# DIAGNOSTIC ASSAYS FOR PARVOVIRUS B19

## Technical Field

The present invention pertains generally to viral diagnostics. In particular, the invention relates to nucleic acid-based assays for accurately diagnosing parvovirus B19 infection and to primers and probes for use in these assays.

## Background Of The Invention

Human parvovirus B19 is a member of the family Parvoviridae, genus Erythrovirus and is a small 22-nm icosahedral nonenveloped virus with a linear single-stranded DNA molecule of approximately 5,600 nucleotides. The viral genome encodes three major proteins, VP1, VP2 and NS1. See, Shade et al., *J. Virol.* (1986) 58:921-936 and Figure 1 herein. VP1 (83kDa) and VP2 (58 kDa) are the structural proteins of the capsid. The two proteins are encoded in overlapping reading frames from about nucleotides 2444 to 4789 and about 3125 to 4789, respectively. VP2 constitutes 95% of the capsid and the larger VP1 protein only 5% of the capsid. VP1 is required for the mature conformation of the virus. NS1 (77 kDa), is a nonstructural protein and is present only in the nuclear fraction of infected cells and absent from the cytoplasm and intact virions in sera.

Parvovirus B19 was first discovered in the sera of normal blood donors and is the only member of the family Parvoviridae known to be pathogenic in humans. The virus is associated with a wide range of disease manifestations. Human parvovirus B19 normally causes an asymptomatic or mild self-limiting infection in children. In adults, parvovirus B19 may cause a rash, transient symmetrical polyarthralgia and arthritis. Parvovirus B19 has been associated with transient aplastic crisis (TAC) in

patients with underlying hemolytic disorders. Chronic B19 infection and persistent anemia have been reported in immunocompromised patients with acute leukemia, congenital immunodeficiencies, AIDS, and following bone marrow transplantation. Parvovirus B19 has also been associated with fetal death in pregnant women.

In most countries, B19 virus infection generally occurs during childhood, with approximately 50% of children having anti-B19 antibodies by the age of 15 years. B19 antibody prevalence may further increase during lifetime and reaches values higher than 90% in elderly individuals.

In human parvovirus B19 infection, initial viral replication is believed to occur in the respiratory tract. The virus then targets cells in the bone marrow. This leads to large-scale viral replication with reported viremia of between $10^2$ to $10^{14}$ particles/ml, occurring 7-10 days after infection but prior to the onset of symptoms. Cessation of viremia coincides with the detection of specific IgM antibodies that remain elevated for two to three months. Anti-B19 IgG antibodies are detected a few days after IgM antibodies appear and persist lifelong.

The absence of a lipid envelope and limited DNA content make parvovirus B19 extremely resistant to physicochemical inactivation. Parvovirus B19, especially at high concentration, can withstand conventional heat treatment of blood products and transmission of B19 through the administration of solvent-detergent-treated factor VIII and steam- or dry-heated factor VIII and IX preparations has been documented.

Human parvovirus B19 cannot be grown in conventional cell cultures making laboratory detection and isolation of the virus extremely difficult. Thus, for many years, the only source of antigen consisted of sera from viremic patients. Recombinant antigens have been produced for use in serological assays in an attempt to circumvent these problems. See, e.g., Sisk and Berman, *Biotechnology* (1987) 5:1077-1080; U.S. Patent No. 6,204,044. Immunoenzymatic IgM capture assays have been used to detect anti-B19 IgM, as well as to diagnose recent B19 infection. The diagnostic performance of a number of commercially available tests, however, is not homogenous. In addition, IgM-based diagnostic tests cannot detect the virus during

the viremic stage of infection and once IgM antibodies are synthesized, they can remain in circulation for several months after the end of viremia.

The high prevalence of B19 antibodies in the normal population together with the fact that high viremia usually persists for only one week, make the use of serological based tests impractical. In addition, in immunocompromised patients, serological diagnosis may be unreliable.

Nucleic acid-based hybridization assays, such as dot blot and *in situ* hybridization have been used for B19 detection. These assays generally have detection limits of 1 to 0.1 pg viral DNA (~$10^4$-$10^5$ viral particles). PCR has greater sensitivity (~100 genome copies). However, DNA hybridization techniques are time consuming and limited in use and PCR is impractical for screening large numbers of samples.

Therefore, there remains a need for the development of reliable diagnostic tests to detect parvovirus B19 in viremic samples, in order to prevent transmission of the virus through blood and plasma derivatives or by close personal contact.

## Summary of the Invention

The present invention is based on the discovery of unique primers and probes for use in nucleic acid-based assays, as well as on the development of a sensitive, reliable nucleic acid-based diagnostic test for the detection of parvovirus B19 DNA in biological samples from potentially infected individuals. The techniques described herein utilize extracted sample DNA as a template for amplification of conserved genomic regions of the B19 sequence using transcription-mediated amplification (TMA), as well as in a 5' nuclease assay, such as the TaqMan™ technique. The methods allow for the detection of B19 DNA in viremic samples having viral titers as low as $10^3$ virus particles/ml. Accordingly, infected samples can be identified and excluded from transfusion, as well as from the preparation of blood derivatives. The probes and primers described herein are also useful in, for example, standard hybridization methods, as well as in PCR-based techniques, nucleic acid sequence-based amplification (NASBA) and in assays that utilize branched DNA-molecules.

Accordingly, in one embodiment, the subject invention is directed to a method of detecting human parvovirus B19 infection in a biological sample. The method comprises:

(a) isolating nucleic acid from a biological sample suspected of containing human parvovirus B19 DNA, wherein the nucleic acid comprises an RNA target sequence;

(b) reacting the isolated parvovirus B19 nucleic acid with a first oligonucleotide which comprises a first primer comprising a complexing sequence sufficiently complementary to the 3'-terminal portion of the RNA target sequence to complex therewith, wherein the first primer further comprises a promoter for a DNA-dependent RNA polymerase 5' and operably linked to the complexing sequence, wherein the reacting is done under conditions that provide for the formation of an oligonucleotide/target sequence complex and initiation of DNA synthesis;

(c) extending the first primer in an extension reaction using the RNA target sequence as a template to give a first DNA primer extension product complementary to the RNA target sequence;

(d) separating the first DNA primer extension product from the RNA target sequence using an enzyme which selectively degrades the RNA target sequence;

(e) treating the DNA primer extension product with a second oligonucleotide which comprises a second primer comprising a complexing sequence sufficiently complementary to the 3'-terminal portion of the DNA primer extension product to complex therewith under conditions that provide for the formation of an oligonucleotide/target sequence complex and initiation of DNA synthesis;

(f) extending the 3'-terminus of the second primer in a DNA extension reaction to give a second DNA primer extension product, thereby producing a template for the DNA-dependent RNA polymerase;

(g) using the template to produce multiple RNA copies of the target sequence using a DNA-dependent RNA polymerase which recognizes the promoter sequence;

and (h) using the RNA copies of step (g), autocatalytically repeating steps (b) to (g)

to amplify the target sequence.

In certain embodiments, the method further comprises the steps of:

(i) adding a labeled oligonucleotide probe to the product of step (h), wherein the oligonucleotide probe is complementary to a portion of the target sequence, under conditions that provide for the hybridization of the probe with the target sequence to form a probe:target complex; and

(j) detecting the presence or absence of label as an indication of the presence or absence of the target sequence.

In additional embodiments, the label is an acridinium ester.

In yet further embodiments, the first and second primers, and the probe used in the methods above are derived from the VP1 region of the human parvovirus B19 genome, such as from the polynucleotide sequence depicted in any one of Figures 2A-2U or 11A-11Z.

In another embodiment, the invention is directed to a method of detecting human parvovirus B19 infection in a biological sample. The method comprises:

(a) isolating nucleic acid from a biological sample suspected of containing human parvovirus B19 DNA, wherein the nucleic acid comprises an RNA target sequence;

(b) reacting the isolated parvovirus B19 nucleic acid with a first oligonucleotide which comprises a first primer comprising a complexing sequence sufficiently complementary to the 3'-terminal portion of the RNA target sequence to complex therewith, wherein the first primer further comprises a promoter for a DNA-dependent RNA polymerase 5' and operably linked to the complexing sequence, wherein the first primer comprises a sequence derived from the polynucleotide sequence depicted in any one of Figures 2A-2U or Figures 11A-11Z and the reacting is done under conditions that provide for the formation of an oligonucleotide/target sequence complex and initiation of DNA synthesis;

(c) extending the first primer in an extension reaction using the RNA target sequence as a template to give a first DNA primer extension product complementary to the RNA target sequence;

(d) separating the first DNA primer extension product from the RNA target sequence using an enzyme which selectively degrades the RNA target sequence;

(e) treating the DNA primer extension product with a second oligonucleotide which comprises a second primer comprising a complexing sequence sufficiently complementary to the 3'-terminal portion of the DNA primer extension product to complex therewith, wherein the second primer is derived from the polynucleotide sequence depicted in any one of Figures 2A-2U or Figures 11A-11Z and the treating is done under conditions that provide for the formation of an oligonucleotide/target sequence complex and initiation of DNA synthesis;

(f) extending the 3'-terminus of the second primer in a DNA extension reaction to give a second DNA primer extension product, thereby producing a template for the DNA-dependent RNA polymerase;

(g) using the template to produce multiple RNA copies of the target sequence using a DNA-dependent RNA polymerase which recognizes the promoter sequence;

and (h) using the RNA copies of step (g), autocatalytically repeating steps (b) to (g)

to amplify the target sequence;

(i) adding an acridinium ester-labeled oligonucleotide probe to the product of step (h), wherein the oligonucleotide probe is complementary to a portion of said target sequence and the probe is derived from the polynucleotide sequence depicted in any one of Figures 2A-2U, wherein the probe is added under conditions that provide for the hybridization of the probe with the target sequence to form a probe:target complex; and

(j) detecting the presence or absence of label as an indication of the presence or absence of the target sequence.

In yet another embodiment, the invention is directed to a method for amplifying a target parvovirus B19 nucleotide sequence. The method comprises:

(a) isolating nucleic acid from a biological sample suspected of containing human parvovirus B19 DNA, wherein the nucleic acid comprises an RNA target sequence;

(b) adding one or more primers capable of hybridizing to the RNA target sequence, wherein the one or more primers are derived from the polynucleotide sequences depicted in any one of Figures 2A-2U and Figures 11A-11Z;

(c) adding an oligonucleotide probe capable of hybridizing to the RNA target sequence 3' relative to the one or more primers;

(d) extending the one or more primers using a polymerase.

In certain embodiments, the RNA target sequence of step (a) is reverse transcribed to provide cDNA and the method can further comprise amplifying the cDNA using polymerase chain reaction (RT-PCR) or asymmetric gap ligase chain reaction (RT-AGLCR). In other embodiments, the polymerase is a thermostable polymerase, such as but not limited to Taq polymerase or Vent polymerase. In additional embodiments, the polymerase is *E. coli* DNA polymerase I, Klenow fragment of *E. coli* DNA polymerase I, or T4 DNA polymerase.

In certain embodiments of the various methods described above, an internal control is provided. The internal control can be derived from the sequence of Figure 12 (SEQ ID NO:92). In additional embodiments, the internal control comprises SEQ ID NO:90.

In additional embodiments, the invention is directed to a method for detecting human parvovirus B19 infection in a biological sample. The method comprises:

(a) isolating nucleic acid from a biological sample suspected of containing human parvovirus B19 DNA, wherein the nucleic acid comprises a target sequence;

(b) reacting the isolated parvovirus B19 nucleic acid with a detectably labeled probe sufficiently complementary to and capable of hybridizing with the target sequence, wherein the probe is derived from the polynucleotide sequences depicted in any one of Figures 2A-2U and Figures 11A-11Z, and further wherein the reacting is done under conditions that provide for the formation of a probe/target sequence complex; and

(c) detecting the presence or absence of label as an indication of the presence or absence of the target sequence.

In further embodiments, the invention is directed to a polynucleotide comprising a nucleotide sequence comprising any one of the nucleotide sequences depicted in Figures 2A-2U or Figures 11A-11Z.

In additional embodiments, the invention is directed to a polynucleotide, as above, wherein the nucleotide sequence consists of the nucleotide sequence depicted in Figures 2A, 2B, 2C, 2D, 2E, 2F, 2G, 2H, 2I, 2J, 2K, 2L, 2M, 2N, 2O, 2P, 2Q, 2R, 2S, 2T, 2U, 11A, 11B, 11C, 11D, 11E, 11F, 11G, 11H, 11I, 11J, 11K, 11L, 11M, 11N, 11O, 11P, 11Q, 11R, 11S, 11T, 11U, 11V, 11W, 11X, 11Y or 11Z.

In still further embodiments, the subject invention is directed to a polynucleotide comprising a nucleotide sequence comprising any one of the nucleotide sequences depicted in Figures 3A-3C or 4A-4C.

In additional embodiments, the invention is directed to a polynucleotide as above, wherein the nucleotide sequence consists of the nucleotide sequence depicted in Figures 3A-3C or in Figures 4A-4C.

In another embodiment, the invention is directed to an oligonucleotide primer consisting of a promoter region recognized by a DNA-dependent RNA polymerase operably linked to a human parvovirus B19-specific complexing sequence of about 10 to about 75 nucleotides. In certain embodiments, the promoter region is the T7 promoter and said polymerase is T7 RNA polymerase. Additionally, the human parvovirus B19-specific sequence may be from the VP1 region of the human parvovirus B19 genome, such as from the polynucleotide sequence depicted in any one of Figures 2A-2U or Figures 11A-11Z.

