CRITICAL REVIEW
Joanne Macdonald, Felix von Stetten et al.
Review: a comprehensive summary of a decade
development of the recombinase polymerase amplification
Review: a comprehensive summary of a decade development of the recombinase polymerase amplification

Jia Li, Joanne Macdonald* and Felix von Stetten*.

Nucleic acid amplification has permeated every field in the life sciences since the introduction of the classic polymerase chain reaction (PCR) method in 1983. Yet, despite its fundamental reach, PCR has been constrained within the walls of a laboratory, due to its requirement for a sophisticated thermocycling machine, limiting external application in low-resource settings. New isothermal amplification strategies are seeking to break through traditional laboratory boundaries by providing nucleic acid replication at constant temperatures. Of these methods, recombinase polymerase amplification (RPA) is one of the fastest developing, experiencing rapid uptake and market, even though it was introduced comparatively late. Critically, RPA’s technology potentiates highly accessible and sensitive nucleic acid amplification outside of laboratory, and even self-testing. Here we provide a comprehensive review of the equipment-free simplicity of RPA over its first decade of development. Our review includes key knowledge of RPA technology, such as its reaction components, mechanism, sensitivities and specificities, and distinctive detection methods. The review also provides know-how for developing RPA assays, and information about commercially available RPA reaction kits and accessories. We summarise critical RPA experimental tips and issues available through data mining the published literature, to assist researchers in mastering the RPA reaction. We also outline influential hotspots of RPA development, and conclude with outlooks for future development and implications for eclipsing PCR and further revolutionising the life sciences.

1. Introduction and overview

Nucleic acid amplification (NAA) in vitro, the artificial replication of genetic material, has infiltrated all areas of life sciences and biotechnology, such as pathogen detection, cancer research, cloning, sequencing, synthetic biology, genotyping, mutagenesis, forensic identification of crimes, drug discovery, molecular archaeology, food testing, wellness and lifestyle testing etc. This explosive revolution began with the invention of the polymerase chain reaction (PCR) by Kary Mullis in 1983. Fundamentally, PCR is a cyclic process that performs exponential amplification from a single nucleic acid molecule to billions of copies in vitro, by providing successive temperatures favourable to nucleic acid replication processes (strand denaturation, primer annealing, and enzymatic extension). Increasing molecular quantities makes the handling and subsequent applications of nucleic acids easier, reducing the requirement for use of toxic radioactive probes to track molecular presence, and spawning immense creativity around applications for use. Yet, as valuable as PCR is, the requirement for a sophisticated thermocycler to provide the cyclic heating and cooling process, has largely bound PCR to implementation within the walls of a laboratory, impeding its application in low-resource settings.

Recent advances in isothermal nucleic acid amplification have provided simplified incubation conditions for artificial nucleic acid replication, requiring only a constant temperature rather than thermocycling. The single temperature incubation reduces equipment requirements, opening new avenues to break through the boundaries of the laboratory and perform amplification in low-resource settings. The elimination of repeated heating and cooling steps also provides a second advantage for low-resource implementation, through reduced amplification times. Faster reactions occur not only because of a reduction in heating and cooling times, but also because multiple molecular reactions can proceed asynchronously rather than being forced to operate sequentially within an arti-
ficial heating and cooling cycle. Since the early 1990s, a plethora of isothermal nucleic acid amplification methods have adopted various reaction mechanisms. The most well-established methods are exemplified by nucleic acid sequence-based amplification (NASBA, also known as transcription mediated amplification, TMA), signal-mediated amplification of ribonucleic acid (RNA) technology (SMART), helicase-dependent amplification (HDA), recombinase polymerase amplification (RPA), rolling circle amplification (RCA), multiple displacement amplification (MDA), loop-mediated isothermal amplification (LAMP) and strand displacement amplification (SDA); readers can refer to details of these methods in a few reviews.2–5 One technology in particular, recombinase polymerase amplification (RPA), is experiencing rapid development and increasing market share (Fig. 1), despite its comparatively late introduction, due to its simplified equipment requirements and fast reaction times.

RPA was first introduced in 2006 by Niall Armes from ASM Scientific Ltd (Cambridge, United Kingdom, founded by the Wellcome Trust Sanger Institute).6 Although RPA has not yet occupied a large market share percentage in the isothermal nucleic acid amplification technology (according to the data from the Grand View Research report,7 Fig. 1A), it is experiencing the most rapid uptake. More than 250 publications about RPA have been published so far, with a consistent increase in RPA publication numbers in the last six years; noticeably, the RPA publication number started growing exponentially from year 2014 (Fig. 1B). Among these publications, five RPA review papers were published in consecutive years from 2014 to 2018, respectively. The review of Zaghloul and El-shahat focuses on the application of RPA for hepatitis C virus diagnosis;8 the review of Moore and Jaykus emphasises RPA assays developed for the detection of enteric viruses;9 the reviews of James and Macdonald,10 Daher et al.11 and Lobato and O’Sullivan12 describe and summarise the characteristics and strengths for applications of RPA in point-of-care (POC) diagnostics. In comparison, here we provide a comprehensive review that focuses on the radical properties and development potential of RPA. Beginning with an introduction of the key aspects of RPA technology, namely reaction components and mechanisms. We subsequently provide know-how about developing RPA assays, including design and selection of oligonucleotides (primer, probe and template); the information about commercially available RPA reaction kits and accessories are also provided. For those interested in the technical implementation of RPA, we summarise critical RPA experimental tips and issues available through data mining the published literature to assist researchers better master RPA reaction. This is followed by elucidating the clinical/field performance of RPA via collated data such as sensitivity and specificity from RPA literature. We also describe some distinctive RPA detection methods for those who want to detect RPA assay signal using the methods other than the commonly used PCR detection methods. To understand the critical significance of this technology for eclipsing PCR and breaking out of the boundaries of the laboratory walls, we discuss the development hotspots of RPA, including quantitative RPA, multiplex RPA reaction, mobile RPA diagnostic, integrated RPA assays on microfluidics and one-step RPA assays. Our review then concludes with outlooks of future development of RPA.

2. Recombinase polymerase amplification (RPA) reaction

The prominence of RPA as revolutionary method to eclipse PCR stems from its specific reaction components (Table 1) and mechanism. For a successful RPA assay, the nuances are hinged on the intrinsic factors, the design of the primers, probe and nucleic acid template; and are related to the extrin-
sic factors, such as reaction temperature and agitation, toler-
ability to mismatches, inhibitors and background DNA. In
addition, the nucleic acid labelling during RPA, and RPA
amplicon clean-up and post-amplification treatment are also
important details for successful RPA detection. This section
provides these practical information summarised from the
RPA literature to serve as a guideline for RPA assay design. In
addition, readers can also get information about commercially
available RPA reaction kits and accessories (Tables 2 and 3). At
the end, this section elucidates the clinical/field performance
of RPA via data mining of RPA literature, which are also suc-
cinctly collated (Tables 4 and 5).

2.1 Reaction components
The fundamental reaction mechanism of RPA relies on a syn-
thetically engineered adaptation of a natural cellular process
called homologous recombination, a key process in DNA
metabolism. The standard RPA reaction reagents comprise
three key proteins (recombinase, recombinase loading factor
and single-stranded binding protein), which subsequently co-
ordinate with ancillary components such as deoxyribonucleic
acid (DNA) polymerase, crowding agent, energy/fuel com-
ponents (e.g. adenosine triphosphate, ATP) and salt molecules
to perform the RPA reaction mechanism (Fig. 2). The detailed
reaction components, and their typical concentration and
function are provided in Table 1:
## Table 1  Summary of RPA reaction components, their typical concentrations and functions

