 250μm in depth above the array, e.g., about 100μm to about 150 μm in depth. The chamber can include a surface that has a reagent delivery port, e.g., for delivery of a sample by manual or automated pipettor.

[0080] **Figure 2** provides a blow-up schematic of an example consumable. In this example, bottom surface layer **1** and upper surface layer **2**, are joined by middle layer **3**. Cutout **4** forms a chamber upon assembly of layers **1**, **2**, and **3**. Port(s) **5** form(s) a convenient way to deliver buffer and reagents to the chamber upon assembly. A high efficiency array can be formed on the top or bottom layer in the region that forms the top or bottom surface of the cutout. In one convenient embodiment, where epifluorescent detection is used for detection of label bound to the array, the array is fabricated on the lower surface, with the consumable being configured to be viewed by detection optics located in the devices and systems of the invention below the lower surface. Generally, either the top or bottom surface (or both) will include a window through which detection optics can view the array.

[0081] Middle layer **3** can take any of a variety of forms, depending on the consumable assembly method to be used. In one convenient embodiment, top and bottom surfaces **1** and **2** are joined by layer 3 formed of a pressure-sensitive adhesive material. Pressure sensitive adhesive layers (e.g., tape) are well known and widely available. See, e.g., Benedek and Feldstein (Editors) (2008) Handbook of Pressure-Sensitive Adhesives and Products: Volume 1: Fundamentals of Pressure Sensitivity, Volume 2: Technology of Pressure-Sensitive Adhesives

and Products, Volume 3: Applications of Pressure-Sensitive Products, CRC Press; 1st edition ISBN-10: 1420059343, ISBN-13: 978-1420059342.

[0082] Other fabrication methods for joining the top and bottom surface to form the chamber can also be used. For example, the top and bottom surfaces can be joined together by a gasket or shaped feature on the upper or lower surface, or both. The gasket or feature is optionally fused or adhered to a corresponding region of the upper or lower surface, or both. Silicon and polymer chip fabrication methods can be applied to form features in the top or bottom surface. For an introduction to feature fabrication methods, including micro-feature fabrication, see, e.g., Franssila (2010) Introduction to Microfabrication Wiley; 2nd edition ISBN-10: 0470749830, ISBN-13: 978-0470749838; Shen and Lin (2009) "Analysis of mold insert fabrication for the processing of microfluidic chip" Polymer Engineering and Science Publisher: Society of Plastics Engineers, Inc. Volume: 49 Issue: 1 Page: 104(11); Abgrall (2009) Nanofluidics ISBN-10: 159693350X, ISBN-13: 978-1596933507; Kaajakari (2009) Practical MEMS: Design of microsystems, accelerometers, gyroscopes, RF MEMS, optical MEMS, and microfluidic systems Small Gear Publishing ISBN-10: 0982299109, ISBN-13: 978-0982299104; Saliterman (2006) Fundamentals of BioMEMS and Medical Microdevices SPIE Publications ISBN-10: 0819459771, ISBN-13: 978-0819459770; Madou (2002) Fundamentals of Microfabrication: The Science of Miniaturization, Second Edition CRC Press; ISBN-10: 0849308267, ISBN-13: 978-0849308260. These fabrication methods can be used to form essentially any feature that is desired on the top or bottom surface, eliminating the need for an intermediate layer. For example, a depression can be formed in the top or bottom surface (or both) and the two layers joined, thereby forming the chamber.

[0083] In some embodiments, the gasket or feature directs flow of a UV or radiation curable adhesive. This adhesive is flowed between the upper and lower surfaces and exposed to UV light or radiation (e.g., electron beam, or "EB" radiation), thereby joining the upper and lower surfaces. For a description of available adhesives, including UV and radiation curable adhesives, see, e.g., Ebnesajjad (2010) Handbook of Adhesives and Surface Preparation: Technology, Applications and Manufacturing William Andrew; 1st edition ISBN-10: 1437744613, ISBN-13: 978-1437744613; Drobny (2010) Radiation Technology for Polymers, Second Edition CRC Press; 2 edition ISBN-10: 1420094041, ISBN-13: 978-1420094046.

[0084] In other embodiments, the upper and lower surfaces can be ultrasonically fused together, with the gasket or surface feature delimiting regions that are fused and the chamber or other structural features to be produced in the consumable. Ultrasonic welding and related techniques useful for fusing materials are taught, e.g., in Astashev and Babitsky (2010) Ultrasonic Processes and Machines: Dynamics, Control and Applications (Foundations of Engineering Mechanics) Springer; 1st Edition. edition ISBN-10: 3642091245, ISBN-13: 978-3642091247; and Leaversuch (2002) "How to use those fancy ultrasonic welding controls," Plastics Technology 48(10): 70-76.

[0085] In another example, the feature is a transparent region on either the upper or lower surface and a corresponding shaded region on a cognate upper or lower surface. In this embodiment, the upper and lower surfaces can be laser welded together by directing laser light through the transparent region and onto the shaded region. Laser welding methods are taught, e.g., in Steen et al. (2010) Laser Material Processing Springer; 4th ed. edition ISBN-10: 1849960615, ISBN-13: 978-1849960618; Kannatey-Asibu (2009) Principles of Laser Materials Processing (Wiley Series on Processing of Engineering Materials) Wiley ISBN-10: 0470177985, ISBN-13: 978-0470177983; and Duley (1998) Laser Welding Wiley-Interscience ISBN-10: 0471246794, ISBN-13: 978-0471246794.

[0086] The capture nucleic acid array is typically coupled to a thermally stable coating on the window. The window itself can include, e.g., glass, quartz, a ceramic, a polymer or other transparent material. A variety of coatings suitable for coating the window are available. In general, the coating is selected based upon compatibility with the array substrate (e.g., whether the chamber surface that the array is attached to is glass or a polymer), ability to be derivatized or treated to include reactive groups suitable for attaching array members, and compatibility with process conditions (e.g., thermostability, photostability, etc.). For example, the coating can include a chemically reactive group, an electrophilic group, an NHS ester, a tetra- or pentafluorophenyl ester, a mono- or dinitrophenyl ester, a thioester, an isocyanate, an isothiocyanate, an acyl azide, an epoxide, an aziridine, an aldehyde, an α,β-unsaturated ketone or amide comprising a vinyl ketone or a maleimide, an acyl halide, a sulfonyl halide, an imidate, a cyclic acid anhydride, a group active in a cycloaddition reaction, an alkene, a diene, an alkyne, an azide, or a combination thereof. For a description of surface coatings and their

use in attaching biomolecules to surfaces see, e.g., Plackett (Editor) (2011) Biopolymers: New Materials for Sustainable Films and Coatings Wiley ISBN-10: 0470683414, ISBN-13: 978-0470683415; Niemeyer (Editor) (2010) Bioconjugation Protocols: Strategies and Methods (Methods in Molecular Biology) Humana Press; 1st Edition. edition ISBN-10: 1617373540, ISBN-13: 978-1617373541; Lahann (Editor) (2009) Click Chemistry for Biotechnology and Materials Science Wiley ISBN-10: 0470699701, ISBN-13: 978-0470699706; Hermanson (2008) Bioconjugate Techniques, Second Edition Academic Press; 2nd edition ISBN-10: 0123705010, ISBN-13: 978-0123705013. Wuts and Greene (2006) Greene's Protective Groups in Organic Synthesis Wiley-Interscience; 4th edition ISBN-10: 0471697540, # ISBN-13: 978-0471697541; Wittmann (Editor) (2006) Immobilisation of DNA on Chips II (Topics in Current Chemistry) Springer; 1st edition ISBN-10: 3540284362, ISBN-13: 978-3540284369; Licari (2003) Coating Materials for Electronic Applications: Polymers, Processing, Reliability, Testing (Materials and Processes for Electronic Applications) William Andrew ISBN-10: 0815514921, ISBN-13: 978-0815514923; Conk (2002) Fabrication Techniques for Micro-Optical Device Arrays Storming Media ISBN-10: 1423509641, ISBN-13: 978-1423509646, and Oil and Colour Chemists' Association (1993) Surface Coatings - Raw materials and their usage, Third Edition Springer; 3rd edition, ISBN-10: 0412552108, ISBN-13: 978-0412552106.