In yet further embodiments, the invention is directed an oligonucleotide primer consisting of a T7 promoter operably linked to a human parvovirus B19-specific complexing sequence of about 10 to about 75 nucleotides, wherein the human parvovirus B19-specific complexing sequence is derived from the polynucleotide sequence depicted in any one of Figures 2A-2U or 11A-11Z.

In another embodiment, the invention is directed to an oligonucleotide probe comprising a parvovirus B19-specific hybridizing sequence of about 10 to about 50 nucleotides linked to an acridinium ester label. In certain embodiments, the human

parvovirus B19-specific hybridizing sequence is from the VP1 region of the human parvovirus B19 genome, such as from the polynucleotide sequence depicted in any one of Figures 2A-2U or Figures 11A-11Z.

In yet an additional embodiment, the invention is directed to a diagnostic test kit comprising one or more oligonucleotide primers described herein, and instructions for conducting the diagnostic test. In certain embodiments, the test kit further comprises an oligonucleotide probe comprising a parvovirus B19-specific hybridizing sequence of about 10 to about 50 nucleotides linked to an acridinium ester label.

These and other aspects of the present invention will become evident upon reference to the following detailed description and attached drawings.

Brief Description of the Figures

Figure 1 is a diagrammatic representation of the human parvovirus B19 genome, depicting the various coding regions of the virus. Three PCR fragments are depicted, one with approximately 700 bp, corresponding to nucleotide positions 2936-3635 of the parvovirus B19 genome described in Shade et al., *J. Virol.* (1986) 58:921-936; one with approximately 370 bp within the 700 bp fragment, corresponding to nucleotide positions 3073-3442 of the parvovirus B19 genome described in Shade et al., *J. Virol.* (1986) 58:921-936; and one with approximately 214 bp corresponding to nucleotide positions 4728-4941 of the parvovirus B19 genome described in Shade et al., *J. Virol.* (1986) 58:921-936.

Figures 2A through 2U (SEQ ID NOS:1-21) depict DNA sequences from various parvovirus B19 isolates which include sequences corresponding to nucleotide positions 2936-3635 of the parvovirus B19 genome described in Shade et al., *J. Virol.* (1986) 58:921-936 (the 700 bp fragment from Figure 1). Figure 2A (SEQ ID NO:1) is the corresponding sequence from isolate CH47-26; Figure 2B (SEQ ID NO:2) is the corresponding sequence from isolate CH48-29; Figure 2C (SEQ ID NO:3) is the corresponding sequence from isolate CH33-2; Figure 2D (SEQ ID NO:4) is the corresponding sequence from isolate CH33-3; Figure 2E (SEQ ID NO:5) is the corresponding sequence from isolate CH33-4; Figure 2F (SEQ ID NO:6) is the

corresponding sequence from isolate CH42-7; Figure 2G (SEQ ID NO:7) is the corresponding sequence from isolate CH42-18; Figure 2H (SEQ ID NO:8) is the corresponding sequence from isolate CH42-19; Figure 2I (SEQ ID NO:9) is the corresponding sequence from isolate CH46-23; Figure 2J (SEQ ID NO:10) is the corresponding sequence from isolate CH1-1; Figure 2K (SEQ ID NO:11) is the corresponding sequence from isolate CH1-6; Figure 2L (SEQ ID NO:12) is the corresponding sequence from isolate CH2-8; Figure 2M (SEQ ID NO:13) is the corresponding sequence from isolate CH2-10; Figure 2N (SEQ ID NO:14) is the corresponding sequence from isolate CH2-11C; Figure 2O (SEQ ID NO:15) is the corresponding sequence from isolate CH5-13; Figure 2P (SEQ ID NO:16) is the corresponding sequence from isolate CH7-22; Figure 2Q (SEQ ID NO:17) is the corresponding sequence from isolate CH13-27; Figure 2R (SEQ ID NO:18) is the corresponding sequence from isolate CH14-33; Figure 2S (SEQ ID NO:19) is the corresponding sequence from isolate CH62-2; Figure 2T (SEQ ID NO:20) is the corresponding sequence from isolate CH64-2; and Figure 2U (SEQ ID NO:21) is the corresponding sequence from isolate CH67-2.

Figures 3A-3C (SEQ ID NO:22) show a sequence for the approximately 4.7 kbp PCR fragment shown in Figure 1 from parvovirus B19 clone 2-B1. The sequence is a 4677 nucleotide fragment corresponding to nucleotide positions 217-4893 of Shade et al., *J. Virol.* (1986) 58:921-936. The sequence depicted contains the parvovirus B19 full-length open reading frame which encodes NS1, VP1 and VP2, plus additional 5' and 3' untranslated sequences.

Figures 4A-4C (SEQ ID NO:23) show a sequence for the approximately 4.7 kbp PCR fragment shown in Figure 1 from parvovirus B19 clone 2-B6. The sequence is a 4677 nucleotide fragment corresponding to nucleotide positions 217-4893 of Shade et al., *J. Virol.* (1986) 58:921-936. The sequence depicted contains the parvovirus B19 full-length open reading frame which encodes NS1, VP1 and VP2, plus additional 5' and 3' untranslated sequences.

Figures 5A (SEQ ID NO:24) and 5B (SEQ ID NO:25) show the NS1 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B1.

Figures 6A (SEQ ID NO:26) and 6B (SEQ ID NO:27) show the VP1 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B1. Figures 7A (SEQ ID NO:28) and 7B (SEQ ID NO:29) show the VP2 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B1. Figures 8A (SEQ ID NO:30) and 8B (SEQ ID NO:31) show the NS1 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B6. Figures 9A (SEQ ID NO:32) and 9B (SEQ ID NO:33) show the VP1 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B6. Figures 10A (SEQ ID NO:34) and 10B (SEQ ID NO:35) show the VP2 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B6.

Figures 11A through 11Z (SEQ ID NOS:62-87) depict DNA sequences from various parvovirus B19 isolates which include sequences corresponding to nucleotide positions 2936-3635 of the parvovirus B19 genome described in Shade et al., *J. Virol.* (1986) 58:921-936 (the 700 bp fragment from Figure 1). Figure 11A (SEQ ID NO:62) is the corresponding sequence from isolate CH80-1; Figure 11B (SEQ ID NO:63) is the corresponding sequence from isolate CH81-3; Figure 11C (SEQ ID NO:64) is the corresponding sequence from isolate B19SCL1-4; Figure 11D (SEQ ID NO:65) is the corresponding sequence from isolate B19SCL2-1; Figure 11E (SEQ ID NO:66) is the corresponding sequence from isolate B19SCL3-1; Figure 11F (SEQ ID NO:67) is the corresponding sequence from isolate B19SCL4-3; Figure 11G (SEQ ID NO:68) is the corresponding sequence from isolate B19SCL5-2; Figure 11H (SEQ ID NO:69) is the corresponding sequence from isolate B19SCL6-2; Figure 11I (SEQ ID NO:70) is the corresponding sequence from isolate B19SCL7-3; Figure 11J (SEQ ID NO:71) is the corresponding sequence from isolate B19SCL8-2; Figure 11K (SEQ ID NO:72) is the corresponding sequence from isolate B19SCL9-1; Figure 11L (SEQ ID NO:73) is the corresponding sequence from isolate B19SCL9-9; Figure 11M (SEQ ID NO:74) is the corresponding sequence from isolate B19SCL10-2; Figure 11N (SEQ ID NO:75) is the corresponding sequence from isolate B19SCL11-1; Figure 11O (SEQ ID NO:76) is the corresponding sequence from isolate B19SCL12-1; Figure 11P (SEQ ID NO:77) is the corresponding sequence from isolate B19SCL13-3;

Figure 11Q (SEQ ID NO:78) is the corresponding sequence from isolate B19SCL14-1; Figure 11R (SEQ ID NO:79) is the corresponding sequence from isolate B19SCL15-3; Figure 11S (SEQ ID NO:80) is the corresponding sequence from isolate B19SCL16-2; Figure 11T (SEQ ID NO:81) is the corresponding sequence from isolate B19SCL17-1; Figure 11U (SEQ ID NO:82) is the corresponding sequence from isolate B19SCL18-1; Figure 11V (SEQ ID NO:83) is the corresponding sequence from isolate B19SCL19-1; Figure 11W (SEQ ID NO:84) is the corresponding sequence from isolate B19SCL20-3; Figure 11X (SEQ ID NO:85) is the corresponding sequence from isolate B19SCL21-3; Figure 11Y (SEQ ID NO:86) is the corresponding sequence from isolate B19SCL22-11; Figure 11Z (SEQ ID NO:87) is the corresponding sequence from isolate B19SCL2-14.

Figure 12 (SEQ ID NO:92) depicts an exemplary sequence from which an internal control (IC) can be derived for target capture and amplification.

Detailed Description of the Invention

The practice of the present invention will employ, unless otherwise indicated, conventional methods of chemistry, biochemistry, recombinant DNA techniques and virology, within the skill of the art. Such techniques are explained fully in the literature. See, e.g., *Fundamental Virology*, 2nd Edition, vol. I & II (B.N. Fields and D.M. Knipe, eds.); A.L. Lehninger, *Biochemistry* (Worth Publishers, Inc., current addition); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); *Methods In Enzymology* (S. Colowick and N. Kaplan eds., Academic Press, Inc.); *Oligonucleotide Synthesis* (N. Gait, ed., 1984); *A Practical Guide to Molecular Cloning* (1984).

It must be noted that, as used in this specification and the appended claims, the singular forms "a", "an" and "the" include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to "an antigen" includes a mixture of two or more antigens, and the like.

The following amino acid abbreviations are used throughout the text:

| | |
|---|---|
| Alanine: Ala (A) | Arginine: Arg (R) |
| Asparagine: Asn (N) | Aspartic acid: Asp (D) |
| Cysteine: Cys (C) | Glutamine: Gln (Q) |
| Glutamic acid: Glu (E) | Glycine: Gly (G) |
| Histidine: His (H) | Isoleucine: Ile (I) |
| Leucine: Leu (L) | Lysine: Lys (K) |
| Methionine: Met (M) | Phenylalanine: Phe (F) |
| Proline: Pro (P) | Serine: Ser (S) |
| Threonine: Thr (T) | Tryptophan: Trp (W) |
| Tyrosine: Tyr (Y) | Valine: Val (V) |

I. Definitions

In describing the present invention, the following terms will be employed, and are intended to be defined as indicated below.

The terms "polypeptide" and "protein" refer to a polymer of amino acid residues and are not limited to a minimum length of the product. Thus, peptides, oligopeptides, dimers, multimers, and the like, are included within the definition. Both full-length proteins and fragments thereof are encompassed by the definition. The terms also include postexpression modifications of the polypeptide, for example, glycosylation, acetylation, phosphorylation and the like. Furthermore, for purposes of the present invention, a "polypeptide" refers to a protein which includes modifications, such as deletions, additions and substitutions (generally conservative in nature), to the native sequence, so long as the protein maintains the desired activity. These modifications may be deliberate, as through site-directed mutagenesis, or may be accidental, such as through mutations of hosts which produce the proteins or errors due to PCR amplification.

A parvovirus B19 polypeptide is a polypeptide, as defined above, derived from a protein encoded by the B19 genome, such as from the nonstructural proteins, NS1 and NS2, as well as from the proteins which form the viral capsid, VP1

(approximately 781 amino acids in length) or VP2 (approximately 554 amino acids in length). Representative NS1, VP1 and VP2 sequences are depicted in Figures 5-10 herein. The polypeptide need not be physically derived from parvovirus B19, but may be synthetically or recombinantly produced. Moreover, the polypeptide may be derived from any of the various parvovirus B19 strains and isolates. A number of conserved and variable regions are known between these strains and isolates and, in general, the amino acid sequences of, for example, epitopes derived from these regions will have a high degree of sequence homology, e.g., amino acid sequence homology of more than 30%, preferably more than 40%, when the two sequences are aligned. Thus, for example, the term "VP1" polypeptide refers to native VP1 from any of the various parvovirus B19 strains and isolates. The complete genotypes and sequences for the above proteins of many parvovirus B19 strains and isolates are known. See, e.g., Shade et al., *J. Virol.* (1986) 58:921-936; Gallinella et al., *J. Virol. Methods* (1993) 41:203-211. Moreover, epitopes from parvovirus B19 derived from these regions are also known. See, e.g., U.S. Patent No. 5,436,127; and International Publication No. WO 91/12269.

The terms "analog" and "mutein" refer to biologically active derivatives of the reference molecule, or fragments of such derivatives, that retain desired activity, such as immunoreactivity in diagnostic assays. In general, the term "analog" refers to compounds having a native polypeptide sequence and structure with one or more amino acid additions, substitutions (generally conservative in nature) and/or deletions, relative to the native molecule, so long as the modifications do not destroy immunogenic activity. The term "mutein" refers to peptides having one or more peptide mimics ("peptoids"), such as those described in International Publication No. WO 91/04282. Preferably, the analog or mutein has at least the same immunoactivity as the native molecule. Methods for making polypeptide analogs and muteins are known in the art and are described further below.