<table>
<thead>
<tr>
<th>Reaction components</th>
<th>Typical concentration</th>
<th>Functions</th>
<th>Ref.</th>
</tr>
</thead>
<tbody>
<tr>
<td>T4 UvsX protein</td>
<td>120 ng μL(^{-1})</td>
<td>Recombinase that possesses pairing and strand-transfer activity that is important in genetic recombination, DNA repair and replication (or E. coli RecA; recombinate is a central component in the related processes of recombinational DNA repair and homologous genetic recombination that is the ortholog of the UvsX protein). Recombinate loading factor that is classified as a recombination-mediator protein that stimulates the single-stranded DNA-dependent ATPase activity of T4 UvsX and lowers the critical concentration of T4 UvsX required for activity. Single-stranded binding (SSB) protein is involved in DNA replication, repair and recombination, and binds preferentially to single-stranded DNA. The T4 UvsX, T4 UvsY and T4 gp32 proteins work co-operatively to initiate the RPA reaction via unwinding, D-loop formation and stabilisation of the DNA template.</td>
<td>13 and 14</td>
</tr>
<tr>
<td>T4 UvsY protein</td>
<td>60 ng μL(^{-1})</td>
<td>DNA polymerase syntheses new DNA templates homologous to the target nucleic acid, by extending nucleotide building blocks from the bound primers, complementary to the original target nucleic acid sequence or “template”.</td>
<td>15</td>
</tr>
<tr>
<td>T4 gp32</td>
<td>600 ng μL(^{-1})</td>
<td>An equimolar solution of dATP, dCTP, dGTP and dTTP are building blocks used by the DNA polymerase to synthesise new templates.</td>
<td>—</td>
</tr>
<tr>
<td>Bacillus subtilis DNA polymerase 1 (Bsa) or Staphylococcus aureus polymerase (Sau)</td>
<td>Bsa: 30 ng μL(^{-1}); Sau: 8.6 or 12.8 μg</td>
<td>Primers are critical to directing the amplification event to the nucleic acid target of interest through homologous binding. After binding, the primers provide the essential 3′-OH for polymerase to perform strand extension.</td>
<td>16 and 17</td>
</tr>
<tr>
<td>Deoxynucleotide triphosphate (dNTP, N = A, T, C, G)</td>
<td>200 μM each</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>Forward and reverse primers</td>
<td>Usually at 420 nM each, but can be varied in the concentration range of 150 nM to 600 nM</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>DNA template</td>
<td>—</td>
<td>The oligonucleotide that the primers bind to for the synthesis of exact new oligonucleotides</td>
<td>—</td>
</tr>
<tr>
<td>Carbowax20M (a high molecular weight polyethylene glycol (PEG))</td>
<td>PEG 35K (5%)</td>
<td>The crowding reagent is a good mimic of the real biomacromolecules condition in vivo and facilitates amplification, as the crowding agents can enhance the catalytic activity of the enzymes. Stabilisation of the enzymes by barying free sulphhydryl groups.</td>
<td>18 and 19</td>
</tr>
<tr>
<td>Dithiothreitol</td>
<td>2 mM</td>
<td>The three components form the energy-supply system for the activities of the recombinase and the DNA polymerase.</td>
<td>20</td>
</tr>
<tr>
<td>Phosphocreatine</td>
<td>50 mM</td>
<td>The two components serve to stabilise and solubilise the DNA in solution.</td>
<td>21</td>
</tr>
<tr>
<td>Creatine kinase</td>
<td>100 ng μL(^{-1})</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>Adenosine triphosphate (ATP)</td>
<td>3 mM</td>
<td>Acting as a cofactor for the performance of the enzymes. The RPA reaction initiates once the magnesium acetate is added.</td>
<td>22</td>
</tr>
<tr>
<td>Tris(hydroxymethyl)aminomethane (Tris)</td>
<td>50 mM (pH 7.9)</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>Potassium acetate</td>
<td>100 mM</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>Magnesium acetate</td>
<td>14 mM</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>L ≈ 1</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>L ≈ 1; 8.6 or 12.8</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>L ≈ 1; 8.6 or 12.8; 15</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>L ≈ 1; 8.6 or 12.8; 15; 8.6 or 12.8 μg</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>L ≈ 1; 8.6 or 12.8; 15; 8.6 or 12.8 μg</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>1 Recombinase that possesses pairing and strand-transfer activity that is important in genetic recombination, DNA repair and replication (or E. coli RecA; recombinase is a central component in the related processes of recombinational DNA repair and homologous genetic recombination that is the ortholog of the UvsX protein). Recombinate loading factor that is classified as a recombination-mediator protein that stimulates the single-stranded DNA-dependent ATPase activity of T4 UvsX and lowers the critical concentration of T4 UvsX required for activity. Single-stranded binding (SSB) protein is involved in DNA replication, repair and recombination, and binds preferentially to single-stranded DNA. The T4 UvsX, T4 UvsY and T4 gp32 proteins work co-operatively to initiate the RPA reaction via unwinding, D-loop formation and stabilisation of the DNA template.</td>
<td>13 and 14</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DNA polymerase syntheses new DNA templates homologous to the target nucleic acid, by extending nucleotide building blocks from the bound primers, complementary to the original target nucleic acid sequence or “template”.</td>
<td>15</td>
<td></td>
<td></td>
</tr>
<tr>
<td>An equimolar solution of dATP, dCTP, dGTP and dTTP are building blocks used by the DNA polymerase to synthesise new templates.</td>
<td>—</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Primers are critical to directing the amplification event to the nucleic acid target of interest through homologous binding. After binding, the primers provide the essential 3′-OH for polymerase to perform strand extension.</td>
<td>20</td>
<td></td>
<td></td>
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<tr>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>The oligonucleotide that the primers bind to for the synthesis of exact new oligonucleotides</td>
<td>—</td>
<td></td>
<td></td>
</tr>
<tr>
<td>The crowding reagent is a good mimic of the real biomacromolecules condition in vivo and facilitates amplification, as the crowding agents can enhance the catalytic activity of the enzymes. Stabilisation of the enzymes by barying free sulphhydryl groups.</td>
<td>6 and 21–24</td>
<td></td>
<td></td>
</tr>
<tr>
<td>The three components form the energy-supply system for the activities of the recombinase and the DNA polymerase.</td>
<td>26</td>
<td></td>
<td></td>
</tr>
<tr>
<td>The two components serve to stabilise and solubilise the DNA in solution.</td>
<td>27 and 28</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Acting as a cofactor for the performance of the enzymes. The RPA reaction initiates once the magnesium acetate is added.</td>
<td>20</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### 2.2 Mechanism

RPA starts with the binding of the T4 UvsX protein (recombinase), assisted by the T4 UvsY (loading factor), to the primers to form a nucleoprotein filament. The resulting complex searches for homologous sequences in duplex DNA (Fig. 2). Once the homology is located, the complex invades the double-stranded DNA, forming a D-loop structure. One side of the D-loop is double-stranded where the primer hybridises with the template strand, initiating a strand exchange reaction, whereas the other side of the D-loop remains single-stranded – the unwound complementary strand that is stabilised by the SSB proteins (T4 gp32). Subsequently, the recombinase disassembles from the nucleoprotein filament and becomes immediately available to initiate another strand displacement reaction with a new primer. Primer incorporation allows the DNA polymerase (Bsa or Sau) to initiate the synthesis from the free 3′-OH at the end of the primer. As the polymerisation continues, the two parental strands continue to separate. Incorporation of both forward and reverse primers enables strand synthesis to occur in both directions simultaneously, and ultimately results in the exponential accumulation of amplified duplex DNA, consisting of the sequence between the forward and reverse primers.

During RPA, the formation of the recombinase-primer complex is the rate limiting for the D-loop formation. It was reported that the D-loop formation was most efficient at the stoichiometries at which the T4 UvsX protein fully coated the DNA template.
primers but did not bind substantially to the double-stranded DNA.\textsuperscript{10} The SSB proteins and the T4 UvsX (together with the ATP) have been shown to be essential for cooperating in strand exchange reaction along with the T4 UvsX protein.\textsuperscript{11,16,32} However, the presence of both of these proteins requires a higher concentration of T4 UvsX protein than what is required in the presence of only one of these proteins.\textsuperscript{29,33,34} The SSB proteins can stimulate the strand exchange reaction if T4 UvsX degrades.\textsuperscript{33} Importantly, the T4 UvsY protein neutralises the competition between the SSB proteins and the T4 UvsX for binding sites on the primers preventing the SSB from binding the primer from initiating the recombination event.\textsuperscript{35} When the primer concentration is low, the SSB proteins inhibits the strand exchange activity of the T4 UvsX protein.\textsuperscript{35} However, once the T4 UvsY protein is supplied, the T4 UvsY protein is able to invade the SSB proteins-covered primers to promote the binding of T4 UvsX protein to primers (from a site that is adjacent to the bound T4 UvsY protein), thereby displacing the SSB proteins from the primers.\textsuperscript{35}