[0087] Methods of making nucleic acid arrays are available and can be adapted to the invention by forming the arrays on an inner chamber surface. Techniques for forming nucleic acid microarrays that can be used to form arrays on an inner chamber surface are described, e.g., in Rampal (Editor) Microarrays: Volume I: Synthesis Methods (Methods in Molecular Biology) Humana Press; 2nd Edition ISBN-10: 1617376639, ISBN-13: 978-1617376634; Müller and Nicolau (Editors) (2010) Microarray Technology and Its Applications (Biological and Medical Physics, Biomedical Engineering) Springer; 1st Edition. ISBN-10: 3642061826, ISBN-13: 978-3642061820; Xing and Cheng (Eds.) (2010) Biochips: Technology and Applications (Biological and Medical Physics, Biomedical Engineering) Springer; 1st Edition. ISBN-10: 3642055850, ISBN-13: 978-3642055850; Dill et al. (eds) (2010) Microarrays: Preparation, Microfluidics, Detection Methods, and Biological Applications (Integrated Analytical Systems) Springer ISBN-10: 1441924906, ISBN-13: 978-1441924902; Whittmann (2010) Immobilisation of DNA on Chips II (Topics in Current Chemistry) Springer; 1st Edition

ISBN-10: 3642066666, ISBN-13: 978-3642066665; Rampal (2010) DNA Arrays: Methods and Protocols (Methods in Molecular Biology) Humana Press; 1st Edition ISBN-10: 1617372048, ISBN-13: 978-1617372049; Schena (Author, Editor) (2007) DNA Microarrays (Methods Express) Scion Publishing; 1st edition, ISBN-10: 1904842151, ISBN-13: 978-1904842156; Appasani (Editor) (2007) Bioarrays: From Basics to Diagnostics Humana Press; 1st edition ISBN-10: 1588294765, ISBN-13: 978-1588294760; and Ulrike Nuber (Editor) (2007) DNA Microarrays (Advanced Methods) Taylor & Francis ISBN-10: 0415358663, ISBN-13: 978-0415358668. Techniques for attaching DNA to a surface to form an array can include any of a variety of spotting methods, use of chemically reactive surfaces or coatings, light-directed synthesis, DNA printing techniques, and many other methods available in the art.

[0088] Methods of quantifying array densities are provided in the references noted above and in Gong et al. (2006) "Multi-technique Comparisons of Immobilized and Hybridized Oligonucleotide Surface Density on Commercial Amine-Reactive Microarray Slides" Anal. Chem. 78:2342-2351.

[0089] The consumable can be packaged in a container or packaging materials to form a kit. The kit can also include components useful in using the consumable, e.g., control reagents (e.g., a control template, control probe, control primers, etc.), buffers, or the like.

DEVICES AND SYSTEMS

[0090] Devices and systems that use the consumable and/or practice the methods of the invention are a feature of the invention as well. The device or system can include the features of the consumable, e.g., a reaction chamber and array (whether formatted as a consumable, or as dedicated portion of the device). Most typically, the device will typically have a receiver, e.g., a stage that mounts the consumable noted above, along with detection optics for monitoring the array, modules for thermocycling the chamber, and a computer with system instructions that control thermocycling, detection, and post-signal processing.

[0091] An example schematic system is illustrated in **Figure 11**. As shown, consumable **10** is mounted on stage **20**. Environmental control module (ECM) **30** (e.g., comprising a Peltier device, cooling fans, etc.) provides environmental control (e.g., thermocycling of temperature). Illumination light is provided by source **40** (e.g., a lamp, arc lamp, LED, laser, or the like). Optical train **50** directs light from illumination source **40** to

consumable **10**. Signals from consumable **10** are detected by the optical train and signal information is transmitted to computer **60**. Computer **60** optionally also controls ECM **30** Signal information can be processed by computer **60**, and outputted to user viewable display **70**, or to a printer, or both. ECM **30** can be mounted above or below consumable **10** and additional viewing optics **80** (located above or below stage **20**) can be included.

[0092] The stage/ receiver is configured to mount the consumable for thermocycling and analysis. The stage can include registration and alignment features such as alignment arms, detents, holes, pegs, etc., that mate with corresponding features of the consumable. The stage can include a cassette that receives and orients the consumable, placing it in operable linkage with other device elements, although this is not necessary in many embodiments, e.g., where the consumable mounts directly to the stage. Device elements are configured to operate with the consumable and can include a fluidic delivery system for delivering buffers and reagents to the consumable, a thermocycling or other temperature control or environmental control module, detection optics, etc. In embodiments where the chamber is build into the device, rather being incorporated into the consumable, the device elements are typically configured to operate on or proximal to the chamber.

[0093] Fluid delivery to the consumable can be done by the device or system, or can be performed prior to loading the consumable into the device or system. Fluid handling elements can be integrated into the device or system, or can be formatted into a separate processing station discrete from the device or system. Fluid handling elements can include pipettors (manual or automated) that deliver reagents or buffers to ports in the consumable, or can include capillaries, microfabricated device channels, or the like. Manual and automated pipettors and pipettor systems that can be used to load the consumable are available from a variety of sources, including Thermo Scientific (USA), Eppendorf (Germany), Labtronics (Canada) and many others. Generally speaking, a variety of fluidic handling systems are available and can be incorporated into the devices and systems of the invention. See, e.g., Kirby (2010) Micro- and Nanoscale Fluid Mechanics: Transport in Microfluidic Devices ISBN-10: 0521119030, ISBN-13: 978-0521119030; Bruus (2007) Theoretical Microfluidics (Oxford Master Series in Physics) Oxford University Press, USA ISBN-10: 0199235090, ISBN-13: 978-0199235094; Nguyen (2006) Fundamentals And Applications of Microfluidics,

Second Edition (Integrated Microsystems) ISBN-10: 1580539726, ISBN-13: 978-1580539722; Wells (2003) High Throughput Bioanalytical Sample Preparation: Methods and Automation Strategies (Progress in Pharmaceutical and Biomedical Analysis) Elsevier Science; 1st edition ISBN-10: 044451029X, ISBN-13: 978-0444510297. The consumable optionally comprises ports that are configured to mate with the delivery system, e.g., ports of an appropriate dimension for loading by a pipette or capillary delivery device.

[0094] The ECM or thermo-regulatory module can include features that facilitate thermocycling, such as a thermoelectric module, a Peltier device, a cooling fan, a heat sink, a metal plate configured to mate with a portion of an outer surface of the chamber, a fluid bath, etc. Many such thermo-regulatory components are available for incorporation into the devices and systems of the invention. See, for example, Kennedy and Oswald (Editors) (2011) PCR Troubleshooting and Optimization: The Essential Guide, Caister Academic Press ISBN-10: 1904455727; ISBN-13: 978-1904455721; Bustin (2009) The PCR Revolution: Basic Technologies and Applications Cambridge University Press; 1st edition ISBN-10: 0521882311, ISBN-13: 978-0521882316; Wittwer et al. (eds.) (2004) Rapid Cycle Real-Time PCR-Methods and Applications Springer; 1 edition, ISBN-10: 3540206299, ISBN-13: 978-3540206293; Goldsmid (2009) Introduction to Thermoelectricity (Springer Series in Materials Science) Springer; 1st edition, ISBN-10: 3642007155, ISBN-13: 978-3642007156; Rowe (ed.) (2005) Thermoelectrics Handbook: Macro to Nano CRC Press; 1 edition, ISBN-10: 0849322642, ISBN-13: 978-0849322648. The thermo regulatory module can, e.g., be formatted into a cassette that receives the consumable, or can be mounted on the stage in operable proximity to the consumable.

