Description

Technical Field

This invention is in the fields of nucleic acid chemistry and biochemical assays. More particularly, it relates to novel nucleic acid multimers and nucleic acid hybridization assays.

Background Art

Nucleic acid hybridizations are now commonly used in genetic research, biomedical research and clinical diagnostics. In the basic nucleic acid hybridization assay, single-stranded analyte nucleic acid (either DNA or RNA) is hybridized to a labeled nucleic acid probe, and resulting labeled duplexes are detected. Both radioactive and nonradioactive labels have been used.

Variations of this basic scheme have been developed to facilitate separation of the duplexes to be detected from extraneous materials and/or to amplify the signal that is detected.

Copending commonly owned EPA Pub. No. 0225807 describes a solution-phase nucleic acid hybridization assay in which the analyte nucleic acid is hybridized to a labeling probe set and to a capturing probe set. The probe-analyte complex is coupled by hybridization with a solid-supported capture probe that is complementary to the capture probe set. This permits the analyte nucleic acid to be removed from solution as a solid phase complex. Having the analyte in the form of a solid phase complex facilitates subsequent separation steps in the assay. The labeling probe set is complementary to a labeled probe that is bound through hybridization to the solid phase/ analyte complex.

PCT Application 84/03520 and EPA 124221 describe a DNA hybridization assay in which: (1) analyte is annealed to a single-stranded DNA probe that has a tail that is complementary to an enzyme-labeled oligonucleotide, and (2) the resulting tailed duplex is hybridized to an enzyme-labeled oligonucleotide. The Enzo Biochem "Bio-Bridge" labeling system appears to be similar to the system described in these two patent applications. The "Bio-Bridge" system uses terminal deoxynucleotide transferase to add unmodified 3'-polyT-tails to a DNA probe. The polyT-tailed probe is hybridized to the target DNA sequence and then to a biotin-modified polyA.

EPA 204510 describes a DNA hybridization assay in which analyte DNA is contacted with a probe that has a tail, such as a polyT-tail, an amplifier strand that has a sequence, e.g., a polyA sequence, that hybridizes to the tail of the probe and is capable of binding a plurality of labeled strands.

The main problem with these prior hybridization assays is that they lack sufficient specificity and/or signal to be useful for detecting very low levels of analyte. A primary object of the present invention is to provide an amplifier for use in nucleic acid hybridizations that provides a high reproducible gain in signal, a high reproducible signal-to-noise ratio and low nonspecific binding, that is itself reproducible, and that is capable of combining specifically with a "universal" signal moiety and an analyte at low concentrations to form a stable complex.

Other aspects are to provide improved hybridization assays for hepatitis B virus (HBV), N. gonorrhoeae, penicillin and tetracycline resistance in N. gonorrhoeae, and Chlamydia trachomatis.

Disclosure of the Invention

One aspect of the invention is a synthetic branched nucleic acid multimer having a minimum of three termini, said multimer comprising:

(a) at least one first single-stranded oligonucleotide unit that is capable of binding specifically to a first single-stranded nucleotide sequence of interest; and
(b) a multiplicity of second single-stranded oligonucleotide units that are capable of binding specifically to a second single-stranded nucleotide sequence of interest, wherein the first single-stranded oligonucleotide is linked directly or indirectly to the second single-stranded oligonucleotide units only via covalent bonds.

Another aspect of the invention is a nucleic acid hybridization assay in which (1) the above-described multimer is hybridized via the first oligonucleotide unit to single-stranded analyte nucleic acid or an oligonucleotide bound to the analyte, and (2) a multiplicity of single-stranded labeled oligonucleotides are then hybridized to the multimer via the multiplicity of second oligonucleotide units.

In performing the invention the following probes are of use : A synthetic oligonucleotide

comprising (a) a first segment having a nucleotide sequence complementary to a segment of the HBV genome and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer;

a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the HBV genome and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;

a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of N. gonorrhoeae pilin DNA and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer;

a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of N. gonorrhoeae pilin DNA and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;

a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the N. gonorrhoeae genomic clone shown in Figure 13 and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer;

a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the N. gonorrhoeae genomic clone shown in Figure 13 and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;

a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the 7.3 kb N. gonorrhoeae family of plasmids carrying the beta-Lactamase TEM-1 gene or said gene and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer;

a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the 7.3 kb N. gonorrhoeae family of plasmids carrying the beta-Lactamase TEM-1 gene or said gene and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;

a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment the tetM gene in a tetracycline resistant organism and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;

a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the tetM gene in a tetracycline resistant organism and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer;

a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the Chlamydia pCHL2 plasmid and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer; and

a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the Chlamydia pCHL2 plasmid and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase.

Still another aspect of the invention is a solution sandwich DNA hybridization for detecting HBV DNA in an analyte comprising:

(a) contacting the analyte under hybridizing conditions with an excess of i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the HBV genome and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the HBV genome and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
(b) contacting under hybridizing conditions the product of step (a) with the oligonucleotide bound to the solid phase;
(c) thereafter separating materials not bound to the solid phase;
(d) contacting under hybridizing conditions the solid phase complex product of step (c) with the nucleic acid multimer of the invention wherein the second oligonucleotide units of said multimer are complementary to a labeled oligonu-

cleotide;
(e) removing unbound multimer;
(f) contacting under hybridizing conditions the solid phase complex product of step (e) with the labeled oligonucleotide;
(g) removing unbound labeled oligonucleotide; and
(h) detecting the presence of label in the solid phase complex product of step (g).

Still another aspect of the invention is a solution sandwich DNA hybridization for detecting N. gonorrhoeae pilin DNA in an analyte comprising:

(a) contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of N. gonorrhoeae pilin DNA genome and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of N. gonorrhoeae pilin DNA and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
(b) contacting under hybridizing conditions the product of step (a) with the oligonucleotide bound to the solid phase;
(c) thereafter separating materials not bound to the solid phase;
(d) contacting under hybridizing conditions the solid phase complex product of step (c) with the nucleic acid multimer, said multimer comprising (i) at least one oligonucleotide unit that is complementary to the second segment of the amplifier probe oligonucleotide and (ii) a multiplicity of second oligonucleotide units that are complementary to a labeled oligonucleotide;
(e) removing unbound multimer;
(f) contacting under hybridizing conditions the solid phase complex product of step (e) with the labeled oligonucleotide;
(g) removing unbound labeled oligonucleotide; and
(h) detecting the presence of label in the solid phase complex product of step (g).

Still another aspect of the invention is a solution sandwich DNA hybridization for detecting N. gonorrhoeae DNA in an analyte comprising:

(a) contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the N. gonorrhoeae genomic clone shown in Figure 13 and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the N. gonorrhoeae genomic clone shown in Figure 13 and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
(b) contacting under hybridizing conditions the product of step (a) with the oligonucleotide bound to the solid phase;
(c) thereafter separating materials not bound to the solid phase;
(d) contacting under hybridizing conditions the solid phase complex product of step (c) with the nucleic acid multimer, said multimer comprising (i) at least one oligonucleotide unit that is complementary to the second segment of the amplifier probe oligonucleotide and (ii) a multiplicity of second oligonucleotide units that are complementary to a labeled oligonucleotide;
(e) removing unbound multimer;
(f) contacting under hybridizing conditions the solid phase complex product of step (e) with the labeled oligonucleotide;
(g) removing unbound labeled oligonucleotide; and
(h) detecting the presence of label in the solid phase complex product of step (g).

Another aspect of the invention is a DNA hybridization assay for detecting N. gonorrhoeae DNA in an analyte comprising contacting the analyte under hybridizing conditions with a DNA probe that is complementary to all or a portion of either strand of the N. gonorrhoeae genomic clone shown in Figure 13 and detecting the presence of duplexes containing the DNA probe.

Still another aspect of the invention is a solution sandwich DNA hybridization for detecting Chlamydia trachomatis DNA in an analyte comprising:

(a) contacting the analyte under hybridizing conditions with an excess of i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the Chlamydia pCHL2 plasmid

and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the Chlamydia pCHL2 plasmid and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
(b) contacting under hybridizing conditions the product of step (a) with the oligonucleotide bound to the solid phase;
(c) thereafter separating materials not bound to the solid phase;
(d) contacting under hybridizing conditions the solid phase complex product of step (c) with the nucleic acid multimer, said multimer comprising (i) at least one oligonucleotide unit that is complementary to the second oligonucleotide unit that is complementary to the second segment of the amplifier probe oligonucleotide and (ii) a multiplicity of second oligonucleotide units that are complementary to a labeled oligonucleotide;
(e) removing unbound multimer;
(f) contacting under hybridizing conditions the solid phase complex product of step (e) with the labeled oligonucleotide;
(g) removing unbound labeled oligonucleotide; and
(h) detecting the presence of label in the solid phase complex product of step (g).

Still another aspect of the invention is a solution sandwich nucleic acid hybridization assay for detecting a first nucleic acid sequence that is part of a nucleic acid segment that includes a second nucleic acid sequence in a sample that contains said segment and another nucleic acid segment that comprises the first nucleic acid sequence but does not include the second nucleic acid sequence comprising:

(a) contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment that is complementary to one of the first nucleic acid sequence or the second nucleic acid sequence and a second segment that is complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment that is complementary to the other of the first nucleic acid sequence or the second nucleic acid sequence and a second segment that is complementary to an oligonucleotide bound to a solid phase;
(b) contacting under hybridizing conditions the product of step (a) with the oligonucleotide bound to the solid phase;
(c) thereafter separating materials not bound to the solid phase;
(d) contacting under hybridizing conditions the solid phase complex product of step (c) with the nucleic acid multimer, said multimer comprising (i) at least one oligonucleotide unit that is complementary to the second segment of the amplifier probe oligonucleotide and (ii) a multiplicity of second oligonucleotide units that are complementary to a labeled oligonucleotide;
(e) removing unbound multimer;
(f) contacting under hybridizing conditions the solid phase complex product of step (e) with the labeled oligonucleotide;
(g) removing unbound labeled oligonucleotide; and
(h) detecting the presence of label in the solid phase complex product of step (g).

Yet another aspect of the invention is a solution sandwich DNA hybridization for detecting the 7.3 kb N. gonorrhoeae plasmid carrying the beta-Lactamase TEM-1 gene or said gene in an analyte comprising:

(a) contacting the analyte under hybridizing conditions with an excess of i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of said plasmid or said gene and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to another segment of said plasmid or said gene and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
(b) contacting under hybridizing conditions the product of step (a) with the oligonucleotide bound to the solid phase;
(c) thereafter separating materials not bound to the solid phase;
(d) contacting under hybridizing conditions the solid phase complex product of step (c) with the nucleic acid multimer, said multimer comprising (i) at least one oligonucleotide unit that is complementary to the second segment of the amplifier probe oligonucleotide and (ii) a multiplicity of second oligonucleotide units that are complementary to a labeled oligonucleotide;
(e) removing unbound multimer;
(f) contacting under hybridizing conditions the solid phase complex product of step (e) with the labeled oligonucleotide;
(g) removing unbound labeled oligonucleotide; and

(h) detecting the presence of label in the solid phase complex product of step (g).

Yet another aspect of the invention is a solution sandwich DNA hybridization for detecting tetM gene DNA suspected of containing DNA of a tetracycline resistant organism in an analyte comprising:

(a) contacting the analyte under hybridizing conditions with an excess of i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the tetM gene and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to another segment of said tetM gene and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
(b) contacting under hybridizing conditions the product of step (a) with the oligonucleotide bound to the solid phase;
(c) thereafter separating materials not bound to the solid phase;
(d) contacting under hybridizing conditions the solid phase complex product of step (c) with the nucleic acid multimer, said multimer comprising (i) at least one oligonucleotide unit that is complementary to the second segment of the amplifier probe oligonucleotide and (ii) a multiplicity of second oligonucleotide units that are complementary to a labeled oligonucleotide;
(e) removing unbound multimer;
(f) contacting under hybridizing conditions the solid phase complex product of step (e) with the labeled oligonucleotide;
(g) removing unbound labeled oligonucleotide; and
(h) detecting the presence of label in the solid phase complex product of step (g).

Brief Description of the Drawings

Figure 1 is a schematic representation of the process for the enzymatic preparation of a linear nucleic acid multimer that is described in Example 1.

Figures 2A and 2B are schematic representations of the processes for the chemical preparation of linear and branched nucleic acid multimers that are described in Example 2.

Figure 3 (Parts A-F), illustrate procedures used in making multimers having "comb-like" and/or bifurcated structures.

Figure 4 is a schematic representation of the sandwich hybridization assay described in Example 3.

Figure 5 is an autoradiogram showing the results of the dot blot screening tests described in the examples.

Figures 6-8 are bar graphs depicting the results of the tests on authentic HBV DNA samples that are described in the examples.

Figure 9 shows the DNA sequence of the coding strand of a portion of a 7.3 kb N. gonorrhoeae plasmid carrying the beta-Lactamase TEM-1 gene.

Figure 10 shows partial nucleotide sequences of the capture and amplifier probes used in the TEM-1NH assay described in section 5 of the examples.

Figure 11 shows partial nucleotide sequences of the capture and amplifier probes used in the TEM-1 assay described in section 5 of the examples.

Figure 12 shows the nucleotide sequence for the tetM gene and partial nucleotide sequences (the 5' ends) of the capture and amplifier probes used in the tetM assay described in section 7 of the examples.

Figure 13 is the DNA sequence of the N. gonorrhoeae genomic sequence SSJK1 described in section 8 of the examples.

Figure 14 shows partial nucleotide sequences of the capture and amplifier probes used in the N. gonorrhoeae assay described in section 8 of the examples.

Modes for Carrying Out the Invention

Description of Multimers

The nucleic acid multimers of the invention are linear or branched polymers of the same repeating single-stranded oligonucleotide unit or different single-stranded oligonucleotide units. At least one of the units has a sequence, length, and composition that permits it to bind specifically to a first single-stranded nucleotide sequence of interest, typically analyte or an oligonucleotide bound to the analyte. In order to achieve such specificity and stability, this unit will normally be 15 to 30 nucleotides in length and have a GC content in the range of 40% to 60%. In addition to such unit(s), the multimer includes a multiplicity of units that are capable of hybridizing specifically and stably to a second single-stranded nucleotide of interest, typically a labeled oligonucleotide or another multimer. These units will also normally be 15 to 30

nucleotides in length and have a GC content in the range of 40% to 60%. When a multimer is designed to be hybridized to another multimer, the first and second oligonucleotide units are heterogeneous (different).

The total number of oligonucleotide units in the multimer will usually be in the range of 3 to 50, more usually 10 to 20. In multimers in which the unit that hybridizes to the nucleotide sequence of interest is different from the unit that hybridizes to the labeled oligonucleotide, the number ratio of the latter to the former will usually be 2:1 to 30:1, more usually 5:1 to 20:1, and preferably 10:1 to 15:1.

The oligonucleotide units of the multimer may be composed of RNA, DNA, modified nucleotides or combinations thereof.

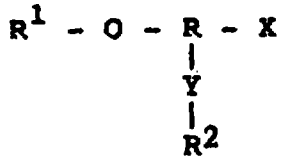
The oligonucleotide units of the multimer may be covalently linked directly to each other through phosphodiester bonds or through interposed linking agents such as nucleic acid, amino acid, carbohydrate or polyol bridges, or through other cross-linking agents that are capable of cross-linking nucleic acid or modified nucleic acid strands. The site(s) of linkage may be at the ends of the unit (in either normal 3'-5' orientation or randomly oriented) and/or at one or more internal nucleotides in the strand. In linear multimers the individual units are linked end-to-end to form a linear polymer. In one type of branched multimer three or more oligonucleotide units emanate from a point of origin to form a branched structure. The point of origin may be another oligonucleotide unit or a multifunctional molecule to which at least three units can be covalently bound. In another type, there is an oligonucleotide unit backbone with one or more pendant oligonucleotide units. These latter-type multimers are "fork-like", "comb-like" or combination "fork-" and "comb-like" in structure. The pendant units will normally depend from a modified nucleotide or other organic moiety having appropriate functional groups to which oligonucleotides may be conjugated or otherwise attached. The multimer may be totally linear, totally branched, or a combination of linear and branched portions. Preferably there will be at least two branch points in the multimer, more preferably at least 3, preferably 5 to 10. The multimer may include one or more segments of double-stranded sequences.

Synthesis of Multimers

The multimers may be prepared by cloning (if linear), enzymatic assembly, chemical cross-linking techniques, direct chemical synthesis or a combination thereof. In the case of linear multimers prepared by cloning, nucleic acid sequences that encode the entire multimer or fragments thereof can be made in single- or double-stranded form by conventional cloning procedures. When made in double-stranded form, the multimers/fragments are ultimately denatured to provide single-stranded multimers/fragments. Multimers may be cloned in single-stranded form using conventional single-stranded phage vectors such as M13. Fragments can be linked enzymatically or chemically to form the multimer. When assembled enzymatically, the individual units are ligated with a ligase such as T4 DNA or RNA ligase, as the case may be. When prepared by chemical cross-linking, the individual units may be synthesized with one or more nucleic acids that have been derivatized to have functional groups that provide linking sites or derivatized after the oligonucleotide has been synthesized to provide such sites. A preferred procedure for chemical cross-linking is to incorporate N^4-modified cytosine bases into the nucleotide as described in commonly owned copending U.S. application Serial No. 945,876 filed 23 December 1986, the disclosure of which is incorporated herein by reference.

When prepared by direct chemical synthesis oligonucleotides containing derivatized nucleic acids or equivalent multifunctional molecules whose functional groups are blocked are made by conventional oligonucleotide synthesis techniques. The functional groups are unblocked and oligonucleotide units are synthesized out from the unblocked site (s).

A generic structure for the molecules used to generate branch points in the multimers is as follows:

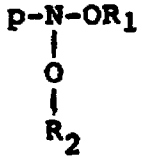


(1)

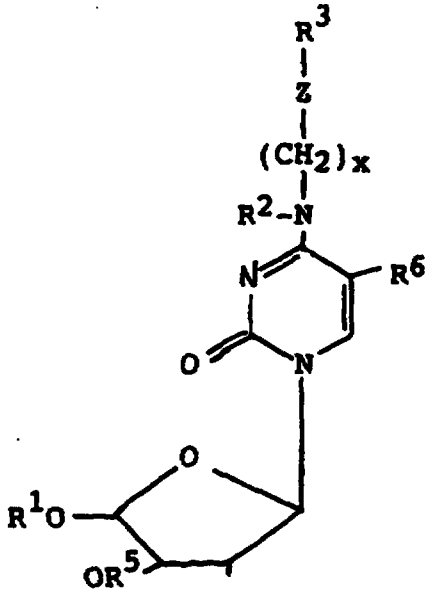
where R is an organic moiety, preferably a nucleic acid, R^1 is a hydroxyl protecting group that can be removed under conditions that do not remove synthetic nucleic acid from a solid phase and do not remove exocyclic nitrogen or phosphate protecting groups, X is a phosphorus-containing group that facilitates nucleic acid synthesis, such as a protected phosphoramidite, phosphonate or phosphate group, Y is a radical derived from a nucleophilic group such as an amino, hydroxyl, sulfhydryl or protected phosphate, and R^2 is R^1 or a blocking or protective group that can be removed and replaced with hydrogen without affecting R^1. In molecules used to generate bifurcated or "fork-like" branching, R^1 and R^2 are the same; whereas in molecules used to generate "comb-like" branching, R^2 is a blocking group that is stable in the presence of an R^1 deblocking reagent. Figure 3 schematically illustrates the procedures used to synthesize multimers having "comb-like" branches, "fork-like" branches, or combinations thereof.

Part A of Figure 3 depicts a conventional oligonucleotide synthesis scheme for preparing a linear oligonucleotide, such as the automated phosphoramidite method (Warner, et al, DNA (1984) 3:401). The dark block represents a solid support, N represents a nucleotide and p-N-OR_1 (R_1 is equivalent to R^1 below), a conventional nucleotide derivative having appropriate protecting groups.

Part B shows the procedure for making a comb-like multimer. The compound

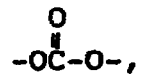


represents a modified base of formula (2) below. An oligomer unit of desired size and sequence is synthesized and left on the support. One or more N^4-modified cytosine bases are then incorporated into the chain by said automated procedure. Preferably, the modified base has the formula

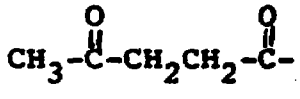


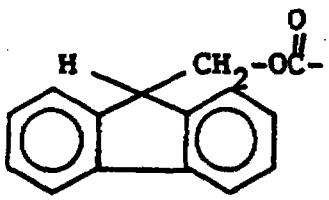
(2)

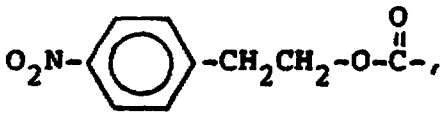
where Z is a nucleophile such as -O-, -NH-, -S-, PO_4=, and

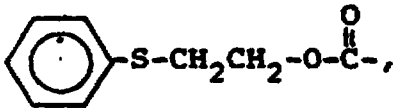


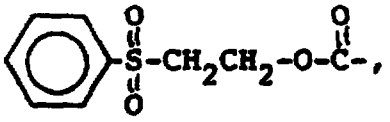
R^1 is a blocking or protective group such as dimethoxytrityl (DMT) or pixyl that is generally base-stable and acid sensitive, R^2 is hydrogen or methyl, R^3 is a blocking or protective group that can be removed and replaced with hydrogen without affecting R^1 such as











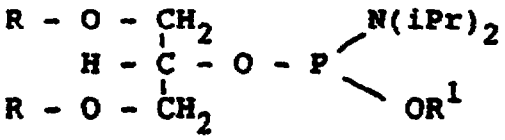
and

$CH_3O\text{-}CH_2\text{-}CH_2\text{-}O\text{-}CH_2\text{-}$,

R^5 is a phosphoramidite or other phosphorus derivative that enables addition of nucleotides to the 5' position of an oligonucleotide chain during chemical synthesis (e.g., a phosphodiester, phosphotriester, etc.), R^6 is methyl, hydrogen, I, Br, or F, and X is an integer in the range of 1 to 8, inclusive. When more than one modified base is incorporated they are preferably spaced by intermediate bases in the chain, most preferably by a -TT- dimer. Additional oligonucleotide units may be incorporated into the backbone followed by additional modified bases and so forth.