<table>
<thead>
<tr>
<th>Product name</th>
<th>Category</th>
<th>Nucleic acid detection</th>
<th>Compatible general detection method</th>
<th>Product information</th>
</tr>
</thead>
<tbody>
<tr>
<td>TwistAmp® Basic</td>
<td>Lyophilised kit</td>
<td>DNA</td>
<td>Gel electrophoresis</td>
<td>The lyophilised kits contain pre-mixed enzymes and reagents necessary for the amplification, the user needs only supply primers and template (and dNTPs for the liquid kits). The RT kits afford one-step RNA amplification, which contain pre-mixed enzymes and reagents necessary for the amplification. The user need only supply primers, template and RNase inhibitor.</td>
</tr>
<tr>
<td>TwistAmp® Liquid Basic</td>
<td>Liquid kit</td>
<td>DNA</td>
<td></td>
<td>Recommended for users who want to combine TwistDx’s RPA amplification technology with the use of TwistDx’s proprietary fluorescent TwistAmp® exo probe in a homogenous format. The lyophilised kits contain pre-mixed enzymes and reagents necessary for the amplification, the user needs only supply primers, probe and template (and dNTPs for the liquid kits). The RT kits afford one-step RNA amplification, which contain pre-mixed enzymes and reagents necessary for the amplification. The user need only supply primers, probe, template and RNase inhibitor.</td>
</tr>
<tr>
<td>TwistAmp® exo RT</td>
<td>Lyophilised kit</td>
<td>DNA</td>
<td>Real-time fluorogenic probe-based</td>
<td>Tailored for users who want to combine TwistDx’s amplification technology with an alternative TwistDx reporter probe system fluorescent TwistAmp® fpg probe other than the TwistAmp® exo probe system in a homogenous format. The kit contains pre-mixed enzymes and reagents necessary for the amplification, the user need only supply primers, probe and template.</td>
</tr>
<tr>
<td>TwistAmp® exo</td>
<td>Lyophilised kit</td>
<td>DNA</td>
<td>Real-time and end-point fluorogenic probe-based</td>
<td>Designed for users who want to detect the amplicons based on sandwich assays. The kit contains pre-mixed enzymes and reagents necessary for the amplification, the user need only supply primers, probe and template.</td>
</tr>
<tr>
<td>TwistAmp® nfo</td>
<td>Lyophilised kit</td>
<td>DNA</td>
<td>Lateral flow strip</td>
<td>The kits contain pre-mixed enzymes, oligos and reagents necessary for detection of specific genes of Listeria monocytogenes and Campylobacter species respectively in less than 10 minutes. User must perform sample preparation.</td>
</tr>
<tr>
<td>TwistAmp® exo ListeriaM</td>
<td>Lyophilised kit</td>
<td>DNA (Listeria monocytogenes hly gene)</td>
<td>Real-time fluorogenic probe-based</td>
<td>The kits contain pre-mixed enzymes, oligos and reagents necessary, users need only add DNA, with provided buffer and magnesium acetate to the reactions. The kits also feature internal control DNA and probes in the lyophilised pellets, and lysis buffer for a two-step lysis of up to 5 µL of sample. The turn-around time of the Glow kit and the Flow kit are less than 10 minutes and approximately 20 minutes, respectively.</td>
</tr>
<tr>
<td>TwistAmp® exo Campylobacter</td>
<td>Lyophilised kit</td>
<td>DNA (Campylobacter species including jejuni and coli)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TwistAmp® exo RT Campylobacter</td>
<td>Liquid kit</td>
<td>DNA</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TwistAmp® exo Salmoneňla</td>
<td>Lyophilised kit</td>
<td>DNA (Salmoneňla enterica INVA gene)</td>
<td>Real-time and end-point fluorogenic probe-based</td>
<td></td>
</tr>
<tr>
<td>TwistAmp® exo RT Salmoneňla</td>
<td>Lyophilised kit</td>
<td>DNA</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TwistAmp® Liquid exo</td>
<td>Liquid kit</td>
<td>DNA</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Table 3  Summary of commercialised RPA devices and accessories by TwistDx™

<table>
<thead>
<tr>
<th>Product name</th>
<th>Category</th>
<th>Compatible general detection method</th>
<th>Product information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Twirla™ Portable Mixing Incubator</td>
<td>Device for incubation</td>
<td>Gel electrophoresis and lateral flow strip</td>
<td>Small and portable, and incubates up to 6 RPA reactions at optimal temperature. Can be powered by battery or mains-power via micro USB. Magnetic mixing of RPA reactions is also possible when fitted with Micro Balls (0.2 mL); dispensed with Micro Ball Dispenser in the reaction tube. Incubates up to 8 RPA reactions with 2 channel fluorescence detection per tube; the testing temperature range is from 37 °C to 65 °C. It can be powered by mains-power via micro USB or PowerGorilla external battery. Magnetic mixing of RPA reactions is also possible when fitted with Micro Balls (0.2 mL); dispensed with Micro Ball Dispenser in the reaction tube. It can also be adapted into a T8-ISO Carry Case when travelling to demanding environments.</td>
</tr>
<tr>
<td>T8-ISO Instrument</td>
<td>Device for incubation and detection</td>
<td>Real-time</td>
<td>An advanced version of the T8-ISO Instrument, which incubates up to 16 RPA reactions with 3 channel fluorescence detection per tube. Single-plex detection designed to detect a biotin and FITC/FAM labelled amplicon. Detection is based on sandwich assay using gold nanoparticles as tracer. Duplex detection designed to simultaneously detect two amplicons labelled with FITC (or FAM)/biotin and/or FITC (or FAM)/DIG. Detection is based on sandwich assay using gold nanoparticles as tracer. Duplex detection designed to simultaneously detect two amplicons labelled with DIG/biotin and/or FITC (or FAM)/biotin. Detection is based on sandwich assay using carbon nanoparticles as tracer. Single-plex detection designed to detect a biotin and FITC (or FAM) labelled amplicon. Detection is based on sandwich assay using carbon nanoparticles as tracer and is performed in an open cartridge.</td>
</tr>
<tr>
<td>T16-ISO Instrument</td>
<td>Device for incubation and detection</td>
<td>Real-time</td>
<td></td>
</tr>
<tr>
<td>Milenia HybriDetect 1</td>
<td>Device for lateral flow detection</td>
<td>Lateral flow strip</td>
<td>Single-plex detection designed to detect a biotin and FITC/FAM labelled amplicon. Detection is based on sandwich assay using gold nanoparticles as tracer. Duplex detection designed to simultaneously detect two amplicons labelled with FITC (or FAM)/biotin and/or FITC (or FAM)/DIG. Detection is based on sandwich assay using gold nanoparticles as tracer. Duplex detection designed to simultaneously detect two amplicons labelled with DIG/biotin and/or FITC (or FAM)/biotin. Detection is based on sandwich assay using carbon nanoparticles as tracer. Single-plex detection designed to detect a biotin and FITC (or FAM) labelled amplicon. Detection is based on sandwich assay using carbon nanoparticles as tracer and is performed in a sealed cartridge.</td>
</tr>
<tr>
<td>Milenia HybriDetect 2</td>
<td>Device for lateral flow detection</td>
<td>Lateral flow strip</td>
<td></td>
</tr>
<tr>
<td>PCRd Nucleic Acid Detection</td>
<td>Device for lateral flow detection</td>
<td>Lateral flow strip</td>
<td></td>
</tr>
<tr>
<td>U-Star disposable nucleic acid lateral flow detection units</td>
<td>Device for lateral flow detection</td>
<td>Lateral flow strip</td>
<td></td>
</tr>
</tbody>
</table>

Table 4  RPA literature reporting analytical sensitivity nearing the single analyte detection limit

<table>
<thead>
<tr>
<th>Analyte(s)</th>
<th>Detection method</th>
<th>Limit of detection</th>
<th>Ref.</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>BlaCTX-M-15</em> antimicrobial resistance gene</td>
<td>Electrowetting-on-dielectric (EWOD)-based digital droplets end-point fluorescent detection</td>
<td>5.6 fg (~a single DNA copy)</td>
<td>80</td>
</tr>
<tr>
<td>RNA polymerase beta subunit (RPOB) gene of <em>Mycobacterium tuberculosis</em></td>
<td>Electrochemical detection using gold nanoparticles on a solid phase</td>
<td>1 CFU&lt;sup&gt;a&lt;/sup&gt;</td>
<td>103</td>
</tr>
<tr>
<td>Early secretory antigenic target-6 (ESAT-6) gene of <em>Mycobacterium tuberculosis</em></td>
<td>Electrochemical detection on a screen-printed carbon electrode (SPCE)</td>
<td>1 CFU&lt;sup&gt;a&lt;/sup&gt;</td>
<td>102</td>
</tr>
<tr>
<td>Serotype-specific Enteritidis sequence fragment <em>sfdJ</em> of <em>Salmonella Enterica</em></td>
<td>Real-time fluorescent detection</td>
<td>1 CFU&lt;sup&gt;a&lt;/sup&gt;</td>
<td>119</td>
</tr>
<tr>
<td>Genomic DNA of <em>Plasmodium falciparum</em> 3D7</td>
<td>Real-time waveguide-based detection</td>
<td>&lt;1 parasite per µL</td>
<td>120</td>
</tr>
<tr>
<td><em>Leishmania donovani</em> kinetoplast minicircle DNA β-Conglutin for Lup an 1 anaphylactic allergen</td>
<td>Real-time fluorescent detection</td>
<td>1 cell</td>
<td>121</td>
</tr>
<tr>
<td><em>CeuE</em> gene of <em>Campylobacter jejuni</em>; <em>hipO</em> gene of <em>Campylobacter coli</em></td>
<td>(Competitive) lateral flow strip detection</td>
<td>0.17 attomol</td>
<td>39</td>
</tr>
<tr>
<td>Lentiviruses harboring genome fragment of Zika virus</td>
<td>Real-time fluorescent detection</td>
<td>1 CFU&lt;sup&gt;a&lt;/sup&gt; ml&lt;sup&gt;−1&lt;/sup&gt; in pure culture and chicken broth without enrichment</td>
<td>122</td>
</tr>
<tr>
<td><em>B1</em> gene of <em>Toxoplasma gondii</em></td>
<td>Clumped regularly interspaced short palindromic repeats (CRISPR)-based end-point fluorescent detection</td>
<td>2 attomol L&lt;sup&gt;−1&lt;/sup&gt;</td>
<td>123</td>
</tr>
<tr>
<td>Small subunit ribosomal RNA (18S RNA) gene of <em>Plasmodium knowlesi</em></td>
<td>Lateral flow strip detection</td>
<td>0.1 oocyst</td>
<td>71</td>
</tr>
<tr>
<td><em>IS6110</em> gene of <em>Mycobacterium tuberculosis</em> H37Rv genomic DNA</td>
<td>Real-time silicon photonic microring-based detection</td>
<td>1 plasmid</td>
<td>124</td>
</tr>
<tr>
<td>3.2 genomic DNA copies (~ single cell of H37Rv)</td>
<td>Real-time silicon photonic microring-based detection</td>
<td>3.2 genomic DNA copies (~ single cell of H37Rv)</td>
<td>113</td>
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</table>