[0095] Typically, the ECM or thermo regulatory module has a feedback enabled control system operably coupled to a computer which controls or is part of the module. Computer directed feedback enabled control is an available approach to instrument control. See, e.g., Tooley (2005) PC Based Instrumentation and Control, Third Edition, ISBN-10: 0750647167, ISBN-13: 978-0750647168; Dix et al. (2003) Human-Computer Interaction (3rd Edition) Prentice Hall, 3rd edition ISBN-10: 0130461091, ISBN-13: 978-0130461094. In general, system control is performed by a computer, which can use, e.g., a script file as an input to generate target temperatures and cycle time periods as well as to specify when images are to be

viewed/ taken by the detection optics. Photo images are typically taken at different times during a reaction and are analyzed by the computer to generate intensity curves as a function of time and thereby derive the concentration of the target.

[0096] The optical train can include any typical optical train components, or can be operably coupled to such components. The optical train directs illumination to the consumable, e.g., focused on an array of the consumable, or an array region. The optical train can also detect light (e.g., a fluorescent or luminescent signal) emitted from the array. For a description of available optical components, See, e.g., Kasap et al. (2009) Cambridge Illustrated Handbook of Optoelectronics and Photonics Cambridge University Press; 1st edition ISBN-10: 0521815967, ISBN-13: 978-0521815963; Bass et al. (2009) Handbook of Optics, Third Edition Volume I: Geometrical and Physical Optics, Polarized Light, Components and Instruments(set) McGraw-Hill Professional; 3rd edition, ISBN-10: 0071498893, ISBN-13: 978-0071498890; Bass et al. (2009) Handbook of Optics, Third Edition Volume II: Design, Fabrication and Testing, Sources and Detectors, Radiometry and Photometry McGraw-Hill Professional; 3rd edition ISBN-10: 0071498907, ISBN-13: 978-0071498906; Bass et al. (2009) Handbook of Optics, Third Edition Volume III: Vision and Vision Optics McGraw-Hill Professional, ISBN-10: 0071498915, ISBN-13: 978-0071498913; Bass et al. (2009) Handbook of Optics, Third Edition Volume IV: Optical Properties of Materials, Nonlinear Optics, Quantum Optics McGraw-Hill Professional, 3rd edition, ISBN-10: 0071498923, ISBN-13: 978-0071498920; Bass et al. (2009) Handbook of Optics, Third Edition Volume V: Atmospheric Optics, Modulators, Fiber Optics, X-Ray and Neutron Optics McGraw-Hill Professional; 3rd edition, ISBN-10: 0071633138, ISBN-13: 978-0071633130; and Gupta and Ballato (2006) The Handbook of Photonics, Second Edition, CRC Press, 2nd edition ISBN-10: 0849330955, ISBN-13: 978-0849330957. Typical optical train components include any of: an excitation light source, an arc lamp, a mercury arc lamp, an LED, a lens, an optical filter, a prism, a camera, a photodetector, a CMOS camera, and/or a CCD array. In one desirable embodiment, an epifluorescent detection system is used. The device can also include or be coupled to an array reader module, which correlates a position of the signal in the array to a nucleic acid to be detected.

[0097] In the context of the mobile substrate embodiments of the invention, in certain aspects, the reaction vessel may be coupled directly to a detection channel, e.g., within an integrated microfluidic channel system, or through an appropriate fluidic interface between the amplification mixture and the detection channel. Alternatively, a fluidic interface, such as are present in conventional flow cytometers, may be provided on the detection channel in order to sample the amplification reaction mixture. The detection channel is typically configured to have a dimension that permits substantially only single beads to traverse the channel at a given time. The detection channel will typically include a detection window allowing excitation of the beads and collection of the fluorescent signals emanating from the beads. In many cases, a fused silica or glass capillary or other transparent microfluidic channel is used as the detection channel.

[0098] The optical detection systems of the invention will typically include one or more excitation light sources capable of delivering excitation light at one or more excitation wavelengths. Also included will be an optical train that is configured to collect the light emanating from the detection channel, and filter excitation light from the fluorescent signals. The optical train also typically includes additional separation elements for transmitting the fluorescent signals, and for separating the fluorescent signal component(s) emanating from the bead and the signal component(s) emanating from the captured probe fragment.

[0099] Figure 14 provides a schematic illustration of an overall detection system 1400. As shown, the system includes first and second excitation light sources, such as lasers 1402 and 1404, that each provide excitation light at different wavelengths. Alternatively, a single broad spectrum light source or multiple narrow spectrum light sources may be used to deliver excitation light at the appropriate wavelength range or ranges to excite the detectable labels in the sample, e.g., those associated with the beads, and those associated with the labeled probe fragments.

[0100] Excitation beams, shown as the solid arrows, from each laser are directed to the detection channel 1408, e.g., through the use of directional optics, such as dichroic 1406. Light that emanates from the beads 1410 in the detection channel 1408, is collected by collection optics, e.g., objective lens 1412. The collected light is then passed through filter 1414 that is configured to pass the emitted fluorescence, shown as the dashed arrows, while rejecting the

collected excitation radiation. The collected fluorescence includes fluorescence emitted from the label on the captured probe fragments at a first emission spectrum, as well as fluorescent signals from the bead label signature, at one or more different emission spectra, depending upon the number of labels used in the beads. The collected fluorescence is then passed through dichroic 1416 that reflects the fluorescence from the captured probe fragments to a first detector 1420. The remaining fluorescent signature from the beads is then subjected to further separation by passing the signal through a second dichroic 1418, that reflects a first bead signal component to a second detector 1422, and passes a second bead signal component to the third detector 1424. The detectors are typically coupled to an appropriate processor or computer for storing signal data associated with detected beads, and analyzing the signal data to determine the identity of the bead, and thus the capture probe and associated target nucleic acid sequence. Additionally, the processor or computer may include programming to quantify signal data and originating target sequence copy number, where time course experiments are performed, e.g., beads are sampled after one or more amplification cycles in an overall amplification reaction.

[0101] The device or system can include or be operably coupled to system instructions, e.g., embodied in a computer or computer readable medium. The instructions can control any aspect of the device or system, e.g., to correlate one or more measurements of signal intensity and a number of amplification cycles performed by the thermo-regulatory module to determine a concentration of a target nucleic acid detected by the device.

[0102] A system can include a computer operably coupled to the other device components, e.g., through appropriate wiring, or through wireless connections. The computer can include, e.g., instructions that control thermocycling by the thermo-regulatory module, e.g., using feedback control as noted above, and/or that specify when images are taken or viewed by the optical train. The computer can receive or convert image information into digital information and/or signal intensity curves as a function of time, determine concentration of a target nucleic acid analyzed by the device, and/or the like. The computer can include instructions for normalizing signal intensity to account for background, e.g., for detecting local background for one or more regions of the array, and for normalizing array signal intensity measurements by correcting for said background. Similarly, the computer can include

instructions for normalizing signal intensity by correcting for variability in array capture nucleic acid spotting, uneven field of view of different regions of the array, or the like.

ADDITIONAL DEFINITIONS

[0103] Before describing the present invention in detail, it is to be understood that this invention is not limited to particular devices or biological systems, which can, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting. As used in this specification and the appended claims, the singular forms "a", "an" and "the" include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to "a surface" e.g., of the consumable chamber discussed herein, optionally includes a combination of two or more surfaces, and the like.

[0104] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. Although any methods and materials similar or equivalent to those described herein can be used in the practice for testing of the present invention, the preferred materials and methods are described herein. In describing and claiming the present invention, the following terminology is used in accordance with the definitions set out below.

[0105] An "amplification primer" is a moiety (e.g., a molecule) that can be extended in a template-dependent amplification reaction. Most typically, the primer will include or will be a nucleic acid that binds to the template under amplification conditions. Typically, the primer will comprise a terminus that can be extended by a polymerase (e.g., by a thermostable polymerase in a polymerase chain reaction), or by a ligase (e.g., as in a ligase chain reaction).