The N^4 nucleophile group is then deprotected (R^3 is removed) and additional oligonucleotide units are generated therefrom by the automated procedure. Residual R^1 groups at the chain terminii are removed and the branched "comb-like" multimer is cleaved from the support.

Part C of Figure 3 depicts the general procedure for making "fork-like" multimers. Again, an oligomer unit of desired size and sequence is synthesized by conventional techniques and left on the support. A blocked, bifunctional phosphorus-containing group (represented as XP in Part C) such as a blocked phosphoramidite, is then incorporated into the chain by the automated procedure. Preferred bifunctional phosphorus-containing groups are blocked phosphoramidites of the formula



where R is said hydroxyl protecting group, iPr is isopropyl, and R^1 is methyl or beta-cyanoethyl. Most preferably R is DMT and R^1 is beta-cyanoethyl.

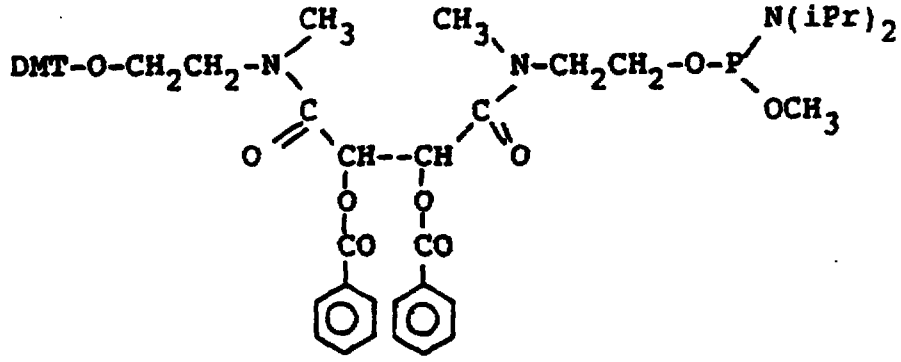
Alternatively, the N^4-modified cytosine base where R_1=R_2 (e.g., DMT) can be used.

The two protecting groups are then removed and additional oligonucleotide units are generated therefrom by the automated procedure. Residual R^1 groups are removed and the bifurcated multimer is cleaved from the support.

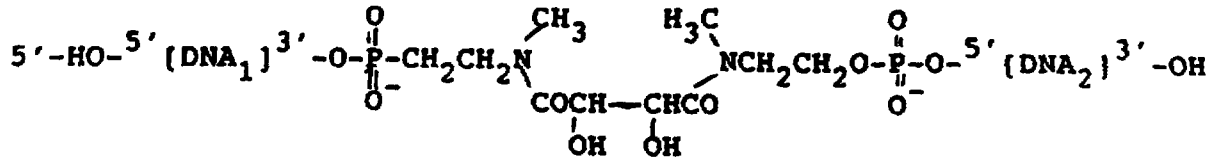
Parts D and E depict procedures where two or more bifurcated multimers, "comb-like" multimers or combinations thereof are spliced together enzymatically or chemically. Generally, the bifurcated and/or "comb-like" multimers are prepared as above and removed from the support. They are then combined in solution using the enzymatic or chemical linkage procedures described above.

Part F shows the procedure for synthesizing a multiple "comb-like" multimer. This procedure is a variation of the procedure shown in Part B and involves incorporating modified bases in the dependent side chains and generating secondary oligonucleotide side chains therefrom.

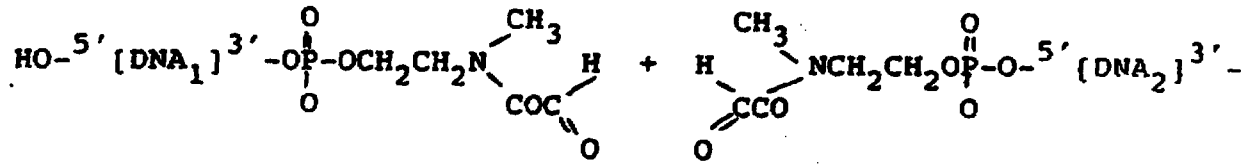
Suitable cleavable linker molecules may be incorporated into the multimers at predetermined sites for the purpose of analyzing the structure of the multimer or as a means for releasing predetermined segments (such as the portion of the multimer that binds to the labeled oligonucleotide). Subsequent to multimer synthesis and purification these linkers can be cleaved specifically without additional degradation of the nucleotide structure of the multimer. A preferred type of linker molecule was designed to contain a 1,2-diol group (which can be cleaved selectively by periodates) as well as a protected hydroxyl and phosphoramidite derived hydroxyl group to permit the linker to be incorporated into any DNA fragment by standard phosphoramidite chemistry protocols. A preferred embodiment of such a linker is the compound:



where DMT and iPr are as defined previously. After incorporation into a DNA fragment and complete deprotection the linker-containing fragment has the following structure:



where DNA_1 and DNA_2 represent DNA subfragments which may be the same or different. Reaction of this fragment with sodium periodate cleaves the fragment into the following subfragments:



Alternatively, the 1,2-diol group may be replaced with linker groups that contain a hydroxylamine-sensitive linkage, a base-sensitive sulfone linkage, or a thiolsensitive disulfide linkage. Such linker groups may be derived from conventional cross-linking agents that are used to conjugate proteins to other entities. Likewise, protecting groups other than DMT may be used.

Hybridization Assays

In nucleic acid hybridization assays, the multimer of the invention is bound to the analyte nucleic acid or to a single-stranded oligonucleotide bound to the analyte. Since the multimer includes a relatively large number of oligonucleotide units that are available for binding with the labeled oligonucleotide, many more label groups may be bound to the analyte than in prior procedures. The large number of label groups decreases the threshold level of detectable analyte, in some instances to the subattomole (10^{-18} mole) level.

The multimers may be used in essentially any of the known nucleic acid hybridization formats, such as those in which the analyte is bound directly to a solid phase or sandwich hybridizations in which the analyte is bound to an oligonucleotide that is in turn bound to a solid phase. It is particularly useful in the solution phase sandwich hybridization assay format described in copending application Serial No. 807,624, (US-A-4,868,105).

In a solution-phase sandwich hybridization assay with a capture step the amplifier is used as follows. Single-stranded analyte nucleic acid is incubated under hybridization conditions with an excess of two single-stranded nucleic acid probes (or probe sets), (1) a capture probe having a first binding sequence complementary to the analyte and a second binding sequence that is complementary to a single-stranded oligonucleotide bound to a solid phase, and (2) an amplifier probe having a first binding sequence that is complementary to the analyte and a second binding sequence that is complementary to an oligonucleotide unit of the amplification multimer. By using an amplifier probe, the multimer may be designed to be a "universal" reagent and different multimers need not be made for each analyte. The resulting product is a three component nucleic acid complex of the two probes hybridized to the analyte by their first binding sequences. The second binding sequences of the probes remain as single-stranded tails as they are not complementary to the analyte. Multiple probes of each type may be used.

This complex is then added under hybridizing conditions to a solid phase having a single-stranded oligonucleotide

bound to it that is complementary to the second binding sequence of the capture probe. The resulting product comprises the complex bound to the solid phase via the duplex formed by the oligonucleotide bound to the solid phase and the second binding sequence of the capture probe. The solid phase with bound complex is then separated from unbound materials.

The multimer is then added to the solid phase-analyte-probe complex under hybridization conditions to permit the multimer to hybridize to the available second binding sequences of the amplifier probe of the complex. The resulting solid phase complex is then separated from any unbound multimer by washing. The labeled oligonucleotide is then added under conditions which permit it to hybridize to the complementary oligonucleotide units of the multimer. The resulting solid phase labeled nucleic acid complex is then separated from excess labeled oligonucleotide, by washing to remove unbound labeled oligonucleotide, and read.

The amplification may be multiplied by the use of more than one multimer in the assay. In such instances a first multimer is designed to bind to the amplifier probe and to a second multimer and the second multimer is designed to bind to the first multimer and to the labeled oligonucleotide. Any number of multimers may be bound in series in this manner to achieve even greater amplification.

The analyte nucleic acids may be from a variety of sources, e.g., biological fluids or solids, food stuffs, environmental materials, etc., and may be prepared for the hybridization analysis by a variety of means, e.g., proteinase K/SDS, chaotropic salts, etc. Also, it may be of advantage to decrease the average size of the analyte nucleic acids by enzymatic, physical or chemical means, e.g., restriction enzymes, sonication, chemical degradation (e.g., metal ions), etc. The fragments may be as small as 0.1 kb, usually being at least about 0.5 kb and may be 1 kb or higher. The analyte sequence is provided in single-stranded form for analysis. Where the sequence is naturally present in single-stranded form, denaturation will not be required. However, where the sequence is present in double-stranded form, the sequence will be denatured. Denaturation can be carried out by various techniques, such as alkali, generally from about 0.05 to 0.2 M hydroxide, formamide, salts, heat, or combinations thereof.

The first binding sequences of the capture probe and amplifier probe that are complementary to the analyte sequence will each be of at least 15 nucleotides (nt), usually at least 25 nt, and not more than about 5 kb, usually not more than about 1 kb, preferably not more than about 100 nt. They will typically be approximately 30 nt. They will normally be chosen to bind to different sequences of the analyte. The first binding sequences may be selected based on a variety of considerations. Depending upon the nature of the analyte, one may be interested in a consensus sequence, a sequence associated with polymorphisms, a particular phenotype or genotype, a particular strain, or the like.

By appropriate selection of the first binding sequences of the amplifier and capture probes they may be used to identify a specific nucleic acid molecule that includes a particular gene or other sequence that is present as part of different nucleic acid molecules. In order to discriminate the nucleic acid molecule of interest from other molecules that also contain the given sequence, one of the probes is made complementary to the given sequence while the other is made complementary to another sequence of the molecule which other sequence is unique to that molecule (i.e., is not present in the other molecules that contain the given sequence). Such a technique is exemplified by the TEM-1NH assay described in the examples, infra.

The second binding sequences of the capture probe and amplifier probe are selected to be complementary, respectively, to the oligonucleotide attached to the solid phase and to an oligonucleotide unit of the multimer and so as to not be encountered by endogenous sequences in the sample/analyte. The second binding sequence may be contiguous to the first binding sequence or be spaced therefrom by an intermediate noncomplementary sequence. The probes may include other noncomplementary sequences if desired. These noncomplementary sequences must not hinder the binding of the binding sequences or cause nonspecific binding to occur.

The capture probe and amplifier probe may be prepared by oligonucleotide synthesis procedures or by cloning, preferably the former.

It will be appreciated that the binding sequences need not have perfect complementarity to provide homoduplexes. In many situations, heteroduplexes will suffice where fewer than about 10% of the bases are mismatches, ignoring loops of five or more nucleotides. Accordingly, as used herein the term "complementary" intends a degree of complementarity sufficient to provide a stable duplex structure.

The solid phase that is used in the assay may be particulate or be the solid wall surface of any of a variety of containers, e.g., centrifugal tubes, columns, microtiter plate wells, filters, tubing, etc. When particles are used, they will preferably be of a size in the range of about 0.4 to 200 microns, more usually from about 0.8 to 4.0 microns. The particles may be any convenient material, such as latex, or glass. Microtiter plates are a preferred solid surface. The oligonucleotide that is complementary to the second binding sequence of the capture probe may be stably attached to the solid surface through functional groups by known procedures.

It will be appreciated that one can replace the second binding sequence of the capture probe and the oligonucleotide attached to the solid phase with an appropriate ligand-receptor pair that will form a stable bond joining the solid phase to the first binding sequence of the capture probe. Examples of such pairs are biotin/ avidin, thyroxine/thyroxine-binding globulin, antigen/ antibody, carbohydrate/lectin, and the like.

The labeled oligonucleotide will include a sequence complementary to the second oligonucleotide units of the multimer. The labeled oligonucleotide will include one or more molecules ("labels"), which directly or indirectly provide for a detectable signal. The labels may be bound to individual members of the complementary sequence or may be present as a terminal member or terminal tail having a plurality of labels. Various means for providing labels bound to the sequence have been reported in the literature. See, for example, Leary et al, Proc Natl Acad Sci USA (1983) 80:4045; Renz and Kurz, Nucl Acids Res (1984) 12:3435; Richardson and Gumport, Nucl Acids Res (1983) 11:6167; Smith et al, Nucl Acids Res (1985) 13:2399; Meinkoth and Wahl, Anal Biochem (1984) 138:267. The labels may be bound either covalently or non-covalently to the complementary sequence. Labels which may be employed include radionuclides, fluorescers, chemiluminescers, dyes, enzymes, enzyme substrates, enzyme cofactors, enzyme inhibitors, enzyme subunits, metal ions, and the like. Illustrative specific labels include fluorescein, rhodamine, Texas red, phycoerythrin, umbelliferone, luminol, NADPH, α-β-galactosidase, horseradish peroxidase, etc.

The labeled oligonucleotide can be conveniently prepared by chemical synthesis such as that described in commonly owned copending application Serial No. 945,876. By providing for a terminal group which has a convenient functionality, various labels may be joined through the functionality. Thus, one can provide for a carboxy, thiol, amine, hydrazine or other functionality to which the various labels may be joined without detrimentally affecting duplex formation with the sequence. As already indicated, one can have a molecule with a plurality of labels joined to the sequence complementary to the labeling sequence. Alternatively, one may have a ligand bound to the labeling sequence and use a labeled receptor for binding to the ligand to provide the labeled analyte complex.

The ratio of capture probe and amplifier probe to anticipated moles of analyte will each be at least stoichiometric and preferably in excess. This ratio is preferably at least about 1.5:1, and more preferably at least 2:1. It will normally be in the range of 2:1 to 10,000:1. Concentrations of each of the probes will generally range from about 10^{-9} to 10^{-6} M, with sample nucleic acid concentrations varying from 10^{-21} to 10^{-12} M. The hybridization steps of the assay will generally take from about 10 minutes to 2 hours, frequently being completed in about 1 hour. Hybridization can be carried out at a mildly elevated temperature, generally in the range from about 20°C to 80°C, more usually from about 35°C to 70°C, particularly 65°C.

The hybridization reaction is usually done in an aqueous medium, particularly a buffered aqueous medium, which may include various additives. Additives which may be employed include low concentrations of detergent (0.1 to 1%), salts, e.g., sodium citrate (0.017 to 0.170 M), Ficoll, polyvinylpyrrolidine, carrier nucleic acids, carrier proteins, etc. Non-aqueous solvents may be added to the aqueous medium, such as dimethylformamide, dimethylsulfoxide, alcohols, and formamide. These other solvents will be present in amounts ranging from 2 to 50%.

The stringency of the hybridization medium may be controlled by temperature, salt concentration, solvent system, and the like. Thus, depending upon the length and nature of the sequence of interest, the stringency will be varied.

The procedure used in the separation steps of the assay will vary depending upon the nature of the solid phase. For particles, centrifugation or filtration will provide for separation of the particles, discarding the supernatant or isolating the supernatant. Where the particles are assayed, the particles will be washed thoroughly, usually from one to five times, with an appropriate buffered medium, e.g., PBS containing a detergent such as SDS. When the separation means is a wall or support, the supernatant may be isolated or discarded and the wall washed in the same manner as indicated for the particles.

Depending upon the nature of the label, various techniques can be employed for detecting the presence of the label. For fluorescers, a large number of different fluorometers are available. For chemiluminescers, luminometers or films are available. With enzymes, a fluorescent, chemiluminescent, or colored product can be provided and determined fluorometrically, luminometric-ally, spectrophotometrically or visually. The various labels which have been employed in immunoassays and the techniques applicable to immunoassays can be employed with the subject assays.

In a hybridization assay in which the analyte nucleic acid is bound directly to a solid phase, such as a "dot blot" assay, the multimer is hybridized directly to the bound analyte. In these instances, the first oligonucleotide unit(s) of the multimer is complementary to a sequence of the analyte and the second oligonucleotide units are complementary to a labeled oligonucleotide. Unbound multimer is removed from the solid phase and the labeled oligonucleotide is then hybridized to the bound analyte-multimer complex. Excess labeled oligomer is removed and the labeled, bound complex is read.

The multimers may also be used in other assays such as direct, indirect, and sandwich immunoassays. In these instances the reagent that plays the role of the labeled antibody or other ligand that is bound directly or indirectly to the analyte has an oligonucleotide that is complementary to the first oligonucleotide unit of the multimer bound to it rather than a label. For instance, in a sandwich immunoassay for an antigen analyte, the analyte sample is incubated with a solid phase to which is bound a first antibody to the antigen. Unbound sample is removed from the solid phase and a second antibody to the antigen and which an oligonucleotide complementary to a unit of the multimer is bound is reacted with the bound complex to form a three-membered complex. Following removal of excess second antibody the multimer is then hybridized to the complex via the oligonucleotide bound to the second antibody. Excess multimer is removed and a labeled oligonucleotide is hybridized to the other oligonucleotide units of the multimer. After removal of excess

labeled oligonucleotide, the complex is read.

Kits for carrying out amplified nucleic acid hybridization assays according to the invention will comprise in packaged combination the following reagents: the multimer; an appropriate labeled oligonucleotide; a solid phase that is capable of binding to the analyte; optionally a capture probe if the assay format is one in which the analyte is bound to the solid phase through an intermediate oligonucleotide or other ligand; and optionally an amplifier probe if the assay format is one in which the multimer is not hybridized directly to the analyte. These reagents will typically be in separate containers in the kit. The kit may also include a denaturation reagent for denaturing the analyte, hybridization buffers, wash solutions, enzyme substrates, negative and positive controls and written instructions for carrying out the assay.

The following examples of the invention are offered by way of illustration and not by way of limitation.

Examples

1. Enzymatic Preparation of Linear Multimer

A linear multimer of an 18-mer that is complementary to amplifier probes (see 3.F. below) was prepared according to the scheme depicted in Figure 1.

Two 18-mers, LLA-1 and LLA-2, were synthesized by an automated phosphoramidite method as described in Warner et al, DNA (1984) 3:401. Purification was carried out according to Sanchez-Pescador and Urdea, DNA (1984) 3:339. Phosphorylation of the 5' end of the LLA-2 was carried out by the chemical phosphorylation procedure described in Example 1 of commonly owned copending EP Application No. 88307358.7, the disclosure of which is incorporated herein by reference. The sequences of LLA-1 and LLA-2 were as follows.

5'-CGTGTCAGGCATAGGACC	LLA-1
TCCGTATCCTGGGCACAG-p-5'	LLA-2

The linear LLA-2 polymer was formed using T4 DNA ligase. The products of such ligations are double-stranded. Single-stranded polymer may be obtained by gel purifying the product under denaturing conditions.

One hundred thousand pmole of each sequence were added to a 1.5 ml tube and evaporated to dryness under vacuum.

The following solution was added to the dried sequences:

100 µl KBTS buffer*
100 µl 10 mM DTT
100 µl 10 mM ATP
50 µl H_2O
50 µl 1M NaCl
500 µl 30% PEG.

*10X (50 mM Tris HCl, pH 7.6, 10 mM $MgCl_2$, 1 mg/ml spermidine)

The tube was vortexed and then heated to 55°C for 30 min. The tube was then cooled to room temperature and the following solution was added

6.7 µl T4 DNA Ligase (New England Nuclear 15 U/µl)
18.8 µl 5X Ligase Dilution Buffer (NEN)
74.5 µl H_2O

Again the tube was vortexed and then incubated at room temperature overnite. The reaction mixture was extracted with n-butanol to a volume of 100 µl, 100 µl of 3X stop mix (25% glycerol, 0.05% bromphenol blue, 0.5% sodium dodecyl sulfate, 25 mM EDTA) was added and then heated to 100°C for 5 min. to denature the sample. Twenty µl portions of this solution were then added to the wells of a 7% denaturing polyacrylamide gel (10 cm X 10 cm X 1.5 mm). The gel was run at 10 V/cm until the bromphenol blue dye was within 0.5 cm of the bottom of the gel. The products formed were made visible by placing the gel on a thin layer chromatography plate containing a UV fluorescing dye covered with Saran wrap and illuminating with a long wave UV lamp. The products absorb the UV irradiation and cast a visible shadow. Bands of increasing length were observed and polymeric products greater than twenty oligomeric units long were cut out. These products were eluted from the gel by soaking in Maxim-Gilbert buffer (0.1 M Tris-HCl, pH 8, 0.5 M NaCl, 5 mM EDTA).

2. Chemical Preparation of Linear and Branched Multimers

A. Preparation of Linear and Branched Multimers

Linear and branched multimers of an 18-mer that are complementary to the amplifier probes (see 3.F. below) were prepared according to the schemes depicted in Figures 2A and 2B.

As indicated, the schemes use oligonucleotide units having derivatized bases that are cross-linked with phenyldiisothiocyanate (DITC).

The oligonucleotide used to prepare the linear multimer had the sequence

3'-XGCACAGTCCGTATCCTGGX-5'

where X represents the N^4-(6-aminocaproyl-2-aminoethyl) derivative of cytidine.