<sup>a</sup> CFU: colony forming unit.
<table>
<thead>
<tr>
<th>Analyte(s)</th>
<th>Detection method</th>
<th>Clinical sensitivity</th>
<th>Clinical specificity</th>
<th>Limit of detection of benchmark method</th>
<th>Limit of detection</th>
<th>Ref.</th>
<th>Clinical field sample(s)</th>
<th>Clinical sensitivity</th>
<th>Clinical specificity</th>
<th>Limit of detection of RPA</th>
<th>Limit of detection of RPA</th>
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</thead>
<tbody>
<tr>
<td>Nucleocapsid (N) gene of bovine coronavirus</td>
<td>Real-time fluorescent detection on the tube scanner</td>
<td>100%</td>
<td>100%</td>
<td>10 to 100 RNA copies by probit analysis</td>
<td>1000 RNA copies</td>
<td>The same</td>
<td>10 to 100 RNA copies by probit analysis</td>
<td>100%</td>
<td>100%</td>
<td>The same</td>
<td>The same</td>
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<tr>
<td>Chlamydia trachomatis CDS2 gene</td>
<td>Lateral flow strip detection</td>
<td>83%</td>
<td>100%</td>
<td>5–12 pathogens per reaction</td>
<td>—</td>
<td>Higher</td>
<td>5–12 pathogens per reaction</td>
<td>Higher</td>
<td>92</td>
<td></td>
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<tr>
<td>Camp Factor (CFb) gene of Group B Streptococci</td>
<td>Real-time fluorescent detection</td>
<td>96%</td>
<td>100%</td>
<td>98 genome copies</td>
<td>—</td>
<td>The same</td>
<td>98 genome copies</td>
<td>The same</td>
<td>92</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DNA target sequence specific to Cryptosporidium spp.</td>
<td>Real-time fluorescent detection</td>
<td>100%</td>
<td>100%</td>
<td>100 oocysts per mL stool</td>
<td>—</td>
<td>The same</td>
<td>100 oocysts per mL stool</td>
<td>The same</td>
<td>92</td>
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</tr>
<tr>
<td>5′-Untranslated region of Yellow fever virus (YFV)</td>
<td>Real-time fluorescent detection on the microfluidic platform</td>
<td>80%</td>
<td>100%</td>
<td>41 genomic copies per reaction in YFV RNA extracts; 21 genomic copies per reaction of YFV-spiked human plasma samples</td>
<td>8 genomic copies per reaction in YFV RNA extracts</td>
<td>Higher</td>
<td>8 genomic copies per reaction in YFV RNA extracts</td>
<td>Higher</td>
<td>117</td>
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<tr>
<td>IS6110 gene of Mycobacterium tuberculosis</td>
<td>Real-time fluorescent detection</td>
<td>87.5%</td>
<td>100%</td>
<td>6.25 fg</td>
<td>—</td>
<td>Higher</td>
<td>6.25 fg</td>
<td>Higher</td>
<td>128</td>
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<tr>
<td>IS1081 gene of Mycobacterium tuberculosis</td>
<td>Real-time fluorescent detection</td>
<td>95.4%</td>
<td>100%</td>
<td>20 fg</td>
<td>—</td>
<td>Higher</td>
<td>20 fg</td>
<td>Higher</td>
<td>128</td>
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<tr>
<td>Giardia beta giardin gene</td>
<td>Lateral flow strip detection</td>
<td>105.4%</td>
<td>96%</td>
<td>10^7–10^10 cysts per mL stool</td>
<td>10^7–10^10 cysts per mL stool</td>
<td>Higher</td>
<td>10^7–10^10 cysts per mL stool</td>
<td>Higher</td>
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<td>Analyte(s)</td>
<td>Detection method</td>
<td>Limit of detection</td>
<td>Clinical/field sample(s)</td>
<td>Clinical sensitivity</td>
<td>Clinical specificity</td>
<td>Benchmark method</td>
<td>Limit of detection of benchmark method compared to RPA</td>
<td>Clinical sensitivity of benchmark method compared to RPA</td>
<td>Clinical specificity of benchmark method compared to RPA</td>
<td>Ref.</td>
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<tr>
<td>IS6110 gene of <em>Mycobacterium tuberculosis</em></td>
<td>Real-time photonic detection</td>
<td>10^{-6}-fold diluted MTB sample</td>
<td>33 clinical samples including 13 smear and culture positive samples and 20 smear and culture negative samples</td>
<td>100%</td>
<td>100%</td>
<td>Conventional microscopy of smear and solid culture</td>
<td>—</td>
<td>The same</td>
<td>The same</td>
<td>130</td>
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<tr>
<td>A highly conserved 3′-untranslated region that cover DENV 1–4</td>
<td>Real-time fluorescent detection</td>
<td>DENV serotype 1: 237 RNA copies; DENV serotype 2: 618 RNA copies; DENV serotype 3: 363 RNA copies; DENV serotype 4: 383 RNA copies</td>
<td>Inactivated DENV 1–4 spiked plasma and 31 DENV positive samples in Kedougou region in Senegal RNA of 90 plasma samples extracted and tested between 2012–2013 by RT-PCR in Bangkok (Thailand)</td>
<td>98%</td>
<td>—</td>
<td>Real-time RT-PCR</td>
<td>—</td>
<td>Higher</td>
<td>—</td>
<td>131</td>
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<tr>
<td>47 kDa gene sequence from the Karp strain of <em>Orientia tsutsugamushi</em> (47-RPA) and the 17 kDa gene sequence from the Wilmington strain of <em>Rickettsia typhi</em></td>
<td>Lateral flow strip detection</td>
<td>47 kDa gene: 53 DNA copies per reaction</td>
<td>10 positive and 10 negative human samples</td>
<td>80%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>47 kDa gene: 10 DNA copies per reaction</td>
<td>Higher</td>
<td>Higher</td>
<td>95</td>
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<tr>
<td>Ribosomal 18S DNA of <em>Entamoeba histolytica</em></td>
<td>Lateral flow strip detection</td>
<td>2.5 fg from serial dilutions of pure DNA extracted from parasites; 40 parasites from spiked stool sample</td>
<td>32 samples of DNA extracted from clinical samples</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>2.5 fg from serial dilutions of pure DNA extracted from parasites</td>
<td>The same</td>
<td>The same</td>
<td>132</td>
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<tr>
<td>A sequence designed based on ITS sequences of the <em>Madurella mycetomatis</em> type strain CBS 109801</td>
<td>Gel electrophoresis detection</td>
<td>0.23 ng of DNA</td>
<td>12 patient biopsy specimens</td>
<td>100%</td>
<td>100%</td>
<td>Conventional PCR</td>
<td>—</td>
<td>The same</td>
<td>The same</td>
<td>133</td>
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<tr>
<td>Ebola virus (EBOV) nucleocapsid sequence</td>
<td>Real-time fluorescent detection</td>
<td>5 genomic copies per reaction of a molecular RNA standard; 15 genomic copies per reaction in EBOV-spiked human plasma samples</td>
<td>928 post-mortem swab samples</td>
<td>100%</td>
<td>100%</td>
<td>Real-time RT-PCR</td>
<td>—</td>
<td>The same</td>
<td>The same</td>
<td>134</td>
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</tr>
<tr>
<td>Orf virus (ORFV) DNA polymerase gene segments</td>
<td>Real-time fluorescent detection</td>
<td>100 DNA copies</td>
<td>22 samples collected from suspected cases of Orf, 8 nasal swabs collected from experimentally infected sheep and 5 samples obtained from healthy goats</td>
<td>86%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>Higher</td>
<td>The same</td>
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<tr>
<td>Analyte(s)</td>
<td>Detection method</td>
<td>Limit of detection</td>
<td>Clinical/field sample(s)</td>
<td>Clinical sensitivity</td>
<td>Clinical specificity</td>
<td>Benchmark method</td>
<td>Limit of detection of benchmark method</td>
<td>Clinical sensitivity of benchmark method compared to RPA</td>
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<tr>
<td>Leader peptidase A (LepA) gene of <em>Streptococcus pneumoniae</em></td>
<td>Real-time fluorescent detection</td>
<td>4.1 genome equivalents per reaction</td>
<td>15 blood samples including 11 confirmed culture positive and 4 confirmed culture negative for <em>Streptococcus pneumoniae</em></td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>5.1 genome equivalents per reaction</td>
<td>The same</td>
<td>The same</td>
<td>97</td>
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<tr>
<td>Orf virus (ORFV) DNA polymerase gene segments</td>
<td>Lateral flow strip detection</td>
<td>80 copies per reaction of DNA plasmid</td>
<td>24 ORFV-spiked tissues samples, 53 samples collected from goats with suspected ORFV infection, 8 nasal swabs samples and 5 tissues from healthy goats</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>The same</td>
<td>The same</td>
<td>64</td>
<td></td>
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<tr>
<td><em>Leishmania donovani</em> (LD) kinetoplast minicircle DNA</td>
<td>Real-time fluorescent detection</td>
<td>100 DNA copies applying the LD DNA linearised plasmid; 1 genomic DNA copy</td>
<td>96 buffy coats and skin biopsies collected from visceral leishmaniasis, asymptomatic and post-kala-azar dermal leishmaniasis</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>The same</td>
<td>The same</td>
<td>121</td>
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<tr>
<td>Highly pathogenic porcine reproductive and respiratory syndrome virus (HP-PRRSV) NSP2 gene</td>
<td>Real-time fluorescent detection</td>
<td>70 RNA copies per reaction</td>
<td>68 tissue samples and 10 serum samples collected from suspected pigs of HP-PRRSV, 35 serum samples and 12 tissue samples collected from healthy pigs</td>
<td>97.6%</td>
<td>100%</td>
<td>Real-time RT&lt;sup&gt;−&lt;/sup&gt;-PCR</td>
<td>—</td>
<td>Higher</td>
<td>The same</td>
<td>136</td>
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<tr>
<td>100% conserved sequence of a major capsid protein gene of all cyprinid herpesvirus 3 strains eAMP factor (efb) gene of Group B Streptococci</td>
<td>Gel electrophoresis detection</td>
<td>10 copies of genomic DNA</td>
<td>12 confirmed latently infected fish and 1 confirmed uninfected fish</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>Lower</td>
<td>The same</td>
<td>66</td>
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</tr>
<tr>
<td>Non-structure protein 1 (nsP1) of Chikungunya virus (CHIKV)</td>
<td>Real-time fluorescent detection</td>
<td>6.25–12.5 genome equivalents</td>
<td>124 clinical samples</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>3.1–6.25 genome equivalents</td>
<td>The same</td>
<td>The same</td>
<td>137</td>
<td></td>
</tr>
<tr>
<td>A sequence designed in NS2A region conserved among all Zika virus lineages</td>
<td>Real-time fluorescent detection</td>
<td>21 RNA copies</td>
<td>25 positive and 9 negative urine samples collected during the Zika virus epidemic in Tuparetama, Brazil</td>
<td>92%</td>
<td>100%</td>
<td>Real-time RT&lt;sup&gt;−&lt;/sup&gt;-PCR</td>
<td>—</td>
<td>Higher</td>
<td>The same</td>
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Table 5 (Contd.)