[0106] A "detection chamber" is a partly or fully enclosed structure in which a sample is analyzed or a target nucleic acids is detected. The chamber can be entirely closed, or can include ports or channels fluidly coupled to the chamber, e.g., for the delivery of reagents or reactants. The shape of the chamber can vary, depending, e.g., on the application and available system equipment. A chamber is "configured to reduce signal background proximal to the array" when it is dimensionally shaped to reduce signal background, e.g., by including a narrow dimension (e.g., chamber depth) near the array (thereby reducing the amount of solution-generated signal proximal to the array), or when the chamber is otherwise configured to reduce

background, e.g., by the use of coatings (e.g., optical coatings) or structures (e.g., baffles or other shaped structures proximal to the array). Typically, the chamber is configured to have a dimension (e.g., depth) proximal to the array, such that signal in solution is low enough to permit signal differences at the array to be detected. For example, in one embodiment, the chamber is less than about 1mm deep above the array; desirably the chamber is less than about 500μm in depth. Typically, the chamber is less than about 400μm, less than about 300μm, less than about 200μm, or less than about 150μm in depth above the array. In one example provided herein, the chamber is about 142μm in depth.

[0107] A "high-efficiency nucleic acid array" is an array of capture nucleic acids that efficiently hybridize to a probe or probe fragment under hybridization conditions. In typical embodiments, the array is formatted on an inner surface of a reaction/ detection chamber. The array can be formed by any conventional array technology, from spotting to chemical or photochemical synthesis on the surface. High efficiency is achieved by controlling the length of the region of the capture probe that recognizes the probe or fragment (shorter probes hybridize more efficiently than long probes, down to a minimum hybridization length for the hybridization conditions), and by controlling the number of capture nucleic acids in each array region. Capture sites can be made more efficient/ available for hybridization by including a linking sequence or structure between the capture site and the surface (thus formatting the capture sites at a selected distance from the surface, which can reduce surface effects on hybridization). For example, nucleic acid sequences or polyethylene glycol linkers (or both) can be used. The number of capture nucleic acids in each array region are distributed such that the number of sites available for hybridization for a given probe or fragment produced as a result of a typical amplification reaction is not rate limiting. As noted previously, this means that the number of sites available for binding labeled probe fragments produced during the amplification reaction is in excess, and preferably substantially in excess of the number of sites that would be saturated by the concentration of probe fragments in the reaction mixture after the amplification reaction.

[0108] A "labeled probe" is a molecule or compound that specifically hybridizes to a target nucleic acid under amplification conditions, and that comprises a moiety that is detectable, or that can be made detectable. Most typically, the labeled probe is a nucleic acid

that comprises an optical label such as a fluorophore, dye, lumophore, quantum dot, or the like. The label can be directly detectable, or can be in a quenched state, e.g., where the probe comprises a quencher moiety. In many embodiments herein, the labeled probe is cleaved during target nucleic acid amplification to release a probe fragment comprising a detectable label. For example, the labeled probe can include a fluorophore and a quencher, e.g., where an amplification reaction results in cleavage of the probe to release the labeled probe fragment. Most typically, the probe will include a "flap" region. This flap region does not base-pair with the target during hybridization, and is cleaved from the rest of the probe by a nuclease (e.g., nuclease activity of a polymerase), thereby forming the probe fragment.

EXAMPLES

[0109] The following examples are offered to illustrate, but not to limit the claimed invention. It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims.

EXAMPLE DETECTION SYSTEM

[0110] The detection system of this example allows for single chamber, multiplexed, real time PCR detection of a target nucleic acid. The system extends the multiplexing capability of real time PCR by moving from traditional spectral discrimination to array-based spatial discrimination to generate real time information specific to each target being amplified.

[0111] Traditionally, single well multiplexing is achieved by using PCR probes such as TAQMAN™ probes that are specific to each amplicon and that are labeled with fluorophores of different wavelengths. This approach limits single-reaction multiplexing capability to a maximum of about 5 targets, due to limits on dye emission spectra and the spectral window.

[0112] The approach described in this example uses a labeled PCR probe that acts as a surrogate for the amplicon to transfer information about the progression of amplification to a surface bound array during the process. Information about the kinetics of amplification is preserved, allowing for both detection and quantitative information to be obtained, based on a cycle number thresholding method.

[0113] During the extension step in the PCR cycle, the 5'-3' nuclease activity of Taq Polymerase cleaves the PCR probe to release a flap nucleic acid that can then preferentially hybridize to a capture probe on the array surface. Each flap and corresponding capture probe is unique to a potential target within the test panel.

Reaction Chamber Depth

[0114] An experiment was conducted to evaluate the relationship of chamber thickness to the Signal to Background Noise Ratio for a given array. Substrates were machined with chambers of varying depths and coated with functionalized polymer. Actual depths of the chambers were measured. The substrates were then spotted with the capture probes and assembled into enclosed reaction chamber using UV cured epoxy. A solution containing 45nM of a synthetic mimic of the labeled probe fragment complementary to each capture probe on the array and 255nM of the corresponding intact probe (to mimic 15% cleavage) was pipetted into each enclosed reaction chamber and the signal vs. background signal was measured after a 3 min hybridization at 30 C. Results for one of the assays is shown in Figure 13. As can be seen, reduction in the thickness of the reaction chamber from 600 microns to below 200 microns showed a dramatic increase in the signal to background noise ratio, with optimal ratios below 300 microns and preferably below 200 microns thickness.

PCR Chamber and Array

[0115] The PCR chamber used in most of the experiments is shown in **Figure 2**. As shown, the chamber consists of a bottom surface containing an array of capture oligos complimentary to the flap sequence of the PCR probes. The capture probes were synthesized by Integrated DNA Technologies Inc. (Coralville, Iowa) and have a 5' terminal amine group for covalent attachment to the substrate forming the bottom of the PCR chamber, along with a polyethylene glycol linker between the attachment chemistry and the oligo sequence. The length of the sequence is the same as the corresponding PCR probe flap. The bottom of the PCR chamber was formed from a commercially available slide. This slide came with a polymeric coating containing active NHS esters for subsequent attachment of the capture probes. Slides included both glass and plastic substrates coated with the polymeric coating.

Both types of slides result in similar experimental data. The capture probes are spotted using a SPOTBOT™ (Arrayit Technologies (Sunnyvale, CA)) according to standard array protocols. The capture probe spots were typically 100μm in diameter with a 200μm center to center pitch between spots.

[0116] After spotting and washing of the capture probes, the PCR chamber was assembled using a pressure sensitive adhesive (PSA) and a polycarbonate top piece with inlet and outlet ports as shown in **Figure 2**. The chamber had a final depth/thickness (or height) of 142 μM and a diameter of 15 mm. The chamber holds a volume of approximately 45 uL of PCR reagents.

Thermocycler and Optics Breadboard.

[0117] The thermocycling and optical detection system included an epifluorescent, single-channel detection system that includes (1) an excitation light source (e.g., a mercury arc lamp or an LED), (2) interference optical filters that are used for the excitation light and for the emission light so that specific combination of fluorophores are detected, such as Cy3, Cy5 or others, and (3) a photo-detector, which is a CCD or CMOS camera.

[0118] The system also included thermocycling components such as a pair of thermoelectric modules, metal plates, heat sinks and powerful cooling fans that were used to rapidly thermocycle an enclosed consumable (e.g., the array and chamber described above) to desired temperatures and for desired times. The thermoelectric modules were controlled to specific temperatures for specific time periods by the use of a feedback enabled control system that used thermistors proximate to the consumable as the feedback to the control system.

[0119] System control was performed by a computer, which used a script file as input to generate the target temperatures and time periods as well as to specify when an image was to be taken by the photo-detector. The resulting images taken at different times during the thermal reaction were analyzed by the computer to generate intensity curves as a function of time and thereby derive the concentration of the target.

[0120] Single-channel fluorescent images were captured from the consumable at various times and temperatures during the progress of the thermal reactions. These fluorescent images were then analyzed to yield quantification of starting target nucleic acid concentrations. The fluorescent images were analyzed using a combination of mean gray intensity

measurements, background correction and baseline adjustments. The background was measured locally for each spot in the array. The background was computed by measuring the fluorescent intensity of a concentric annulus of the solution surrounding the spot of interest. The signal from each spot was then corrected to account for the local background. The corrected signal from each spot was further normalized to account for variability in spotting as well as uneven illumination in the field of view. The average of the corrected intensity measurements obtained from the first few cycles, typically between cycle 5 and 15, were then used to adjust the baseline and normalize measurements from each spot.