The oligonucleotide used for the branched multimer had the sequence

5'-XTGGTCCTATGCCTGACACGTXTGGTCCTATGCCTGACACGTXT-3'

where X is as above.

The N^4-(6-aminocaproyl-2-aminoethyl) derivative of cytidine was prepared as described in commonly owned copending application Serial No. 945,876 (US-A-5093232). The oligomers were synthesized and purified as described in Example 1.

A sample of 0.2 OD260 units of either fragment was dissolved in 0.5 µl of 0.1 M sodium borate, pH 9.3, to which 9.5 µl of DITC in dimethylformamide (2 mg/ml) was added. The solution was vortexed and set at room temperature overnight in the dark. After the addition of 300 µl of n-butanol and mixing, 300 µl of water was added. The mixture was vortexed and centrifuged to separate the layers. The sample was extracted several times until the aqueous phase was lowered to a volume of approximately 50 µl and then vacuumed to dryness. The polymer was then treated with 10 µl of 1 M glycine, pH 9.5, for 2 hr to modify any remaining isothiocyanate groups. The mixture was loaded onto a 10 ml Sephadex G-25 column, eluted with water, collected, evaporated to dryness, taken up in 1% SDS and loaded onto a 7% polyacrylamide gel (vertical 2% agarose gels are preferred for preparation runs). The gel was run at 60 ma and then stained with ethidium bromide. Bands estimated to comprise 10-25 units of the oligomer were cut, electroeluted and precipitated.

B. Preparation of Comb-like and Bifurcated Multimers

In this section DMT = dimethoxytrityl; T = deoxythymidine; DMF = dimethylformamide; BDMS = t-butyldimethylsilyl; C = deoxycytidine; TLC = thin-layer chromatography; DMAP = N,N-dimethylaminopyridine; THF = tetrahydrofuran; DIPEA = diisopropylethylamine; LEV = levulinic ester; DCA = dichloroacetic acid; DCC = dicyclohexylcarbodiimide; DCHU = dicyclohexylurea; TEA = triethylamine; TMS = trimethylsilyl; FMOC = 9-fluorenyl-methoxycarbonyl.

B.1A. Synthesis of Nucleotide for Forming Comb-Like Branch Points

5'-DMT-T-OH (27.3 g, 50 mmole) and imidazole (10 g, 150 mmole) were coevaporated with 200 ml DMF. The residue was dissolved in 250 ml DMF, and BDMS chloride (75 mmol) was added. The reaction mixture was stirred for 18 hr at 20°C. Methanol (50 ml) was added and after 30 min the solvents were removed in vacuo. The oily residue was dissolved in 50 ml ethyl acetate, and the organic phase extracted with 5% aqueous $NaHCO_3$ (2 x 500 ml) and 80% saturated aqueous NaCl (500 ml) and finally dried over solid Na_2SO_4. The solvent was removed in vacuo to give 35 g (50 mmole) 5'-DMT-3'BDMS T (100% yield). This material was used without further purification.

Triazole (25.6 g) was suspended in 400 ml of CH_3CN (at 0°C) and $POCl_3$ (8 ml) was added with rapid stirring. Then triethylamine (60 ml) was added dropwise over 15 min to the slurry stirred at 0°C for 30 min. 5'-DMT-3'BDMS T (25 mmole crude) dissolved in 100 ml CH_3CN was added dropwise to the above stirred slurry at 0°C. The ice-water bath was removed and stirring continued at 20°C for one hour. The reaction mixture was diluted with 800 ml ethyl acetate, and the organic phase was extracted with 5% $NaHCO_3$ (2 x 500 ml) and 80% saturated aqueous NaCl (500 ml). After drying the organic phase over solid Na_2SO_4 solvents were removed in vacuo. The resulting residue was coevaporated with toluene (400 ml) and CH_3CN (400 ml) to give 5'-DMT-3'-BDMS-5-methyl-4-triazoyl β-D-2-deoxyribofuranosyl-2(1H)-pyrimidinone as a white foam in quantitative yield. This material was used without further purification.

To a solution of 6-aminohexanol (11.7 g, 100 mmole) in 400 ml CH_3CN was added dropwise 5'-DMT-3'-BDMS-5-methyl-4-triazoyl β-D-2-deoxyribofuranosyl-2(1H)-pyrimidinone (8.7 g, 12 mmole) dissolved in 100 ml CH_3CN and the reaction mixture stirred at 20°C. The progress of the reaction was monitored by TLC (every 30 min) and when the starting

material had completely disappeared (usually in 1-2 hours), the reaction mixture was diluted with 500 ml ethyl acetate, which was extracted with 5% aqueous $NaHCO_3$ and 80% saturated aqueous NaCl as described above. After drying of the organic phase over Na_2SO_4, the solvent was removed in vacuo to give 7.0 g (9.2 mmole) of product 5'-DMT-3'-BDMS-5-methyl-N^4-6-hydroxyhexyl deoxycytidine (yield 77%). This material was used without further purification.

To a solution of 5'-DMT-3'-BDMS-5-methyl-N^4-6-hydroxyhexyl deoxycytidine (7 g, 9.2 mmole) in 100 ml THF was added $(CH_3COCH_2CH_2CO)_2O$ (50 mmole) dissolved in 100 ml THF and then 10 ml 6.5% DMAP in 2,6-lutidine/THF. The reaction mixture was left stirring for 30 min. The analysis showed that starting material had been completely consumed. The reaction mixture was diluted with 700 ml ethyl acetate which was diluted with 700 ml ethyl acetate which was extracted with 5% aqueous $NaHCO_3$ (3 x 500 ml) and 80% saturated aqueous NaCl (500 ml) as described above. After drying over solid Na_2SO_4, the solvent was removed and the residue coevaporated with toluene (200 ml) and CH_3CN (200 ml) to give 12.3 g of crude product.

This crude product was dissolved in 100 ml THF, and 10 ml of-a 1.1 M solution of tetrabutylammonium fluoride in THF was added. The progress of the reaction was monitored by TLC; it is usually over in 30 min but may take longer. When starting material had been consumed, the reaction mixture was diluted with 700 ml ethyl acetate, which was extracted with $NaHCO_3$ and NaCl solutions, as above. Removal of the solvent afforded 8.5 g crude product 5'-DMT-5-methyl-N^4(O-levulinyl-6-oxyhexyl)-2'-deoxycytidine. This material was subjected to silica gel chromatography. The purified product was isolated by elution with 4% methanol in CH_2Cl_2 to give 5.0 g of a slightly brownish foam (6.7 mmole; 73% yield).

Silica-purified 5'-DMT-5-methyl-N^4(O-levulinyl-6-oxyhexyl)-2'-deoxycytidine (7.7 mmole) was coevaporated twice with CH_3CN. The resulting dry powder was dissolved in 70 ml CH_2Cl_2 containing 4.9 ml DIPEA in a flask under argon. After cooling to 0°C, 1.65 ml (8.5 mmole) N,N-diisopropylaminomethoxy chlorophosphine was added with a syringe and the mixture stirred at 0° for 30 min. After dilution with 400 ml ethyl acetate, the organic phase was washed 4 times with 400 ml 80% saturated aqueous NaCl, then dried over solid Na_2SO_4 and filtered. The solvent was removed in vacuo and the resulting residue coevaporated twice with toluene to give an oil. This oil was dissolved in 30 ml toluene and added dropwise into 400 ml cold hexane (~-20°C). The precipitate was quickly collected by filtration and dried in vacuo for 18 hr to give 5.45 g of phosphoramidite (6.0 mmole; 78% yield).

B.1B. Synthesis of Alternative, Preferred Nucleotide for Forming Comb-Like Branch Points

To a solution of 5'-DMT-3'-BDMS-5-methyl-N^4-6-hydroxyhexyl deoxycytidine (34 g, 50 mmole) prepared as described above in 200 ml CH_2Cl_2 was added 1.5 g N,N-dimethylaminopyridine and 25 ml triethylamine. To this solution at 0°C was added dropwise DMT-Cl (75 mmole, 25.5 g) dissolved in CH_2Cl_2 (100 ml). The reaction mixture was left stirring for 1 hour. The analysis showed that starting material had been completely consumed. Then 50 ml of methanol was added. After 30 min the reaction mixture was diluted with 800 ml ethyl acetate which was extracted with 5% $NaHCO_3$ (2 x 500 ml) and 80% saturated aqueous NaCl (500 ml) described above. After drying over solid Na_2SO_4 the solvent was removed in vacuo and the residue coevaporated with toluene (200 ml) and CH_3CN (200 ml).

This crude product was dissolved in 200 ml THF, and 200 ml of a 1.1 M solution of tetrabutylammonium fluoride in THF was added. The progress of the reaction was monitored by TLC; it is usually over in 30 min but may take longer. When starting material had been consumed, the reaction mixture was diluted with 700 ml ethyl acetate, which was extracted with $NaHCO_3$ and NaCl solutions, as above. Removal of the solvent afforded 36 g crude product, 5'-DMT-5-methyl-N^4(O-DMT-6-oxyhexyl)deoxy-cytidine. This material was subjected to silica gel chromatography. The purified product was isolated by elution with 2-4% methanol in CH_2Cl_2 to give 32.7 g of pure product (34 mmole; yield based on 5'-DMT-T-OH: 69%).

Silica-purified 5'-DMT-5-methyl-N^4(O-DMT-6-oxyhexyl)-2'-deoxycytidine (34 mmole) was coevaporated twice with CH_3CN. The resulting dry powder was dissolved in 100 ml CH_2Cl_2 containing 7.5 ml DIPEA in a flask under argon. After cooling to 0°C, 7.37 ml (38 mmole) N,N-diisopropylaminomethoxy chlorophosphine was added with a syringe and the mixture stirred at 0° for 30 min. After dilution with 800 ml ethyl acetate, the organic phase was washed 4 times with 800 ml 80% saturated aqueous NaCl, then dried over solid Na_2SO_4 and filtered. The solvent was removed in vacuo and the resulting residue coevaporated twice with toluene to give an oil. This oil was dissolved in 80 ml toluene and added dropwise into 700 ml cold hexane (~-20°C). The precipitate was quickly collected by filtration and dried in vacuo for 18 hr to give 31.8 g of phosphoramidite (28.7 mmole; 84% yield).

5'-DMT-T-OH (16.4, 30 mmole) was dissolved in dry 200 ml CH_3CN and 1-(TMS)imidazole (14.6 ml, 100 mmole) was added. After 60 min the solvents were removed in vacuo. The oily residue was dissolved in 700 ml ethyl acetate, and the organic phase extracted with 5% aqueous $NaHCO_3$ (2 x 500 ml) and 80% saturated aqueous NaCl (500 ml) and finally dried over solid Na_2SO_4. The solvent was removed in vacuo to give 30 mmole 5'-DMT-3'-TMS-T (100% yield). This material was used without further purification.

Triazole (37.8 g) was suspended in 450 ml of CH_3CN (at 0°C) and $POCl_3$ (12 ml) was added with rapid stirring.

Then triethylamine (90 ml) was added dropwise over 15 min to the slurry stirred at 0°C for 30 min. 5'- DMT-3'-TMS-T (30 mmole crude) dissolved in 100 ml CH_3CN was added dropwise to the above stirred slurry at 0°C. The ice-water bath was removed and stirring continued at 20°C for one hour. The reaction mixture was diluted with 800 ml ethyl acetate, and the organic phase was extracted with 5% $NaHCO_3$ (2 x 500 ml) and 80% saturated aqueous NaCl (500 ml). After drying the organic phase over solid Na_2SO_4 solvents were removed in vacuo. The resulting residue was coevaporated with toluene (400 ml) and CH_3CN (400 ml) to give 5'-DMT-3'-TMS-5-methyl-4-triazoyl β-D-2-deoxyribofuranosyl-2(1H) -pyrimidinone as a white foam in quantitative yield. This material was used without further purification.

To a solution of 6-aminohexanol (23 g, 200 mmole) in 400 ml CH_3CN was added dropwise 5'-DMT-3'-TMS-5-methyl-4-triazoyl β -D-2-deoxyribofuranosyl-2(1H)-pyrimidinone (20 g, 30 mmole) dissolved in 100 ml CH_3CN and the reaction mixture stirred at 20°C. The progress of the reaction was monitored by TLC (every 30 min) and when the starting material had completely disappeared (usually in 1-2 hours), the reaction mixture was diluted with 800 ml ethyl acetate, which was extracted with 5% aqueous $NaHCO_3$ and 80% saturated aqueous NaCl as described above. After drying of the organic phase over Na_2SO_4, the solvent was removed in vacuo to give 20.3 g (~30 mmole) of product 5'-DMT-3'-TMS-5-methyl-N^4-6-hydroxyhexyl deoxycytidine. This material was used without further purification.

To a solution of 5'-DMT-3'-TMS-5-methyl-N^4(6-hydroxyhexyl)deoxycytidine in 250 ml methanol was added 25 ml concentrated aqueous NH_4OH and the reaction mixture left stirring in a closed round-bottom flask to 1 hour. The solvent was then removed in vacuo and coevaporated with 1 x 200 ml ethanol, 1 x 100 ml toluene and 1 x 100 ml CH_3CN to give 5'-DMT-5-methyl-N^4(6-hydroxylhexyl)deoxy-cytidine in quantitative yield. This material was used without further purification. This material was dissolved in 200 ml CH_2Cl_2 and 4 ml of pyridine was added followed by dropwise addition of FMOC-Cl (7.8 g, 30 mmole) dissolved in CH_2Cl_2 (50 ml). The reaction mixture was left stirring for 30 min. The analysis showed that starting material had been completely consumed. The reaction mixture was diluted with 500 ml ethyl acetate which was extracted with 5% aqueous $NaHCO_3$ (3 x 500 ml) and 80% saturated aqueous NaCl (500 ml) as described above. After drying over solid Na_2SO_4, the solvent was removed and the residue coevaporated with toluene (200 ml) and CH_3CN (200 ml) to give 23.7 g of crude product. This crude product was subjected to silica gel chromatography. The purified product eluted with about 4% methanol in CH_2C_{l2} to give 13.3 g (15.3 mmole) of pure 5'-DMT-5-methyl-N^4 (O-FMOC-6-oxyhexyl)deoxycytidine (50% yield based on 5'-DMT-TOH).

Silica-purified 5'-DMT-5-DMT-5-methyl-N^4(O-FMOC-6-oxyhexyl)-2'-deoxycytidine (15.3 mmole) was coevaporated twice with CH_3CN. The resulting dry powder was dissolved in 60 ml CH_2Cl_2 containing 4.1 ml DIPEA in a flask under argon. After cooling to 0°C, 3.19 ml (16.5 mmole) N,N-diisopropylaminomethoxy chlorophosphine was added with a syringe and the mixture stirred at 0° for 30 min. After dilution with 400 ml ethyl acetate, the organic phase was washed 4 times with 400 ml 80% saturated aqueous NaCl, then dried over solid Na_2SO_4 and filtered. The solvent was removed in vacuo and the resulting residue coevaporated twice with toluene to give an oil. This oil was dissolved in 50 ml toluene and added dropwise into 400 ml cold hexane (~-20°C). The precipitate was quickly collected by filtration and dried in vacuo for 18 hr to give 12.15 g of phosphoramidite (11.8 mmole; 77% yield). Removal of O-FMOC group during solid phase synthesis: t-butylamine/pyridine (1:10 v/v) for 1 hour at 20°. Removal of O-levulinyl group: 0.5 M hydrazine hydrate in pyridine/glacial acetic acid (4:1 v/v) 15 minutes at 20°C.

B.2. Synthesis of a Multifunctional Phosphoramidite for Forming Bifurcated Branch Points

Glycerol (10 mmole) was dried by coevaporation with pyridine. The resulting oil was dissolved in 50 ml pyridine and DMT-Cl (6.8 g, 20 mmole) was added, and the reaction mixture was stirred at 20°C for 18 hr. After addition of methanol (10 ml), the solvent was removed on a rotary evaporator. The resulting oil was dissolved in 250 ml ethyl acetate and the organic phase was washed with 5% aqueous $NaHCO_3$ (2 x 250 ml), 80% saturated aqueous NaCl (l x 250 ml) and then dried over solid Na_2SO_4. The solvent was removed in vacuo and the residue coevaporated with 100 ml toluene and 100 ml CH_3CN. The product was isolated by silica gel chromatography to give 2.5 g (3.6 mmole) O,O-bis DMT glycerol (35% yield). Product elutes with 0-1% MeOH.

The bis-DMT glycerol (2.3 mmole) was dissolved in CH_2Cl_2 (10 ml) containing DIPEA (0.8 ml) under argon, and N,N-diisopropylamino-2-cyanoethoxy-chlorophosphine (1 ml) was added by syringe. After 30 minutes the mixture was diluted with ethyl acetate (200 ml) and the organic phase washed with 200 ml 80% saturated aqueous NaCl. After drying over solid Na_2SO_4, the solvent was removed in vacuo, and the residue coevaporated with 100 ml toluene and 100 ml dry CH_3CN to give 2.15 g (2.3 mmole; 100% yield) of bis-DMT glycerol phosphoramidite. The product was dispensed with dry CH_3CN into small septum-capped vials and after removal of the solvent stored at -20°C under argon.

B.3. Synthesis of Periodate-Cleavable Linker Phosphoramidite

O,O-Dibenzoyl tartaric acid monohydrate (18.8g, 50 mmole) was dissolved in 250 ml CH_3CN and the solvent was removed in vacuo. This process was repeated. The resulting oil was dissolved in 250 ml THF and DCC (10.6g, 50 mmole) dissolved in 50 ml THF was added. A precipitate started forming in a few minutes. After stirring for 18 hr at 20°C

the reaction mixture was filtered, and the precipitate washed with THF. The precipitate was dried in high vacuum to give 10.8g (50 mmole) DCHU. To the combined filtrate was added 2-(N-methyl)aminoethanol (4.0 ml, 50 mmole) and the reaction mixture was stirred for 1 hr at 20°C. DCC (10.6g, 50 mmole) in 50 ml THF was then added. A small precipitate formed. After about 1 hr, 2-(N-methyl)aminoethanol (4.0 ml, 50 mmole) was added and the reaction mixture stirred for 18 hours at 20°C.

The formed precipitate was filtered off and washed with THF. The dried precipitate of DCHU weighed 10.8g. The combined filtrate was evaporated to an oil. Chromatography on silica afforded 8g (17 mmole) of O,O-dibenzoyl tartaric di(N-methyl-2-hydroxyethyl)amide (this product elutes with 6% MeOH/CH_2Cl_2).

To the amide product (8.6 mmole) in 50 ml CH_2Cl_2 containing DMAP (0.11 g) and TEA (2.4 ml) was added dropwise, DMT-Cl (8.6 mmole) dissolved in 50 ml CH_2Cl_2. After addition of DMT-Cl the reaction mixture was stirred for 1 hr at 20°C, then the solvent was removed by evaporation. The residue was dissolved in 600 ml ethyl acetate and the organic phase washed with 400 ml 5% $NaHCO_3$ and 400 ml 80% saturated aqueous NaCl. The organic phase was dried over solid Na_2SO_4. After 30 min the Na_2SO_4 was filtered off, and the supernatant was concentrated to an oil, then coevaporated with toluene and CH_3CN. The crude material was subjected to silica gel chromatography using n-butanol/CH_2Cl_2 for elution. The pure mono-DMT product eluted with 2-3% n-butanol/CH_2Cl_2 to give 1.53 g (2 mmole) of O,O-dibenzoyl tartaric 2-(O-dimethoxytrityl)hydroxy-ethyl-N,N-dimethyl, N-methyl-2-hydroxyethyldiamide.

This material was dissolved in 20 ml CH_2Cl_2 containing DIPEA (3 mmole). After cooling to 10°C, 2.2 mmole methoxy-N,N-diisopropylaminochlorophosphine was added under argon. After 15 min, ethyl acetate was added, and the organic phase washed with 80% saturated aqueous NaCl, dried over solid Na_2SO_4 and evaporated to dryness. After coevaporation with toluene and dry CH_3CN, the phosphoramidite residue was dissolved in 10 ml dry CH_3CN. This solution was aliquoted into 19 dry Weaton vials and the solvent removed in vacuo. The vials were closed with septum screw caps and stored at -20°C.

This phosphoramidite may be coupled to oligonucleotides using standard DNA synthesis techniques and equipment. After deprotection the resulting linker-containing DNA may be cleaved at the 1,2-diol site as described above.

B.4. Synthesis of a Four-Site Bifurcated Amplification Multimer

For synthesis of branched fragments, a 2000 A control pore glass (CPG) support (30 mg of 7.3 µmole of nucleoside/g) was used. The CPG support was synthesized as described in the commonly owned copending EP Application EP-A- 304 215. An automated methyl phosphoramidite coupling procedure was employed for DNA synthesis as above, except that during the addition of the branched oligonucleotide segments 2.5% (v/v) DCA in toluene (instead of CH_2Cl_2) was used for detritylation.

Fragment LLA-2 (GACACGGGTCCTATGCCT; see above) was synthesized on the CPG, then removed from the automated synthesizer and placed into a sintered glass funnel. Manual phosphoramidite couplings were then performed as described (Urdea, M.S., Methods in Enzymol (1987) 146:22-41). A 100 µmole aliquot of the DMT_2-glycerol phosphoramidite (2-cyanoethyl form) and 250 µmoles of tetrazole were added to the 5'-deprotected fragment and incubated for 15 min. This process was then repeated. Two T methyl phosphoramidites were then added manually and an additional glycerol phosphate was added. The CPG was then placed back on the automated synthesizer and the fragment GATGTGGTTGTCGTACTTTT was synthesized off of each branch. The standard deprotection and purification as above was then employed.