Particularly preferred analogs include substitutions that are conservative in nature, i.e., those substitutions that take place within a family of amino acids that are related in their side chains. Specifically, amino acids are generally divided into four

families: (1) acidic -- aspartate and glutamate; (2) basic -- lysine, arginine, histidine; (3) non-polar -- alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar -- glycine, asparagine, glutamine, cysteine, serine threonine, tyrosine. Phenylalanine, tryptophan, and tyrosine are sometimes classified as aromatic amino acids. For example, it is reasonably predictable that an isolated replacement of leucine with isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar conservative replacement of an amino acid with a structurally related amino acid, will not have a major effect on the biological activity. For example, the polypeptide of interest may include up to about 5-10 conservative or non-conservative amino acid substitutions, or even up to about 15-25 conservative or non-conservative amino acid substitutions, or any integer between 5-25, so long as the desired function of the molecule remains intact. One of skill in the art may readily determine regions of the molecule of interest that can tolerate change by reference to Hopp/Woods and Kyte-Doolittle plots, well known in the art.

By "isolated" is meant, when referring to a polypeptide, that the indicated molecule is separate and discrete from the whole organism with which the molecule is found in nature or is present in the substantial absence of other biological macro-molecules of the same type. The term "isolated" with respect to a polynucleotide is a nucleic acid molecule devoid, in whole or part, of sequences normally associated with it in nature; or a sequence, as it exists in nature, but having heterologous sequences in association therewith; or a molecule disassociated from the chromosome.

A polynucleotide "derived from" or "specific for" a designated sequence refers to a polynucleotide sequence which comprises a contiguous sequence of approximately at least about 6 nucleotides, preferably at least about 8 nucleotides, more preferably at least about 10-12 nucleotides, and even more preferably at least about 15-20 nucleotides corresponding, i.e., identical or complementary to, a region of the designated nucleotide sequence. The derived polynucleotide will not necessarily be derived physically from the nucleotide sequence of interest, but may be generated in any manner, including, but not limited to, chemical synthesis, replication,

reverse transcription or transcription, which is based on the information provided by the sequence of bases in the region(s) from which the polynucleotide is derived. As such, it may represent either a sense or an antisense orientation of the original polynucleotide.

"Homology" refers to the percent similarity between two polynucleotide or two polypeptide moieties. Two DNA, or two polypeptide sequences are "substantially homologous" to each other when the sequences exhibit at least about 50% , preferably at least about 75%, more preferably at least about 80%-85%, preferably at least about 90%, and most preferably at least about 95%-98% sequence similarity over a defined length of the molecules. As used herein, substantially homologous also refers to sequences showing complete identity to the specified DNA or polypeptide sequence.

In general, "identity" refers to an exact nucleotide-to-nucleotide or amino acid-to-amino acid correspondence of two polynucleotides or polypeptide sequences, respectively. Percent identity can be determined by a direct comparison of the sequence information between two molecules by aligning the sequences, counting the exact number of matches between the two aligned sequences, dividing by the length of the shorter sequence, and multiplying the result by 100.

Readily available computer programs can be used to aid in the analysis of homology and identity, such as ALIGN, Dayhoff, M.O. in *Atlas of Protein Sequence and Structure* M.O. Dayhoff ed., 5 Suppl. 3:353-358, National biomedical Research Foundation, Washington, DC, which adapts the local homology algorithm of Smith and Waterman *Advances in Appl. Math.* 2:482-489, 1981 for peptide analysis. Programs for determining nucleotide sequence homology are available in the Wisconsin Sequence Analysis Package, Version 8 (available from Genetics Computer Group, Madison, WI) for example, the BESTFIT, FASTA and GAP programs, which also rely on the Smith and Waterman algorithm. These programs are readily utilized with the default parameters recommended by the manufacturer and described in the Wisconsin Sequence Analysis Package referred to above. For example, percent homology of a particular nucleotide sequence to a reference sequence can be

determined using the homology algorithm of Smith and Waterman with a default scoring table and a gap penalty of six nucleotide positions.

Another method of establishing percent homology in the context of the present invention is to use the MPSRCH package of programs copyrighted by the University of Edinburgh, developed by John F. Collins and Shane S. Sturrok, and distributed by IntelliGenetics, Inc. (Mountain View, CA). From this suite of packages the Smith-Waterman algorithm can be employed where default parameters are used for the scoring table (for example, gap open penalty of 12, gap extension penalty of one, and a gap of six). From the data generated the "Match" value reflects "sequence homology." Other suitable programs for calculating the percent identity or similarity between sequences are generally known in the art, for example, another alignment program is BLAST, used with default parameters. For example, BLASTN and BLASTP can be used using the following default parameters: genetic code = standard; filter = none; strand = both; cutoff = 60; expect = 10; Matrix = BLOSUM62; Descriptions = 50 sequences; sort by = HIGH SCORE; Databases = non-redundant, GenBank + EMBL + DDBJ + PDB + GenBank CDS translations + Swiss protein + Spupdate + PIR. Details of these programs can be found at the following internet address: http://www.ncbi.nlm.gov/cgi-bin/BLAST.

Alternatively, homology can be determined by hybridization of polynucleotides under conditions which form stable duplexes between homologous regions, followed by digestion with single-stranded-specific nuclease(s), and size determination of the digested fragments. DNA sequences that are substantially homologous can be identified in a Southern hybridization experiment under, for example, stringent conditions, as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Sambrook et al., *supra*; *DNA Cloning, supra*; *Nucleic Acid Hybridization, supra.*

"Operably linked" refers to an arrangement of elements wherein the components so described are configured so as to perform their desired function. Thus, a given promoter operably linked to a nucleic acid sequence is capable of effecting the transcription, and in the case of a coding sequence, the expression of the coding

sequence when the proper transcription factors, etc., are present. The promoter need not be contiguous with the nucleic acid sequence, so long as it functions to direct the transcription and/or expression thereof. Thus, for example, intervening untranslated yet transcribed sequences can be present between the promoter sequence and the coding sequence, as can transcribed introns, and the promoter sequence can still be considered "operably linked" to the coding sequence.

"Recombinant" as used herein to describe a nucleic acid molecule means a polynucleotide of genomic, cDNA, viral, semisynthetic, or synthetic origin which, by virtue of its origin or manipulation is not associated with all or a portion of the polynucleotide with which it is associated in nature. The term "recombinant" as used with respect to a protein or polypeptide means a polypeptide produced by expression of a recombinant polynucleotide. In general, the gene of interest is cloned and then expressed in transformed organisms, as described further below. The host organism expresses the foreign gene to produce the protein under expression conditions.

A "control element" refers to a polynucleotide sequence which aids in the transcription and/or translation of a nucleotide sequence to which it is linked. The term includes promoters, transcription termination sequences, upstream regulatory domains, polyadenylation signals, untranslated regions, including 5'-UTRs and 3'-UTRs and when appropriate, leader sequences and enhancers, which collectively provide for the transcription and translation of a coding sequence in a host cell.

A "promoter" as used herein is a regulatory region capable of binding a polymerase and initiating transcription of a downstream (3' direction) nucleotide sequence operably linked thereto. For purposes of the present invention, a promoter sequence includes the minimum number of bases or elements necessary to initiate transcription of a sequence of interest at levels detectable above background. Within the promoter sequence is a transcription initiation site, as well as protein binding domains (consensus sequences) responsible for the binding of RNA or DNA polymerase. For example, promoter may be a nucleic acid sequence that is recognized by a DNA-dependent RNA polymerase ("transcriptase") as a signal to bind to the nucleic acid and begin the transcription of RNA at a specific site. For

binding, such transcriptases generally require DNA which is double-stranded in the portion comprising the promoter sequence and its complement; the template portion (sequence to be transcribed) need not be double-stranded. Individual DNA-dependent RNA polymerases recognize a variety of different promoter sequences which can vary markedly in their efficiency in promoting transcription. When an RNA polymerase binds to a promoter sequence to initiate transcription, that promoter sequence is not part of the sequence transcribed. Thus, the RNA transcripts produced thereby will not include that sequence.

A control sequence "directs the transcription" of a nucleotide sequence when RNA or DNA polymerase will bind the promoter sequence and transcribe the adjacent sequence.

A "DNA-dependent DNA polymerase" is an enzyme that synthesizes a complementary DNA copy from a DNA template. Examples are DNA polymerase I from *E. coli* and bacteriophage T7 DNA polymerase. All known DNA-dependent DNA polymerases require a complementary primer to initiate synthesis. Under suitable conditions, a DNA-dependent DNA polymerase may synthesize a complementary DNA copy from an RNA template.

A "DNA-dependent RNA polymerase" or a "transcriptase" is an enzyme that synthesizes multiple RNA copies from a double-stranded or partially-double stranded DNA molecule having a (usually double-stranded) promoter sequence. The RNA molecules ("transcripts") are synthesized in the 5' to 3' direction beginning at a specific position just downstream of the promoter. Examples of transcriptases are the DNA-dependent RNA polymerase from *E. coli* and bacteriophages T7, T3, and SP6.

An "RNA-dependent DNA polymerase" or "reverse transcriptase" is an enzyme that synthesizes a complementary DNA copy from an RNA template. All known reverse transcriptases also have the ability to make a complementary DNA copy from a DNA template; thus, they are both RNA- and DNA-dependent DNA polymerases. A primer is required to initiate synthesis with both RNA and DNA templates.

"RNAse H" is an enzyme that degrades the RNA portion of an RNA:DNA duplex. These enzymes may be endonucleases or exonucleases. Most reverse transcriptase enzymes normally contain an RNAse H activity in addition to their polymerase activity. However, other sources of the RNAse H are available without an associated polymerase activity. The degradation may result in separation of RNA from a RNA:DNA complex. Alternatively, the RNAse H may simply cut the RNA at various locations such that portions of the RNA melt off or permit enzymes to unwind portions of the RNA.

The terms "polynucleotide," "oligonucleotide," "nucleic acid" and "nucleic acid molecule" are used herein to include a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, the term includes triple-, double- and single-stranded DNA, as well as triple-, double- and single-stranded RNA. It also includes modifications, such as by methylation and/or by capping, and unmodified forms of the polynucleotide. More particularly, the terms "polynucleotide," "oligonucleotide," "nucleic acid" and "nucleic acid molecule" include polydeoxyribonucleotides (containing 2-deoxy-D-ribose), polyribonucleotides (containing D-ribose), any other type of polynucleotide which is an N– or C-glycoside of a purine or pyrimidine base, and other polymers containing nonnucleotidic backbones, for example, polyamide (e.g., peptide nucleic acids (PNAs)) and polymorpholino (commercially available from the Anti-Virals, Inc., Corvallis, Oregon, as Neugene) polymers, and other synthetic sequence-specific nucleic acid polymers providing that the polymers contain nucleobases in a configuration which allows for base pairing and base stacking, such as is found in DNA and RNA. There is no intended distinction in length between the terms "polynucleotide," "oligonucleotide," "nucleic acid" and "nucleic acid molecule," and these terms will be used interchangeably. These terms refer only to the primary structure of the molecule. Thus, these terms include, for example, 3'-deoxy-2',5'-DNA, oligodeoxyribonucleotide N3' P5' phosphoramidates, 2'-O-alkyl-substituted RNA, double- and single-stranded DNA, as well as double- and single-stranded RNA, DNA:RNA hybrids, and hybrids between PNAs and DNA or RNA,

and also include known types of modifications, for example, labels which are known in the art, methylation, "caps," substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoramidates, carbamates, etc.), with negatively charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), and with positively charged linkages (e.g., aminoalklyphosphoramidates, aminoalkylphosphotriesters), those containing pendant moieties, such as, for example, proteins (including nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., alpha anomeric nucleic acids, etc.), as well as unmodified forms of the polynucleotide or oligonucleotide. In particular, DNA is deoxyribonucleic acid.

As used herein, the term "target nucleic acid region" or "target nucleic acid" denotes a nucleic acid molecule with a "target sequence" to be amplified. The target nucleic acid may be either single-stranded or double-stranded and may include other sequences besides the target sequence, which may not be amplified. The term "target sequence" refers to the particular nucleotide sequence of the target nucleic acid which is to be amplified. The target sequence may include a probe-hybridizing region contained within the target molecule with which a probe will form a stable hybrid under desired conditions. The "target sequence" may also include the complexing sequences to which the oligonucleotide primers complex and be extended using the target sequence as a template. Where the target nucleic acid is originally single-stranded, the term "target sequence" also refers to the sequence complementary to the "target sequence" as present in the target nucleic acid. If the "target nucleic acid" is originally double-stranded, the term "target sequence" refers to both the plus (+) and minus (-) strands.

The term "primer" or "oligonucleotide primer" as used herein, refers to an oligonucleotide which acts to initiate synthesis of a complementary DNA strand when placed under conditions in which synthesis of a primer extension product is induced,

i.e., in the presence of nucleotides and a polymerization-inducing agent such as a DNA or RNA polymerase and at suitable temperature, pH, metal concentration, and salt concentration. The primer is preferably single-stranded for maximum efficiency in amplification, but may alternatively be double-stranded. If double-stranded, the primer is first treated to separate its strands before being used to prepare extension products. This denaturation step is typically effected by heat, but may alternatively be carried out using alkali, followed by neutralization. Thus, a "primer" is complementary to a template, and complexes by hydrogen bonding or hybridization with the template to give a primer/template complex for initiation of synthesis by a polymerase, which is extended by the addition of covalently bonded bases linked at its 3' end complementary to the template in the process of DNA synthesis.