EXAMPLE 1: THREE STEP AMPLIFICATION REACTION

[0121] The amplification reagent mix contained standard PCR reagents including two PCR amplification primers specific to each target being amplified, as well as a PCR probe specific to each target being amplified. The structure of typical probe is schematically shown in **Figure 1A**. As shown, **Figure 1A** probe region (A) represents a nucleic acid region of the probe that is complimentary to a target amplicon, designed using the same rules as is typical for a traditional real time PCR probe (e.g., as in a TAQMAN™ probe). Probe region (B) represents an orthogonal nucleic acid "flap" sequence that is complimentary to a corresponding capture probe (discussed below), but not the target nucleic acid. For purposes of illustration, this sequence is designed in one example to have a T_m of between 40° and 46° C, although other probe designs can be substituted. In one example, the sequence length is about 13 or 14 bases. Probe region (C) represents a nucleic acid with a sequence that is complimentary to a portion of the sequence of nucleic acid region (B). This sequence is designed to facilitate the formation of a secondary structure of the full-length probe, e.g., with a T_m of between 47 and 51 C. Quencher (D) represents an optional quencher molecule. Label (E) represents a fluorophore or other optically detectable label. The fluorophore Cy3 was used for the data presented below.

[0122] For the data in this example, PCR was performed with the following reagent formulation: 200 nM primers, 1X FAST START™ PCR buffer (available from Roche), 2-6 mM MgCl2, 0.5 mg/mL BSA, 0.2 units/uL FAST START™ Taq polymerase (Roche), and 150 nM of PCR Probe.

[0123] 100 uL PCR reactions were prepared using the formulation described above. The PCR Probe sequence that was used in this example was: NNNNNNNNNNNN**CCTGTTGCCAATTTCAGAGTGTTTTGCTTAAC**NNNNNNNN NGAT (SEQ ID NO:1).

[0124] The 5' and 3' flaps are denoted in underline/double underline and the traditional TaqMan sequence is shown in bold. The double underlined sequences denote the homologous regions designed to form secondary structure. The predicted melting temperature of the secondary structure was 51 °C, as determined by mFold (idtdna.com) using the PCR buffer conditions. The PCR probe was labeled with a 5' Cy3 fluorophore and a Black Hole Quencher 2 moiety on the 3' end.

[0125] The capture probe sequence attached to the bottom substrate of the PCR chamber was: NNN NNNNNNNNN N with a T_m of 42 °C using the PCR buffer conditions.

[0126] DNA plasmids comprising a target sequence were added to each PCR reaction at a concentration of 10^6, 10^4, and 10^2 copies/uL. The solution was then degassed by heating to 95 °C. After degassing, polymerase was added and the reaction was loaded into the PCR chamber using a pipette. Left over solution was loaded onto an Applied Biosystems 7500 for parallel analysis.

[0127] The cycling conditions for the array based PCR were as follows:

Temp	Time	Purpose
95 °C	120 sec	Fast Start Enzyme activation
95°C	15 sec	denaturation
60°C	60 sec	polymerase extension
30°C	120 sec	Flap hybridization and optical reading

(denaturation and extension were performed for 5 cycles, and then denaturation/ extension/ flap hybridization and optical reading are repeated for 8 cycles).

[0128] The Cycling conditions for the ABI 7500 were as follows:

Temp	Time	Purpose
95 °C	120 sec	Fast Start Enzyme activation
95 °C	15 sec	denaturation

60 °C 60sec polymerase extension and optical reading

Denaturation/ extension and reading were performed for 40 cycles.

[0129] The results for the copy number titrations are shown in **Figure 3** for the array based PCR and **Figure 4** for the solution phase PCR. As can be seen from the figures, the results are comparable, giving similar behavior for the titrations.

EXAMPLE 2: TWO STEP AMPLIFICATION REACTION

[0130] As with Example 1, above, the amplification reagent mix contained standard PCR reagents including two PCR primers (200nM) complementary to each target being amplified as well as a PCR probe (300nM) having a sequence complementary to each target being amplified. The structure of typical probe is shown in Figure 1B. As shown, the labeled probe again includes a nucleic acid fragment (A) that is complimentary to a target amplicon designed using the same rules as is typical for a traditional real time PCR probe (i.e. TaqMan). Also included is orthogonal nucleic acid "flap" sequence (B) that is complimentary to a corresponding capture probe on the capture array. The probe also includes a fluorescent label (C) coupled to the flap portion B and a quencher moiety (D) coupled to the target specific portion (A).

[0131] For the two step amplification, the orthogonal flap (B) comprises a sequence that was designed to have a T_m with its complement on the capture array of 70° C. Typically the sequence length is 25 to 27 bases. As with Example 1, above, the overall probe is designed so that the most stable secondary structure has a T_m no higher than 10° C below the extension and measurement temperature in the buffer conditions used for PCR. The oligo was designed using the unafold software available at www[dot]idtdna[dot]com. The following PCR probe sequence was used in this example:

NNN NNNNNNNNNNNNNNN N/Cy3/NN NNNNNNATG GCC GTT AGC TTC AGT CAA TTC AAC AG/BHQ_2/ (SEQ ID NO:2)

[0132] Where the double underlined sequence constitutes the orthogonal flap and the non-underlined sequence is homologous to the amplicon. The most stable secondary structure

probes are deposited onto the bottom substrate of the PCR chamber corresponding to the 5' flap sequence of each of the 5 PCR probes. Third, after the 10th PCR cycle the temperature was dropped to the surface hybridization temperature of 30 °C every 2 cycles instead of every 5 cycles as in Example 1. This allows for a higher frequency of optical interrogation during the PCR amplification.

[0137] The PCR probe and capture probe sequences are shown below:

PCR Probes:

Flu A: NNNNNNNNNNNNNCCCCAT GGAATGTTAT
CTCCCTTTTAAGCTTCTNNNNNNNN (SEQ ID NO:4) (T_m of 50.3°)

A/H1: NNNNNNNNNNNNNACCTTGGC GCTATTAGAT TTCCATTTGC CNNNNNNNN
(SEQ ID NO:5) (T_m of 51.2°)

A/H3: NNNNNNNNNNNNNNCCTGTT GCCAATTT CAGAGTGTT
TTGCTTAACNNNNNNNNNNNN (SEQ ID NO:6) (T_m of 51°)

FluB: NNNNNNNNNNNNNNTCAAAGC CAATTCGAG CAGCTGAAAC TNNNNNNNN
(SEQ ID NO: 7) (T_m of 51°)

phiMS2: NNNNNNNNNNNNNTCGCTGAA CAAGCAACC
GTTACCCNNNNNNNNNNNN (SEQ ID NO:8) (T_m of 52°)

Capture Probes

FluA:	NNN NNNNNNNNN N	(T_m of 46°)
A/H1:	NNN NNNNNNNNN N	($T_m$of 45°)
A/H3:	NNN NNNNNNNNN N	($T_m$of 42°)
FluB:	NNN NNNNNNNNN N	($T_m$of 46°)
phiMS2:	NNN NNNNNNNNN N	($T_m$of 43°)

[0138] 5 targets plasmids encompassing the sequences specific to the primers and PCR probes above were added to a 100uL PCR reaction and the solution was prepped and loaded as described in above. The resulting real time array based PCR data is shown in **Figure 6**.

EXAMPLE 5: HIGH LEVEL MULTIPLEXING

[0139] This example demonstrates single chamber multiplexing for detection of multiple targets that can be any of the ten potential targets included in the panel of this example. This level of multiplexing – a panel of more than five potential targets – cannot be achieved in traditional solution phase PCR.