B.5. Synthesis of a Four-Site Comb Amplification Multimer

Using the methods described above, the fragment TTOTTOTTOTTGACACGGGTCCTATGCCT (O = 5'-DMT-N^4-[LevO$(CH_2)_6$]-5-Me cytidine methyl phosphoramidite) was synthesized. The fragment was then removed from the machine and treated for 1 hr at room temperature with 0.5 M hydrazine monohydrate in 8:2 (v/v) pyridine/concentrated acetic acid. The CPG was then washed with pyridine, then 1:1:2 (v/v/v) H_2O/lutidine/THF. The support was then placed back on the automated synthesizer and the fragment was synthesized off of each O in the above formula. The standard deprotection and purification as above was then employed. Note that one copy of the labeled probe (LLA-2) binding fragment is at the 5'-end of the multimer and three copies of the fragment are at the O residues.

3. Sandwich Hybridization Assay for Hepatitis B Virus (HBV) DNA Using Multimer

Figure 3 schematically depicts the assay procedure.

A. Standard Analyte HBV DNA

The plasmid pHE63 composed of the entire 3.2 kb HBV genome cloned into the EcoRI site of plasmid pBR325

linearized with EcoRI and diluted into normal human serum was used as standard analyte. The analyte is designated 11 in Figure 3.

B. Solid Phase Oligonucleotide Complex (C in Figure 3)

A 21 base oligomer, 5'-XCACCACTTTCTCCAAAGAAG-3', where X is as defined above, was synthesized as described in Example 1 and biotinylated using N-hydroxysuccinimdyl biotin in 0.1 M sodium phosphate, pH 7.5. A 5 µl aliquot of this biotinylated fragment (800 pmoles) was added to a 1.5 ml Eppendorf tube containing 500 µl of 0.25% (w/v) 2.8 micron avidin polystyrene beads in 1x PBS. After a 1 h incubation at 37°C, the beads were washed 3 times with 500 µl of 0.1% SDS, 4x SSC by centrifugation then resuspended and stored in the same solution until used.

C. Labeled Oligomer (E in Figure 3)

An 18 base oligomer, 5'-XGGTCCTAGCCTGACAGC-3', where X is defined as above, was synthesized, modified with DITC in 95:5 (v/v) dimethylformamide:0.1 M sodium borate, pH 9.3, extracted with n-butanol, and combined with horseradish peroxidase (HRP).

D. Capture Probes (A in Figure 3)

A set of 12 single-stranded oligomers each having a varying 30 base long portion complementary to a specific sequence of the HBV genome and a constant 20 base long 3'-portion complementary to the oligonucleotide bound to the solid phase was synthesized by the procedures described in Example 1.

E. Amplifier Probes (B in Figure 3)

A set of 36 single-stranded oligomers each consisting of a varying 30 base long portion complementary to a specific sequence of the HBV genome and a constant 20 base long 3'-portion complementary to the multimer (D in Figure 3) were synthesized by the procedures described in Example 1.

Both the capture and amplifier probes were designed for the constant ds region of the HBV virus.

F. Bead Assay Procedure

10 µl samples of analyte were placed in 1.5 ml Eppendorf tubes and treated with 12.5 µl of proteinase K/ SDS (Gene (1987) 61:254) at 37°C for 30 min. To each sample, 5 µl of 1 M NaOH containing 50 fmoles each of the 48 HBV oligonucleotide probes (12 capture probes and 36 amplifier probes) were added and the tubes were heated to 100°C for 10 min. The samples were set on ice for 5 min, microfuged for 10 sec and neutralized with 0.38 M acetic acid, 12.3x SSC (final 4x SSC). Annealing of the probes to the analyte was conducted at 55°C for 1 h. Subsequently, 25 µl of the capture beads were added and the solution was left at 55°C for an additional 15 min. Two washes were performed by adding 500 µl of wash solution (0.1% SDS, 4x SSC), vortexing, centrifuging for 1 min and decanting. To each tube, 20 µl containing 50 fmoles of multimer (D in Figure 3) in HM buffer (0.1% SDS, 4x SSC, 1 mg/ml sonicated salmon sperm DNA, 1 mg/ml poly-A, 10 mg/ml BSA) was added. After vortexing, the tubes were left at 55°C for 15 min and washed twice as above. Labeling was conducted with 20 µl containing 250 fmoles of probe Type E in HM for 1 h at 37°C. After three washes as above, the beads were thoroughly drained by inversion onto Kimwipes, treated with the appropriate substrate and measured as described below. The total time required for the analysis from addition of the proteinase K/SDS solution to readout was 3 h 50 min in the chemiluminescent format.

The enhanced chemiluminescence method for HRP detection reported by Matthews et al., Anal Biochem (1985) 151:205-209, was employed. Beads were taken up in 15 µl of chemiluminescent substrate solution (luminol with p-hydroxycinnamic acid) and then transferred to 8 x 50 mm Evergreen polypropylene tubes containing 5 µl of 4 mM H_2O_2. After 30 sec, tubes were read on a Turner TD-20e luminometer (delay, 10 sec; integration, 20 sec; smoothing, 20 sec). Output was given as the full integral of the light produced during the reaction.

To each tube, a 100 µl aliquot of a fresh o-phenylenediamine solution (OPD; in tablet form from Sigma Chemicals; 50 mg dissolved in 5 ml of 50 mM sodium citrate, pH 5.1, containing 3 µl of 30% H_2O_2) was added. After 20 min at 37°C, 50 µl of 4 N H_2SO_4 was added to quench the reaction. The beads were then pelleted by centrifugation and the supernatant was transferred to a microtiter dish well. The dish was then read on a Biotek EL310 plate reader set at 490 nm. Longer incubations did not improve the signal to noise ratios.

G. Microtiter Dish Assay Procedure

A microtiter dish assay procedure was employed. Microtiter dishes were prepared as follows. Two types of microtiter dish wells were prepared: (1) N wells for sample work-up and negative controls, and (2) S wells for capture of the probe-analyte complex from samples and positive controls.

N wells were produced as follows: 300 µl of HM buffer was added to Immulon II Remov-a-wells (Dynatech Inc.). The well strips were covered and left standing at room temperature for 1 hour. The HM buffer was removed by aspiration and the wells were washed 3 times with 400 µl of 1 x PBS. The strips were covered with plastic wrap and stored at 4°C until used. Alternatively, wells were coated with poly-phenylalanyl-lysine then with HM buffer, as below.

S wells were prepared from the Immulon II strips as follows. To each well, 200 µl of a 200 µg/ml solution of poly-phenylalanyl-lysine (Sigma Chemical Inc.) in water. The covered strips were left at room temperature for 30 min to 2 hr, then washed as above. A 10 OD_{260} sample of the oligonucleotide of 3B above in 60 µl of 1 x PBS was treated with 140 µl of DMF containing 10 mg of ethylene glycolbis(succinimidylsuccinate) (Pierce Chemicals Inc.). The mixture was vortexed and incubated in the dark at room temperature. After 15 min, the solution was passed over a Sephadex G-25 column (PD-10 from Pharmacia), previously equilibrated with 30 ml of 1 x PBS. The void volume of the column was diluted to a final volume of 35 ml with 1 x PBS. To each well, a 50 µl aliquot of the capture probe solution was added. After covering with plastic wrap, the wells were incubated at room temperature in the dark for 30 min to ovemight. The wells were washed with 1 x PBS, then coated with H buffer, washed, and stored as above.

Label oligonucleotides were derivatized with alkaline phosphatase (AP) as follows. Calf intestinal AP (3 mg in buffer; immunoassay grade, Boehringer-Mannheim) was placed in a Centricon 30 Microconcentrator. Approximately 2 ml of 0.1 M sodium borate, pH 9.5, was then added and the device was spun at 3500 rpm until a final volume of 40 µl was obtained. The alkylamino oligonucleotide (Section 3C) was then activated with DITC, extracted with butanol, and combined with the protein as described for the HRP probe. PAGE, elution (with 0.1 M Tris, pH 7.5, 0.1 M NaCl, 10 mM $MgCl_2$, 0.1 mM $ZnCl_2$), and concentration as described for the HRP conjugates were employed. The final product was stored at 4°C.

For duplicate analyses, 20 µl of each sample was placed into 2 N wells, then treated with 25 µl of proteinase K/SDS solution. The wells were covered with a Linbro-Titertek microtiter plate sealer, gently agitated, and incubated at 65°C for 30 min in a water bath. The capture and amplifier probe sets in 1 M NaOH were added in 10 µl to each well. After sealing, the samples were incubated for 10-30 min at 65°C to 72°C as above. The solutions were neutralized with 26 µl 0.38 M acetic acid (or 0.76 M 3-[N-Morpholino]propane sulfonic acid (MOPS), free acid), 12.3 x SSC, then incubated for an additional 15-30 min covered at 65°C. From each N well, 40 µl of sample was transferred to a new S well containing the solid supported capture probe. The wells were sealed and set at 65°C for 1-2 hours. Each well was then washed 2 times by aspiration with 0.1% SDS, 0.1 x SSC. A solution of amplification multimer (for N. gonorrhoeae, penicillin-resistant N. gonorrhoeae, tetracycline resistant N. gonorrhoeae and Chlamydia tests; a five-site comb structure (section 2.B.5) was employed) in HM buffer was then added and the samples set sealed in a 55°C water bath for 15 min to 1 hour. After washing as above, 20 µl of the enzyme-labeled probe in HM buffer was added. Incubation for the HRP probe was carried out for 15 min at 42°C, while the alkaline phosphatase probe was used at 55°C for 15 min. After washing as above, the appropriate detection reagents were added.

For HRP, the enhanced luminol reagent (see 3F) was used as above.

For AP detection, an enzyme-triggered dioxetane (Schaap et al. (1987) Tet. Lett. 28: 1159-1162 and EPA Publication No. 0254051), obtained from Lumigen Inc., was employed. The detection procedure was as follows. For the labeling step 20 µl MM buffer with the AP probe was added to each well and the wells were incubated at 55°C for 15 min. The supernatant was removed and the wells were washed 2 x with 380 µl of 0.1 x SSC-0.1% SDS. The wells were then washed 2 x with 380 µl of 0.1 x SSC to remove any remaining SDS. 20 µl of 3.3×10^{-4} M dioxetane in CTAB buffer was added to each well. The wells were tapped lightly so that the reagent would fall to the bottom and gently swirled to distribute the reagent evenly over the bottom. The wells were covered with the microtiter plate sealer and incubated in a 37°C oven for one hour. The wells are then read with a luminometer.

Results

A. Tests on Standard Analyte

The above described assay was carried out on samples containing known amounts of the standard analyte HBV DNA using the multimers of Examples 1-2A. For comparison purposes a three piece assay (bound analyte; oligonucleotide complementary to both analyte and labeled probe; and HRP-labeled probe) was carried out. The comparison assay was assigned a gain value of 1. Gain is the ratio of signal obtained in an amplified assay to signal obtained in an unamplified three piece assay.

The results of these assays are reported in the table below. S/N = signal-to-background ratio.

TABLE 1

AMPLIFIER	ASSAY TYPE	GAIN	SIGNAL	BACKGROUND	S/N
Enzymatically Ligated Multimer (Ex. 1)	HBV Serum Assay	29	56.2 ± 24.4 @ 10 amole	12.9 ± 4.73	4.4
Chemically Cross-linked Linear Multimer (Ex. 2)	HBV Serum Assay	25	617 ± 116 @ 50 amole	432 ± 53	1.4
Chemically Cross-linked Branched Multimer (Ex. 2)	HBV Serum Assay	102	168 ± 31 @ 10 amole	17 ± 2	9.9
HRP Probe Without Amplifier	3 Piece Assay	1	32.9 ± 5.7 @ 100 amole	18.2 ± 1.5	1.8

B. Tests on Authentic HBV DNA Samples

Authentic HBV DNA samples were identified as follows.

A dot blot screening was conducted for the presence of HBV DNA in 49 HBV surface antigen positive samples using the protein-DNA complex extraction technique of Zyzik et al, Eur J Chem Microbiol (1986) 5:330-335. Figure 4 presents

the analysis of the six DNA positive sera found in the set of 49 using ^{32}P nick translated pHE63 as a probe. Each sample was blotted and probed in duplicate directly (10^0), diluted 1:10 (10^1) and 1:100 (10^2) in pooled normal human sera. Samples of pHE63 were blotted in duplicate in pooled normal sera or in buffer (10X SSC). Five separate blotting experiments of these sera with dilutions and plasmid standards were performed to establish the ranges calculated. These samples were used in the evaluation of the sandwich hybridization assay of the invention.

Figure 5 presents the results obtained for the chemiluminescent readout format of the bead capture assay method with the HBV DNA positive samples described above. Analysis of a 4 pg sample of pHE63 is also shown. Two shaded values are given for each sample. The shaded bar represents the absolute signal (S) obtained for each sample and is expressed as the mean for two sets of triplicate samples (6 total samples). The open bar indicates the same number of control samples run on the same sera using beads that do not contain the Type C capture probe. This control, which is not possible in a blotting assay format, was used to determine nonspecific binding or noise (N) for each sample matrix that might lead to false positive signals. The specific signal for each sample can be expressed as the ratio of S and N as defined. An S/N ratio of 1 indicated no specific binding. Minimal S/N ratios indicating a positive sample are discussed below.

S/N ratios ranged from 3.9 to 49 for sera containing between 0.2 and 8 pg of HBV DNA. Assays conducted on two and four fold dilutions of sera 4825 and 3657 into pooled normal human sera resulted in a near linear decrease in the absolute signals for each sample, substantiating the presumed specific nature of the method. Excellent run to run reproducibility was found for all samples with different lots of beads and reagents. Although samples were read only 30 sec after addition of the chemiluminescent substrate solution, equivalent results were obtained for up to 45 min. Also, longer signal integrations did not improve S/N ratios. The sera employed ranged from cloudy to clear in appearance, were stored frozen and freeze-thawed many times. No attempt was made to clarify the samples prior to hybridization analysis. Increased solution hybridization or bead capture times (up to 18 h) did not significantly increase the S/N ratios.

In Figure 6 the analysis of subpicogram HBV DNA samples are compared to known negative sera and large quantities of heterologous nucleic acids in pooled sera. Although the S value for the lowest positive serum employed (upper panel; 1 to 10 dilution of serum 3657) is slightly higher than the highest S for a negative serum (0092) or non-HBV DNA (HIV), no clear cutoff to differentiate between true and false positives below the pg level was possible based on absolute S alone. However, if the S/N was compared for these same samples (lower panel), a cutoff of S/N = 2.5 permitted a clear distinction to be made. No negative sample had a value higher than 1.7, yet the lowest positive at 0.2 pg had an S/N = 4.3. This clearly demonstrates the value of using a nonspecific binding control for each sample.

In Figure 7, a comparison is made between an assay conducted on HBV DNA positive and negative sera using both the luminol-p-hydroxycinnamic acid (given as relative luminescence, RL) and o-phenylenediamine (OPD) detection. Although the methods were comparable in sensitivity, the chemiluminescent method was preferred for several reasons. Firstly, using the bead format, the best colorimetric results were obtained by conducting the OPD reactions in Eppendorf tubes and transferring the solution to a microtiter dish for reading on an ELISA reader since the scattering from beads proved to be a significant source of background. In contrast, beads did not interfere with the chemiluminescent readout on the luminometer. Secondly, the chemiluminescent method was considerably faster. As opposed to waiting 30 min after addition of OPD before the detection, the chemiluminescent reactions could be read rapidly 30 sec after addition of the substrate. Lastly, there was a 1.5 to 2 fold increase in the S/N using RL versus OPD.

4. Sandwich Hybridization for N. gonorrhoeae DNA

Based on the N. gonorrhoeae pilin sequence described by Bergstrom, S., et al. PNAS USA (1986) 83:3890-3894, twelve amplifier DNA probes and three capture DNA probes were synthesized by the automated phosphoramidite method as described by Warner, et al., supra. Purification was carried out according to Sanchez-Pescador and Urdea, supra. The 5'-portions of the probes were complementary to segments of the pilin sequence and were as follows:

Probe Designation	5'-Sequence
Amplifier	
GCP-LLA2C-1	ATACTTATGGGAAGTTTTTCCGAAATGGGA
GCP-LLA2C-2	GCTCGACTACTAACACTAGCGATAGCAGCC
GCP-LLA2C-3	AAACCGCAATCAGCGGGAAGGGCGGATGGT
GCP-LLA2C-5	GGAAAACCGGCTTCCAGTTTTTAGTCGGCA
GCP-LLA2C-6	GCTCATAATGGACTTAAGGCCGTTTACCGG
GCP-LLA2C-7	TTTGTTGTGAAGACGGCCGCACCGTAGGGG
GCP-LLA2C-9	ACTTCAATTTTTGCCGCAGCAATGGCGGTG
GCP-LLA2C-10	CGAAAGTTCGCCGCATTTGTTACTAATGTT
GCP-LLA2C-11	GTTTTTTGAGAGGGACACCCGGTCCGCACT
GCP-LLA2C-13	ATGCGCGTGGCTGCTGCTGTGGCAACGGCT
GCP-LLA2C-14	GTTTCTGCCGTTTCTTTAGCTGTGGTTCGT
GCP-LLA2C-15	CGGCAGTTGGACGGCGCTATTCCGTAGACT
Capture	
GCP-XT1-4	GATGTGGCGGGCGCGCGTTCAAAGGCTTCG
GCP-XT1-8	GAGGCTGTAGTTTCCGTTTATACAATTTCT
GCP-XT1-12	GCCAAGCCATTTTACCAAGACGCCTGTCGG

The 3'-portion of each amplifier probe was constructed to be complementary to the linear multimer of 2A above.

The 3'-portion of each capture probe was constructed to be complementary to the sequence of the oligonucleotide of the solid phase oligonucleotide complex of 3.B above.

Analyte DNA isolated from an N. gonorrhoeae strain, an N. meningitiditis strain, and several nonpathogenic commensal strains of Neisseria were tested using the N. gonorrhoeae amplifier and capture probes according to the assay format described in 3.G above. The results of these tests are reported in the table below.

Assay Signal Response of Neisseria Species

Sample	S/N[a]
Positive[b] species:	
N. gonorrhoeae	
(1) Clinical isolates[c]	6.8 - 187.0
(2) Geographical distribution[d]	48.6 - 239.5
N. meningitiditis	
(1) Serogroup A (#9205)	5.8
(2) Serogroup B (#9206)	15.4
(3) Serogroup C (#9207)	12.9
(4) Serogroup 29E (#9218)	18.1
(5) Serogroup X (#9210)	31.2
(6) Serogroup Z (#9211)	15.5
Negative[b] species:	
N. meningitiditis	
(1) Serogroup E (#9209)	2.1
(2) Serogroup W135 (#9212)	1.9
N. cererea	
(1) #36263	0.92
(2) #33683	0.76
(3) #32824	0.83
(4) #32828	0.99
(5) #30003	2.1
N. lactamica	
(1) #30011	0.92
(2) #36016	1.1
(3) #37168	1.7
(4) #37170	0.72
(5) #37174	0.97

[a] Signal obtained with $6x10^6$ to $2x10^8$ cells. Noise was defined as the relative luminescence obtained for buffer alone.
[b] A sample with a S/N > 3 was defined as positive; and a sample with a S/N < 3 was defined as negative.
[c] Urethral swab samples, 46 male and 56 female, were obtained from Highland Hospital, Oakland, California.
[d] Samples were obtained from Boston, Denver, New York, Indianapolis, Peoria, Portland, San Diego, San Francisco, Kentucky, Minnesota and North Carolina.

As indicated by the results shown in the table, only the DNA from the N. gonorrhoeae and N. meningitiditis strains exhibited positive (above background) signals in these tests. The assay is rapid (about 4 hr for 96 samples) and has a sensitivity similar to ^{32}P-based dot blot methods. DNA from over 100 clinical isolates of N. gonorrhoeae were tested and all were detected.

5. Sandwich Hybridization Test for TEM-1 beta-Lactamase DNA in N. gonorrhoeae

Molecular analyses have revealed that the penicillin resistance observed in N. gonorrhoeae is mostly due to the

presence of a TEM-1 beta-Lactamase gene in a non-conjugative plasmid of 3-7 Mdal. (This plasmid is homologous to those found in H. ducreyi, H. parainfluenzae, and occasionally H. influenzae.) Probes were thus developed to detect TEM-1 DNA in N. gonorrhoeae (or the other mentioned bacteria carrying homologous plasmids) for the purpose of determining penicillin resistance.

The 7.3 Kb N. gonorrhoeae plasmid carrying the TEM-1 gene was obtained as described by Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory (1982). This plasmid was transformed into E. coli HB101 and purified. The plasmid was digested with BamHI and a 2390 bp BamHI fragment was purified and partially sequenced. A total of 1811 bp were sequenced, corresponding to 80% of the structural TEM-1 gene and 1181 bp of adjacent sequences from the H. parainfluenzae plasmid related to pHPA300 DNA. The sequenced portion is shown in Figure 8.

Amplifier probes and capture probes were synthesized and purified by the procedures described above. The 5'-portions of the amplifier probes were complementary to sequences of the coding region; whereas the 5'-portions of the capture probes were complementary to sequences of pHPA300. The sequences of the probes are shown in Figure 8.

Amplifier and capture probes were also prepared using a similar strategy to that used for the HBV and N. gonorrhoeae probes in which both sets of probes are directed to the TEM-1 gene. The sequences of these probes are shown in Figure 9.

The assay format of 3.G. above was used to assay crude cellular lysates from different bacteria. The results of these tests are tabulated below with the designations "TEM-1" indicating tests using the probes directed only to the TEM-1 gene and "TEM-1NH" indicating the tests where the probes are directed, respectively, to the TEM-1 gene and pHPA300 sequences.