As used herein, the term "probe" or "oligonucleotide probe" refers to a structure comprised of a polynucleotide, as defined above, that contains a nucleic acid sequence complementary to a nucleic acid sequence present in the target nucleic acid analyte. The polynucleotide regions of probes may be composed of DNA, and/or RNA, and/or synthetic nucleotide analogs. When an "oligonucleotide probe" is to be used in a 5' nuclease assay, such as the TaqMan™ technique, the probe will contain at least one fluorescer and at least one quencher which is digested by the 5' endonuclease activity of a polymerase used in the reaction in order to detect any amplified target oligonucleotide sequences. In this context, the oligonucleotide probe will have a sufficient number of phosphodiester linkages adjacent to its 5' end so that the 5' to 3' nuclease activity employed can efficiently degrade the bound probe to separate the fluorescers and quenchers. When an oligonucleotide probe is used in the TMA technique, it will be suitably labeled, as described below.

It will be appreciated that the hybridizing sequences need not have perfect complementarity to provide stable hybrids. In many situations, stable hybrids will form where fewer than about 10% of the bases are mismatches, ignoring loops of four or more nucleotides. Accordingly, as used herein the term "complementary" refers to an oligonucleotide that forms a stable duplex with its "complement" under assay conditions, generally where there is about 90% or greater homology.

The terms "hybridize" and "hybridization" refer to the formation of complexes between nucleotide sequences which are sufficiently complementary to form complexes via Watson-Crick base pairing. Where a primer "hybridizes" with target (template), such complexes (or hybrids) are sufficiently stable to serve the priming function required by, e.g., the DNA polymerase to initiate DNA synthesis.

As used herein, the term "binding pair" refers to first and second molecules that specifically bind to each other, such as complementary polynucleotide pairs capable of forming nucleic acid duplexes. "Specific binding" of the first member of the binding pair to the second member of the binding pair in a sample is evidenced by the binding of the first member to the second member, or vice versa, with greater affinity and specificity than to other components in the sample. The binding between the members of the binding pair is typically noncovalent. Unless the context clearly indicates otherwise, the terms "affinity molecule" and "target analyte" are used herein to refer to first and second members of a binding pair, respectively.

The terms "specific-binding molecule" and "affinity molecule" are used interchangeably herein and refer to a molecule that will selectively bind, through chemical or physical means to a detectable substance present in a sample. By "selectively bind" is meant that the molecule binds preferentially to the target of interest or binds with greater affinity to the target than to other molecules. For example, a DNA molecule will bind to a substantially complementary sequence and not to unrelated sequences.

The "melting temperature" or "Tm" of double-stranded DNA is defined as the temperature at which half of the helical structure of DNA is lost due to heating or other dissociation of the hydrogen bonding between base pairs, for example, by acid or alkali treatment, or the like. The $T_m$ of a DNA molecule depends on its length and on its base composition. DNA molecules rich in GC base pairs have a higher $T_m$ than those having an abundance of AT base pairs. Separated complementary strands of DNA spontaneously reassociate or anneal to form duplex DNA when the temperature is lowered below the $T_m$. The highest rate of nucleic acid hybridization occurs approximately 25 °C below the $T_m$. The $T_m$ may be estimated using the following

relationship: $T_m = 69.3 + 0.41(GC)\%$ (Marmur et al. (1962) *J. Mol. Biol.* 5:109-118).

As used herein, a "biological sample" refers to a sample of tissue or fluid isolated from a subject, that commonly includes antibodies produced by the subject. Typical samples that include such antibodies are known in the art and include but not limited to, blood, plasma, serum, fecal matter, urine, bone marrow, bile, spinal fluid, lymph fluid, samples of the skin, secretions of the skin, respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, blood cells, organs, biopsies and also samples of *in vitro* cell culture constituents including but not limited to conditioned media resulting from the growth of cells and tissues in culture medium, e.g., recombinant cells, and cell components.

As used herein, the terms "label" and "detectable label" refer to a molecule capable of detection, including, but not limited to, radioactive isotopes, fluorescers, chemiluminescers, chromophores, enzymes, enzyme substrates, enzyme cofactors, enzyme inhibitors, chromophores, dyes, metal ions, metal sols, ligands (e.g., biotin, avidin, strepavidin or haptens) and the like. The term "fluorescer" refers to a substance or a portion thereof which is capable of exhibiting fluorescence in the detectable range.

## II. Modes of Carrying out the Invention

Before describing the present invention in detail, it is to be understood that this invention is not limited to particular formulations or process parameters as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments of the invention only, and is not intended to be limiting.

Although a number of compositions and methods similar or equivalent to those described herein can be used in the practice of the present invention, the preferred materials and methods are described herein.

As noted above, the present invention is based on the discovery of novel primers and probes and diagnostic methods for accurately detecting parvovirus B19 infection in a biological sample. The methods rely on sensitive nucleic-acid-based

detection techniques that allow identification of parvovirus B19 target nucleic acid sequences in samples containing small amounts of virus.

In particular, the inventors herein have characterized regions within the parvovirus B19 genome which are desirable targets for diagnostic tests. Primers and probes derived from these regions are extremely useful for detection of parvovirus B19 infection in biological samples.

Parvovirus B19 primers and probes described above are used in nucleic acid-based assays for the detection of human parvovirus B19 infection in biological samples.

In particular, primers and probes for use in these assays are preferably derived from the approximately 4.7 kb fragment of the parvovirus B19 genome corresponding to nucleotide positions 217-4678 of Shade et al., *J. Virol.* (1986) 58:921-936. The nucleotide sequences of this region from two different parvovirus B19 isolates are depicted in Figures 3A-3C and 4A-4C herein. As explained above, this fragment contains the NS1, VP1 and VP2 coding regions.

Particularly preferred primers and probes for use with the present assays are designed from highly conserved regions of the parvovirus B19 genome to allow detection of parvovirus B19 infection caused by a variety of isolates. As described herein, a highly conserved region of the parvovirus B19 genome is found within the 700 bp region spanning nucleotide positions 2936-3635, numbered relative to the parvovirus B19 genome described in Shade et al., *J. Virol.* (1986) 58:921-936. This region is found within the VP1 region of the genome. The sequence of this region from 21 different parvovirus B19 isolates is shown herein in Figures 2A-2U. The sequences from an additional 26 isolates are shown in Figures 11A-11Z herein. A comparison of the sequences shows that this region displays from about 98% to 99.5% sequence homology from isolate to isolate, making it a highly desirable target sequence. Also desirable for the design of primers and probes is the 370 bp region found within VP1 which spans approximately nucleotide positions 3073-3442, numbered relative to Shade et al., *J. Virol.* (1986) 58:921-936, as well as the 214 bp fragment depicted in Figure 1 which occurs within the 3' portion of the 4.7 kb

fragment and spans nucleotide positions 4728-4941, numbered relative to Shade et al., *J. Virol.* (1986) 58:921-936.

The 4.7 kbp, 700 bp and 370 bp regions are readily obtained from additional isolates using portions of the parvovirus B19 sequence found within these particular regions as primers in PCR reactions such as those described herein, as well as in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,889,818, and based on the sequences provided herein. Another method of obtaining nucleotide sequences with the desired sequences is by annealing complementary sets of overlapping synthetic oligonucleotides produced in a conventional, automated polynucleotide synthesizer, followed by ligation with an appropriate DNA ligase and amplification of the ligated nucleotide sequence via PCR. See, e.g., Jayaraman et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:4084-4088. Once the sequences have been prepared or isolated, they can be cloned into any suitable vector or replicon. Numerous cloning vectors are known to those of skill in the art, and the selection of an appropriate cloning vector is a matter of choice. Suitable vectors include, but are not limited to, plasmids, phages, transposons, cosmids, chromosomes or viruses which are capable of replication when associated with the proper control elements.

Recombinant clones are readily identified by restriction enzyme analysis and polyacryamide or agarose gel electrophresis, using techniques well known in the art, and described in the examples below.

Primers and probes for use in the assays herein are derived from these sequences and are readily synthesized by standard techniques, e.g., solid phase synthesis via phosphoramidite chemistry, as disclosed in U.S. Patent Nos. 4,458,066 and 4,415,732; Beaucage et al. (1992) *Tetrahedron* 48:2223-2311; and Applied Biosystems User Bulletin No. 13 (1 April 1987). Other chemical synthesis methods include, for example, the phosphotriester method described by Narang et al., *Meth. Enzymol.* (1979) 68:90 and the phosphodiester method disclosed by Brown et al., *Meth. Enzymol.* (1979) 68:109. Poly(A) or poly(C), or other non-complementary nucleotide extensions may be incorporated into probes using these same methods. Hexaethylene oxide extensions may be coupled to probes by methods known in the

art. Cload et al. (1991) *J. Am. Chem. Soc.* 113:6324-6326; U.S. Patent No. 4,914,210 to Levenson et al.; Durand et al. (1990) *Nucleic Acids Res.* 18:6353-6359; and Horn et al. (1986) *Tet. Lett.* 27:4705-4708. Typically, the primer sequences are in the range of between 10-75 nucleotides in length, such as 15-60, 20-40 and so on, more typically in the range of between 18-40 nucleotides long, and any length between the stated ranges. The typical probe is in the range of between 10-50 nucleotides long, such as 15-40, 18-30, and so on, and any length between the stated ranges.

Moreover, the probes may be coupled to labels for detection. There are several means known for derivatizing oligonucleotides with reactive functionalities which permit the addition of a label. For example, several approaches are available for biotinylating probes so that radioactive, fluorescent, chemiluminescent, enzymatic, or electron dense labels can be attached via avidin. See, e.g., Broken et al., *Nucl. Acids Res.* (1978) 5:363-384 which discloses the use of ferritin-avidin-biotin labels; and Chollet et al. *Nucl. Acids Res.* (1985) 13:1529-1541 which discloses biotinylation of the 5' termini of oligonucleotides via an aminoalkylphosphoramide linker arm. Several methods are also available for synthesizing amino-derivatized oligonucleotides which are readily labeled by fluorescent or other types of compounds derivatized by amino-reactive groups, such as isothiocyanate, N-hydroxysuccinimide, or the like, see, e.g., Connolly (1987) *Nucl. Acids Res.* 15:3131-3139, Gibson et al. (1987) *Nucl. Acids Res.* 15:6455-6467 and U.S. Patent No. 4,605,735 to Miyoshi et al. Methods are also available for synthesizing sulfhydryl-derivatized oligonucleotides which can be reacted with thiol-specific labels, see, e.g., U.S. Patent No. 4,757,141 to Fung et al., Connolly et al. (1985) *Nucl. Acids Res.* 13:4485-4502 and Spoat et al. (1987) *Nucl. Acids Res.* 15:4837-4848. A comprehensive review of methodologies for labeling DNA fragments is provided in Matthews et al., *Anal. Biochem.* (1988) 169:1-25.

For example, probes may be fluorescently labeled by linking a fluorescent molecule to the non-ligating terminus of the probe. Guidance for selecting appropriate fluorescent labels can be found in Smith et al., *Meth. Enzymol.* (1987) 155:260-301; Karger et al., *Nucl. Acids Res.* (1991) 19:4955-4962; Haugland (1989)

*Handbook of Fluorescent Probes and Research Chemicals* (Molecular Probes, Inc., Eugene, OR). Preferred fluorescent labels include fluorescein and derivatives thereof, such as disclosed in U.S. Patent No. 4,318,846 and Lee et al., *Cytometry* (1989) 10:151-164, and 6-FAM, JOE, TAMRA, ROX, HEX-1, HEX-2, ZOE, TET-1 or NAN-2, and the like.

Additionally, probes can be labeled with an acridinium ester (AE) using the techniques described below. Current technologies allow the AE label to be placed at any location within the probe. See, e.g., Nelson et al. (1995) "Detection of Acridinium Esters by Chemiluminescence" in *Nonisotopic Probing, Blotting and Sequencing*, Kricka L.J.(ed) Academic Press, San Diego, CA; Nelson et al. (1994) "Application of the Hybridization Protection Assay (HPA) to PCR" in *The Polymerase Chain Reaction*, Mullis et al. (eds.) Birkhauser, Boston, MA; Weeks et al., *Clin. Chem.* (1983) 29:1474-1479; Berry et al., *Clin. Chem.* (1988) 34:2087-2090. An AE molecule can be directly attached to the probe using non-nucleotide-based linker arm chemistry that allows placement of the label at any location within the probe. See, e.g., U.S. Patent Nos. 5,585,481 and 5,185,439.

In certain embodiments, an internal control (IC) or an internal standard is added to serve as a control for target capture and amplification. Preferably, the IC includes a sequence that differs from the target sequence, is capable of hybridizing with the probe sequences used for separating the oligonucleotides specific for the organism from the sample, and is capable of amplification. The use of the IC permits the control of the separation process, the amplification process, and the detection system, and permits the monitoring of assay performance and quantification for the sample(s). A representative sequence from which the IC can be obtained is shown in Figure 12. The IC can be included at any suitable point, for example, in the lysis buffer. In one embodiment, the IC comprises M13 ssDNA containing a nucleotide sequence from a parvovirus B19 and a unique sequence that hybridizes with the probe, for example, comprising sequences from the VP1 region, where the target sequence is modified by substituting or deleting 5-20 bases or more, preferably 5-15 bases, such as 5, 10 or 15, bases or any number within these ranges. The substituted

or deleted bases preferably occur over the entire length of the target sequence such that only 2 or 3 consecutive sequences are replaced. Thus for example, if the target sequence is CTACTTGCTGCGGGAGAAAAACACCT (SEQ ID NO:91), then the sequence may be substituted with, for example, AGCTAGACCTGCATGTCACTG (SEQ ID NO:90) in the IC.