[0140] The experimental materials and procedures were the same as that above except for the following: first, 10 Primer sets and PCR probes were incorporated into PCR reaction in the same concentrations as above. The sequences of the PCR probes and capture probes are given below:

PCR Probes:

FluA: NNNNNNNNNNNNNCCCCATGG AATGTTATCT CCCTTTTAAG
CTTCTNNNNNNNN (SEQ ID NO:9) (T_m of 50.3°)

A/H1: NNNNNNNNNNNNNNACCTTGGCGCT ATTAGATTTC
CATTTGCCNNNNNNNN (SEQ ID NO:10) ($T_m$of 51.2°)

A/H3: NNNNNNNNNNNNNCCTGTTGCCA ATTTCAGAG TGTTTTGCT
TAACNNNNNNNNNN (SEQ ID NO:11) ($T_m$of 51°)

FluB-v2: NNNNNNNNNNNNNTCAAAGCC AATTCGAGCA GCTGAAAC TNNNNNNNN
(SEQ ID NO:12) ($T_m$of 51°)

phiMS2: NNNNNNNNNNNNNTCGCTG AACAAGCAA CCGTTACCC NNNNNNNN
(SEQ ID NO:13) ($T_m$of 52°)

MPV: NNNNNNNNNNNNNNATGG CCGTTAGCTT CAGTCAATTC AACAGNNNNNNN
(SEQ ID NO:14) ($T_m$of 48.4°)

PIV1: NNNNNNNNNNNNNTTGGAATT GTCTCGACA ACAATCTTTG
GCCTNNNNNNNNN (SEQ ID NO:15) ($T_m$of 50.4°)

PIV2: NNNNNNNNNNNNNCCATTT ACCTAAGTGA TGGAATCAAT
CGCAAAAGNNNNNNNN (SEQ ID NO:16) (T_m of 48.8°)

PIV3: NNNNNNNNNNNNNNNACATAA GCTTTGATC AACCCTATG
CTGCACNNNNNNNNN (SEQ ID NO:17) ($T_m$of 49.9°)

RSV: NNNNNNNNNNNNNTTCGAAGGCTC CACATACACAG CTGCTGNNNNNNNNN
(SEQ ID NO:18) ($T_m$of 49.9°)

RSV-v2: NNNNNNNNNNNNNTCGAAGGC TCCACATACA CAGCTGCTGNNNNNNNN
(SEQ ID NO:19) ($T_m$of 51°)

OPC1: NNNNNNNNNNNNNTTCGGCAT TTCCTGGATTGAGT
CGGTACTANNNNNNNN (SEQ ID NO:20) ($T_m$of 48.7°)

Capture Probes

	Capture Probe T_m	
FluA	NNN NNNNNNNNN N	(T_m of 46°)
A/H1	NNN NNNNNNNNN N	(T_m of 45°)
A/H3	NNN NNNNNNNNN N	(T_m of 42°)
FluB-v2	NNN NNNNNNNNN N	(T_m of 46°)
phiMS2	NNN NNNNNNNNN N	(T_m of 43°)

MPV	NNN NNNNNNNNN N
PIV1	NNN NNNNNNNNN N
PIV2	NNN NNNNNNNNN N
PIV3	NNN NNNNNNNNN N
RSV	NNN NNNNNNNNN N
RSV-v2	NNN NNNNNNNNN N
OPC1	NNN NNNNNNNNN N

[0141] **Figure 7** shows the resulting real time array-based PCR curves when no target was added to the PCR reactions (No Template Control). As can be seen from the figure, no signal was obtained from a solution containing all PCR components except target. **Figure 8** shows the same experiment with 3 plasmid targets (MPV, OPC-1, PIV2) added at 10,000 copies/uL.

EXAMPLE 6: DEMONSTRATION OF FAST HYBRIDIZATION KINETICS

[0142] A PCR chamber was constructed as described above. The following amine, pegylated capture probe sequence was deposited on the bottom substrate: NNN NNNNNNNNNN.

[0143] A solution containing the PCR buffer described above was prepared containing the following oligo sequence (100 nM) which mimics the 5' flap portion of the PCR probe, labeled with a Cy3 fluorophore on the 5' end and complimentary to the capture probe: NNN NNNNNNNNN N.

[0144] The solution was loaded into the PCR chamber and the chamber was heated to 60 °C (15 degrees above the T_m of the duplex) and then cooled back down to 30 °C. This mimics the conditions during the hybridization step of the PCR protocol. An optical reading was taken every 20 sec for 2 min. The resulting data is shown in **Figure 9**.

[0145] One interesting aspect of the data shows that there is already significant hybridization occurring at the instant that the internal temperature reaches 30 °C.

[0146] The approach outlined in herein has multiple advantages not found in previous approaches. The systems of the invention allow for single chamber, highly multiplexed,

quantitative PCR by efficiently transferring information from solution phase PCR to a surface confined array in real time during the amplification process. This allows for a much higher level of multiplexing while preserving the efficiency and leveraging the immense body of knowledge accumulated for solution phase real time PCR. In order to achieve this, multiple novel aspects of the system had to be developed.

[0147] For example, one feature of the invention is the use of an amplicon surrogate to bridge the solution phase and the solid phase. Previous teachings aimed towards the goal of array based real time PCR have generally relied upon hybridization of the amplicon itself to the solid phase array. This presents multiple issues that complicate the system, hinder the efficiency, and require more expensive components to elucidate the required information. In a multiplexed PCR environment, it is very hard to design amplicons of similar lengths and hybridization efficiencies. The use of a PCR probe with a cleavable 5' flap homogenizes the species that transfers the information from each amplicon to the surface by employing a very short sequence that is ideal for hybridization kinetics. This approach also makes the capture probe sequences on the array independent of the sequence of the amplicon to be detected. This allows for selection of the most advantageous capture sequences and the possibility of a universal array that can be used for many different target panels, simplifying the design and manufacturing approach.

[0148] As disclosed here, the PCR probe also leverages the design rules that have already been developed for probe based solution phase real time PCR. The use of a very short sequence for hybridization (e.g., 13-14 bases) makes the hybridization very efficient, allowing for high signal on the array in the low salt environment of standard PCR buffers. Thus the system can work very well in a single chamber where surface hybridization has to be coupled with optimal solution phase PCR.

[0149] Another feature of the invention is the discrimination of surface hybridized signal from solution phase background fluorescence. This aspect of the invention is important in extracting relevant information from the array. Previous teachings employ complicated or expensive optical approaches to overcome this problem, such the use of total internal reflectance or confocal microscopy to isolate the surface signal from the solution background. By contrast, this invention provides the use of simple standard optical equipment that require

no optical "tricks" to achieve discrimination. The ability to discriminate the signal arises from multiple sources. The surface chemistry that is used in the array provides a very high capture probe density and thus hybridized target density. It has been shown that the surface can approach 100% capture efficiency of target nucleic acid. This high capture density and efficiency serves to concentrate the surface signal, aiding in surface/solution phase discrimination. The use of a short target nucleic acid serves to dramatically enhance this effect.

[0150] Another aspect of the invention that aids in the signal discrimination is the use of a very thin PCR chamber. The background signal from the solution is linearly related to the height of solution above the array. The use of a thin chamber takes advantage of this effect.

[0151] Another aspect of the invention is the use of fast hybridization kinetics to allow for real time transfer of the solution phase information to the surface array. The system described in these examples demonstrates extremely fast solid phase hybridization. This phenomenon facilitates the technology and can be attributed to multiple aspects of the invention, including the short 5' flap target, the optimal solid phase surface chemistry, the thin consumable and the temperature gradient produced during the thermocycling temperature program.

[0152] While the foregoing invention has been described in some detail for purposes of clarity and understanding, it will be clear to one skilled in the art from a reading of this disclosure that various changes in form and detail can be made without departing from the true scope of the invention. For example, all the techniques and apparatus described above can be used in various combinations. All publications, patents, patent applications, and/or other documents cited in this application are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent, patent application, and/or other document were individually indicated to be incorporated by reference for all purposes.

WHAT IS CLAIMED IS:

1. A method of detecting a target nucleic acid, the method comprising:

providing a detection chamber that has at least one high efficiency nucleic acid detection array on at least one surface of the chamber;

loading a sample into the detection chamber, which sample comprises one or more copies of the target nucleic acid to be detected;

hybridizing an amplification primer and a probe to the one or more copies;

amplifying at least a portion of one or more of the target nucleic acid copies in an amplification primer dependent amplification reaction, wherein the amplification reaction results in cleavage of the probe and release of a first probe fragment;

hybridizing the first probe fragment to the high-efficiency array; and,

detecting a signal produced by binding the first probe fragment to the array, thereby detecting the target nucleic acid, wherein the detecting step is carried out under conditions that reduce background signal proximal to the array.