Table 2

Screening of Penicillin-Resistant Bacteria

	TEM-1		TEM-1NH	
Species	Pos.	Neg.	Pos.	Neg.
Neisseria gonorrhoeae	2	0	97	0
Haemophilus parainfluenzae[1]	nd[2]	nd	3	0
Haemophilus influenzae[3]	2	0	0	2
Haemophilus ducreyi	nd	nd	3	0
Salmonella typhi	2	0	0	2
Shigella sonnei	1	0	0	1
Branhamella catarrhalis	0	4	0	4
Escherichia coli	1	0	0	1

1. Isolated from respiratory tract.
2. Not determined.
3. Isolated from genital tract.

Based on the above tests and additional tests, the specificities of the TEM-1 and TEM-1NH assays may be defined as follows:

Penicillin Resistant Organisms Positive with the TEM-1 Assay: Penicillinase Producing Neisseria gonorrhoeae (PPNG), H. influenzae, H. patainfluenzae, S. typhi, S. sonnei, E. coli.

Penicillin Resistant Organisms Positive with the TEM-1NH Assay: PPNG, H. influenzae, H. parainfluenzae, H. ducreyi.

Penicillin Resistant Organisms Negative with the TEM-1NH Assay: H. influenzae, S. typhi, S. sonnei, E. coli, B. catarrhalis non-TEM-1 β-lactamase.

Penicillin Sensitive Organisms Negative with the TEM-1NH Assay: N. gonorrhoeae, B. catarrhalis, H. ducreyi, N. cinerea, Clostridium albians, N. lactamica, N. mucosa, N. sicca, N. subflava, N. meningitidis, H. influenzae, Streptococcus faecalis, Mycoplasma hominis, Treponema pallidum.

This TEM-1 assay is thus a powerful clinical tool that will enable medical personnel to identify penicillin-resistant infections and prevent treatment failure by choosing the appropriate antibiotic for therapy.

6. Sandwich Hybridization for Chlamydia trachomatis

A. Probes/Multimers

Amplification and capture probe sets were prepared using the same strategy as that used to prepare the HBV and TEM-1 probes and were designed to hybridize to the Chlamydia pCHL2 plasmid. (Palmer and Falkow (1986) Plasmid 16; 52-62.) Each probe of the set was a 50 mer, with the first 30 nucleotides (5' to 3') being complementary to pCHL2 sequences and the last 20 nucleotides being the amplifier and capture sequences used in the TEM-1 and TEM-1NH assays. The pCHL2 sequences for these probes are given below:

Probe Designation

Amplifier	Sequence (3' to 5')
pCHL2.C LLA2C-2	CTACTAAACTCGCACACATCGCGACTTCTT
pCHL2.C LLA2C-3	AACTCATTAAAGTAAAAGGCGAGCAAATTA
pCHL2.C LLA2C-4	ATGTTACTTTTAGGTAACGCATCTAGAGGC
pCHL2.C LLA2C-6	TCACGATATCGTTTCTGAAAAAGATAAGCG
pCHL2.C LLA2C-7	CGATCTCCGGCCAGATAAATACTATATAAG
pCHL2.C LLA2C-8	GTCAGTCTTTAACCTCACGACCGAGCATAT
pCHL2.C LLA2C-10	AGAAAGAAACTACGGAAGGGTTGTCCTATG
pCHL2.C LLA2C-11	CTATAACTACTATTTCCTCAATAGAATCGA
pCHL2.C LLA2C-12	CCATTAAAGCACTAATATCGTCGATCCGGT
pCHL2.C LLA2C-14	TATTTAGAACGCCAATGAGTTGTCGCATCT
pCHL2.C LLA2C-15	CCAAAGGATAGAGATCTTTACTCGCGTCCA
pCHL2.C LLA2C-16	TAACAACTCGCCTAATAACGATTAAATTGT
pCHL2.C LLA2C-18	AGATTTCTTCTTAATAAGGCTCATCTTCTT
pCHL2.C LLA2C-19	CCTCTTTGTCAATCTCTTAGTGTAAAAATA
Capture	
pCHL2.CXTI-1	TTCGAATCTAGGCAAAGAGTATGCCAAAAG
pCHL2.CXTI-5	GATAACGAACTCGCATATTTCCCTTCCGAA
pCHL2.CXTI-9	TTTTCTGCTCGTTGCAAGAGACTCTTAGTT
pCHL2.CXTI-13	TATCCCTTTTGACGAAATCGATATCTGTAC
pCHL2.CXTI-17	TATAGACCACTTTTTAATGTTTCTCCCCTA

B. Samples Tested and Results

Assays were performed on isolated elementary bodies (EB) of Serovar L_2. The concentration of EB in standard samples was determined by spreading dilutions in 1 x PBS onto a slide and staining with the Syva Microtrak Immunofluorescence Kit. By microscopic examination, six random fields were counted and the total EB per ml was calculated.

The sample preparation procedure for Chlamydia differed from the HBV or Neisseria. One of two methods was employed: 12.5 µl of either (1) lysozyme (4 mg/ml in 50 mM glucose, 25 mM Tris, pH 8.0, 10 mM EDTA) or (2) 10 mM DTT in 1 x PBS was added to each well containing 10 µl of sample. After incubation at 65°C for 30 min, 1.2 µl of 10% SDS was added. The assay was then conducted as described above. Prior to the capture step, 10 µl of horse serum was added to the N and S wells. Also, for the amplification and labeling steps, horse serum instead of water was used in the HM buffer. The alkaline phosphatase/phosphate dioxetane system was employed for detection, as above. The results were as follows.

Number of EB	Signal
3×10^6	22.67+/-1.63
6×10^5	5.39+/-0.12
3×10^5	2.07+/-0.11
1.5×10^5	1.63+/-0.03
0	0.57+/-0.06

It will be appreciated that the invention assay may be adapted to conduct multiple assays for different analytes simultaneously. In one format, by changing the label and the labeling probe sequences, amplification multimer and labeled probe sequences for a new analyte, it should prove possible to detect two different analytes in the same sample on the same solid phase. Alternatively, by synthesizing analyte specific capture probe and attaching the specific complementary capture probes to different positions on a membrane strip, it is possible to perform several different assays simultaneously with the same label.

7. Sandwich Hybridization Test for tetM Determinant in N. gonorrhoeae

N. gonorrhoeae strains resistant to high levels of tetracycline resistance exhibiting MIC (minimum inhibitory concentration) values above 16 µg/ml have been found to have acquired the tetM determinant in a 24.5 Md conjugative plasmid (Annual Review of Microbiology (1984) 38:111-133 and Antimicrobe Agents Chemother. (1986) Vol 30:664-670). An assay was thus developed to detect the tetM determinant in N. gonorrhoeae to permit direct diagnosis of tetM mediated tetracycline resistance in clinical samples. The assay allows detection of tetM from large numbers of samples, gives "same day" results, and is capable of detecting as few as 15×10^3 cells.

Ten µl of tetracycline resistant N. gonorrhoeae (TRNG) cells suspended in either GC broth or skimmed milk were mixed with 12.5ul of lysis solution (2 mg/ml proteinase K in 10 mM Tris-HCl, 150 mM NaCl, 10 mM EDTA, 1% SDS, pH 8.0) in a clear Immulon II well (Dynatech), and incubated at 65°C for 20 min.

Amplification and capture probes sets were prepared using the same strategy as that used to prepare the HBV and TEM-1 probes and were designed to hybridize to the tetM structural gene. The sequences of the probes were based on the tetM gene sequence from the streptococcal conjugative shuttle transposon Tn1545 described in Nucleic Acids Research (1986) 14:7047-7058. The sequence of the tetM gene together with the capture probe (A) and amplifier probe (B) sequences are shown in Figure 12. Each probe was a 50 mer with the first 30 nucleotides (5' to 3') being complementary to the tetM gene (as shown in Figure 12) and the last 20 nucleotides (extended at the 3' end) being CTTCTTTGGAGAAAGTGGTG for the capture probes and TTAGGCATAGGACCCGTGTC for the amplifier probes.

The test procedure was similar to the microtiter dish assay procedure of 3.G. above. Five µl of 1 M NaOH containing 0.2 pm of each capture and labeling probes were added and the mixture was incubated at 65°C for 20 min. Thirteen µl of neutralizing solution (2M MOPS, 12.3 x SSC(1 x SSC = 0.15 M NaCl, 15 mM sodium citrate) were added and the mixture was incubated at 65°C for 15 min. After ten µl of heat inactivated horse serum was added to each well, the solutions were mixed and transferred to Immulon I white wells previously coated with a synthetic oligonucleotide complementary to the capture probes. The wells were incubated at 65°C for 2 hours after which the mixture was removed from the wells and discarded. The wells were washed twice with 0.1% SDS, 0.1 x SSC. Forty µl of a solution of amplification multimer (see 3.G. above) were added and the wells were incubated at 55°C for 15 min. The wells were then washed twice as above and 40 µl of an alkaline phosphatase labeled oligonucleotide probe (see 3.G. above) solution were added. The wells were further incubated at 55°C for 15 min, washed twice as above and washed twice with 0.1 x SSC. Detection was achieved with a dioxetane chemiluminescent substrate (see 3.G. above). Luminescence was re-

corded either by using a microtiter dish reading luminometer (Dynatech) or by exposing the wells at Polaroid 57 instant black and white film in a dark chamber at 37°C for 10 min. The signal to noise ratio (S/N) is defined as the light counts emitted by a well containing a sample divided by the light counts emitted by a well containing buffer alone. A sample was considered positive when the S/N ratio was ≥ 3.

For comparison, tetracycline sensitive (TC^s) strains and commensal strains known to carry tetM were also tested. The table below presents the results of the tests.

strain[1]	tetM positive	tetM negative
N. gonorrhoeae	132	0
N. gonorrhoeae(Tc^S)	0	45
N. mucosa	4	0
N. mucosa/perflava	1	0
N. perflava/sicca	9	0
K. denitrificans	3	0
E. corrodens	1	0

1. -All organisms were resistant to tetracycline (MIC ≥ 16 µg/ml) except where indicated.

As shown in the table, a total of 132 TRNG strains were tested using the tetM hybridization assay. All of these strains showed positive values when read with the luminometer or with instant film. Commensal strains known to carry tetM, such as N. mucosa, N. mucosa/perflava, N. perflava/sicca, Kingella denitrificans and Eikenella corrodens, were also positive in the assay. On the other hand, none of the 45 Tc^S strains tested showed positive values.

This assay may be used to detect any tetM mediated tetracycline resistant organism. By designing the capture and amplifier probes to bind to both the tetM gene and the 24.5 Md plasmid in an appropriate arrangement (as in the TEM-1NH assay described above), reactivity may be limited to TRNG. The use of the tetM test, together with the TEM-1 test reported above considerably reduces the time required to screen for antibiotic resistant microorganisms where TEM-1 or tetM mediated resistance is suspected. These procedures obviate the need for subculturing primary cultures in the presence of the appropriate antibiotic. These assays require minimal sample preparation and involve very simple manipulations similar to ELISA procedures. In combination with the assay for N. gonorrhoeae, detection of N. gonorrhoeae and antibiotic resistance characterization can be conducted in a few hours. All the components of the assay, including the microtiter wells, are universal (analyte independent) with the exception of the capture and amplifier probes. As a result, the simultaneous analysis of a sample for the infectious agent and the antibiotic resistance can be performed in parallel, within the same time frame, and with the same manipulations.

8. Sandwich Hybridization Assay for N. gonorrhoeae DNA using Probes Based on N. gonorrhoeae Genomic Sequence SSJK1.

A new genomic sequence designated SSJK1 having a high degree of specificity for N. gonorrhoeae was identified by screening genomic clones against N. gonorrhoeae DNA and N. meningitidis DNA and selecting sequences that reacted with the former but not the latter. The DNA sequence of SSJK1 is shown in Figure 13. This sequence was checked against available DNA libraries and has not been reported previously.

Based on the SSJK1 sequence, capture and amplifier probes were synthesized as in section 4 above. The 5' portions of the sequences are shown in Fig. 14. The 3' portions of the sequences were the same as those described in the TEM-1 assay described above (see Fig. 11). Both 5' portions and 3' portions are shown in Fig. 14. The assay format of 3.G. above was used to assay crude cellular lysates and genomic DNA from different bacteria. The results of tests with DNA samples are tabulated below.

Sample		S/N
1)	Negative samples[a]	
a)	Branhamella catarrhallis	0.97
b)	Neisseria sicca	1.12
c)	Neisseria subflava	1.08
d)	Neisseria mucosa	1.02
e)	Neisseria lactamica	1.94
f)	Neisseria flavescens	1.09
g)	Neisseria cinerea (#33683)	2.21
h)	Neisseria cinerea (#32828)	2.23
i)	Neisseria meningitidis, serogroup A	1.94
j)	Neisseria meningitidis, serogroup B	1.12
k)	Neisseria meningitidis, serogroup C	1.19
l)	Neisseria meningitidis, serogroup D	0.92
2)	Positive samples[b]	
	Neisseria gonorrhoeae (17 strains represeenting various serotypes were tested)	3.67-26.64

[a]Samples with an S/N < 3 were defined as negative. All negative samples were tested using 10 µg of genomic DNA.
[b]Samples with an S/N > 3 were defined as positive. All positive samples were tested using 100 ng of genomic DNA.

Due to the specificity of the SSJK1 sequence for N. gonorrhoeae it will be appreciated that probes based upon the entire sequence or fragments thereof may be used in other DNA hybridization assays. Accordingly, in general DNA probes based upon the SSJK1 sequence are intended to be within the invention. Such probes may be labeled directly or indirectly depending upon the particular hybridization assay format used.

Due to the low interference observed from the presence of heterologous nucleic acids and sample components, the invention method presented here is useful in the detection of a variety of organisms in crude materials with minimal sample preparation. Except for the solution phase hybridization probes which are unmodified synthetic oligonucleotides, all assay components are universal (analyte sequence independent); therefore, a new assay simply requires a new set of oligonucleotides. In principle, the chemiluminescent form of the analysis system presented is sufficiently sensitive to permit single gene detection in 5 µg of mammalian DNA in 4 h.

Modifications of the above-described modes for carrying out the invention that are obvious to those of skill in nucleic acid chemistry, biochemical assays, and related fields are intended to be within the scope of the following claims.

Claims

Claims for the following Contracting States : AT, BE, CH, DE, FR, GB, GR, IT, LI, LU, NL, SE

1. A synthetic branched nucleic acid multimer having a minimum of three termini, said multimer comprising:

(a) at least one first single-stranded oligonucleotide unit that is capable of binding specifically to a first sin-

Sample		S/N
1)	Negative samples[a]	
a)	Branhamella catarrhallis	0.97
b)	Neisseria sicca	1.12
c)	Neisseria subflava	1.08
d)	Neisseria mucosa	1.02
e)	Neisseria lactamica	1.94
f)	Neisseria flavescens	1.09
g)	Neisseria cinerea (#33683)	2.21
h)	Neisseria cinerea (#32828)	2.23
i)	Neisseria meningitidis, serogroup A	1.94
j)	Neisseria meningitidis, serogroup B	1.12
k)	Neisseria meningitidis, serogroup C	1.19
l)	Neisseria meningitidis, serogroup D	0.92
2)	Positive samples[b]	
	Neisseria gonorrhoeae (17 strains repreeenting various serotypes were tested)	3.67-26.64

[a]Samples with an S/N < 3 were defined as negative. All negative samples were tested using 10 μg of genomic DNA.
[b]Samples with an S/N > 3 were defined as positive. All positive samples were tested using 100 ng of genomic DNA.

Due to the specificity of the SSJK1 sequence for N. gonorrhoeae it will be appreciated that probes based upon the entire sequence or fragments thereof may be used in other DNA hybridization assays. Accordingly, in general DNA probes based upon the SSJK1 sequence are intended to be within the invention. Such probes may be labeled directly or indirectly depending upon the particular hybridization assay format used.

Due to the low interference observed from the presence of heterologous nucleic acids and sample components, the invention method presented here is useful in the detection of a variety of organisms in crude materials with minimal sample preparation. Except for the solution phase hybridization probes which are unmodified synthetic oligonucleotides, all assay components are universal (analyte sequence independent); therefore, a new assay simply requires a new set of oligonucleotides. In principle, the chemiluminescent form of the analysis system presented is sufficiently sensitive to permit single gene detection in 5 μg of mammalian DNA in 4 h.

Modifications of the above-described modes for carrying out the invention that are obvious to those of skill in nucleic acid chemistry, biochemical assays, and related fields are intended to be within the scope of the following claims.

Claims

Claims for the following Contracting States : AT, BE, CH, DE, FR, GB, GR, IT, LI, LU, NL, SE

1. A synthetic branched nucleic acid multimer having a minimum of three termini, said multimer comprising:

(a) at least one first single-stranded oligonucleotide unit that is capable of binding specifically to a first sin-

* C L M S *

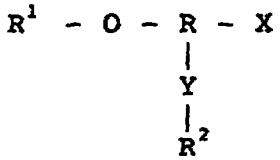
gle-stranded nucleic acid sequence of interest; and
(b) a multiplicity of second single-stranded oligonucleotide units that are capable of binding specifically to a second single-stranded nucleic acid sequence of interest, wherein the first single-stranded oligonucleotide is linked directly or indirectly to the second single-stranded oligonucleotide units only via covalent bonds.

2. The nucleic acid multimer of claim 1 wherein the first oligonucleotide unit has a different sequence than the second oligonucleotide unit and the number of second oligonucleotide units is at least about two-fold the number of first oligonucleotide units.

3. The nucleic acid multimer of claim 1 wherein the nucleotide sequence of the first oligonucleotide unit is the same as the nucleotide sequence of the second oligonucleotide unit and the combined number of units is at least about 3.

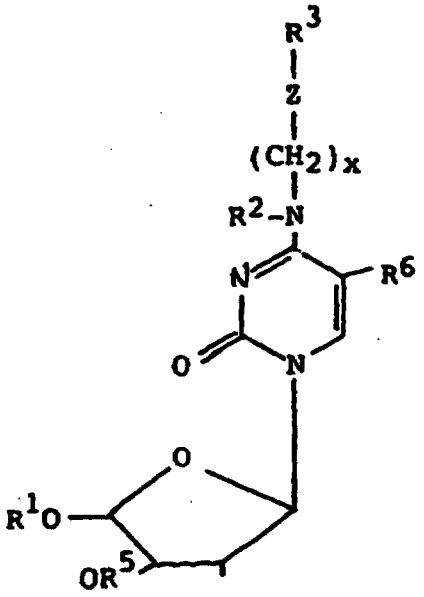
4. The nucleic acid multimer of claim 1, 2 or 3 wherein the multimer has a branched structure.

5. The nucleic acid multimer of claim 1, 2, 3 or 4 wherein at least a portion of the oligonucleotide units of the multimer are linked via a multifunctional moiety derived from a compound of the formula (1)



(1)

where R is an organic moiety, preferably a nucleic acid, R^1 is a hydroxyl protecting group that can be removed under conditions that do not remove synthetic nucleic acid from a solid phase and do not remove exocyclic nitrogen or phosphate protecting groups, X is a phosphorus-containing group that facilitates nucleic acid synthesis, Y is a radical derived from a nucleophilic group, and R^2 is R^1 or a blocking or protective group that can be removed and replaced with hydrogen without affecting R^1, wherein at least a portion of the oligonucleotide units are linked via a multifunctional moiety derived from a compound of the formula (2)



(2)

where Z is a nucleophile, R^1 is a protective group that is generally base-stable and acid sensitive, R^2 is hydrogen or methyl, R^3 is a protective group that can be removed and replaced with hydrogen without affecting R^1, R^5 is a phosphorus derivative that enables addition of nucleotides to the 5′ position of an oligonucleotide chain during chemical synthesis, R^6 is methyl, hydrogen, I, Br, or F, and X is an integer in the range of 1 to 8, inclusive.

6. The nucleic acid multimer of claim 1, 2, 3, 4 or 5 wherein the first single-stranded nucleotide sequence of interest is analyte nucleic acid, or wherein the first single-stranded nucleotide sequence of interest is an oligonucleotide that is bound to analyte acid.

* C L M S *

7. The nucleic acid multimer of claim 1, 2, 3, 4, 5 or 6 wherein the second single-stranded nucleotide sequence of interest is a sequence of a single-stranded labelled oligonucleotide.

8. The nucleic acid multimer of claim 1, 2, 3, 4, 5, 6 or 7 wherein there is a chemically cleavable linker in each of the second single-stranded oligonucleotide units.

9. A process for conducting a nucleic hybridization assay comprising

(a) hybridizing the multimer of claim 7 via the first oligonucleotide unit to single-stranded analyte nucleic acid bound to a solid phase or to a single-stranded oligonucleotide bound to the analyte;
(b) removing unbound multimer;
(c) hybridizing a single-stranded labelled oligonucleotide to the multimer via the second oligonucleotide units;
(d) removing unbound labelled oligonucleotide; and
(e) detecting the presence of label bound to the multimer.

10. A process for conducting a solution sandwich nucleic acid hybridization assay for detecting a first nucleic acid sequence that is part of a nucleic acid segment that includes a second nucleic acid sequence in a sample that contains said segment and another nucleic acid segment that comprises the first nucleic acid sequence but does not include the second nucleic acid sequence comprising:

(a) contacting the analyte under hybrizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment that is complementary to one of the first nucleic acid sequence or the second nucleic acid sequence and a second segment that is complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment that is complementary to the other of the first nucleic acid sequence or the second nucleic acid sequence and a second segment that is complementary to an oligonucleotide bound to a solid phase;
(b) contacting under hybridizing conditions the product of step (a) with the oligonucleotide bound to the solid phase;
(c) thereafter separating materials not bound to the solid phase;
(d) contacting under hybridizing conditions the solid phase complex product of step (c) with a nucleic acid multime according to any one of claims 1 to 8 wherein the second oligonucleotide units of said multimer are complementary to a labelled oligonucleotide;
(e) removing unbound multimer;
(f) contacting under hybrizing conditions the solid phase complex product of step (e) with the labelled oligonucleotide;
(g) removing unbound labelled oligonucleotide; and
(h) detecting the presence of label in the solid phase complex product of step (g).