The solid support may additionally include probes specific to the internal standard (IC probe), thereby facilitating capture when using the IC probe. The IC probe can optionally be coupled with a detectable label that is different from the detectable label for the target sequence. In embodiments where the detectable label is a fluorophore, the IC can be quantified spectrophotometrically and by limit of detection studies. Typically, the copy number of the IC which does not interfere with the target detection is determined by titrating the IC with a fixed IU of target, preferably at the lower end, and a standard curve is generated by diluting a sample of internationally accepted IU. For parvovirus B19 quantitation, an eight member panel of 8000 IU - 125 IU can be used.

In another embodiment, an IC, as described herein, is combined with RNA isolated from the sample according to standard techniques known to those of skill in the art, and described herein. The RNA is then reverse-transcribed using a reverse transcriptase to provide copy DNA. The cDNA sequences can be optionally amplified (e.g., by PCR) using labeled primers. The amplification products are separated, typically by electrophoresis, and the amount of radioactivity (proportional to the amount of amplified product) is determined. The amount of mRNA in the sample is then calculated by comparison with the signal produced by the known standards.

The primers and probes described above may be used in polymerase chain reaction (PCR)-based techniques to detect parvovirus B19 infection in biological samples. PCR is a technique for amplifying a desired target nucleic acid sequence contained in a nucleic acid molecule or mixture of molecules. In PCR, a pair of primers is employed in excess to hybridize to the complementary strands of the target nucleic acid. The primers are each extended by a polymerase using the target nucleic

acid as a template. The extension products become target sequences themselves after dissociation from the original target strand. New primers are then hybridized and extended by a polymerase, and the cycle is repeated to geometrically increase the number of target sequence molecules. The PCR method for amplifying target nucleic acid sequences in a sample is well known in the art and has been described in, e.g., Innis et al. (eds.) *PCR Protocols* (Academic Press, NY 1990); Taylor (1991) *Polymerase chain reaction: basic principles and automation,* in *PCR: A Practical Approach*, McPherson et al. (eds.) IRL Press, Oxford; Saiki et al. (1986) *Nature* 324:163; as well as in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,889,818.

In particular, PCR uses relatively short oligonucleotide primers which flank the target nucleotide sequence to be amplified, oriented such that their 3' ends face each other, each primer extending toward the other. The polynucleotide sample is extracted and denatured, preferably by heat, and hybridized with first and second primers which are present in molar excess. Polymerization is catalyzed in the presence of the four deoxyribonucleotide triphosphates (dNTPs -- dATP, dGTP, dCTP and dTTP) using a primer- and template-dependent polynucleotide polymerizing agent, such as any enzyme capable of producing primer extension products, for example, *E. coli* DNA polymerase I, Klenow fragment of DNA polymerase I, T4 DNA polymerase, thermostable DNA polymerases isolated from *Thermus aquaticus* (*Taq*), available from a variety of sources (for example, Perkin Elmer), *Thermus thermophilus* (United States Biochemicals), *Bacillus stereothermophilus* (Bio-Rad), or *Thermococcus litoralis* ("Vent" polymerase, New England Biolabs). This results in two "long products" which contain the respective primers at their 5' ends covalently linked to the newly synthesized complements of the original strands. The reaction mixture is then returned to polymerizing conditions, e.g., by lowering the temperature, inactivating a denaturing agent, or adding more polymerase, and a second cycle is initiated. The second cycle provides the two original strands, the two long products from the first cycle, two new long products replicated from the original strands, and two "short products" replicated from the long products. The short products have the sequence of the target sequence with a primer

at each end. On each additional cycle, an additional two long products are produced, and a number of short products equal to the number of long and short products remaining at the end of the previous cycle. Thus, the number of short products containing the target sequence grow exponentially with each cycle. Preferably, PCR is carried out with a commercially available thermal cycler, e.g., Perkin Elmer.

RNAs may be amplified by reverse transcribing the mRNA into cDNA, and then performing PCR (RT-PCR), as described above. Alternatively, a single enzyme may be used for both steps as described in U.S. Patent No. 5,322,770. mRNA may also be reverse transcribed into cDNA, followed by asymmetric gap ligase chain reaction (RT-AGLCR) as described by Marshall et al. (1994) *PCR Meth. App.* 4:80-84.

The fluorogenic 5' nuclease assay, known as the TaqMan™ assay (Perkin-Elmer), is a powerful and versatile PCR-based detection system for nucleic acid targets. Hence, primers and probes derived from regions of the parvovirus B19 genome described herein can be used in TaqMan™ analyses to detect the presence of infection in a biological sample. Analysis is performed in conjunction with thermal cycling by monitoring the generation of fluorescence signals. The assay system dispenses with the need for gel electrophoretic analysis, and has the capability to generate quantitative data allowing the determination of target copy numbers.

The fluorogenic 5' nuclease assay is conveniently performed using, for example, AmpliTaq Gold™ DNA polymerase, which has endogenous 5' nuclease activity, to digest an internal oligonucleotide probe labeled with both a fluorescent reporter dye and a quencher (see, Holland et al., *Proc. Natl. Acad.Sci. USA* (1991) 88:7276-7280; and Lee et al., *Nucl. Acids Res.* (1993) 21:3761-3766). Assay results are detected by measuring changes in fluorescence that occur during the amplification cycle as the fluorescent probe is digested, uncoupling the dye and quencher labels and causing an increase in the fluorescent signal that is proportional to the amplification of target DNA.

The amplification products can be detected in solution or using solid supports. In this method, the TaqMan™ probe is designed to hybridize to a target sequence

within the desired PCR product. The 5' end of the TaqMan™ probe contains a fluorescent reporter dye. The 3' end of the probe is blocked to prevent probe extension and contains a dye that will quench the fluorescence of the 5' fluorophore. During subsequent amplification, the 5' fluorescent label is cleaved off if a polymerase with 5' exonuclease activity is present in the reaction. Excision of the 5' fluorophore results in an increase in fluorescence which can be detected.

In particular, the oligonucleotide probe is constructed such that the probe exists in at least one single-stranded conformation when unhybridized where the quencher molecule is near enough to the reporter molecule to quench the fluorescence of the reporter molecule. The oligonucleotide probe also exists in at least one conformation when hybridized to a target polynucleotide such that the quencher molecule is not positioned close enough to the reporter molecule to quench the fluorescence of the reporter molecule. By adopting these hybridized and unhybridized conformations, the reporter molecule and quencher molecule on the probe exhibit different fluorescence signal intensities when the probe is hybridized and unhybridized. As a result, it is possible to determine whether the probe is hybridized or unhybridized based on a change in the fluorescence intensity of the reporter molecule, the quencher molecule, or a combination thereof. In addition, because the probe can be designed such that the quencher molecule quenches the reporter molecule when the probe is not hybridized, the probe can be designed such that the reporter molecule exhibits limited fluorescence unless the probe is either hybridized or digested.

Accordingly, the present invention relates to methods for amplifying a target parvovirus B19 nucleotide sequence using a nucleic acid polymerase having 5' to 3' nuclease activity, one or more primers capable of hybridizing to the target B19 sequence, and an oligonucleotide probe capable of hybridizing to the target B19 sequence 3' relative to the primer. During amplification, the polymerase digests the oligonucleotide probe when it is hybridized to the target sequence, thereby separating the reporter molecule from the quencher molecule. As the amplification is conducted, the fluorescence of the reporter molecule is monitored, with fluorescenee

corresponding to the occurrence of nucleic acid amplification. The reporter molecule is preferably a fluorescein dye and the quencher molecule is preferably a rhodamine dye.

While the length of the primers and probes can vary, the probe sequences are selected such that they have a lower melt temperature than the primer sequences. Hence, the primer sequences are generally longer than the probe sequences. Typically, the primer sequences are in the range of between 10-75 nucleotides long, more typically in the range of 20-45. The typical probe is in the range of between 10-50 nucleotides long, more typically 15-40 nucleotides in length.

If a solid support is used, the oligonucleotide probe may be attached to the solid support in a variety of manners. For example, the probe may be attached to the solid support by attachment of the 3' or 5' terminal nucleotide of the probe to the solid support. More preferably, the probe is attached to the solid support by a linker which serves to distance the probe from the solid support. The linker is usually at least 15-30 atoms in length, more preferably at least 15-50 atoms in length. The required length of the linker will depend on the particular solid support used. For example, a six atom linker is generally sufficient when high cross-linked polystyrene is used as the solid support.

A wide variety of linkers are known in the art which may be used to attach the oligonucleotide probe to the solid support. The linker may be formed of any compound which does not significantly interfere with the hybridization of the target sequence to the probe attached to the solid support. The linker may be formed of a homopolymeric oligonucleotide which can be readily added on to the linker by automated synthesis. Alternatively, polymers such as functionalized polyethylene glycol can be used as the linker. Such polymers are preferred over homopolymeric oligonucleotides because they do not significantly interfere with the hybridization of probe to the target oligonucleotide. Polyethylene glycol is particularly preferred.

The linkages between the solid support, the linker and the probe are preferably not cleaved during removal of base protecting groups under basic conditions at high temperature. Examples of preferred linkages include carbamate and amide linkages.

Examples of preferred types of solid supports for immobilization of the oligonucleotide probe include controlled pore glass, glass plates, polystyrene, avidin-coated polystyrene beads, cellulose, nylon, acrylamide gel and activated dextran.

For a detailed description of the TaqMan™ assay, reagents and conditions for use therein, see, e.g., Holland et al., *Proc. Natl. Acad. Sci, U.S.A.* (1991) 88:7276-7280; U.S. Patent Nos. 5,538,848, 5,723,591, and 5,876,930.

The parvovirus B19 sequences described herein may also be used as a basis for transcription-mediated amplification (TMA) assays. TMA provides a method of identifying target nucleic acid sequences present in very small amounts in a biological sample. Such sequences may be difficult or impossible to detect using direct assay methods. In particular, TMA is an isothemal, autocatalytic nucleic acid target amplification system that can provide more than a billion RNA copies of a target sequence. The assay can be done qualitatively, to accurately detect the presence or absence of the target sequence in a biological sample. The assay can also provide a quantitative measure of the amount of target sequence over a concentration range of several orders of magnitude. TMA provides a method for autocatalytically synthesizing multiple copies of a target nucleic acid sequence without repetitive manipulation of reaction conditions such as temperature, ionic strength and pH.

Generally, TMA includes the following steps: (a) isolating nucleic acid, including RNA, from the biological sample of interest suspected of being infected with parvovirus B19; and (b) combining into a reaction mixture (i) the isolated nucleic acid, (ii) first and second oligonucleotide primers, the first primer having a complexing sequence sufficiently complementary to the 3' terminal portion of an RNA target sequence, if present (for example the (+) strand), to complex therewith, and the second primer having a complexing sequence sufficiently complementary to the 3' terminal portion of the target sequence of its complement (for example, the (-) strand) to complex therewith, wherein the first oligonucleotide further comprises a sequence 5' to the complexing sequence which includes a promoter, (iii) a reverse transcriptase or RNA and DNA dependent DNA polymerases, (iv) an enzyme activity which selectively degrades the RNA strand of an RNA-DNA complex (such as an

RNAse H) and (v) an RNA polymerase which recognizes the promoter.

The components of the reaction mixture may be combined stepwise or at once. The reaction mixture is incubated under conditions whereby an oligonucleotide/target sequence is formed, including DNA priming and nucleic acid synthesizing conditions (including ribonucleotide triphosphates and deoxyribonucleotide triphosphates) for a period of time sufficient to provide multiple copies of the target sequence. The reaction advantageously takes place under conditions suitable for maintaining the stability of reaction components such as the component enzymes and without requiring modification or manipulation of reaction conditions during the course of the amplification reaction. Accordingly, the reaction may take place under conditions that are substantially isothermal and include substantially constant ionic strength and pH. The reaction conveniently does not require a denaturation step to separate the RNA-DNA complex produced by the first DNA extension reaction.

Suitable DNA polymerases include reverse transcriptases, such as avian myeloblastosis virus (AMV) reverse transcriptase (available from, e.g., Seikagaku America, Inc.) and Moloney murine leukemia virus (MMLV) reverse transcriptase (available from, e.g., Bethesda Research Laboratories).

Promoters or promoter sequences suitable for incorporation in the primers are nucleic acid sequences (either naturally occurring, produced synthetically or a product of a restriction digest) that are specifically recognized by an RNA polymerase that recognizes and binds to that sequence and initiates the process of transcription whereby RNA transcripts are produced. The sequence may optionally include nucleotide bases extending beyond the actual recognition site for the RNA polymerase which may impart added stability or susceptibility to degradation processes or increased transcription efficiency. Examples of useful promoters include those which are recognized by certain bacteriophage polymerases such as those from bacteriophage T3, T7 or SP6, or a promoter from *E. coli*. These RNA polymerases are readily available from commercial sources, such as New England Biolabs and Epicentre.