2. The method of claim 1, wherein the probe comprises a labeled probe and the first probe fragment comprises a labeled probe fragment.

3. The method of claim 2, wherein the labeled probe fragment comprises a label that produces a detectable signal upon hybridizing to the array.

4. The method of claim 1, wherein the detection chamber is configured to reduce signal background proximal to the array.

5. The method of claim 1, wherein the detection chamber is less than 500 μm in at least one dimension proximal to the array.

6. The method of claim 1, wherein the detection chamber is between about 10 μm and about 200 μm in at least one dimension proximal to the array.

7. The method of claim 1, wherein the array comprises a non-rate limiting number of capture nucleic acids that hybridize to the first probe fragment.

8. The method of claim 1, wherein the first probe fragment is not complementary to the target nucleic acid.

9. The method of claim 7, wherein the first probe fragment that hybridizes to the capture nucleic acids of the array is less than about 30 nucleotides in length.

10. The method of claim 7, wherein the first probe fragment that hybridizes to the capture nucleic acids of the array is less than about 20 nucleotides in length.

11. The method of claim 7, wherein the first probe fragment that hybridizes to the capture nucleic acids of the array is about 15 nucleotides or less in length.

12. The method of claim 1, wherein the sample is loaded through at least one port or fluidic channel in operable communication with the chamber.

13. The method of claim 1, wherein the target nucleic acid is amplified for at least 5 amplification cycles prior to said detecting.

14. The method of claim 1, wherein the target nucleic acid is amplified in a plurality of amplification cycles prior to said detecting, wherein the target nucleic acid portion is additionally amplified after said detecting, in the presence of additional copies of the probe, with resulting released first probe fragments being subsequently hybridized to the array and detected, wherein detected signal intensity is correlated to a quantity of the target nucleic acid present in the sample.

15. The method of claim 1, wherein the signal is detected by detecting one or more optical signal wavelengths.

16. The method of claim 1, wherein detecting the signal comprises detecting a plurality of optical signal wavelengths from a plurality of signals.

17. The method of claim 1, wherein the hybridization temperature is less than the temperature of the amplification reaction.

18. The method of claim 1, wherein the first probe comprises a first orthogonal flap that is not complimentary to the target nucleic acid, which flap is cleaved from the labeled probe to produce the labeled probe fragment.

19. The method of claim 14, wherein the probe comprises a second orthogonal flap which is at least partially complimentary to the first flap, wherein the second flap has a higher T_m for binding to the first flap than the first flap has for binding to the array.

20. The method of claim 2, wherein the labeled probe comprises a fluorescent or luminescent label.

21. The method of claim 20, wherein the label is a fluorescent dye.

22. The method of claim 1, wherein the probe comprises a label and a label quencher, wherein cleavage of the probe results in separation of the label and the quencher, thereby unquenching the label.

23. The method of claim 1, wherein the probe comprises an unquenched label.

24. The method of claim 1, wherein the signal is an optical signal.

25. The method of claim 24, wherein the signal detected comprises a signal from an intercalating dye indicating hybridization of the first probe fragment to the high-efficiency array.

26. The method of claim 1, comprising detecting local background for one or more regions of the array, and normalizing signal intensity measurements by correcting for said background.

27. The method of claim 1, wherein the signal detected in the detecting step has a signal to background noise ratio of greater than 2.5.

28. The method of claim 1,wherein the signal detected in the detecting step has a signal to background noise ratio of greater than 5.

29. The method of claim 26, further comprising normalizing signal intensity by correcting for variability in array capture nucleic acid spotting, or uneven field of view of different regions of the array.

30. The method of claim 1, wherein the sample comprises a plurality of target nucleic acids and the array comprises a plurality of capture nucleic acid types.

31. The method of claim 30, wherein the capture nucleic acid types are spatially separated on the array.

32. The method of claim 30, comprising incubating a plurality of amplification probes, each specific for a different nucleic acid target, with the target nucleic acids.

33. The method of claim 30, wherein there are between about 5 and about 100 capture nucleic acid types, and between about 5 and about 100 corresponding labeled probe

types in the amplification reaction, wherein up to 5 to 100 different signals can be detected based upon positioning of the signals in the array.

34. The method of claim 30, wherein the capture nucleic acids are arrayed at a density of about between about 350 fmoles/cm^2 and about 5,000 fmoles/cm^2 or greater.

35. The method of claim 30, wherein the capture nucleic acids are arrayed at a density greater than 2000 fmoles/cm^2.

36. The method of claim 32, comprising incubating a plurality of labeled probes, each specific for a different target nucleic acid, with the target nucleic acids, wherein amplifying at least a portion of the target nucleic acids in the amplification primer dependent amplification reaction results in cleavage of a plurality of labeled probe types and resulting release of a plurality of labeled probe fragment types, wherein said hybridizing comprises hybridizing the plurailty of probe fragment types to the array, wherein each of the different probe fragment types hybridizes to a spatially discrete capture nucleic acid type, and wherein detecting the label signal comprises detecting a plurality of label signals from a plurality of spatially discrete regions corresponding to the spatially discrete capture nucleic acids on the array.

37. The method of claim 36, wherein the labeled probe types comprise the same label moiety.

38. The method of claim 36, wherein the labeled probe types comprise a plurality of different label moieties.

39. The method of claim 36, wherein the labeled probe types comprise one or more different label moieties, wherein the number of different moieties is less than the number of labeled probe types.

40. The method of claim 1, wherein the amplifying step and the step of hybridizing the first probe fragment to the high-efficiency array are carried out at the same temperature.

41. A method of analyzing a sample for a plurality of target nucleic acid sequences, comprising:

contacting the sample with a first plurality of labeled probes, each of the first plurality labeled probes comprising a first portion complementary to a different target sequence of interest in a first panel of target nucleic acid sequences and a second portion complementary to a different capture probe on a high efficiency probe array, wherein the second portion has a label attached thereto and is not complementary to the target sequence of interest;

amplifying any target sequences from the first panel of target nucleic acid sequences that are present in the sample, in an amplification primer dependent amplification reaction, wherein the amplification reaction results in cleavage of labeled probes hybridized to the target sequences and release of the second portion of the labeled probes bearing the label;

hybridizing the released second portion of the labeled probes to the high-efficiency array;

detecting binding of the second portion of the labeled probe to a capture probe in the high efficiency array; and

identifying the target sequences present in the sample from the second portions of the labeled probes that hybridize to the high efficiency array.

42. The method of claim 41, further comprising:

contacting the sample with a second plurality of labeled probes, each of the second plurality labeled probes comprising the second portion, and a third portion complementary to a different target sequence of interest in a second panel of target nucleic acid sequences;

amplifying any target sequences from the second panel of target nucleic acid sequences that are present in the sample, in an amplification primer dependent amplification reaction, wherein the amplification reaction results in cleavage of labeled probes hybridized to the target sequences and release of the second portion of the labeled probes bearing the label; and

repeating the hybridizing, detecting and identifying steps.

43. A nucleic acid detection device, comprising:

a detection chamber that comprises at least one high efficiency nucleic acid detection array on at least one surface of the chamber, wherein the chamber is configured to reduce signal background for signals detected from the array;

a thermo-regulatory module operably coupled to the detection chamber, which module regulates temperature within the chamber during operation of the device; and,

an optical train that detects a signal produced at the array during operation of the device.

44. The nucleic acid detection device of claim 43, wherein the device is less than about 500μm in depth in at least one dimension proximal to the array.

45. The nucleic acid detection device of claim 43, wherein the device is between about 10μm and about 200μm in depth in at least one dimension proximal to the array.

46. The nucleic acid detection device of claim 43, wherein the surface is composed of a ceramic, glass, quartz, or a polymer.

47. The nucleic acid detection device of claim 43, wherein capture nucleic acids are present in the array at a non-rate limiting density during operation of the device.

48. The nucleic acid detection device of claim 47, wherein the capture nucleic acids are coupled to a thermostable coating on the surface of the chamber.