11. A process according to claim 10

(A) for detecting N. gonorrhoeae pilin DNA in an analyte wherein step (a) comprises contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of N. gonorrhoeae pilin DNA and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of N. gonorrhoeae pilin DNA and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
or (B) for detecting N. gonorrhoeae DNA in an analyte wherein step (a) comprises contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the N. gonorrhoeae genomic clone shown in Figure 13 and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the N. gonorrhoeae genomic clone shown in Figure 13 and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
or (C) for detecting the 7.3 kb N. gonorrhoeae family of plasmids carrying the beta-Lactamase TEM-1 gene or said gene in an analyte wherein step (a) comprises contacting the analyte under hyridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of said plasmid or gene and a second segment having a nucleotide sequence com-

* C L M S *

plementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to another segment of said plasmid or gene and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;

or (D) for detecting HBV DNA in an analyte wherein step (a) comprises contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of a conserved region of the HBV genome and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a another segment of a conserved region of the HBV genome and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;

or (E) for detecting Chlamydia trachomatis DNA in an analyte wherein step (a) comprises contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the Chlamydia pCHL2 plasmid and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a another segment of a conserved region of the HBV genome and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;

or (F) for detecting tetM gene DNA suspected of containing DNA of a tetracycline resistant organism in an analyte wherein step (a) comprises contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the tetM gene and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a another segment of said tetM gene and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;

12. Use of a synthetic oligonucleotide comprising :

(a) a first segment having a nucleotide sequence complementary to a segment of a conserved region of the HBV genome or complementary to a segment of N. gonorrhoeae pilin DNA and
(b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer; as a component of an assay process according to any one of claims 9, 10 or 11.

13. Use of a synthetic oligonucleotide comprising :

(a) a first segment having a nucleotide sequence complementary to a segment of a conserved region of the HBV genome or complementary to a segment of N. gonorrhoeae pilin DNA, and
(b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase; as a component of an assay process according to any one of claims 9, 10 or 11.

14. Use of a synthetic oligonucleotide comprising

(a) a first segment having a nucleotide sequence complementary to a segment of the N. gonorrhoeae genomic clone shown in Figure 13 and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase; as a component of an assay process according to any one of claims 9, 10 or 11.

15. Use of a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the 7.3 kb N. gonorrhoeae plasmid carrying the beta-Lactamase TEM-1 gene or said gene and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer; as a component of an assay process according to any one of claims 9, 10 or 11.

16. Use of a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the 7.3 kb N. gonorrhoeae family of plasmids carrying the beta-Lactamase TEM-1 gene or said gene and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase; as a component of an assay process according to any one of claims 9, 10 or 11.

17. Use of a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to

* C L M S *

a segment of the tetM gene in a tetracycline resistant organism and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase or haying a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer; as a component of an assay process according to any one of claims 9, 10 or 11.

18. Use of a synthetic oligonucleotide comprising :

(a) a first segment having a nucleotide sequence complementary to a segment of the Chlamydia pCHL2 plasmid, and
(b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase; as a component of an assay process according to any one of claims 9, 10 or 11.

19. A process for conducting an immunosassay for an analyte immunochemical comprising:

(a) binding a ligand specifically and directly or indirectly to the analyte, said ligand having a single-stranded oligonucleotide that is complementary to the first oligonucleotide unit of the multimer any one of claims 1 to 8 bound thereto;
(b) removing unbound ligand;
(c) hybridizing said multimer to the ligand;
(d) hybridizing a labelled oligonucleotide to the second oligonucleotide units of the bound multimer;
(e) removing unbound labelled oligonucleotide;
(f) detecting the presence of label bound to the bound multimer.

Claims for the following Contracting State : ES

1. a process for conducting a nucleic acid hybridization assay comprising

(a) hybridizing a nucleic acid multimer via the first oligonucleotide unit to single-stranded analyte nucleic acid bound to a solid phase or to a single-stranded oligonucleotide bound to the analyte;
(b) removing unbound multimer;
(c) hybridizing a single-stranded labelled oligonucleotide to the multimer via the second oligonucleotide units;
(d) removing unbound labelled oligonucleotide; and
(e) detecting the presence of label bound to the multimer; wherein said multimer is a synthetic branched nucleic acid multimer having a minimum of three termini, said multimer comprising:

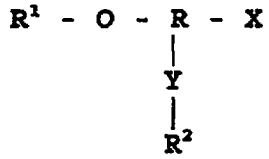
(i) at least one first single-stranded oligonucleotide unit that is capable of binding specifically to a first single-stranded nucleic acid sequence of interest; and
(ii) a multiplicity of second single-stranded oligonucleotide units that are capable of binding specifically to a second single-stranded nucleic acid sequence of interest, wherein the first single-stranded oligonucleotide is linked directly or indirectly to the second single-stranded oligonucleotide units only via covalent bonds.

2. The process of claim 1 wherein the first oligonucleotide unit of the multimer has a different sequence than the second oligonucleotide unit and the number of second oligonucleotide units is at least about two-fold the number of first oligonucleotide units.

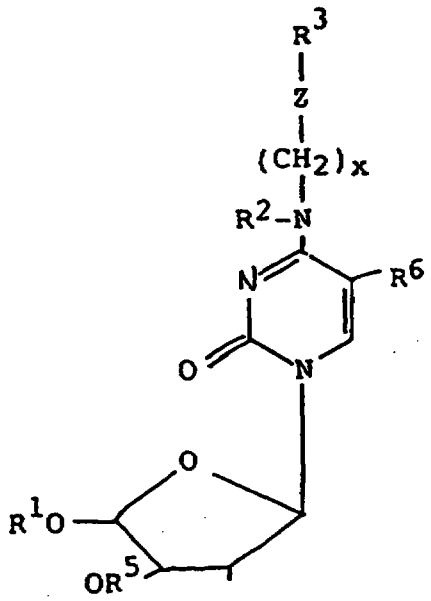
3. The process of claim 1 wherein the nucleotide sequence of the first oligonucleotide unit of the multimer is the same as the nucleotide sequence of the second oligonucleotide unit and the combined number of units is at least about 3.

4. The process of claims 1, 2 or 3 wherein the multimer has a branched structure.

5. The process of claims 1, 2, 3 or 4 wherein at least a portion of the oligonucleotide units of the multimer are linked via a multifunctional moiety derived from a compound of the formula (I)



where R is an organic moiety, preferably a nucleic acid, R^1 is a hydroxyl protecting group that can be removed under conditions that do not remove synthetic nucleic acid from a solid phase and do not remove exocyclic nitrogen or phosphate protecting groups, X is a phosphorus-containing group that facilitates nucleic acid synthesis, Y is a radical derived from a nucleophilic group, and R^2 is R^1 or a blocking or protective group that can be removed and replaced with hydrogen without affecting R^1, wherein at least a portion of the oligonucleotide units are linked via a multifunctional moiety derived from a compound of the formula (2)



(2)

where z is a nucleophile, R^1 is a protective group that is generally base-stable and acid sensitive, R^2 is hydrogen or methyl, R^3 is a protective group that can be removed and replaced with hydrogen without affecting R^1, R^5 is a phosphorus derivative that enables addition of nucleotides to the 5' position of an oligonucleotide chain during chemical synthesis, R^6 is methyl, hydrogen, I, Br, or F, and X is an integer in the range of 1 to 8, inclusive.

6. The process of claim 1, 2, 3, 4 or 5 wherein the first single-stranded nucleotide sequence of interest is analyte nucleic acid, or wherein the first single-stranded nucleotide sequence of interest is an oligonucleotide that is bound to analyte acid.

7. The process of claims 1, 2, 3, 4, 5 or 6 wherein the second single-stranded nucleotide sequence of interest is a sequence of a single-stranded labelled oligonucleotide.

8. The process of claims 1, 2, 3, 4, 5, 6 or 7 wherein there is a chemically cleavable linker in each of the second single-stranded oligonucleotide units.

9. A process for conducting a solution sandwich nucleic acid hybridization assay for detecting a first nucleic acid sequence that is part of a nucleic acid segment that includes a second nucleic acid sequence in a sample that contains said segment and another nucleic acid segment that comprises the first nucleic acid sequence but does not include the second nucleic acid sequence comprising:

(a) contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment that is complementary to one of the first nucleic acid sequence or the second nucleic acid sequence and a second segment that is complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment that is complementary to the other of the

* C L M S *

first nucleic acid sequence or the second nucleic acid sequence and a second segment that is complementary to an oligonucleotide bound to a solid phase;
(b) contacting under hybridizing conditions the product of step (a) with the oligonucleotide bound to the solid phase;
(c) thereafter separating materials not bound to the solid phase;
(d) contacting under hybridizing conditions the solid phase complex product of step (c) with a nucleic acid multimer as defined in any one of claims 1 to 8 wherein the second oligonucleotide units of said multimer are complementary to a labelled oligonucleotide;
(e) removing unbound multimer;
(f) contacting under hybrizing conditions the solid phase complex product of step (e) with the labelled oligonucleotide;
(g) removing unbound labelled oligonucleotide; and
(h) detecting the presence of label in the solid phase complex product of step (g).

10. A process according to claim 9

(A) for detecting N. gonorrhoeae pilin DNA in an analyte wherein step (a) comprises contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of N. gonorrhoeae pilin DNA and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of N. gonorrhoeae pilin DNA and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
or (B) for detecting N. gonorrhoeae DNA in an analyte wherein step (a) comprises contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the N. gonorrhoeae genomic clone shown in Figure 13 and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the N. gonorrhoeae genomic clone shown in Figure 13 and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
or (C) for detecting the 7.3 kb N. gonorrhoeae family of plasmids carrying the beta-Lactamase TEM-1 gene or said gene in an analyte wherein step (a) comprises contacting the analyte under hyridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of said plasmid or gene and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to another segment of said plasmid or gene and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
or (D) for detecting HBV DNA in an analyte wherein step (a) comprises contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of a conserved region of the HBV genome and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a another segment of a conserved region of the HBV genome and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
or (E) for detecting Chlamydia trachomatis DNA in an analyte wherein step (a) comprises contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the Chlamydia pCHL2 plasmid and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a another segment of a conserved region of the HBV genome and a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase;
or (F) for detecting tetM gene DNA suspected of containing DNA of a tetracycline resistant organism in an analyte wherein step (a) comprises contacting the analyte under hybridizing conditions with an excess of (i) an amplifier probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a segment of the tetM gene and a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer and (ii) a capture probe oligonucleotide comprising a first segment having a nucleotide sequence complementary to a another segment of said tetM gene and a second segment having

* C L M S *

a nucleotide sequence complementary to an oligonucleotide bound to a solid phase.

11. Use of a synthetic oligonucleotide comprising:

(a) a first segment having a nucleotide sequence complementary to a segment of a conserved region of the HBV genome or complementary to a segment of N. gonorrhoeae pilin DNA and
(b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer; as a component of an assay process according to any one of claims 1 to 10.

12. Use of a synthetic oligonucleotide comprising:

(a) a first segment having a nucleotide sequence complementary to a segment of a conserved region of the HBV genome or complementary to a segment of N. gonorrhoeae pilin DNA, and
(b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase; as a component of an assay process according to any one of claims 1 to 10.

13. Use of a synthetic oligonucleotide comprising
(a) a first segment having a nucleotide sequence complementary to a segment of the N. gonorrhoeae genomic clone shown in Figure 13 and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase; as a component of an assay process according to any one of claims 1 to 10.

14. Use of a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the 7.3 kb N. gonorrhoeae plasmid carrying the beta-Lactamase TEM-1 gene or said gene and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer; as a component of an assay process according to any one of claims 1 to 10.

15. A synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the 7.3 kb N. gonorrhoeae family of plasmids carrying the beta-Lactamase TEM-1 gene or said gene and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase; as a component of an assay process according to any one of claims 1 to 10.

16. Use of a synthetic oligonucleotide comprising (a) a first segment having a nucleotide sequence complementary to a segment of the tetM gene in a tetracycline resistant organisms and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase or having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer; as a component of an assay process according to any one of claims 1 to 10.

17. A synthetic oligonucleotide comprising: (a) a first segment having a nucleotide sequence complementary to a segment of the Chlamydia pCHL2 plasmid, and (b) a second segment having a nucleotide sequence complementary to an oligonucleotide unit of a nucleic acid multimer having a nucleotide sequence complementary to an oligonucleotide bound to a solid phase; as a component of an assay process according to any one of claims 1 to 10.

18. A process for conducting an immunoassay for an analyte immunochemical comprising:

(a) binding a ligand specifically and directly or indirectly to the analyte, said ligand having a single-stranded oligonculeotide that is complementary to the first oligonucleotide unit of the multimer as defined in any one of claims 1 to 8 bound thereto;
(b) removing unbound ligand;
(c) hybridizing said multimer to the ligand;
(d) hybridizing a labelled oligonucleotide to the second oligonucleotide units of the bound multimer;
(e) removing unbound labelled oligonucleotide;
(f) detecting the presence of label bound to the bound multimer.

Patentansprüche

Patentansprüche für folgende Vertragsstaaten : AT, BE, CH, DE, FR, GB, GR, IT, LI, LU, NL, SE

1. Synthetisches verzweigtes Nukleinsäure-Multimeres mit einem Minimum von drei Enden, umfassend:

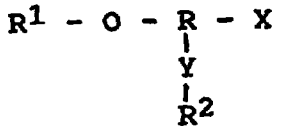
   (a) mindestens eine erste einzelsträngige Oligonukleotideinheit, die spezifisch an eine erste einzelsträngige Nukleinsäuresequenz von Interesse binden kann, und
   (b) eine Vielzahl von zweiten einzelsträngigen Oligonukleotideinheiten, die spezifisch an eine zweite einzelsträngige Nukleinsäuresequenz von Interesse binden können, wobei das erste einzelsträngige Oligonukleotid direkt oder indirekt an die zweiten einzelsträngigen Oligonukleotideinheiten nur über covalente Bindungen gebunden ist.

2. Nukleinsäure-Multimeres nach Anspruch 1, worin die erste Oligonukleotideinheit eine andere Sequenz als die zweite Oligonukleotideinheit besitzt, und die Anzahl der zweiten Oligonukleotideinheiten mindestens etwa das zweifache der Anzahl der ersten Oligonukleotideinheiten beträgt.

3. Nukleinsäure-Multimeres nach Anspruch 1, worin die Nukleotidsequenz der ersten Oligonukleotideinheit die gleiche wie die Nukleotidsequenz der zweiten Oligonukleotideinheit ist, und die gemeinsame Anzahl der Einheiten mindestens etwa 3 beträgt.

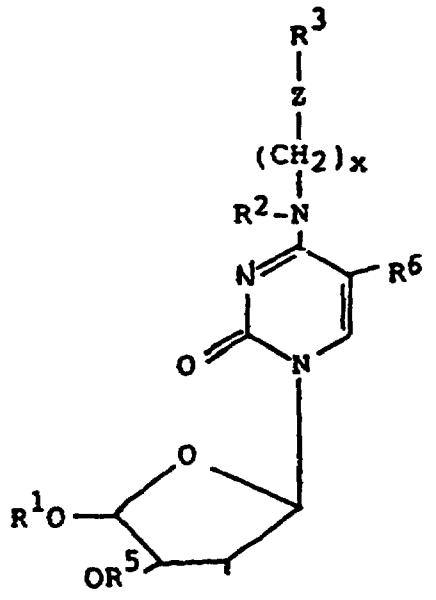
4. Nukleinsäure-Multimeres nach Anspruch 1, 2 oder 3, worin das Multimere eine verzweigte Struktur besitzt.

5. Nukleinsäure-Multimeres nach Anspruch 1, 2, 3 oder 4, worin mindestens ein Anteil der Oligonukleotideinheiten des Multimeren über eine multifunktionelle Einheit gebunden ist, die von einer Verbindung der Formel (1)



(1)

abgeleitet ist, worin R eine organische Einheit, bevorzugt eine Nukleinsäure, ist, R^1 eine Hydroxylschutzgruppe ist, die unter Bedingungen entfernt werden kann, die die synthetische Nukleinsäure von einer festen Phase nicht entfernen und die Schutzgruppen des exocyclischen Stickstoffs oder Phosphats nicht entfernen, X eine Phosphor-enthaltende Gruppe ist, die die Nukleinsäuresynthese erleichtert, Y ein Rest, abgeleitet von einer nukleophilen Gruppe, ist, und R^2 R^1 oder eine blockierende oder schützende Gruppe ist, die entfernt werden und durch Wasserstoff ersetzt werden kann, ohne R^1 zu beeinträchtigen, wobei mindestens ein Anteil der Oligonukleotideinheiten über eine multifunktionelle Einheit verknüpft ist, die von einer Verbindung der Formel (2)



(2)

abgeleitet ist, worin Z ein Nukleophil ist, R^1 eine Schutzgruppe ist, die im allgemeinen basenstabil und säurelabil ist, R^2 Wasserstoff oder Methyl bedeutet, R^3 eine Schutzgruppe ist, die entfernt und durch Wasserstoff ersetzt werden kann, ohne R^1 zu beeinträchtigen, R^5 ein Phosphorderivat ist, das die Addition von Nukleotiden an die 5'-Position einer Oligonukleotidkette während der chemischen Synthese erlaubt, R^6 Methyl, Wasserstoff, I, Br oder F bedeutet, und X eine ganze Zahl im Bereich von 1 bis 8 einschließlich bedeutet.

6. Nukleinsäure-Multimeres nach Anspruch 1, 2, 3, 4 oder 5, worin die erste einzelsträngige Nukleotidsequenz von Interesse eine Analyt-Nukleinsäure ist, oder worin die erste einzelsträngige Nukleotidsequenz von Interesse ein Oligonukleotid ist, das an eine Analyt-Säure gebunden ist.

7. Nukleinsäure-Multimeres nach Anspruch 1, 2, 3, 4, 5 oder 6, worin die zweite einzelsträngige Nukleotidsequenz von Interesse eine Sequenz eines einzelsträngigen markierten Oligonukleotids ist.

8. Nukleinsäure-Multimeres nach Anspruch 1, 2, 3, 4, 5, 6 oder 7, worin ein chemisch spaltbarer Linker in jeder der zweiten einzelsträngigen Oligonukleotideinheiten vorhanden ist.

9. Verfahren zur Durchführung eines Nukleinsäure-Hybridisierungsassays, wobei man

(a) das Multimere von Anspruch 7 über die erste Oligonukleotideinheit an die einzelsträngige Analyt-Nukleinsäure, die an eine feste Phase gebunden ist, oder an ein einzelsträngiges Nukleotid, das an den Analyt gebunden ist, hybridisiert,
(b) nichtgebundenes Multimeres entfernt,
(c) ein einzelsträngiges markiertes Oligonukleotid an das Multimere über die zweiten Oligonukleotideinheiten hybridisiert,
(d) nichtgebundenes markiertes Oligonukleotid entfernt, und
(e) das Vorhandensein des an das Multimere gebundenen Markers nachweist.

10. Verfahren zur Durchführung eines Sandwich-Nukleinsäure-Hybridisierungsassays in Lösung zum Nachweis einer ersten Nukleinsäuresequenz, die Teil eines Nukleinsäuresegments ist, das eine zweite Nukleinsäuresequenz umfaßt, in einer Probe, die das Segment und ein weiteres Nukleinsäuresegment enthält, welches die erste Nukleinsäuresequenz umfaßt, aber nicht die zweite Nukleinsäuresequenz einschließt, wobei man

(a) den Analyt unter hybrisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment, das entweder der ersten Nukleinsäuresequenz oder der zweiten Nukleinsäuresequenz komplementär ist, und ein zweites Segment, das einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementär ist, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment, das dem anderen der ersten Nukleinsäuresequenz oder der zweiten Nukleinsäuresequenz komplementär ist, und ein zweites Segment, das einem an eine feste Phase gebundenen Oligonukleotid komplementär

* C L M S *

ist, in Kontakt bringt,
(b) unter hybridisierenden Bedingungen das Produkt von Stufe (a) mit dem an die feste Phase gebundenen Oligonukleotid in Kontakt bringt,
(c) anschließend die an die feste Phase nichtgebundenen Materialien abtrennt,
(d) unter hybridisierenden Bedingungen das Festphasen-gebundene Komplexprodukt der Stufe (c) mit einem Nukleinsäure-Multimeren nach einem der Ansprüche 1 bis 8 in Kontakt bringt, wobei die zweiten Oligonukleotideinheiten des Multimeren einem markierten Oligonukleotid komplementär sind,
(e) nichtgebundenes Multimeres entfernt,
(f) unter hybridisierenden Bedingungen das Festphasen-gebundene Komplexprodukt der Stufe (e) mit dem markierten Oligonukleotid in Kontakt bringt,
(g) nichtgebundenes markiertes Oligonukleotid entfernt, und
(h) die Anwesenheit des Markers in dem Festphasen-gebundenen Komplexprodukt der Stufe (g) nachweist.