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<tr>
<th>Analyte(s)</th>
<th>Detection method</th>
<th>Limit of detection</th>
<th>Clinical/field sample(s)</th>
<th>Clinical sensitivity</th>
<th>Clinical specificity</th>
<th>Benchmark method</th>
<th>Limit of detection of benchmark method compared to RPA</th>
<th>Clinical sensitivity of benchmark method compared to RPA</th>
<th>Ref.</th>
</tr>
</thead>
<tbody>
<tr>
<td>G-protein-coupled chemokine receptor (GPCR) gene of lumpy skin disease virus (LSDV)</td>
<td>Real-time fluorescent detection</td>
<td>100 DNA copies (179 DNA copies by probit analysis)</td>
<td>12 negative skin samples and 22 skin nodules of suspected LSDV-infected cattle collected during the summer of 2012 in Dakahlia Governorate, Egypt</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>37 DNA copies</td>
<td>The same</td>
<td>139</td>
</tr>
<tr>
<td>IS9000 gene of <em>Mycobacterium avium</em> subsp. <em>paratuberculosis</em> (MAP)</td>
<td>Real-time fluorescent detection</td>
<td>16 plasmid copies per µL; 500 fg genomic DNA/reaction</td>
<td>Archived DNA of MAP positive blood (<em>n</em> = 14), sperm (<em>n</em> = 18), faecal (<em>n</em> = 12) and tissue (<em>n</em> = 4) samples and 20 MAP-negative faecal samples</td>
<td>89.5%</td>
<td>—</td>
<td>Real-time PCR</td>
<td>1 plasmid copies per µL; 50 fg genomic DNA/reaction</td>
<td>Higher</td>
<td>140</td>
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<tr>
<td>T1E4 gene of prostate cancer</td>
<td>Real-time fluorescent detection</td>
<td>1000 RNA copies</td>
<td>9 urine samples obtained from prostate cancer and 2 urine samples from healthy individuals</td>
<td>90%</td>
<td>100%</td>
<td>Real-time RT&lt;sup&gt;a&lt;/sup&gt;-PCR</td>
<td>—</td>
<td>The same</td>
<td>141</td>
</tr>
<tr>
<td>NS1 gene of porcine parvovirus (PPV)</td>
<td>Real-time fluorescent detection</td>
<td>300 DNA copies</td>
<td>101 clinical tissue samples (serum, liver, kidney, lymph node, spleen and duodenum) collected from pig farms with suspected cases of PPV in Gansu province, China, and 27 clinical samples (serum, kidney and duodenum) collected from healthy pigs</td>
<td>94.4%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>Higher</td>
<td>54</td>
</tr>
<tr>
<td>Nucleocapsid gene of type 2 porcine reproductive and respiratory syndrome virus (PRRSV)</td>
<td>Real-time fluorescent detection</td>
<td>100 RNA copies (690 RNA copies by probit analysis)</td>
<td>60 clinical samples (lymph node, lung, spleen and liver) collected from diseased pigs suspected of having PRRS from 5 pigs farms in Hebei province, China from 2015–2016</td>
<td>100%</td>
<td>100%</td>
<td>Real-time RT&lt;sup&gt;a&lt;/sup&gt;-PCR</td>
<td>100 RNA copies</td>
<td>The same</td>
<td>142</td>
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<tr>
<td>Cytochrome b gene of <em>Theileria annulata</em></td>
<td>Lateral flow strip detection</td>
<td>2 pg genomic DNA</td>
<td>17 anticoagulated blood samples collected from tropical theileriosis endemic areas in Gansu province, China</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>The same</td>
<td>67</td>
</tr>
<tr>
<td>Analyte(s)</td>
<td>Detection method</td>
<td>Limit of detection</td>
<td>Clinical/field sample(s)</td>
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<td>Clinical specificity</td>
<td>Benchmark method</td>
<td>Limit of detection of benchmark method compared to RPA</td>
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<td>Clinical specificity of benchmark method compared to RPA</td>
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<tr>
<td>pirA-like gene of <em>Vibrio owensii</em></td>
<td>Real-time fluorescent detection</td>
<td>2 plasmid copies (2.84 plasmid copies by probit analysis)</td>
<td>138 clinical shrimp obtained from immersion bioassay, including 70 shrimp acute hepatopancreatic necrosis disease (AHPND) infected shrimp and 68 non-AHPND infected shrimp</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>Lower</td>
<td>Lower</td>
</tr>
<tr>
<td>rRNA gene of <em>Fasciola hepatica</em></td>
<td>Gel electrophoresis detection</td>
<td>1.6 pg µL⁻¹ DNA copies</td>
<td>102 human stool samples selected from banked specimens</td>
<td>87.8%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>1.6 pg µL⁻¹ DNA copies</td>
<td>Lower</td>
<td>The same</td>
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<tr>
<td></td>
<td>Lateral flow strip detection</td>
<td>1.0 pg µL⁻¹ DNA copies</td>
<td></td>
<td>95.2%</td>
<td>90.4%</td>
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<tr>
<td>N gene of pest des petits ruminants virus (PPRV)</td>
<td>Real-time fluorescent detection</td>
<td>100 plasmid copies</td>
<td>32 clinical samples collected from suspected cases of PPRV in Gansu province, China and 5 samples obtained from healthy sheep</td>
<td>90%</td>
<td>100%</td>
<td>Real-time RT²-PCR</td>
<td>150 plasmid copies</td>
<td>Higher</td>
<td>The same</td>
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<td>Lateral flow strip detection</td>
<td>10 plasmid copies</td>
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<td>90%</td>
<td>100%</td>
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<tr>
<td>ITS2 gene of <em>Phytophthora infestans</em></td>
<td>Real-time fluorescent detection</td>
<td>50 fg µL⁻¹ of genomic DNA</td>
<td>24 potato leaf samples collected from fields with and without visible symptoms of late blight infections in New Brunswick and Quebec provinces, Canada, respectively</td>
<td>60%</td>
<td>100%</td>
<td>LAMP</td>
<td>50 fg µL⁻¹ of genomic DNA</td>
<td>Higher</td>
<td>Lower</td>
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<tr>
<td>ORF2 gene of porcine circovirus type 2 (PCV2)</td>
<td>Real-time fluorescent detection</td>
<td>100 plasmid copies</td>
<td>65 clinical samples collected from suspected PCV2 infection pigs from 8 pig farms in Shandong province, China; 37 clinical samples (inguinal lymph node, tonsil, lung and serum) collected from Gansu Province, China, and 10 PCV1 positive samples conserved in the laboratory</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>80 plasmid copies</td>
<td>The same</td>
<td>The same</td>
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<tr>
<td></td>
<td>Lateral flow strip detection</td>
<td>100 plasmid copies</td>
<td></td>
<td>100%</td>
<td>100%</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Analyte(s)</td>
<td>Detection method</td>
<td>Limit of detection</td>
<td>Clinical/field sample(s)</td>
<td>Clinical sensitivity</td>
<td>Clinical specificity</td>
<td>Benchmark method</td>
<td>Limit of detection of benchmark method compared to RPA</td>
<td>Clinical sensitivity of benchmark method compared to RPA</td>
<td>Clinical specificity of benchmark method compared to RPA</td>
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<tr>
<td>gD gene of pseudorabies virus</td>
<td>Real-time fluorescent detection</td>
<td>100 DNA copies</td>
<td>76 clinical samples (tonsil, heart, spleen, lymph nodes, lung and serum) collected from pig farms in Shandong province, China, and 26 clinical samples (lymph nodes, tonsil and serum) collected from healthy pigs</td>
<td>93.3%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>Higher</td>
<td>The same</td>
</tr>
<tr>
<td>B1 gene of <em>Toxoplasma gondii</em></td>
<td>Lateral flow strip detection</td>
<td>0.1 oocysts per reaction 93.3%</td>
<td>100%</td>
<td>Nested PCR</td>
<td>1 oocyst/reaction</td>
<td>The same</td>
<td>The same</td>
<td>71</td>
<td></td>
</tr>