49. The nucleic acid detection device of claim 48, wherein the coating comprises one or more of: a chemically reactive group, an electrophilic group, an NHS ester, a tetra- or pentafluorophenyl ester, a mono- or dinitrophenyl ester, a thioester, an isocyanate, an isothiocyanate, an acyl azide, an epoxide, an aziridine, an aldehyde, an α,β-unsaturated ketone or amide comprising a vinyl ketone or a maleimide, an acyl halide, a sulfonyl halide, an

imidate, a cyclic acid anhydride, a group active in a cycloaddition reaction, an alkene, a diene, an alkyne, an azide, or a combination thereof.

50. The nucleic acid detection device of claim 43, wherein the array comprises a plurality of capture nucleic acid types, wherein different types are localized to spatially distinct regions of the array.

51. The nucleic acid detection device of claim 43, wherein more than 5 different capture nucleic acid types are present on the array.

52. The nucleic acid detection device of claim 43, wherein between about 5 and about 100 different capture nucleic acid types are present on the array.

53. The nucleic acid detection device of claim 43, wherein the capture nucleic acids are arrayed at a density greater than 2000 fmoles/cm^2.

54. The nucleic acid detection device of claim 43, wherein the thermo-regulatory module comprises one or more of: a thermoelectric module, a Peltier device, a cooling fan, a heat sink, or a metal plate configured to mate with a portion of an outersurface of the chamber.

55. The nucleic acid detection device of claim 54, wherein the thermo regulatory module comprises a feedback enabled control system operably coupled to a computer.

56. The nucleic acid detection device of claim 43, wherein the optical train comprises or is operably coupled to an epifluorescent detection system.

57. The nucleic acid detection device of claim 43, wherein the optical train comprises one or more of: an excitation light source, an arc lamp, a mercury arc lamp, an LED, a lens, an optical filter, a prism, a camera, a photodetector, a CMOS camera, or a CCD array.

58. The nucleic acid detection device of claim 43, comprising an array reader module, which reader module correlates a position of the signal in the array to a nucleic acid to be detected.

59. The nucleic acid detection device of claim 43, wherein the device comprises or is operably coupled to system instructions embodied in a computer or computer readable medium that correlates one or more measurements of signal intensity and a number of amplification cycles performed by the thermo-regulatory module to determine a concentration of a target nucleic acid detected by the device.

60. A system comprising the device of claim 43, operably coupled to a computer, which computer comprises instructions that control the thermocycling by the thermo-regulatory module, and to specify when images are taken or viewed by the optical train, which computer further comprises instructions to convert image information into signal intensity curves as a function of time, and/or to determine concentration of a target nucleic acid analyzed by the device.

61. The system of claim 60, wherein the computer comprises instructions for detecting local background for one or more regions of the array, and for normalizing signal intensity measurements by correcting for said background.

62. The system of claim 60, wherein the computer comprises instructions for normalizing signal intensity by correcting for variability in array capture nucleic acid spotting, or uneven field of view of different regions of the array.

63. A nucleic acid detection consumable, comprising: a thin chamber less than about 500μm in depth, which chamber comprises an optically transparent window that comprises a high efficiency capture nucleic acid array disposed on an inner surface of the window, which chamber additionally comprises at least one reagent delivery port fluidly coupled to the

chamber, wherein the consumable is configured to permit thermocycling of fluid within the chamber.

64. The consumable of claim 63, wherein the nucleic acid array comprises a plurality of different capture nucleic acid types, which types are located in spatially distinct regions of the array.

65. The consumable of claim 63, wherein the chamber comprises a first upper surface comprising the reagent delivery port, and a bottom transparent surface comprising the window, wherein the top and bottom surface are joined by sidewalls comprising a pressure-sensitive adhesive material.

66. The consumable of claim 63, wherein the chamber comprises a first upper surface comprising the reagent delivery port, and a bottom transparent surface comprising the window, wherein the top and bottom surface are joined together by a gasket or shaped feature on the upper or lower surface, or both, wherein the gasket or feature is fused or adhered to a corresponding region of the upper or lower surface, or both.

67. The consumable of claim 66, wherein the upper and lower surfaces are ultrasonically fused together, wherein the gasket or feature delimits regions that are fused.

68. The consumable of claim 66, wherein the feature is a transparent region on either the upper or lower surface and a corresponding shaded region on a cognate upper or lower surface, wherein the upper and lower surfaces are laser welded together by directing laser light through the transparent region and onto the shaded region.

69. The consumable of claim 66, wherein the gasket or feature directs flow of a UV curable adhesive, which adhesive is flowed between the upper and lower surfaces and exposed to UV light, thereby joining the upper and lower surfaces.

70. The consumable of claim 65, wherein the capture nucleic acid array is coupled to a thermally stable coating on the window.

71. The consumable of claim 70, wherein the coating comprises a chemically reactive group, an electrophilic group, an NHS ester, a tetra- or pentafluorophenyl ester, a mono- or dinitrophenyl ester, a thioester, an isocyanate, an isothiocyanate, an acyl azide, an epoxide, an aziridine, an aldehyde, an α,β-unsaturated ketone or amide comprising a vinyl ketone or a maleimide, an acyl halide, a sulfonyl halide, an imidate, a cyclic acid anhydride, a group active in a cycloaddition reaction, an alkene, a diene, an alkyne, an azide, or a combination thereof.

72. The consumable of claim 65, wherein the capture nucleic acid array is arrayed at a density greater than 2000 fmoles/cm^2.

73. The consumable of claim 65, wherein the capture nucleic acid array is arrayed at a density greater than 2500 fmoles/cm^2.

74. The consumable of claim 70, wherein the window comprises glass, quartz, a ceramic, or a polymer.

75. The consumable of claim 63, wherein the chamber is between about 10μm and about 200μm in depth.

76. The consumable of claim 63, wherein the chamber is about 140 μm in depth or less.

77. The consumable of claim 63, wherein the chamber is about 100 μm in depth or less.

78. The consumable of claim 63, wherein the chamber is between about 1 mm and about 50 mm in average diameter.

79. The consumable of claim 63, wherein the chamber is between about 10 mm and about 20 mm in average diameter.

80. A kit comprising the consumable of claim 63, packaged in packaging material, the kit optionally comprising one or more control reagents.

81. A method of detecting the presence of a target nucleic acid sequence in a sample, comprising:

performing an amplification reaction on the sample with a polymerase enzyme that possesses nuclease activity, in the presence of a first labeled probe that comprises a first portion complementary to a first target nucleic acid sequence and a second labeled portion not complementary to the first target nucleic acid sequence, such that the second portion is cleaved from the first portion when the target nucleic acid sequence is amplified;

hybridizing the second labeled portion to a substrate that comprises a capture probe complementary to the second portion; and

detecting the presence of the second labeled portion hybridized to the capture probe on the substrate.

82. The method of claim 81, wherein the substrate comprises a planar substrate.

83. The method of claim 81, wherein the substrate comprises a bead.

84. The method of claim 82, further comprising providing a plurality of labeled probes, each of the plurality of labeled probes having a first portion complementary to a different target nucleic acid sequence, and a second labeled portion where each second labeled portion comprises a different sequence that is not complementary to any of the different target

nucleic acid sequences, such that the second labeled portion is cleaved from the first portion when the different target nucleic acid sequences is amplified;

hybridizing the second labeled portions cleaved during the amplification reaction to a plurality of different capture probes complementary to each different labeled second portion, wherein each different capture probe is disposed at a different known location on the planar substrate; and

identifying the presence of a target nucleic acid sequence in the sample from a location at which a labeled second portion hybridizes to the capture probe on the substrate.

85. The method of claim 83, further comprising providing a plurality of labeled probes, each of the plurality of labeled probes having a first portion complementary to a different target nucleic acid sequence, and a second labeled portion where each second labeled portion comprises a different sequence that is not complementary to any of the different target nucleic acid sequences, such that the second labeled portion is cleaved from the first portion when the different target nucleic acid sequences is amplified;

hybridizing the second labeled portions cleaved during the amplification reaction to a plurality of different capture probes complementary to each different labeled second portion, wherein each different capture probe is disposed on a different bead bearing a unique label; and

detecting the presence of a given target nucleic acid sequence by identifying the bead to which it binds.