Some of the reverse transcriptases suitable for use in the methods herein have

an RNAse H activity, such as AMV reverse transcriptase. It may, however, be preferable to add exogenous RNAse H, such as *E. coli* RNAse H, even when AMV reverse transcriptase is used. RNAse H is readily available from, e.g., Bethesda Research Laboratories.

The RNA transcripts produced by these methods may serve as templates to produce additional copies of the target sequence through the above-described mechanisms. The system is autocatalytic and amplification occurs autocatalytically without the need for repeatedly modifying or changing reaction conditions such as temperature, pH, ionic strength or the like.

Detection may be done using a wide variety of methods, including direct sequencing, hybridization with sequence-specific oligomers, gel electrophoresis and mass spectrometry. these methods can use heterogeneous or homogeneous formats, isotopic or nonisotopic labels, as well as no labels at all.

One preferable method of detection is the use of target sequence-specific oligonucleotide probes, derived from the 4.7 kbp, 700 bp, 370 bp and 214 bp fragments described above. The probes may be used in hybridization protection assays (HPA). In this embodiment, the probes are conveniently labeled with acridinium ester (AE), a highly chemiluminescent molecule. See, e.g., Nelson et al. (1995) "Detection of Acridinium Esters by Chemiluminescence" in *Nonisotopic Probing, Blotting and Sequencing*, Kricka L.J.(ed) Academic Press, San Diego, CA; Nelson et al. (1994) "Application of the Hybridization Protection Assay (HPA) to PCR" in *The Polymerase Chain Reaction*, Mullis et al. (eds.) Birkhauser, Boston, MA; Weeks et al., *Clin. Chem.* (1983) 29:1474-1479; Berry et al., *Clin. Chem.* (1988) 34:2087-2090. One AE molecule is directly attached to the probe using a non-nucleotide-based linker arm chemistry that allows placement of the label at any location within the probe. See, e.g., U.S. Patent Nos. 5,585,481 and 5,185,439. Chemiluminescence is triggered by reaction with alkaline hydrogen peroxide which yields an excited N-methyl acridone that subsequently collapses to ground state with the emission of a photon. Additionally, AE causes ester hydrolysis which yields the nonchemiluminescent –methyl acridinium carboxylic acid.

When the AE molecule is covalently attached to a nucleic acid probe, hydrolysis is rapid under mildly alkaline conditions. When the AE-labeled probe is exactly complementary to the target nucleic acid, the rate of AE hydrolysis is greatly reduced. Thus, hybridized and unhybridized AE-labeled probe can be detected directly in solution, without the need for physical separation.

HPA generally consists of the following steps: (a) the AE-labeled probe is hybridized with the target nucleic acid in solution for about 15 to about 30 minutes. A mild alkaline solution is then added and AE coupled to the unhybridized probe is hydrolyzed. This reaction takes approximately 5 to 10 minutes. The remaining hybrid-associated AE is detected as a measure of the amount of target present. This step takes approximately 2 to 5 seconds. Preferably, the differential hydrolysis step is conducted at the same temperature as the hybridization step, typically at 50 to 70 °C. Alternatively, a second differential hydrolysis step may be conducted at room temperature. This allows elevated pHs to be used, for example in the range of 10-11, which yields larger differences in the rate of hydrolysis between hybridized and unhybridized AE-labeled probe. HPA is described in detail in, e.g., U.S. Patent Nos. 6,004,745; 5,948,899; and 5,283,174.

TMA is described in detail in, e.g., U.S. Patent No. 5,399,491. In one example of a typical assay, an isolated nucleic acid sample, suspected of containing a parvovirus B19 target sequence, is mixed with a buffer concentrate containing the buffer, salts, magnesium, nucleotide triphosphates, primers, dithiothreitol, and spermidine. The reaction is optionally incubated at about 100 °C for approximately two minutes to denature any secondary structure. After cooling to room temperature, reverse transcriptase, RNA polymerase, and RNAse H are added and the mixture is incubated for two to four hours at 37 °C. The reaction can then be assayed by denaturing the product, adding a probe solution, incubating 20 minutes at 60 °C, adding a solution to selectively hydrolyze the unhybridized probe, incubating the reaction six minutes at 60 °C, and measuring the remaining chemiluminescence in a luminometer.

The oligonucleotide molecules of the present invention may also be used in

nucleic acid sequence-based amplification (NASBA). This method is a promoter-directed, enzymatic process that induces *in vitro* continuous, homogeneous and isothermal amplification of a specific nucleic acid to provide RNA copies of the nucleic acid. The reagents for conducting NASBA include a first DNA primer with a 5' tail comprising a promoter, a second DNA primer, reverse transcriptase, RNAse-H, T7 RNA polymerase, NTP's and dNTP's. Using NASBA, large amounts of single-stranded RNA are generated from either single-stranded RNA or DNA, or double-stranded DNA. When RNA is to be amplified, the ssRNA serves as a template for the synthesis of a first DNA strand by elongation of a first primer containing an RNA polymerase recognition site. This DNA strand in turn serves as the template for the synthesis of a second, complementary, DNA strand by elongation of a second primer, resulting in a double- stranded active RNA-polymerase promoter site, and the second DNA strand serves as a template for the synthesis of large amounts of the first template, the ssRNA, with the aid of a RNA polymerase. The NASBA technique is known in the art and described in, e.g., European Patent 329,822, International Patent Application No. WO 91/02814, and U.S. Patent Nos. 6,063,603, 5,554,517 and 5,409,818.

The parvovirus B19 sequences described herein are also useful in nucleic acid hybridization and amplification techniques that utilize branched DNA molecules. In a basic nucleic acid hybridization assay, single-stranded analyte nucleic acid is hybridized to a labeled single-stranded nucleic acid probe and resulting labeled duplexes are detected. 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. One method for amplifying the signal uses amplification multimers that are polynucleotides with a first segment that hybridizes specifically to the analyte nucleic acid or a strand of nucleic acid bound to the analyte and iterations of a second segment that hybridizes specifically to a labeled probe. The amplification is theoretically proportional to the number of iterations of the second segment. The multimers may be either linear or branched. Two general types of branched multimers are useful in these techniques: forked and combed.-Methods for

making and using branched nucleic acid molecules are known in the art and described in, e.g., U.S. Patent No. 5,849,481.

In another aspect of the invention, two or more of the tests described above are performed to confirm the presence of the organism. For example, if the first test used the transcription mediated amplification (TMA) to amplify the nucleic acids for detection, then an alternative nucleic acid testing (NAT) assay is performed, for example, by using PCR amplification, RT PCR, and the like, as described herein. Thus, parvovirus B19 can be specifically and selectively detected even when the sample contains other organisms, such as HIV, and Hepatitis B virus, for example.

As is readily apparent, design of the assays described herein are subject to a great deal of variation, and many formats are known in the art. The above descriptions are merely provided as guidance and one of skill in the art can readily modify the described protocols, using techniques well known in the art.

The above-described assay reagents, including the primers, probes, solid support with bound probes, as well as other detection reagents, can be provided in kits, with suitable instructions and other necessary reagents, in order to conduct the assays as described above. The kit will normally contain in separate containers the combination of primers and probes (either already bound to a solid matrix or separate with reagents for binding them to the matrix), control formulations (positive and/or negative), labeled reagents when the assay format requires same and signal generating reagents (e.g., enzyme substrate) if the label does not generate a signal directly. Instructions (e.g., written, tape, VCR, CD-ROM, etc.) for carrying out the assay usually will be included in the kit. The kit can also contain, depending on the particular assay used, other packaged reagents and materials (i.e. wash buffers and the like). Standard assays, such as those described above, can be conducted using these kits.

III. Experimental

Below are examples of specific embodiments for carrying out the present invention. The examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

Efforts have been made to ensure accuracy with respect to numbers used (e.g., amounts, temperatures, etc.), but some experimental error and deviation should, of course, be allowed for.

In the following examples, enzymes were purchased from commercial sources, and used according to the manufacturers' directions. Nitrocellulose filters and the like were also purchased from commercial sources.

In the isolation of DNA fragments, except where noted, all DNA manipulations were done according to standard procedures. See, Sambrook et al., *supra*. Restriction enzymes, $T_4$ DNA ligase, *E. coli*, DNA polymerase I, Klenow fragment, and other biological reagents can be purchased from commercial suppliers and used according to the manufacturers' directions. Double stranded DNA fragments were separated on agarose gels.

Example 1

Parvovirus B19 Nucleic Acid Extraction for PCR

Human serum samples that had previously tested positive for human parvovirus B19 by either IgM or PCR tests were obtained from commercial sources and used to isolate DNA for subsequent PCR experiments. Samples were stored at -80 °C until used.

DNA was extracted from 0.2 mL of serum using the QIAamp DNA Blood Mini Kit (QIAGEN, Valencia, CA) following the manufacturer's specifications with the following considerations. Carrier DNA was added to the lysis buffer to enhance nucleic acid binding and yield. In particular, an amount of 5.6 μg per sample of poly-adenylic acid 5' (Sigma, St. Louis, MO) or poly-dA (Roche, Indianapolis, IN) was added. Additionally, parvovirus B19 DNA was eluted with 200 μL of buffer AE (Qiagen) instead of water.

Example 2

Detection of Parvovirus B19 Nucleic Acid-Positive Samples by PCR

Two different PCR procedures were used to amplify parvovirus B19 fragments. One method, described in detail below, was used to amplify fragments of approximately 700 bp, 370 bp and 214 bp (see, Figure 1). High Fidelity Expand PCR (Roche) was used to amplify fragments of approximately 4.7 kb. The approximately 700 bp fragment corresponds to nucleotide positions 2936-3635 of the parvovirus B19 genome described in Shade et al., *J. Virol.* (1986) 58:921-936. The approximately 370 bp occurs within the 700 bp fragment at nucleotide positions 3073-3442. The approximately 4.7 kb fragment is a 4677 nucleotide fragment corresponding to nucleotide positions 217-4893 of Shade et al., *J. Virol.* (1986) 58:921-936.

In order to amplify the B19 fragments of approximately 700 bp, 370 bp and 214 bp, the primers shown in Table 1 were used.

**Table 1**

| Primer region | Sequence | PCR product | Genomic |
|---|---|---|---|
| VP-5 | AGGAAGTTTGCCGGAAGTTC (SEQ ID NO:36) | 370 bp | VP1 |
| VP-3 | GTGCTGAAACTCTAAAGGTG (SEQ ID NO:37) | 370bp | VP1 |
| VP2-5 | GACATGGATATGAAAAGCCTGAAG (SEQ ID NO:38) | 214 bp | VP1/VP2 |
| VP2-3 | GTTGTTCATATCTGGTTAAGTACT (SEQ ID NO:39) | 214 bp | VP1/VP2 |
| K-1sp | ATAAATCCATATACTCATT (SEQ ID NO:40) | 700 bp | VP1/VP2 |
| K-2sp | CTAAAGTATCCTGACCTTG (SEQ ID NO:41) | 700 bp | VP1/VP2 |

For this experiment, PCR was performed in a final volume of 100 μL using 2 μL of purified parvovirus B19 DNA (purified as described above), 0.2 mM of each deoxy nucleotide triphosphate and 1.25 units of Pfu DNA polymerase (Stratagene, La Jolla, CA). The amplification profile involved denaturation at 94 °C for 2 min., primer annealing at 37 °C for 3 min. and extension at 72 °C for 3 min. for 35 cycles. A 3-min. preincubation at 94 °C to ensure initial denaturation and a final 7-min. incubation at 72 °C to ensure the full extension of fragments preceded and followed, respectively, the 35 PCR cycles. PCR products were electrophoresed on 7% polyacrylamide gels, stained with ethidium bromide and visualized under an UV source. Purification of amplified fragments was carried out using the QiaQuick PCR purification kit (QIAGEN).

Nested PCR to amplify the 370 bp B19 fragment was performed when the 700 bp band was not visualized on the polyacrylamide gels. The 700 bp DNA material was used for the nested PCR using primers shown in Table 1.

High Fidelity Expand PCR (Roche) was used to amplify the parvovirus B19 fragment of 4.7 kb as follows. The High Fidelity Expand PCR kit (Roche) and primers Hicks-5 (5'CCCGCCTTATGCAAATGGGCAG3') (SEQ ID NO:42) and Hicks-3 (5'TTGTGTTAGGCTGTCTTATAGG3') (SEQ ID NO:43) were used following the vendor's recommendations. Amplification conditions were 94 °C for 1 min., 50 °C for 2 min. and 68 °C for 4 min. for 35 or 45 cycles. A pre-incubation at 94 °C for 2 min. and a post incubation at 75 °C for 7 min. were also included. The PCR products were separated on 1% agarose gels and purified using the PCR Purification kit (Promega, Madison, WI).

## Example 3

### Cloning of Parvovirus B19 DNA Fragments

The PCR fragments were cloned into TOPO-TA vectors (Invitrogen, Carlsbad, CA). Cloning into these vectors is highly facilitated when the amplified DNA contains a single deoxyadenosine (A) at its 3' end. Accordingly, a catalytic reaction to add the 3' (A) overhead was used. The reaction mix contained 1.25 mM of dATP, 0.5 units of Taq polymerase (Perkin Elmer, Boston, MA) and proceeded at 72 °C for 15 min.