11. Verfahren nach Anspruch 10, wobei man

(A) zum Nachweis von N. gonorrhoeae pilin-DNA in einem Analyt in der Stufe (a) den Analyt unter hybridisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer Nukleotidsequenz, die einem Segment der N. gonorrhoeae pilin-DNA komplementär ist, und ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment von N. gonorrhoeae pilin-DNA komplementären Nukleotidsequenz, und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz in Kontakt bringt,
oder (B) zum Nachweis von N. gonorrhoeae-DNA in einem Analyt in Stufe (a) den Analyt unter hybridisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment des in Figur 13 gezeigten genomischen N. gonorrhoeae-Clons komplementären Nukleotidsequenz und einem zweiten Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Nukleotid, umfassend ein erstes Segment mit einer einem Segment des in Figur 13 gezeigten genomischen N. gonorrhoeae-Clons komplementären Nukleotidsequenz, und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz in Kontakt bringt,
oder (C) zum Nachweis der 7,3 kb-Plasmidfamilie von N. gonorrhoeae, die das β-Lactamase TEM-1-Gen tragen, oder zum Nachweis dieses Gens in einem Analyt in Stufe (a) den Analyt unter hybridisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment des Plasmids oder Gens komplementären Nukleotidsequenz und ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem weiteren Segment des Plasmids oder Gens komplementären Nukleotidsequenz und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz in Kontakt bringt,
oder (D) zum Nachweis von HBV-DNA in einem Analyt in Stufe (a) den Analyt unter hybrisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment einer konservierten Region des HBV-Genoms komplementären Nukleotidsequenz und ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem weiteren Segment einer konservierten Region des HBV-Genoms komplementären Nukleotidsequenz und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz in Kontakt bringt,
oder (E) zum Nachweis von Chlamydia trachomatis-DNA in einem Analyt in Stufe (a) den Analyt unter hybridisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment des Chlamydia-Plasmids pCHL2 komplementären Nukleotidsequenz und ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem weiteren Segment einer konservierten Region des HBV-Genoms komplementären Nukleotidsequenz und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz in Kontakt bringt,
oder (F) zum Nachweis von tetM-Gen-DNA, die vermutlich DNA eines Tetracyclin-resistenten Organismus enthält, in einem Analyt in Stufe (a) den Analyt unter hybridisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment des

* C L M S *

tetM-Gens komplementären Nukleotidsequenz und ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem weiteren Segment des tetM-Gens komplementären Nukleotidsequenz und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz in Kontakt bringt.

12. Verwendung eines synthetischen Oligonukleotids, umfassend

(a) ein erstes Segment mit einer Nukleotidsequenz, die einem Segment einer konservierten Region des HBV-Genoms komplementär ist oder einem Segment der N. gonorrhoeae pilin-DNA komplementär ist, und
(b) ein zweites Segment mit einer Nukleotidsequenz, die einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementär ist, als Komponente eines Assayverfahrens nach einem der Ansprüche 9, 10 oder 11.

13. Verwendung eines synthetischen Oligonukleotids, umfassend

(a) ein erstes Segment mit einer Nukleotidsequenz, die einem Segment einer konservierten Region des HBV-Genoms komplementär ist oder einem Segment der N. gonorrhoeae pilin-DNA komplementär ist, und
(b) ein zweites Segment mit einer Nukleotidsequenz, die einem an eine feste Phase gebundenen Oligonukleotid komplementär ist, als Komponente eines Assayverfahrens nach einem der Ansprüche 9, 10 oder 11.

14. Verwendung eines synthetischen Oligonukleotids, umfassend

(a) ein erstes Segment mit einer einem Segment des in Figur 13 gezeigten genomischen Clons von N. gonorrhoeae komplementären Nukleotidsequenz, und
(b) ein zweites Segment mit einer Nucleotidsequenz, die einer Oligonukleotideinheit eines Nukleinsäure-Multimeren mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz komplementär ist, als Komponente eines Assayverfahrens nach einem der Ansprüche 9, 10 oder 11.

15. Verwendung eines synthetischen Oligonukleotids, umfassend

(a) ein erstes Segment mit einer einem Segment des 7,3 kb-N. gonorrhoeae-Plasmids, das das β-Lactamasegen TEM-1 trägt, oder dem Gen komplementären Nukleotidsequenz, und
(b) ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nucleotidsequenz als Komponente eines Assayverfahrens nach einem der Ansprüche 9, 10 oder 11.

16. Verwendung eines synthetischen Oligonukleotids, umfassend

(a) ein erstes Segment mit einer einem Segment des 7,3 kb-N. gonorrhoeae-Plasmids, das das β-Lactamasegen TEM-1 trägt oder dem Gen komplementären Nukleotidsequenz, und
(b) ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz als Komponente eines Assayverfahrens nach einem der Ansprüche 9, 10 oder 11.

17. Verwendung eines synthetischen Oligonukleotids, umfassend

(a) ein erstes Segment mit einer einem Segment des tetM-Gens in einem Tetracyclin-resistenten Organismus komplementären Nukleotidsequenz, und
(b) ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz oder mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz als Komponente eines Assayverfahrens nach einem der Ansprüche 9, 10 oder 11.

18. Verwendung eines synthetischen Oligonukleotids, umfassend

(a) ein erstes Segment mit einer einem Segment des Chlamydia-Plasmids pCHL2 komplementären Nukleotidsequenz, und
(b) ein zweites Segment mit einer Nucleotidsequenz, die einer Oligonukleotideinheit eines Nukleinsäure-Multimeren mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz komplementär ist, als Komponente eines Assayverfahrens nach einem der Ansprüche 9, 10 oder 11.

* C L M S *

19. Verfahren zur Durchführung eines Immunoassays auf einen immunchemischen Analyten, wobei man

(a) einen Liganden spezifisch und direkt oder indirekt an den Analyt bindet, wobei der Ligand ein einzelsträngiges Oligonukleotid besitzt, das der ersten Oligonukleotideinheit des daran gebundenen Multimeren nach einem der Ansprüche 1 bis 8 komplementär ist,
(b) den nichtgebundenen Liganden entfernt,
(c) das Multimere an den Liganden hybridisiert,
(d) ein markiertes Oligonukleotid an die zweiten Oligonukleotideinheiten des gebundenen Multimeren hybridisiert,
(e) nichtgebundenes markiertes Oligonukleotid entfernt,
(f) die Anwesenheit des an das gebundene Multimere gebundenen Markers nachweist.

Patentansprüche für folgenden Vertragsstaat : ES

1. Verfahren zur Durchführung eines Nukleinsäure-Hybridisierungsassays, wobei man

(a) ein Nukleinsäure-Multimeres über die erste Oligonukleotideinheit an die an eine feste Phase gebundene einzelsträngige Analyt-Nukleinsäure oder an ein an den Analyt gebundenes einzelsträngiges Oligonukleotid hybridisiert,
(b) nichtgebundenes Multimeres enfernt,
(c) ein einzelsträngiges markiertes Oligonukleotid an das Multimere über die zweiten Oligonukleotideinheiten hybridisiert,
(d) nichtgebundenes markiertes Oligonukleotid entfernt, und
(e) das Vorhandensein des an das Multimere gebundenen Markers nachweist, wobei das Multimere ein synthetisches verzweigtes Nukleinsäure-Multimeres mit einem Minimum von drei Enden ist, wobei das Multimere

(i) mindestens eine erste einzelsträngige Oligonukleotideinheit, die spezifisch an eine erste einzelsträngige Nukleinsäuresequenz von Interesse binden kann, und

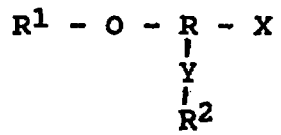
(ii) eine Vielzahl von zweiten einzelsträngigen Oligonukleotideinheiten, die spezifisch an eine zweite einzelsträngig Nukleinsäuresequenz von Interesse binden können, umfaßt, wobei das erste einzelsträngige Oligonukleotid direkt oder indirekt an die zweiten einzelsträngigen Oligonukleotideinheiten nur über covalente Bindungen gebunden ist.

2. Verfahren nach Anspruch 1, wobei die erste Oligonukleotideinheit des Multimeren eine andere Sequenz als die zweite Oligonukleotideinheit besitzt, und die Anzahl der zweiten Oligonukleotideinheiten mindestens zweimal die Anzahl der ersten Oligonukleotideinheiten ist.

3. Verfahren nach Anspruch 1, wobei die Nukleotidsequenz der ersten Oligonukleotideinheit des Multimeren die gleiche wie die Nukleotidsequenz der zweiten Oligonukleotideinheit ist, und die kombinierte Anzahl der Einheiten mindestens etwa 3 beträgt.

4. Verfahren nach den Ansprüchen 1, 2 oder 3, wobei das Multimere eine verzweigte Struktur besitzt.

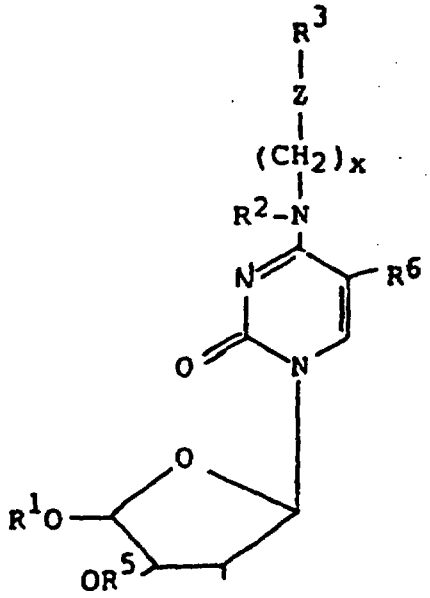
5. Verfahren nach den Ansprüchen 1, 2, 3 oder 4, wobei mindestens ein Anteil der Oligonukleotideinheiten des Multimeren über eine multifunktionelle Einheit gebunden ist, die von einer Verbindung der Formel (I)



abgeleitet ist, worin R eine organische Einheit, bevorzugt eine Nukleinsäure, ist, R^1 eine Hydroxylschutzgruppe ist, die unter Bedingungen entfernt werden kann, die die synthetische Nukleinsäure von einer festen Phase nicht entfernen und die Schutzgruppen des exocyclischen Stickstoffs oder Phosphats nicht entfernen, X eine Phosphor-enthaltende Gruppe ist, die die Nukleinsäuresynthese erleichtert, Y ein Rest, abgeleitet von einer nukleophilen Gruppe, ist, und R^2 R^1 oder eine blockierende oder schützende Gruppe ist, die entfernt werden und durch Wasserstoff ersetzt

* C L M S *

werden kann, ohne R^1 zu beeinträchtigen, wobei mindestens ein Anteil der Oligonukleotideinheiten über eine multifunktionelle Einheit verknüpft ist, die von einer Verbindung der Formel (2)



(2)

abgeleitet ist, worin Z ein Nukleophil ist, R^1 eine Schutzgruppe ist, die im allgemeinen basenstabil und säurelabil ist, R^2 Wasserstoff oder Methyl bedeutet, R^3 eine Schutzgruppe ist, die entfernt und durch Wasserstoff ersetzt werden kann, ohne R^1 zu beeinträchtigen, R^5 ein Phosphorderivat ist, das die Addition von Nukleotiden an die 5'-Position einer Oligonukleotidkette während der chemischen Synthese erlaubt, R^6 Methyl, Wasserstoff, I, Br oder F bedeutet, und X eine ganze Zahl im Bereich von 1 bis 8 einschließlich bedeutet.

6. Verfahren nach Anspruch 1, 2, 3, 4 oder 5, wobei die erste einzelsträngige Nukleotidsequenz von Interesse eine Analyt-Nukleinsäure ist, oder wobei die erste einzelsträngige Nukleotidsequenz von Interesse ein Oligonukleotid ist, das an eine Analyt-Säure gebunden ist.

7. Verfahren nach Anspruch 1, 2, 3, 4, 5 oder 6, wobei die zweite einzelsträngige Nukleotidsequenz von Interesse eine Sequenz eines einzelsträngigen markierten Oligonukleotids ist.

8. Verfahren nach Anspruch 1, 2, 3, 4, 5, 6 oder 7, wobei ein chemisch spaltbarer Linker in jeder der zweiten einzelsträngigen Oligonukleotideinheiten vorhanden ist.

9. Verfahren zur Durchführung eines Sandwich-Nukleinsäure-Hybridisierungsassays in Lösung zum Nachweis einer ersten Nukleinsäuresequenz, die Teil eines Nukleinsäuresegments ist, das eine zweite Nukleinsäuresequenz umfaßt, in einer Probe, die das Segment und ein weiteres Nukleinsäuresegment enthält, welches die erste Nukleinsäuresequenz umfaßt, aber nicht die zweite Nukleinsäuresequenz einschließt, wobei man

(a) den Analyt unter hybrisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment, das entweder der ersten Nukleinsäuresequenz oder der zweiten Nukleinsäuresequenz komplementär ist, und ein zweites Segment, das einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementär ist, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment, das dem anderen der ersten Nukleinsäuresequenz oder der zweiten Nukleinsäuresequenz komplementär ist, und ein zweites Segment, das einem an eine feste Phase gebundenen Oligonukleotid komplementär ist, in Kontakt bringt,
(b) unter hybridisierenden Bedingungen das Produkt von Stufe (a) mit dem an die feste Phase gebundenen Oligonukleotid in Kontakt bringt,
(c) anschließend die an die feste Phase nichtgebundenen Materialien abtrennt,
(d) unter hybridisierenden Bedingungen das Festphasen-gebundene Komplexprodukt der Stufe (c) mit einem Nukleinsäure-Multimeren nach einem der Ansprüche 1 bis 8 in Kontakt bringt, wobei die zweiten Oligonukleotideinheiten des Multimeren einem markierten Oligonukleotid komplementär sind,
(e) nichtgebundenes Multimeres entfernt,

* C L M S *

(f) unter hybridisierenden Bedingungen das Festphasen-gebundene Komplexprodukt der Stufe (e) mit dem markierten Oligonukleotid in Kontakt bringt,
(g) nichtgebundenes markiertes Oligonukleotid entfernt, und
(h) die Anwesenheit des Markers in dem Festphasengebundenen Komplexprodukt der Stufe (g) nachweist.

10. Verfahren nach Anspruch 9, wobei man

(A) zum Nachweis von N. gonorrhoeae pilin-DNA in einem Analyt in der Stufe (a) den Analyt unter hybridisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer Nukleotidsequenz, die einem Segment der N. gonorrhoeae pilin-DNA komplementär ist, und ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment von N. gonorrhoeae pilin-DNA komplementären Nukleotidsequenz, und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz, in Kontakt bringt,
oder (B) zum Nachweis von N. gonorrhoeae-DNA in einem Analyt in Stufe (a) den Analytn unter hybridisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment des in Figur 13 gezeigten genomischen N. gonorrhoeae-Clons komplementären Nukleotidsequenz und einem zweiten Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Nukleotid, umfassend ein erstes Segment mit einer einem Segment des in Figur 13 gezeigten genomischen N. gonorrhoeae-Clons komplementären Nukleotidsequenz, und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz in Kontakt bringt,
oder (C) zum Nachweis der 7,3 kb-Plasmidfamilie von N. gonorrhoeae, die das β-Lactamase TEM-1-Gen tragen, oder zum Nachweis dieses Gens in einem Analyt in Stufe (a) den Analyt unter hybridisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment des Plasmids oder Gens komplementären Nukleotidsequenz und ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem weiteren Segment des Plasmids oder Gens komplementären Nukleotidsequenz und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz in Kontakt bringt,
oder (D) zum Nachweis von HBV-DNA in einem Analyt in Stufe (a) den Analyten unter hybrisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment einer konservierten Region des HBV-Genoms komplementären Nukleotidsequenz und ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem weiteren Segment einer konservierten Region des HBV-Genoms komplementären Nukleotidsequenz und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz in Kontakt bringt,
oder (E) zum Nachweis von Chlamydia trachomatis-DNA in einem Analyt in Stufe (a) den Analyt unter hybridisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment des Chlamydia-Plasmids pCHL2 komplementären Nukleotidsequenz und ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem weiteren Segment einer konservierten Region des HBV-Genoms komplementären Nukleotidsequenz und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz in Kontakt bringt,
oder (F) zum Nachweis von tetM-Gen-DNA, die vermutlich DNA eines Tetracyclin-resistenten Organismus enthält, in einem Analyt in Stufe (a) den Analyt unter hybridisierenden Bedingungen mit einem Überschuß an (i) einem Amplifikator-Sonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem Segment des tetM-Gens komplementären Nukleotidsequenz und ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz, und (ii) einem Einfangssonden-Oligonukleotid, umfassend ein erstes Segment mit einer einem weiteren Segment des tetM-Gens komplementären Nukleotidsequenz und ein zweites Segment mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz in Kontakt bringt.

11. Verwendung eines synthetischen Oligonukleotids, umfassend

* C L M S *

(a) ein erstes Segment mit einer Nukleotidsequenz, die einem Segment einer konservierten Region des HBV-Genoms komplementär ist oder einem Segment der N. gonorrhoeae pilin-DNA komplementär ist, und
(b) ein zweites Segment mit einer Nukleotidsequenz, die einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementär ist, als Komponente eines Assayverfahrens nach einem der Ansprüche 1 bis 10.

12. Verwendung eines synthetischen Oligonukleotids, umfassend

(a) ein erstes Segment mit einer Nukleotidsequenz, die einem Segment einer konservierten Region des HBV-Genoms komplementär ist oder einem Segment der N. gonorrhoeae pilin-DNA komplementär ist, und
(b) ein zweites Segment mit einer Nukleotidsequenz, die einem an eine feste Phase gebundenen Oligonukleotid komplementär ist, als Komponente eines Assayverfahrens nach einem der Ansprüche 1 bis 10.

13. Verwendung eines synthetischen Oligonukleotids, umfassend

(a) ein erstes Segment mit einer einem Segment des in Figur 13 gezeigten genomischen Clons von N. gonorrhoeae komplementären Nukleotidsequenz, und
(b) ein zweites Segment mit einer Nucleotidsequenz, die einer Oligonukleotideinheit eines Nukleinsäure-Multimeren mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz, komplementär ist, als Komponente eines Assayverfahrens nach einem der Ansprüche 1 bis 10.

14. Verwendung eines synthetischen Oligonukleotids, umfassend

(a) ein erstes Segment mit einer einem Segment des 7,3 kb-N. gonorrhoeae-Plasmids, das das β-Lactamasegen TEM-1 trägt, oder dem Gen komplementären Nukleotidsequenz, und

(b) ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nucleotidsequenz als Komponente eines Assayverfahrens nach einem der Ansprüche 1 bis 10.

15. Synthetisches Oligonukleotid, umfassend

(a) ein erstes Segment mit einer einem Segment der 7,3 kb-Plasmidfamilie von N. gonorrhoeae, die das β-Lactamasegen TEM-1 trägt, oder dem Gen komplementären Nukleotidsequenz, und

(b) ein zweites Segment mit einer einem Oligonukleotid, das an eine feste Phase gebunden ist, komplementären Nukleotidsequenz als Komponente eines Assayverfahrens nach einem der Ansprüche 1 bis 10.

16. Verwendung eines synthetischen Oligonukleotids, umfassend

(a) ein erstes Segment mit einer einem Segment des tetM-Gens in einem Tetracyclin-resistenten Organismus komplementären Nukleotidsequenz, und
(b) ein zweites Segment mit einer einem Oligonukleotid, das an eine feste Phase gebunden ist, komplementären Nukleotidsequenz oder mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren komplementären Nukleotidsequenz als Komponente eines Assayverfahrens nach einem der Ansprüche 1 bis 10.

17. Synthetisches Oligonukleotid, umfassend

(a) ein erstes Segment mit einer einem Segment des Chlamydia-Plasmids pCHL2 komplementären Nukleotidsequenz, und
(b) ein zweites Segment mit einer einer Oligonukleotideinheit eines Nukleinsäure-Multimeren mit einer einem an eine feste Phase gebundenen Oligonukleotid komplementären Nukleotidsequenz als Komponente eines Assayverfahrens nach einem der Ansprüche 1 bis 10.

18. Verfahren zur Durchführung eines Immunoassays auf einen immunchemischen Analyten, wobei man

(a) einen Liganden spezifisch und direkt oder indirekt an den Analyt bindet, wobei der Ligand ein einzelsträngiges Oligonukleotid besitzt, das der ersten Oligonukleotideinheit des daran gebundenen Multimeren nach einem der Ansprüche 1 bis 8 komplementär ist,
(b) den nichtgebundenen Liganden entfernt,

* C L M S *

(c) das Multimere an den Liganden hybridisiert,
(d) ein markiertes Oligonukleotid an die zweiten Oligonukleotideinheiten des gebundenen Multimeren hybridisiert,
(e) nichtgebundenes markiertes Oligonukleotid entfernt,
(f) die Anwesenheit des an das gebundene Multimere gebundenen Markers nachweist.

Revendications

Revendications pour les Etats contractants suivants : AT, BE, CH, DE, FR, GB, GR, IT, LI, LU, NL, SE

1. Multimère d'acide nucléique synthétique ramifié ayant un minimum de trois extrémités, ledit multimère comprenant :

   (a) au moins une première unité oligonucléotidique simple brin qui est capable de se lier spécifiquement à une première séquence d'acide nucléique simple brin d'intérêt; et

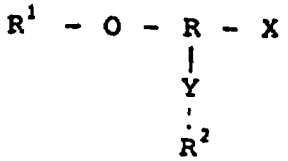
   (b) une pluralité de secondes unités oligonucléotidiques simple brin qui sont capables de se lier spécifiquement à une seconde séquence d'acide nucléique simple brin d'intérêt, où le premier oligonucléotide simple brin est lié directement ou indirectement aux secondes unités oligonucléotidiques simple brin uniquement via des liaisons covalentes.

2. Multimère d'acide nucléique de la revendication 1 dans lequel la première unité oligonucléotidique a une séquence différente de la seconde unité oligonucléotidique et le nombre de secondes unités oligonucléotidiques est au moins environ le double du nombre de premières unités oligonucléotidiques.