<tr>
<td>RNA transcript of TMPRSS2:ERG (a fusion gene for prostate cancer)</td>
<td>RPA fluoccellation assay</td>
<td>10⁷ RNA copies</td>
<td>Clinical urine specimens from 10 metastatic castration-resistant promising prostate cancer patients and 5 healthy control patients</td>
<td>70%</td>
<td>100%</td>
<td>Conventional RT²-PCR</td>
<td>—</td>
<td>The same</td>
<td>The same</td>
</tr>
<tr>
<td>VP2 gene of porcine parvovirus</td>
<td>Real-time fluorescent detection</td>
<td>100 DNA copies (103 DNA copies by probit analysis)</td>
<td>115 clinical samples (lymph node, lung, spleen, kidney and duodenum collected from pigs with reproductive disorders, diarrhea or respiratory disease in Hebei province, China from 2014 to 2016</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>100 DNA copies</td>
<td>The same</td>
<td>The same</td>
</tr>
<tr>
<td>G-protein-coupled chemokine receptor (GPCR) gene of <em>Capripoxvirus</em></td>
<td>Real-time fluorescent detection</td>
<td>300 plasmid copies</td>
<td>107 clinical samples (liver, lung, kidney, spleen, skin and blood) collected from 14 suspected sheep and 6 suspected goats in Gansu province which were characterised by pyrexia, excessive salivation and generalised pock lesions in the skin during the period of October 2014 to August 2015</td>
<td>97%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>Higher</td>
<td>The same</td>
</tr>
<tr>
<td>Analyte(s)</td>
<td>Detection method</td>
<td>Limit of detection</td>
<td>Clinical/field sample(s)</td>
<td>Clinical sensitivity</td>
<td>Clinical specificity</td>
<td>Benchmark method</td>
<td>Limit of detection of benchmark method compared to RPA</td>
<td>Clinical sensitivity of benchmark method compared to RPA</td>
<td>Ref.</td>
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<td>------------------------------------------------</td>
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<tr>
<td>Nucleocapsid protein gene of canine distemper virus</td>
<td>Real-time fluorescent detection</td>
<td>9.4 RNA copies (31.8 RNA copies by probit analysis)</td>
<td>32 nasal/oropharyngeal swabs collected from 20 dogs of both sexes (various breeds and ages) from the animal hospital of Agricultural University of Hebei and 12 raccoon dogs from the farms in Hebei Province, China from 2014 to 2016</td>
<td>100%</td>
<td>100%</td>
<td>Real-time RT&lt;sup&gt;q&lt;/sup&gt;-PCR</td>
<td>94 RNA copies</td>
<td>The same</td>
<td>149</td>
</tr>
<tr>
<td>imp gene of Candidatus Phytoplasma oryzae</td>
<td>Real-time fluorescent detection</td>
<td>1–10 plasmid copies</td>
<td>66 Napier grass samples from various geographical locations in western Kenya</td>
<td>100%</td>
<td>57.1%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>Lower</td>
<td>The same</td>
</tr>
<tr>
<td>imp gene of Candidatus Phytoplasma mali</td>
<td>Real-time fluorescent detection</td>
<td>10–100 plasmid copies</td>
<td>38 roots of field samples from apple (&lt;i&gt;Malus domestica&lt;/i&gt;) trees collected in autumn 2014, in spring 2015 and in June 2016 in private orchards or in the experimental field of the Institute for Fruit Growing in Samochwałowic, Belarus</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>The same</td>
<td>The same</td>
</tr>
<tr>
<td>N gene of rabies</td>
<td>Real-time fluorescent detection</td>
<td>1000 RNA copies per µL of strains SAD B19, Bobcat USA and Kelev 1% to 100% of the mutant cells</td>
<td>A panel of RNA from 33 field samples</td>
<td>97%</td>
<td>—</td>
<td>Real-time PCR</td>
<td>1 RNA copies per µL of strains SAD B19, Bobcat USA and Kelev 30% to 100% of the mutant cells</td>
<td>Higher</td>
<td>—</td>
</tr>
<tr>
<td>KRAS oncogenic mutation gene G12D on Exon 12</td>
<td>Real-time silicon photonic microroring-based detection</td>
<td>70 frozen tissues samples from colorectal cancer patients in Bio-Resource Center of Asian Medical Center, including 24 samples with the G12D mutation (34.3%), 26 samples with G13D mutation (37.1%) and 20 samples with no mutation (28.6%)</td>
<td>100% to 100% of the mutant cells</td>
<td>100%</td>
<td>100%</td>
<td>Conventional PCR</td>
<td>Lower</td>
<td>The same</td>
<td>151</td>
</tr>
<tr>
<td>KRAS oncogenic mutation genes G13D on Exon 13</td>
<td>Real-time silicon photonic microroring-based detection</td>
<td>70 frozen tissues samples from colorectal cancer patients in Bio-Resource Center of Asian Medical Center, including 24 samples with the G12D mutation (34.3%), 26 samples with G13D mutation (37.1%) and 20 samples with no mutation (28.6%)</td>
<td>100% to 100% of the mutant cells</td>
<td>100%</td>
<td>100%</td>
<td>Conventional PCR</td>
<td>Lower</td>
<td>The same</td>
<td>151</td>
</tr>
<tr>
<td>Analyte(s)</td>
<td>Detection method</td>
<td>Limit of detection</td>
<td>Clinical/field sample(s)</td>
<td>Clinical sensitivity</td>
<td>Clinical specificity</td>
<td>Benchmark method</td>
<td>Limit of detection of benchmark method compared to RPA</td>
<td>Clinical sensitivity of benchmark method compared to RPA</td>
<td>Clinical specificity of benchmark method compared to RPA</td>
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<tr>
<td>A consensus region that covers all 7 S-segment clades of Crimean-Congo Hemorrhagic fever virus (CCHFV)</td>
<td>Real-time fluorescent detection</td>
<td>500 RNA copies (251 RNA copies by probit analysis)</td>
<td>21 extracted patient sera samples obtained in relation to outbreaks of CCHFV in 2013–2015 in Tajikistan</td>
<td>88%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>—</td>
<td>Higher</td>
<td>The same</td>
</tr>
<tr>
<td>Canine parvovirus 2 (CPV-2) nucleocapsid protein gene (BEFV) G gene of bovine ephemeral fever virus (BEFV)</td>
<td>Real-time fluorescent detection</td>
<td>10 copies of recombinant plasmid</td>
<td>91 fecal swab samples collected from the dogs from 2012 to 2016 104 clinical blood specimens and 24 tissue samples including 16 lung tissue specimens, 8 lymph gland specimens collected from suspected dairy cattle cases of BEFV infections in eastern China</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>10 copies of recombinant plasmid</td>
<td>The same</td>
<td>The same</td>
</tr>
<tr>
<td>IS900 gene of Mycobacterium avium subsp. paratuberculosis</td>
<td>Lateral flow strip detection</td>
<td>8 plasmid copies per reaction</td>
<td>320 individual fecal samples collected between September 2016 and September 2017 from 10 different dairy farms located in 10 distinct geographic regions of Shandong province, China</td>
<td>100%</td>
<td>97.63%</td>
<td>Real-time PCR</td>
<td>8 plasmid copies per reaction</td>
<td>The same</td>
<td>Higher</td>
</tr>
<tr>
<td>Pho FSC771 hypothetical protein gene of Francisella noatunensis subsp. Orientalis</td>
<td>Real-time fluorescent detection</td>
<td>10 plasmid copies (15 plasmid copies by probit analysis)</td>
<td>Samples of spleen (n = 78), head kidney (n = 78) and water (n = 5)</td>
<td>100%</td>
<td>84.89%</td>
<td>Real-time PCR</td>
<td>10 plasmid copies (11 plasmid copies by probit analysis)</td>
<td>The same</td>
<td>Higher</td>
</tr>
<tr>
<td>VP1 gene of Enterovirus 71 subgenotype C4 (EV71-C4)</td>
<td>Real-time fluorescent detection</td>
<td>3.767 log 10 genomic copies (LGC)</td>
<td>Stool samples (n = 44) collected in 2017 by Shenzhen Center for Disease Control and Prevention</td>
<td>100%</td>
<td>100%</td>
<td>Real-time PCR</td>
<td>2.026 log 10 genomic copies (LGC)</td>
<td>The same</td>
<td>The same</td>
</tr>
</tbody>
</table>
2.3 Template, primers, probe and their designs