PCR fragments were cloned into the pCR2.1-TOPO vector using Invitrogen's TA cloning kit (TOPO™ TA Cloning® Kit with One Shot TOP10 Electrocompetent Cells) following the manufacturer's specifications. Bacterial cells were incubated at 37 °C on Luria Broth plates containing ampicillin at 100 µg/ml, 0.66 mM IPTG and 0.033% X-Gal. A number of white colonies were inoculated in 4 mL of Luria-Broth ampicillin (100 µg/ml ) and incubated overnight at 37 °C with shaking. Three mL of the overnight cultures were used to prepare plasmid DNA using the QIAprep Miniprep kit (QIAGEN). Recombinant clones were identified by restriction enzyme

analysis with *Eco*RI (New England and Biolabs) and 7% polyacryamide or 1% agarose gel electrophresis as described above.

In order to determine the DNA sequences of the clones, large amounts of plasmids from recombinant clones were prepared as above and the DNA suspended in TE (10 mM Tris-HCl, pH 8.0, 1 mM EDTA) at 0.2 mg/ml. Nucleotide sequence determination of the parvovirus B19 fragments was performed using an Applied Biosystems Model 373 (or Model 377) DNA Sequencer system.

Figures 2A through 2U (SEQ ID NOS:1-21) depict DNA sequences from 21 parvovirus B19 isolates, purified, amplified and sequenced as described above, which correspond to nucleotide positions 2936-3635 of the parvovirus B19 genome described in Shade et al., *J. Virol.* (1986) 58:921-936 (the 700 bp fragment from Figure 1 and described above). Figure 2A (SEQ ID NO:1) is the sequence from isolate CH47-26; Figure 2B (SEQ ID NO:2) is the sequence from isolate CH48-29; Figure 2C (SEQ ID NO:3) is the sequence from isolate CH33-2; Figure 2D (SEQ ID NO:4) is the sequence from isolate CH33-3; Figure 2E (SEQ ID NO:5) is the sequence from isolate CH33-4; Figure 2F (SEQ ID NO:6) is the sequence from isolate CH42-7; Figure 2G (SEQ ID NO:7) is the sequence from isolate CH42-18; Figure 2H (SEQ ID NO:8) is the sequence from isolate CH42-19; Figure 2I (SEQ ID NO:9) is the sequence from isolate CH46-23; Figure 2J (SEQ ID NO:10) is the sequence from isolate CH1-1; Figure 2K (SEQ ID NO:11) is the sequence from isolate CH1-6; Figure 2L (SEQ ID NO:12) is the sequence from isolate CH2-8; Figure 2M (SEQ ID NO:13) is the sequence from isolate CH2-10; Figure 2N (SEQ ID NO:14) is the sequence from isolate CH2-11C; Figure 2O (SEQ ID NO:15) is the sequence from isolate CH5-13; Figure 2P (SEQ ID NO:16) is the sequence from isolate CH7-22; Figure 2Q (SEQ ID NO:17) is the sequence from isolate CH13-27; Figure 2R (SEQ ID NO:18) is the sequence from isolate CH14-33; Figure 2S (SEQ ID NO:19) is the sequence from isolate CH62-2; Figure 2T (SEQ ID NO:20) is the sequence from isolate CH64-2; and Figure 2U (SEQ ID NO:21) is the sequence from isolate CH67-2.

Figures 11A through 11Z (SEQ ID NOS:62-87) depict DNA sequences

from an additional 26 parvovirus B19 isolates, purified, amplified and sequenced as described above, which correspond to nucleotide positions 2936-3635 of the parvovirus B19 genome described in Shade et al., *J. Virol.* (1986) 58:921-936 (the 700 bp fragment from Figure 1 and described above). Figure 11A (SEQ ID NO:62) is the sequence from isolate CH80-1; Figure 11B (SEQ ID NO:63) is the sequence from isolate CH81-3; Figure 11C (SEQ ID NO:64) is the sequence from isolate B19SCL1-4; Figure 11D (SEQ ID NO:65) is the sequence from isolate B19SCL2-1; Figure 11E (SEQ ID NO:66) is the sequence from isolate B19SCL3-1; Figure 11F (SEQ ID NO:67) is the sequence from isolate B19SCL4-3; Figure 11G (SEQ ID NO:68) is the sequence from isolate B19SCL5-2; Figure 11H (SEQ ID NO:69) is the sequence from isolate B19SCL6-2; Figure 11I (SEQ ID NO:70) is the sequence from isolate B19SCL7-3; Figure 11J (SEQ ID NO:71) is the sequence from isolate B19SCL8-2; Figure 11K (SEQ ID NO:72) is the sequence from isolate B19SCL9-1; Figure 11L (SEQ ID NO:73) is the sequence from isolate B19SCL9-9; Figure 11M (SEQ ID NO:74) is the sequence from isolate B19SCL10-2; Figure 11N (SEQ ID NO:75) is the sequence from isolate B19SCL11-1; Figure 11O (SEQ ID NO:76) is the sequence from isolate B19SCL12-1; Figure 11P (SEQ ID NO:77) is the sequence from isolate B19SCL13-3; Figure 11Q (SEQ ID NO:78) is the sequence from isolate B19SCL14-1; Figure 11R (SEQ ID NO:79) is the sequence from isolate B19SCL15-3; Figure 11S (SEQ ID NO:80) is the sequence from isolate B19SCL16-2; Figure 11T (SEQ ID NO:81) is the sequence from isolate B19SCL17-1; Figure 11U (SEQ ID NO:82) is the sequence from isolate B19SCL18-1; Figure 11V (SEQ ID NO:83) is the sequence from isolate B19SCL19-1; Figure 11W (SEQ ID NO:84) is the sequence from isolate B19SCL20-3; Figure 11X (SEQ ID NO:85) is the sequence from isolate B19SCL21-3; Figure 11Y (SEQ ID NO:86) is the sequence from isolate B19SCL22-11; Figure 11Z (SEQ ID NO:87) is the sequence from isolate B19SCL2-14.

Sequence comparisons revealed approximately 98% to 99.5% sequence homology of this 700 bp sequence between the various isolates.

Figures 3A-3C (SEQ ID NO:22) show the sequence for the approximately 4.7 kbp PCR fragment shown in Figure 1 and described above from parvovirus B19 clone

2-B1. The sequence depicted in the figures is a 4677 nucleotide fragment corresponding to nucleotide positions 217-4893 of Shade et al., *J. Virol.* (1986) 58:921-936. The sequence depicted contains the parvovirus B19 full-length open reading frame which encodes NS1, VP1 and VP2, plus additional 5' and 3' untranslated sequences. The fragment sequenced contained an additional nucleotide in the 5' non-coding region between nucleotide position 367 and 368 of the B19 sequence reported by Shade et al., *J. Virol.* (1986) 58:921-936.

Figures 4A-4C (SEQ ID NO:23) show the sequence for the approximately 4.7 kbp PCR fragment shown in Figure 1 from parvovirus B19 clone 2-B6. The sequence is a 4677 nucleotide fragment corresponding to nucleotide positions 217-4893 of Shade et al., *J. Virol.* (1986) 58:921-936. The sequence depicted contains the parvovirus B19 full-length open reading frame which encodes NS1, VP1 and VP2, plus additional 5' and 3' untranslated sequences. The fragment sequenced contained an additional nucleotide in the 5' non-coding region between nucleotide position 367 and 368 of the B19 sequence reported by Shade et al., *J. Virol.* (1986) 58:921-936.

## Example 4

## Cloning and Expression of Parvovirus B19 NS1, VP1 and VP2 Recombinant Proteins.

Fragments encoding NS1, VP1 and VP2 (see Figure 1) were amplified using the 4.7 kb fragment of parvovirus B19 cloned in pCR2.1-TOPO (described above). In particular, PCR primers (see below) were designed to PCR out the NS1, VP1, and VP2 regions of parvovirus B19. To facilitate the cloning of these regions into yeast expression vectors, *Xba*I, *Hind*III and *Sal*I restriction sites were introduced in the primers as required.

The primers used to clone and amplify parvovirus B19 fragments for yeast expression of NS1, VP1 and VP2 recombinant proteins were based on the sequences obtained above and were as follows:

NS1-5 (sense primer)

5'ATACTCTCTAGACAAAACAAAATGGAGCTATTTAGAGGGGTGCTTCAAGTTTCT3'

(SEQ ID NO:44)

NS1-3 (anti-sense primer)
5' GAGTATGTCGACTTACTCATAATCTACAAAGCTTTGCAATCCAGACAG3' (SEQ ID NO:45)

VP1-5SN (sense primer)
5'ATACTCAAGCTTACAAAACAAAATGAGTAAAGAAAGTGGCAAATGGTGGGAAAGT3' (SEQ ID NO:46)

VPALL-3 (anti-sense primer)
5'GAGTATGTCGACTTACAATGGGTGCACACGGCTTTTGGCTGTCCACAATTC3' (SEQ ID NO:47)

VP2-5SN (sense primer)
5'ATACTCAAGCTTACAAAACAAAATGACTTCAGTTAATTCTGCAGAAGCCAGCACT3' (SEQ ID NO:48)

PCR primers were synthesized, purified and suspended in 300 µL of $dH_20$ and their optical densities at 260 nm determined. The reaction mix contained 0.25 ng of template, 100 pmol of each primer, 10µL of 1.25 mM of each dNTP and 1 unit of Taq polymerase (Perkin Elmer, Boston, MA) in a final volume of 50 µL. Amplification conditions were 94°C for 1 min., 50°C for 2 min. and 68°C for 4 min. for 35 cycles. A 7-min. post-incubation at 75°C was added to ensure the full extension of fragments. Aliquots of 5 µL were used to check PCR synthesis by electrophoresis on 1% agarose gels. The entire PCR product was then electrophoresed and fragments exhibiting the expected sizes were purified from the gels using the PCR Purification kit (Promega) following the vendor's recommendations. Approximately 0.8 µg of purified PCR DNA was digested with the appropriate restriction enzymes (Roche) for 3h at 37°C and the products were further purified using the Promega PCR Purification kit.

Plasmid pBS24.1 was used for heterologous expression of the parvovirus B19 recombinant proteins. This yeast expression vector contains 2µ sequences and inverted repeats (IR) for autonomous replication in yeast, the α-factor terminator to

ensure transcription termination, and the yeast *leu2-d* and URA3 for selection. The ColE1 origin of replication and the β-lactamase gene are also present for propagation and selection in *E. coli* (Pichuantes et al. (1996) "Expression of Heterologous Gene Products in Yeast." In: *Protein Engineering: A Guide to Design and Production*, Chapter 5. J. L. Cleland and C. Craik, eds., Wiley-Liss, Inc., New York, N.Y. pp. 129-161. Plasmid pBS24.1 was digested with *Bam*HI/*Sal*I and dephosphorylated with 10 units of calf intestine alkaline phosphatase (Boheringer Manheim, Indianapolis, IN) under the conditions recommended by the vendor. The digested and purified PCR fragments were mixed with *Bam*HI/*Sal*I digested pBS24.1 and with a DNA fragment containing the yeast hybrid promoter ADH2/GAPDH (Cousens et al., *Gene* (1987) 61:265- 275) digested with either *Bam*HI/*Sfu*I or a *Bam*HI/*Hind*III, depending on the restriction sites present in the PCR fragments to be cloned. Ligation was carried out with the Roche Rapid Ligation kit and protocol. The ligation mix was then used to transform *E. coli* HB101 competent cells and transformants were selected in Luria-Broth plates containing ampicillin at 100 μg/ml after an overnight incubation at 37°C. Several colonies of each transformation were picked and inoculated in 3mL of Luria-Broth with ampicillin at 100 μg/ml and incubated at 37°C with shaking overnight.

Plasmid DNA was prepared using 1.5 mL of cultures and the QIAprep Miniprep kit (QIAGEN). Recombinant clones were identified by analytical restriction enzyme analysis with *Bam*HI-*Sal*I. Large-scale preparations of recombinant plasmids were made to perform sequencing to confirm the nucleotide sequence of the cloned parvovirus B19 fragments.

Yeast expression plasmids exhibiting the expected sequence for NS1, VP1 and VP2 were used for yeast transformation as follows. Competent *Saccharomyces cerevisiae* AD3 cells [*Mat a, trp1+, ura3-52, prb1-1122, pep4-3, prc1-407, [cir$^0$],::pDM15(pGAP/ADR1::G418$^R$)], leu2(ΔAD)*] were transformed with plasmid DNAs encoding for NS1, VP1 or VP2, cloned as described above. Selection of yeast recombinants was achieved by two rounds of uracil-deficient plates followed by one round of leucine-deficient plates after incubation at 30 °C for 48-72 hours. Cultures were then grown in leucine-deficient media and then in YEP supplemented with 2%

glucose (Pichuantes et al., *Proteins: Struct. Funct. Genet.* (1989) 6:324-337) for 48h before checking expression of the recombinant proteins.

The sequences for the various proteins from two different isolates are shown in Figures 5-10. In particular, Figures 5A (SEQ ID NO:24) and 5B (SEQ ID NO:25) show the NS1 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B1. Figures 6A (SEQ ID NO:26) and 6B (SEQ ID NO:27) show the VP1 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B1. Figures 7A (SEQ ID NO:28) and 7B (SEQ ID NO:29) show the VP2 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B1. Figures 8A (SEQ ID NO:30) and 8B (SEQ ID NO:31) show the NS1 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B6. Figures 9A (SEQ ID NO:32) and 9B (SEQ ID NO:33) show the VP1 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B6. Figures 10A (SEQ ID NO:34) and 10B (SEQ ID NO:35) show the VP2 nucleotide and protein sequences, respectively, from parvovirus B19 clone 2-B6.