3. Multimère d'acide nucléique de la revendication 1 dans lequel la séquence nucléotidique de la première unité oligonucléotidique est la même que la séquence nucléotidique de la seconde unité oligonucléotidique et le nombre combiné d'unités est d'au moins environ 3.

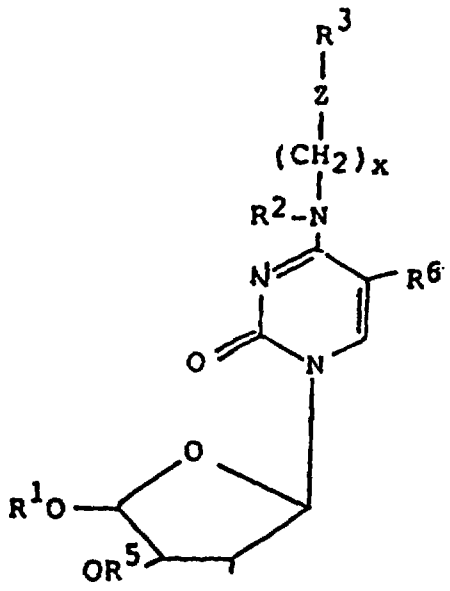
4. Multimère d'acide nucléique de la revendication 1, 2 ou 3 dans lequel le multimère a une structure ramifiée.

5. Multimère d'acide nucléique de la revendication 1, 2, 3 ou 4 dans lequel au moins une partie des unités oligonucléotidiques du multimère sont liées via une partie multifonctionnelle dérivée d'un composé de formule (1)



(1)

dans laquelle R est une partie organique, de préférence un acide nucléique, R^1 est un groupe protecteur de groupe hydroxyle qui peut être éliminé dans des conditions qui ne déplacent pas l'acide nucléique synthétique d'une phase solide et qui n'éliminent pas les groupes protecteurs d'azote exocyclique ou de phosphate, X est un groupe contenant du phosphore qui facilite la synthèse d'acide nucléique, Y est un radical dérivé d'un groupe nucléophile, et R^2 est R^1 ou un groupe bloquant ou protecteur qui peut être éliminé et remplacé par un atome d'hydrogène sans affecter R^1, où au moins une partie des unités oligonucléotidiques sont liées via une partie multifonctionnelle dérivée d'un composé de la formule (2)



(2)

dans laquelle Z est un groupe nucléophile, R^1 est un groupe protecteur qui est habituellement stable en présence de bases et sensible aux acides, R^2 est un atome d'hydrogène ou un groupe méthyle, R^3 est un groupe protecteur qui peut être éliminé et remplacé par un atome d'hydrogène sans affecter R^1, R^5 est un dérivé du phosphore qui permet l'addition de nucléotides en position 5' d'une chaîne oligonucléotidique durant la synthèse chimique, R^6 est un groupe méthyle, un atome d'hydrogène, I, Br ou F, et X est un nombre entier dans la gamme de 1 à 8, y compris ces nombres.

6. Multimère d'acide nucléique de la revendication 1, 2, 3, 4 ou 5 dans lequel la première séquence nucléotidique simple brin d'intérêt est un acide nucléique à analyser, ou dans lequel la première séquence nucléotidique simple brin d'intérêt est un oligonucléotide qui est lié à un acide à analyser.

7. Multimère d'acide nucléique de la revendication 1, 2, 3, 4, 5 ou 6 dans lequel la seconde séquence nucléotidique simple brin d'intérêt est une séquence oligonucléotidique simple brin marquée.

8. Multimère d'acide nucléique de la revendication 1, 2, 3, 4, 5, 6 ou 7 dans lequel se trouve un linker qui peut être clivé chimiquement dans chacune des secondes unités oligonucléotidiques simple brin.

9. Procédé pour effectuer un test d'hybridation nucléique comprenant les étapes consistant à

(a) hybrider le multimère de la revendication 7 via la première unité oligonucléotidique avec un acide nucléique simple brin à analyser lié à une phase solide ou avec un oligonucléotide simple brin lié à la substance à analyser;

(b) éliminer le multimère non lié;

(c) hybrider un oligonucléotide simple brin marqué avec le multimère via les secondes unités oligonucléotidiques;

(d) éliminer l'oligonucléotide marqué non lié; et

(e) détecter la présence de marqueur lié au multimère.

10. Procédé pour effectuer un test sandwich en solution d'hybridation d'acides nucléiques pour détecter une première séquence d'acide nucléique qui fait partie d'un segment d'acide nucléique qui comprend une seconde séquence d'acide nucléique dans un échantillon qui contient ledit segment et un autre segment d'acide nucléique qui comprend la première séquence d'acide nucléique mais ne comprend pas la seconde séquence d'acide nucléique, comprenant les étapes consistant à :

(a) mettre en contact la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligo-

* C L M S *

nucléotide sonde amplificateur comprenant un premier segment qui est complémentaire de l'une de la première séquence d'acide nucléique ou de la seconde séquence d'acide nucléique et un second segment qui est complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment qui est complémentaire de l'autre de la première séquence d'acide nucléique ou de la seconde séquence d'acide nucléique et un second segment qui est complémentaire d'un oligonucléotide lié à une phase solide;

(b) mettre en contact dans des conditions d'hybridation le produit de l'étape (a) avec l'oligonucléotide lié à la phase solide;

(c) ensuite séparer les substances non liées à la phase solide ;

(d) mettre en contact dans des conditions d'hybridation le complexe obtenu en phase solide à l'étape (c) avec un multimère d'acide nucléique selon l'une quelconque des revendications 1 à 8 où les secondes unités oligonucléotidiques dudit multimère sont complémentaires d'un oligonucléotide marqué;

(e) éliminer le multimère non lié;

(f) mettre en contact dans des conditions d'hybridation le complexe obtenu en phase solide à l'étape (e) avec l'oligonucléotide marqué ;

(g) éliminer l'oligonucléotide marqué non lié; et

(h) détecter la présence de marqueur dans le complexe obtenu en phase solide à l'étape (g).

11. Procédé selon la revendication 10

(A) pour détecter de l'ADN de piline de N. gonorrhoeae dans une substance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment d'ADN de piline de N.gonorrhoeae et un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment d'ADN de piline de N. gonorrhoeae et un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide;

ou (B) pour détecter de l'ADN de N. gonorrhoeae dans une subtance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment du clone génomique de N. gonorrhoeae présenté à la Figure 13 et un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment du clone génomique de N. gonorrhoeae présenté à la Figure 13 et un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide;

ou (C) pour détecter la famille de plasmides de 7,3 kb de N. gonorrhoeae portant le gène TEM-1 de la β-lactamase ou ledit gène dans une substance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment dudit plasmide ou gène et un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un autre segment dudit plasmide ou gène et un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide;

ou (D) pour détecter de l'ADN de HBV dans une substance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment d'une région conservée du génome de HBV et un second segment ayant une séquence nucléotidique

* C L M S *

complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucleotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un autre segment d'une région conservée du génome de HBV et un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide ;

ou (E) pour détecter de l'ADN de Chlamydia trachomatis dans une substance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment du plasmide pCHL2 de Chlamydia et un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un autre segment d'une région conservée du génome de HBV et un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide;

ou (F) pour détecter de l'ADN du gène tetM soupçonnée de contenir de l'ADN d'un organisme résistant à la tétracycline dans une substance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment du gène tetM et un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un autre segment dudit gène tetM et un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide;

12. Utilisation d'un oligonucléotide synthétique comprenant :

(a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment d'une région conservée du génome de HBV ou complémentaire d'un segment d'ADN de piline de N. gonorrhoeae et

(b) un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique; en tant que composant d'un procédé de test selon l'une quelconque des revendications 9, 10 ou 11.

13. Utilisation d'un oligonucléotide synthétique comprenant :

(a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment d'une région conservée du génome de HBV ou complémentaire d'un segment d'ADN de piline de N. gonorrhoeae, et

(b) un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide; en tant que composant d'un procédé de test selon l'une quelconque des revendications 9, 10 ou 11.

14. Utilisation d'un oligonucléotide synthétique comprenant
(a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment du clone génomique de N.gonorrhoeae présenté à la Figure 13 et (b) un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide; en tant que composant d'un procédé de test selon l'une quelconque des revendications 9, 10 ou 11.

15. Utilisation d'un oligonucléotide synthétique comprenant (a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment du plasmide de 7,3 kb de N. gonorrhoeae portant le gène TEM-1 de la β-lactamase ou dudit gène et (b) un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique; en tant que composant d'un procédé de test selon l'une quelconque des revendications 9, 10 ou 11.

16. Utilisation d'un oligonucléotide synthétique comprenant (a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment de la famille de plasmides de 7,3 kb de N. gonorrhoeae portant le gène TEM-1 de la β-lactamase ou dudit gène et (b) un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide; en tant que composant d'un procédé de test selon l'une quelconque des revendications 9, 10 ou 11.

* C L M S *

17. Utilisation d'un oligonucléotide synthétique comprenant (a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment du gène tetM dans un organisme résistant à la tétracycline et (b) un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide ou ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique; en tant que composant d'un procédé de test selon l'une quelconque des revendications 9, 10 ou 11.

18. Utilisation d'un oligonucléotide synthétique comprenant :

(a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment du plasmide pCHL2 de Chlamydia, et

(b) un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide; en tant que composant d'un procédé de test selon l'une quelconque des revendications 9, 10 ou 11.

19. Procédé pour effectuer un test immunologique pour une substance immunochimique à analyser comprenant les étapes consistant à :

(a) lier un ligand spécifiquement et directement ou indirectement à la substance à analyser, ledit ligand ayant un oligonucléotide simple brin qui est complémentaire de la première unité oligonucléotidique du multimère de l'une quelconque des revendications 1 à 8 lié à celui-ci;

(b) éliminer le ligand non lié;

(c) hybrider ledit multimère avec le ligand;

(d) hybrider un oligonucléotide marqué avec les secondes unités oligonucléotidiques du multimère lié;

(e) éliminer l'oligonucléotide marqué non lié;

(f) détecter la présence de marqueur lié au multimère lié.

Revendications pour l'Etat contractant suivant : ES

1. Procédé pour effectuer un test d'hybridation d'acides nucléiques comprenant les étapes consistant à

(a) hybrider un multimère d'acide nucléique via la première unité oligonucléotidique avec un acide nucléique à analyser simple brin lié à une phase solide ou avec un oligonucléotide simple brin lié à la substance à analyser;

(b) éliminer le multimère non lié;

(c) hybrider un oligonucléotide marqué simple brin avec le multimère via les secondes unités oligonucléotidiques;

(d) éliminer l'oligonucléotide marqué non lié; et

(e) détecter la présence de marqueur lié au multimère ; où ledit multimère est un multimère d'acide nucléique ramifié synthétique ayant un minimum de trois extrémités, ledit multimère comprenant :

(i) au moins une première unité oligonucléotidique simple brin qui est capable de se lier spécifiquement à une première séquence d'acide nucléique simple brin d'intérêt; et

(ii) une pluralité de secondes unités oligonucléotidiques simple brin qui sont capables de se lier spécifiquement à une seconde séquence d'acide nucléique simple brin d'intérêt, où le premier oligonucléotide simple brin est lié directement ou indirectement aux secondes unités oligonucléotidiques simple brin uniquement via des liaisons covalentes.

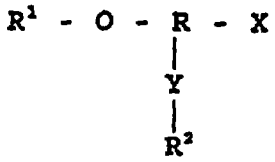
* C L M S *

2. Procédé de la revendication 1 dans lequel la première unité oligonucléotidique du multimère a une séquence différente de celle de la seconde unité oligonucléotidique et le nombre de secondes unités oligonucléotidiques est au moins environ le double du nombre de premières unités oligonucléotidiques.

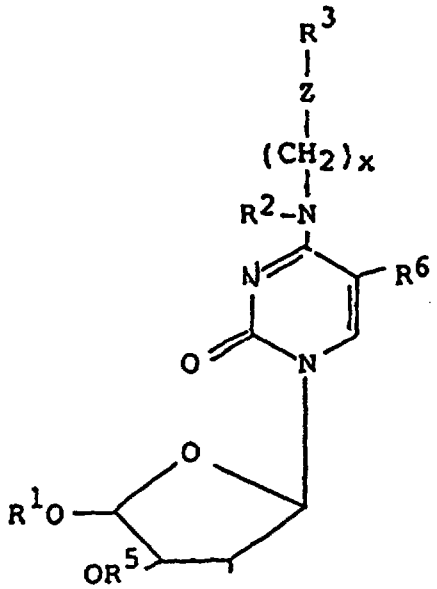
3. Procédé de la revendication 1 dans lequel la séquence nucléotidique de la première unité oligonucléotidique du multimère est la même que la séquence nucléotidique de la seconde unité oligonucléotidique et le nombre combiné d'unités est d'au moins environ 3.

4. Procédé des revendications 1, 2 ou 3 dans lequel le multimère a une structure ramifiée.

5. Procédé des revendications 1, 2, 3 ou 4 dans lequel au moins une partie des unités oligonucléotidiques du multimère sont liées via une partie multifonctionnelle dérivée d'un composé de formule (I)



dans laquelle R est une partie organique, de préférence un acide nucléique, R^1 est un groupe protecteur de groupe hydroxyle qui peut être éliminé dans des conditions qui ne déplacent pas l'acide nucléique synthétique d'une phase solide et qui n'éliminent pas les groupes protecteurs d'azote exocyclique ou de phosphate, X est un groupe contenant du phosphore qui facilite la synthèse d'acide nucléique, Y est un radical dérivé d'un groupe nucléophile, et R^2 est R^1 ou un groupe bloquant ou protecteur qui peut être éliminé et remplacé par un atome d'hydrogène sans affecter R^1, où au moins une partie des unités oligonucléotidiques sont liées via une partie multifonctionnelle dérivée d'un composé de la formule (2)



(2)

dans laquelle Z est un groupe nucléophile, R^1 est un groupe protecteur qui est habituellement stable en présence de bases et sensible aux acides, R^2 est un atome d'hydrogène ou un groupe méthyle, R^3 est un groupe protecteur qui peut être éliminé et remplacé par un atome d'hydrogène sans affecter R^1, R^5 est un dérivé du phosphore qui permet l'addition de nucléotides en position 5' d'une chaîne oligonucléotidique durant la synthèse chimique, R^6 est un groupe méthyle, un atome d'hydrogène, I, Br, ou F, et X est un nombre entier dans la gamme de 1 à 8, y compris ces nombres.

6. Procédé selon la revendication 1, 2, 3, 4 ou 5 dans lequel la première séquence nucléotidique simple brin d'intérêt est un acide nucléique à analyser, ou dans lequel la première séquence nucléotidique simple brin d'intérêt est un oligonucléotide qui est lié à un acide à analyser.

* C L M S *

7. Procédé selon les revendications 1, 2, 3, 4, 5 ou 6 dans lequel la seconde séquence nucléotidique simple brin d'intérêt est une séquence oligonucléotidique simple brin marquée.

8. Procédé selon les revendications 1, 2, 3, 4, 5, 6 ou 7 dans lequel il y a un linker qui peut être chimiquement clivé dans chacune des secondes unités oligonucléotidiques simple brin.

9. Procédé pour effectuer un test sandwich en solution d'hybridation d'acides nucléiques pour détecter une première séquence d'acide nucléique qui fait partie d'un segment d'acide nucléique qui comprend une seconde séquence d'acide nucléique dans un échantillon qui contient ledit segment et un autre segment d'acide nucléique qui comprend la première séquence d'acide nucléique mais ne comprend pas la seconde séquence d'acide nucléique, comprenant les étapes consistant à :

(a) mettre en contact la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment qui est complémentaire de l'une de la première séquence d'acide nucléique ou de la seconde séquence d'acide nucléique et un second segment qui est complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment qui est complémentaire de l'autre de la première séquence d'acide nucléique ou de la seconde séquence d'acide nucléique et un second segment qui est complémentaire d'un oligonucléotide lié à une phase solide;

(b) mettre en contact dans des conditions d'hybridation le produit de l'étape (a) avec l'oligonucléotide lié à la phase solide;

(c) séparer ensuite les substances non liées à la phase solide;

(d) mettre en contact dans des conditions d'hybridation le complexe obtenu en phase solide à l'étape (c) avec un multimère d'acide nucléique tel que défini dans l'une quelconque des revendications 1 à 8 où les secondes unités oligonucléotidiques dudit multimère sont complémentaires d'un oligonucléotide marqué;

(e) éliminer le multimère non lié;

(f) mettre en contact dans des conditions d'hybridation le complexe obtenu en phase solide à l'étape (e) avec l'oligonucléotide marqué ;

(g) éliminer l' oligonucléotide marqué non lié; et

(h) détecter la présence de marqueur dans le complexe obtenu en phase solide à l'étape (g).

10. Procédé selon la revendication 9

(A) pour détecter de l'ADN de piline de N. gonorrhoeae dans une substance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment d'ADN de piline de N.gonorrhoeae et un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment d'ADN de piline de N. gonorrhoeae et un second segment ayant une séquence nucléotidique complémentaire d' un oligonucléotide lié à une phase solide;

ou (B) pour détecter de l'ADN de N. gonorrhoeae dans une substance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment du clone génomique de N. gonorrhoeae présenté à la Figure 13 et un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment du clone génomique de N. gonorrhoeae présenté à la Figure 13 et un second segment ayant une séquence nucléotidique complémentaire d' un oligonucléotide lié à une phase solide;

* C L M S *

ou (C) pour détecter la famille de plasmides de 7,3 kb de N. gonorrhoeae portant le gène TEM-1 de la β-lactamase ou ledit gène dans une substance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment dudit plasmide ou gène et un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un autre segment dudit plasmide ou gène et un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide;

ou (D)pour détecter de l'ADN de HBV dans une substance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment d'une région conservée du génome de HBV et un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un autre segment d'une région conservée du génome de HBV et un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide;

ou (E) pour détecter de l'ADN de Chlamydia trachomatis dans une substance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment du plasmide pCHL2 de Chlamydia et un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un autre segment d'une région conservée du génome de HBV et un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide;

ou (F) pour détecter de l'ADN du gène tetM soupçonnée de contenir de l'ADN d'un organisme résistant à la tétracycline dans une substance à analyser où l'étape (a) comprend la mise en contact de la substance à analyser dans des conditions d'hybridation avec un excès de (i) un oligonucléotide sonde amplificateur comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un segment du gène tetM et un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique et (ii) un oligonucléotide sonde de capture comprenant un premier segment ayant une séquence nucléotidique complémentaire d'un autre segment dudit gène tetM et un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide.

11. Utilisation d'un oligonucléotide synthétique comprenant:

(a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment d'une région conservée du génome de HBV ou complémentaire d'un segment d'ADN de piline de N. gonorrhoeae et

(b) un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique; en tant que composant d'un procédé de test selon l'une quelconque des revendications 1 à 10.

12. Utilisation d'un oligonucléotide synthétique comprenant :

(a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment d'une région conservée du génome de HBV ou complémentaire d'un segment d'ADN de piline de N. gonorrhoeae, et

(b) un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide; en tant que composant d'un procédé de test selon l'une quelconque des revendications 1 à 10.

13. Utilisation d'un oligonucléotide synthétique comprenant

(a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment du clone génomique de N.gonorrhoeae présenté à la Figure 13 et (b) un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique ayant une séquence nucléotidique

* C L M S *

complémentaire d'un oligonucléotide lié à une phase solide; en tant que composant d'un procédé de test selon l'une quelconque des revendications 1 à 10.

14. Utilisation d'un oligonucléotide synthétique comprenant (a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment du plasmide de 7,3 kb de N. gonorrhoeae portant le gène TEM-1 de la β-lactamase ou dudit gène et (b) un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique; en tant que composant d'un procédé de test selon l'une quelconque des revendications 1 à 10.

15. Oligonucléotide synthétique comprenant (a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment de la famille de plasmides de 7,3 kb de N. gonorrhoeae portant le gène TEM-1 de la β-lactamase ou dudit gène et (b) un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide; en tant que composant d'un procédé de test selon l'une quelconque des revendications 1 à 10.

16. Utilisation d'un oligonucléotide synthétique comprenant (a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment du gène tetM dans un organisme résistant à la tétracycline et (b) un second segment ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide ou ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique; en tant que composant d'un procédé de test selon l'une quelconque des revendications 1 à 10.

17. Oligonucléotide synthétique comprenant: (a) un premier segment ayant une séquence nucléotidique complémentaire d'un segment du plasmide pCHL2 de Chlamydia, et (b) un second segment ayant une séquence nucléotidique complémentaire d'une unité oligonucléotidique d'un multimère d'acide nucléique ayant une séquence nucléotidique complémentaire d'un oligonucléotide lié à une phase solide; en tant que composant d'un procédé de test selon l'une quelconque des revendications 1 à 10.

18. Procédé pour effectuer un test immunologique pour une substance immunochimique à analyser comprenant les étapes consistant à :

(a) lier un ligand spécifiquement et directement ou indirectement à la substance à analyser, ledit ligand ayant un oligonucléotide simple brin qui est complémentaire de la première unité oligonucléotidique du multimère tel que défini dans l'une quelconque des revendications 1 à 8 lié à celui-ci ;

(b) éliminer le ligand non lié;

(c) hybrider ledit multimère avec le ligand;

(d) hybrider un oligonucléotide marqué avec les secondes unités oligonucléotidiques du multimère lié;

(e) éliminer l'oligonucléotide marqué non lié;

(f) détecter la présence de marqueur lié au multimère lié.