RPA was initially demonstrated to be a nucleic acid amplification method for DNA,\(^6\) later it was shown that RNA also could be the template by addition of reverse transcriptase (e.g. Murine Leukemia virus (MuLV) reverse transcriptase) in the same reaction tube.\(^{46}\) Regardless of nucleic acid template type, the recommended RPA amplicon length should be below 500 nucleotides for efficient amplification. Most published RPA papers have applied amplicon lengths between 100 and 250 nucleotides, which usually incur fast and efficient amplification. However, shorter amplicons (79 nucleotides\(^{37}\) 94 nucleotides\(^{38-40}\) and longer amplicon up to 1500 nucleotides\(^{41}\) have also been reported.

Unlike PCR, the length of RPA primers is relatively long (a recommended minimum of 30 nucleotides, but typically between 32 and 35 nucleotides). Shorter PCR primers (typically between 18 and 25 nucleotides) can also be used in the RPA reaction but may decrease the reaction speed and sensitivity.\(^{42}\)

Application of short PCR primers in RPA has been demonstrated by Mayboroda \(\textit{et al.},^{43}\) Martorell \(\textit{et al.},^{37}\) Wang \(\textit{et al.}\)\(^44\) and Fuller \(\textit{et al.}\)\(^45\) The latter two authors have shown that the PCR primers used in RPA resulted higher analytical sensitivity of detection compared to their usage in PCR: RPA detected 100 DNA copies of genetically modified GTS 40-3-2 soybean and 3.5 pg of genomic DNA of Agrobacterium\(^46\) and Fuller \(\textit{et al.}\)\(^45\) The latter two authors have shown that the PCR primers used in RPA resulted higher analytical sensitivity of detection compared to their usage in PCR: RPA detected 100 DNA copies of genetically modified GTS 40-3-2 soybean and 3.5 pg of genomic DNA of Agrobacterium spp. respectively, while the benchmark method PCR detected 1000 DNA copies and 350 pg of genomic DNA respectively.\(^44,45\)

The company that sells the commercialised RPA reagents, TwistDx\(^{\text{TM}}\) Ltd (see section 2.4 and Tables 2 and 3 for more details) provides additional probes that can be incorporated during the RPA reaction. The TwistAmp\(^{\text{TM}}\) exo probe (typically between 46 and 52 nucleotides) and the TwistAmp\(^{\text{®}}\) fpg probe (typically between 32 and 35 nucleotides) are used for fluorogenic real-time detection (Fig. 3A and B). These two probes are usually labelled with a fluorophore, a quencher (e.g. Black Hole Quencher) that is in close proximity to the fluorophore, to temporarily deter the fluorescent signal, and a blocker (e.g. C3-spacer, a phosphate, a biotin-TEG or an amine) at the 3'-end serving to prevent polymerase extension from the 3'-end (Fig. 3A and B). The real-time detection is based on cleavage of fluorogenic probes at an abasic site (also known as an apurinic/apyrimidinic site that is a location in DNA (less often in RNA), which has neither a purine nor a pyrimidine base) between the fluorophor and the quencher. The abasic site can either be tetrahydrofuran (THF) or a dSpacer (a derivative of the THF) or a dR group (the deoxyribose of the abasic site) between the fluorophore and the quencher. The TwistAmp\(^{\text{TM}}\)™ exo probe at a THF or a dSpacer site, while the TwistAmp\(^{\text{®}}\)™ fpg probe cleaves the TwistAmp\(^{\text{TM}}\)™ fpg probe at the dR group (the deoxyribose of the abasic site via a C–O–C linker). The \(E.\ \text{coli}\) exonuclease III cleaves the TwistAmp\(^{\text{TM}}\)™ exo probe at a THF or a dSpacer site, while the glycosylase/lyase \(E.\ \text{coli}\) fpg cleaves the TwistAmp\(^{\text{TM}}\)™ fpg probe at the dR position (Fig. 3A and B). After the enzymatic cleavage, the TwistAmp\(^{\text{®}}\)™ exo probe can serve as a forward primer. However, the TwistAmp\(^{\text{TM}}\)™ fpg probe cannot serve as a primer due to different catalytic mode (beta-elimination) of the glycosylase/lyase \(E.\ \text{coli}\) fpg protein, which does not generate an extendable 3'-OH group but a 3'-phosphate group.\(^{46}\)

**Table 5 (Contd.)**

<table>
<thead>
<tr>
<th>Analyte(s)</th>
<th>Clinical sensitivity of method compared to RPA</th>
<th>Ref.</th>
<th>Limit of detection of benchmark method</th>
<th>Limit of detection of RPA method</th>
</tr>
</thead>
<tbody>
<tr>
<td>56 Kda gene of a Karp-like strain of Orientia tsutsugamushi</td>
<td>100%</td>
<td>The same</td>
<td>The same</td>
<td>The same</td>
</tr>
<tr>
<td>23S RNA gene of (C.\ \text{burchardii})</td>
<td>100%</td>
<td>The same</td>
<td>The same</td>
<td>The same</td>
</tr>
</tbody>
</table>

\(\text{RT: reverse transcription.}\)

[A link to the article online]
A third probe, the TwistAmp™ LF (typically between 46 and 52 nucleotides), is used for lateral flow strip detection (Fig. 3C). This probe is labelled at the 5′-end (e.g. with fluorescein), has a blocker at the 3′-end, and an internal abasic site (THF or dSpacer). The Nfo endonucleases IV cleaves at this abasic site of the TwistAmp™ LF probe, and generates an extendable 3′-OH group for polymerisation. However, unlike the E. coli exonuclease III which degrades most of the amplicons during RPA reaction, the Nfo endonuclease IV generates a slower signal and incomplete cleavage to avoid amplicon degradation (also see section 2.8). Therefore, the TwistAmp™ LF probe can also be used for cases when gel electrophoresis (GE) is chosen as a detection method.