## Example 5

### Detection and Quantitation of Parvovirus B19 DNA by TaqMan™

A sensitive diagnostic method for the detection of parvovirus B19 infection was designed as follows. In particular, TaqMan™ PCR technology was used to detect and quantitate parvovirus B19 DNA. Quantitative PCR requires efficient extraction of nucleic acid. The volume of plasma/serum used for DNA extraction also influences the sensitivity of detection. Two approaches were used to isolate nucleic acid from 0.5 ml of plasma/serum. In particular, DNA was extracted by (a) binding to silica; and (b) annealing to target-specific oligonucleotides.

#### (a) Isolation of nucleic acid by binding to silica.

In the presence of high concentrations of chaotropic salt such as guanidinium isothiocyanate, nucleic acids bind to silica. Small sized nucleic acids bind more efficiently to silica under conditions of acidic pH. The bound nucleic acids are

efficiently eluted in low salt, alkaline pH buffer at high temperatures. The substitution of magnetized silica for regular silica greatly facilitates washing and elution steps of nucleic acid isolation. A magnetic base was used to capture the nucleic acid-bound silica particles, thus eliminating centrifugations required to sediment regular silica particles.

The lysis buffer used was from Organon-Teknika (Durham, NC). This lysis buffer contains guanidinium isothiocyanate to solubilize proteins and inactivate RNases and DNases. The detergent Triton X-100 further facilitates the process of solubilization and disintegration of cell structure and nuclear proteins, thus releasing nucleic acid. The lysis reagent was acidified to enhance nucleic acid binding, and 50 µl of alkaline elution buffer was used to elute the bound nucleic acid. Following nucleic acid isolation, the presence of parvovirus DNA was determined by performing TaqMan™ PCR, as described below.

(b) Isolation of nucleic acid by annealing to target-specific oligonucleotides.

Although use of magnetized silica greatly facilitates rapid and easy handling during the washing and elution steps, isolation of nucleic acid is still laborious and time consuming. Therefore one-step capture of specific nucleic acid target from plasma or serum using magnetic beads was used. In order to make this applicable for a wide variety of viral nucleic acid capture tests, generic magnetic beads coupled with oligo dT were used. Sera-Mag magnetic oligo (dT) beads (Seradyn, Indianapolis, IN) with an oligo dT length of 14mers were used in combination with Capture oligonucleotides containing 20 poly A's at 3' end contiguous with the parvovirus-specific sequence used (designated at the end of the sequence specified below).

The antisense capture oligonucleotides used were derived from the 700 bp fragment and were as follows:

VSPC1 - AAAAAAAAAAAAAAAAAAAAATCCTTAACAGCAATTTCTGATA (nt 3492-3514) (*) (SEQ ID NO:49)

VSPC2 - AAAAAAAAAAAAAAAAAAAACGCCCTGTAGTGCTGTCAG (nt 3549-3568) (SEQ ID NO:50)

VSPC3 - AAAAAAAAAAAAAAAAAAAATATACCCAAATAGGAAGTTCTG (nt 3639-3660) (SEQ ID NO:51)

VSPC4 - AAAAAAAAAAAAAAAAAAAATAAAATGCTGATTCTTCACTTGC (nt 3737-3759) (SEQ ID NO:52)

VSPC5 - AAAAAAAAAAAAAAAAAAAATGCTGTACCTCCTGTACCTA (nt 3789-3808) (SEQ ID NO:53)

VSPC6 - AAAAAAAAAAAAAAAAAAAAAGCCCTCTAAATTTTCTGGG (nt 3838-3857) (SEQ ID NO:54)

VSPC7 - AAAAAAAAAAAAAAAAAAAACTCCTAATGTGTCAGGAACC (nt 3910-3929) (SEQ ID NO:55)

(*) Nucleotide numbers are according to Shade et al., *J. Virol.* (1986) 58:921-936.

The magnetic beads were suspended in Novagen lysis buffer (Madison, WI) and a series of seven capture oligonucleotides (VSPC1-VSPC7, described above) were tested individually or in combination, to capture parvovirus B19 DNA from a panel obtained from the FDA Center for Biologic Evaluation and Research, U.S. Department of Health and Human Services (FDA-CBER).

(c) Washing the beads with a wash buffer.

Following capture, the beads were washed with a buffer containing 10 mM Hepes buffered to pH 7.5 in 0.3 M NaCl., and 0.5% NP-40. After treatment of serum with lysis buffer, hybridization, magnetic adsorption of beads, and removal of lysis buffer, 1.5 ml of the wash buffer was added to the beads. Following the usual vortexing, magnetic adsorption, and removal of the wash buffer, the beads were washed a second time in 0.5 ml of the same buffer, so that the magnetic beads can be

compacted, for easy suspension in 100 ml of Universal PCR buffer containing all the reagents for the Taqman assay. The beads with the captured DNA were transferred to a TaqMan™ plate for detection by TaqMan™ PCR as described below. Several oligonucleotide combinations were efficient at capturing B19 as detected by TaqMan™ assay.

In particular, the TaqMan™ technology amplifies captured target nucleic acid as DNA amplicons. An alternative is amplifying the captured target as RNA. For this, amplification oligonucleotides consisted of a parvovirus B19-specific primer with a T7 promoter sequence, in order to generate RNA amplicons using T7 RNA polymerase. Three amplification primers (VSA1-A3, described below), derived from the 700 bp sequence corresponding to nucleotides 2936-3635 of the parvovirus B19 genome described in Shade et al., *J. Virol.* (1986) 58:921-936 were tested for their ability to amplify. The primers were as follows:

Sense strand amplification primers

VSA1-AATTCTAATACGACTCACTATAGGGAGAAGGCCATATACTCATTGGACTGT (nt 2942-2961) (SEQ ID NO:56)

VSA2 - AATTCTAATACGACTCACTATAGGGAGAAGGCCAGAGCACCATTATAA (nt 3272-3288) (SEQ ID NO:57)

VSA3 -AATTCTAATACGACTCACTATAGGGAGAAGGCACAATGCCAGTGGAAA (nt 3317-3333) (SEQ ID NO:58)

VSP2-GTGCTGAAACTCTAAAGGT (Anti-sense Primer- nt 3424-3442) (SEQ ID NO:59)

RNamplifire kit (Qiagen) reagents were used to examine amplification efficiency using 50 copies of the parvovirus DNA as target in a final volume of 20 mLs. The amplification primers were tested individually or in combination using VSP2 as the second primer. Following one hour incubation at 42 °C as recommended by the manufacturer, an aliquot of the amplified material was diluted 100 fold, for detection by the TaqMan™ assay to assess the efficiency of the amplification primers.

A combination of two amplification primers, VSA2 and VSA3 with VSP2, was highly efficient at generating RNA amplicons.

The sensitivity of the TaqMan™ assay, the suitability of the PCR primers and the optimum reaction conditions were established using plasmid DNA containing the 4.7 kb fragment described above. This fragment includes the VP1 region, as well as the NS1 and VP2 regions (see, Figure 1). PCR amplification primers derived from the VP1 region, as detailed below, were used. The numbering is relative to Shade et al., *J. Virol.* (1986) 58:921-936. X represents 5'-fluorescein phosphoramidite and Z represents DABCYL-dT, both obtained from Glen Research Corporation, Sterling, VA. The numbers designated to the right of the sequence refer to the nucleotides in the primers from the parvovirus B19 sequence.

VSP1- GGAGGCAAAGGTTTGCA (Sense Primer- nt 3334-3350) (SEQ ID NO:60)

VSP2-GTGCTGAAACTCTAAAGGT (Anti-sense Primer-nt 3424-3442) (SEQ ID NO:59)

VSPPR1-XCCCATGGAGATATTTAGATTZ (Probe-nt 3379-3398) (SEQ ID NO:61)

Vpara 8: TCCATATGACCCAGAGCACCA (nt3262-3460) (SEQ ID NO: 88)

Vpara 9: TTTCCACTGGCATTGTGGC (Anti-sense Primer- nt 3313-3331)(SEQ ID NO: 89)

Vpara10: X AGCTAGACCTGCATGTCACTG Z, where X is Fam and Z is Tamra. (nt3286-3310) (SEQ ID NO: 90)

The plasmid DNA concentration was estimated spectrophotometrically, and serial dilution was performed to obtain 5,000-10 copies/20 µl. The reaction mix in a final volume of 50 µl contained 20 µl sample, 1X Gold Taq amplification buffer (Perkin Elmer) with 3.2 mM $MgCl_2$, 300 µM each of dNTPs, 1 pmol each of the amplification primers, 0.4 pmol of the probe, and 1 unit of AmpliTaq enzyme. The reaction conditions included 10 min at 95 $^0$C to activate the enzyme followed by 45 cycles of 30 secs at 95

$^0$C, alternating with 60 $^0$C in an ABI 7700 Sequence Detector.

Using the primer pair VSP1 and VSP2 which generated a 109 bp PCR product and the probe VSPPR1, as few as 10 copies/assay were detectable. Since the sample volume was 20 μL in a final volume of 50 μLs, this suggests that plasma samples containing as few as 50 copies/ml of parvovirus B19 DNA could be extracted and detected by TaqMan™ technology. Since parvovirus is a high titer virus, plasma/serum volumes of 50 μL could be extracted and used for analysis.

Using the FDA-CBER parvovirus B19 DNA positive sample ($10^6$ copies/ml) TaqMan™ technology detected as few as 50 copies per assay. In an attempt to correlate the nucleic acid and immunotiter, the viral DNA load was quantitated in several antibody-positive samples.

Accordingly, novel human parvovirus B19 sequences and detection assays using these sequences have been disclosed. From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope thereof.

AMENDED CLAIMS

1. (Amended) A method for detecting human parvovirus B19 in a biological sample, the method comprising:

isolating nucleic acids from a biological sample suspected of containing human parvovirus wherein the nucleic acids are isolated from the biological sample by a method comprising (i) contacting a solid support comprising magnetic beads that comprise capture nucleic acids associated therewith with the biological sample under hybridizing conditions wherein target nucleic acid strands, if present in the biological sample, hybridize with the capture nucleic acids, and (ii) separating the solid support from the sample;

amplifying the isolated nucleic acids using a sense and an antisense primer wherein each

(a) the sense primer consists of SEQ ID NO:88;

(b) the antisense primer consists of SEQ ID NO:89; and detecting the presence of the amplified nucleic acids as an indication of the presence of human parvovirus B19 in the sample,

wherein amplifying uses a fluorogenic 5' nuclease assay using the sense primer and the antisense primer and detecting is done using at least one probe comprising a detectable label.

2. (Amended) The method of claim 1, wherein the capture nucleic acids further comprise a homopolymer chain to link the capture nucleic acids to the solid support.

3. (Amended) The method of claim 2, wherein the homopolymer chain is a polyA chain.

4. (Amended) The method of claim 3, wherein the capture nucleic acids comprise the oligonucleotide of SEQ ID NO:55 or a nucleotide sequence having at least 90% sequence identity to SEQ ID NO:55.

5. (Amended) The method of claim 1, wherein the detectable label is a fluorescent label selected from the group consisting of 6-carboxyfluorescein (6-FAM), tetramethyl rhodamine (TAMRA), and 2', 4', 5', 7',- tetrachloro -4-7- dichlorofluorescein (TET).

6. (Amended) The method of claim 5, wherein the probe further comprises detectable labels at the 5'-end and at the 3'-end.

7. (Amended) The method of claim 1, wherein an internal control sequence is present.

8. (Amended) The method of claim 7, wherein the internal control sequence is derived from the nucleotide sequence of SEQ ID NO:92.

9. (New)The method of claim 8, further comprising a detectably labeled probe sequence for the internal control sequence.

10. (New) The method of Claim 4, wherein the capture nucleic acids comprise the oligonucleotide of SEQ ID NO:55.

11. (New) The method of claim 10, wherein the capture nucleic acids comprise the oligonucleotide of SEQ ID NO:55 and one or more of the oligonucleotides of SEQ ID NOS: 49-54.

12. (New) The method of claim 11, wherein the capture nucleic acids comprise the oligonucleotides of SEQ ID NOS:49 and 55.

13. (New) The method of claim 11, wherein the capture nucleic acids comprise the oligonucleotides of SEQ ID NOS:50 and 55.

14. (New) The method of claim 11, wherein the capture nucleic acids comprise the oligonucleotides of SEQ ID NOS:51 & 55.

15. (New) The method of claim 11, wherein the capture nucleic acids comprise the oligonucleotides of SEQ ID NOS:52 & 55.

16. (New) The method of claim 11, wherein the capture nucleic acids comprise the oligonucleotides of SEQ ID NOS:53 & 55.

17. (New) The method of claim 11, wherein the capture nucleic acids comprise the oligonucleotides of SEQ ID NOS:54 & 55.

18. (New) The method of claim 11, wherein the capture nucleic acids comprise the oligonucleotides of SEQ ID NOS:49, 52, 53 & 55.

19. (New) The method of claim 1, wherein the capture nucleic acids comprises the oligonucleotides of SEQ ID NO: 55 and one or more of the oligonucleotides of SEQ ID NOS: 49 – 54.

20. (New) The method of claim 19, wherein the capture nucleic acids comprises the oligonucleotides of SEQ ID NOS:49, 52, 53 & 55.