To select suitable RPA templates and to design primers and probes, users can refer to the criteria suggested in the TwistAmp™ reaction kit manual. In brief, (1) GC content of the DNA template should be between 40% and 60%, and should avoid long homo-polymer tracks, few direct/inverted repeats and palindromes; (2) GC content of the primers should be between 30% and 70%, and should avoid long tracks of guanines at the 5′-end but recommend cytidines; and (3) guanines and cytidines are recommended at 3′-end of the primer for improved performance. From the RPA literature, it is further recommended that users evaluate the melting temperature, hybridisation stability, secondary structures and dimer formations among these oligonucleotides. Specific softwares such as BioEdit version 7.0.5.3, Primer3, UNAFold, mFOLD, Oligoanalyzer 3.1 (IDT, Leuven, Belgium), PrimerQuest software (Integrated DNA Technologies, Coralville, IA) and Visual OMP (DNA software, MI, USA) have been used in the literature for analysing RPA oligonucleotide properties. An effective way to avoid primer dimer formation is to employ self-avoiding molecular recognition systems (SAMRS), by including SAMRS nucleotides 2-aminopurine-2′-deoxyriboside (A*), 2′-deoxy-2-thiothymidine (T*), 2′-deoxyinosine (G*) and N4-thyl-2′-deoxycytidine (C*) in the primers. The inclusion of these SAMRS nucleotides strategically replaces the hydrogen-bonding units from natural A pairs with T (and G pairs with C) to SAMRS A* pairs with natural T, SAMRS T* pairs with natural A, SAMRS G* pairs with natural C and SAMRS C* pairs with natural G. However, the SAMRS A* and SAMRS G* nucleotides do not interact with the SAMRS T* and SAMRS C* nucleotides respectively no matter what their concentration, and in this way, the undesired products due to primer dimer can be avoided during nucleic acid amplification. Such SAMRS system has been demonstrated in RPA.
RPA probes. A: TwistAmp™ exo probe. This probe is cleaved by the E. coli exonuclease III at the abasic site (e.g. tetrahydrofuran, THF) to depart the fluorophore from the quencher and generate an extensible 3’-OH group for polymerisation. B: TwistAmp™ fpg probe. This probe is cleaved by the glycosylase/lyase E. coli fpg at the dR position (the deoxyribose of the abasic site via a C–O–C linker) to depart the fluorophore from the quencher and generate a 3’-phosphate group which is non-extensible for polymerisation. C: TwistAmp™ LF probe. This probe is cleaved by the Nfo endonucleases IV at the abasic site (e.g. tetrahydrofuran, THF) to generate an extensible 3’-OH group for polymerisation. The DNA polymerases extend and displace from 3’-ends of the primers and cleaved probe to produce the minor amplicons (from the forward and reverse primers) and a displaced strand. The displaced strand combines with the labelled reverse primer, and leads to the production of a dual-labelled amplicon (the major amplicon) for the downstream sandwich assay detection.31

2.4 Commercial kits and instrumentation by TwistDx™

All the RPA reagents are available for commercial purchase through TwistDx™, a subsidiary of Abbott.56 The company provides various kits for RPA reactions that can be customised towards specific applications by the end user. The company also sells RPA kits for the detection of specific food-borne pathogens (e.g. Listeria monocytogenes, Campylobacter and Salmonella enterica) (Table 2). The company not only provides RPA reagents in liquid format, but also in lyophilised pellet format which allows in-field application. These lyophilised pellets have shelf-lives up to 12 weeks at 25 °C or up to 3 weeks at 45 °C.57 In addition, TwistDx™ offers a custom freeze-drying service to create RPA reaction pellets containing primers, probes, and concentrations of protein components or other components (e.g. internal control DNA or RNA species), which can be encased in various holding vessels with different volumes.58

Apart from various RPA reaction kits, TwistDx™ also develops tailor-made devices and accessories for RPA reactions; these devices and accessories enable incubation, dispensing, mixing, detection, power supply and portability (Table 3 and Fig. 4). The Twirla™ device is a hand-held sized battery-powered incubator, which allows up to six parallel RPA reactions and subsequent end-point detection (e.g. gel electrophoresis and lateral flow strip detection; Fig. 4A) (note that the Twirla™ is an upgraded version of an earlier Twista® device that does not support constant mixing during incubation, which has now been discontinued). Alternatively, the T8-ISO allows up to eight parallel incubations and two-channel real-time fluorescent detection per tube (Fig. 4B). The T16-ISO is an advanced version of the T8-ISO, which supports up to sixteen parallel reactions with three-channel fluorescent detection per tube (Fig. 4C). The T8-ISO and the T16-ISO can be powered by mains-power supply, micro USB, or PowerGorilla external battery (Fig. 4D). Moreover, all three incubators mentioned so far support magnetic mixing (programmed or constant) when fitted with Micro Ball(s) (0.2 mL; dispensed with Micro Ball Dispenser) in the reaction tube (Fig. 4E). For lateral flow strip detection, TwistDx™ provides four different lateral flow devices: Milenia HybriDetect 1, Milenia HybriDetect 2 (Fig. 4F), PCRD Nucleic Acid Detection (Fig. 4G) and U-Star Disposable Nucleic Acid Lateral Flow Detection Units (Fig. 4H). The Milenia HybriDetect 1 and the U-Star Disposable Nucleic Acid Lateral Flow Detection Units allow
single-plex detection while the other two devices allow duplex detection. All the lateral flow devices except for the PCRD Nucleic Acid Detection device are based on sandwich assay using gold nanoparticles as tracer; the PCRD Nucleic Acid Detection device employs carbon nanoparticles, which can be more sensitive than the gold nanoparticles.59,60 The Milenia HybriDetect are provided as strips, whereas the PCRD Nucleic Acid Detection strips are encased in a semi-sealed cartridge, and the U-Star Disposable Nucleic Acid Lateral Flow Detection strips are embedded in a sealed cartridge designed to enable the RPA reaction to flow to the strips in a completely closed environment that prevents cross-contamination of amplified products.

2.5 Influence of temperature and agitation

For RPA reactions to achieve optimal efficiency and analytical sensitivity, the choice of target sequence and the designs of corresponding primers and probe are the intrinsic determinants, however, the reaction temperature and agitation during RPA reaction are two of the most important contributing extrinsic factors.

The recommended RPA reaction temperature is between 37 °C and 42 °C,42 and Crannell et al.61 and Wang et al.44 have also demonstrated that RPA reaction can be performed using body temperature, which can be used advantageously for in-field application. However, several research groups have studied RPA reaction temperatures that lie outside of the recommended range.38,44,45,60,62–78 The largest temperature range was tested between 15 °C and 50 °C;62,64,69,70,76 and results indicated the marginal reaction temperature to produce a positive result should be greater than 30 °C.62–64,66,67,69,71,74,76,77 However, Sun et al.65 and Poulton and Webster60 showed that temperature as low as 25 °C could still generate a positive signal after RPA amplification and subsequent lateral flow strip detection. Moreover, Lillis et al.63 showed that the ambient temperature also had an effect on RPA reaction: the RPA reaction was unstable if the ambient temperature was below 10 °C, however, extension of the reaction time could improve positive results attainability. Such reaction tempera-
ture range studies indicate that RPA reaction does not require precise temperature control.

While reaction temperature provides a suitable working environment for the RPA enzymes, agitation increases the interactions among the RPA components in a homogenous reaction solution. TwistDx™ recommends the user performing two times mixing steps for the RPA reaction, one is at the beginning of the process and the other is after 4 minutes of the reaction. The former is to mix all the RPA reagents to initiate the reaction, the latter is to prevent from local depletion of the reaction reagents, thereby increasing the reaction rate. Wambua et al. reported that threshold fluorescence values were reached in 5–8 minutes when agitation was performed after 4 minutes, whereas the time to reach detectable levels ranged between 8 and 14 minutes without this agitation. In addition, constant shaking throughout the RPA reaction has been shown to further accelerate the RPA reaction rate, achieve more stable positive results and improve sensitivity, especially when the template concentration is close to the limit of detection. Kersting et al. reported that constant shaking resulted in faster and more stable signals on the lateral flow strips than with the recommended two-shaking event. Kalsi et al. also reported that continuous mixing of microdroplets from a RPA exo assay led to faster time to result, increased fluorescence and improved sensitivity. In addition, Moody et al. built up a mathematical model and showed that mechanical stirring is better than manually shaking to eliminate inter-operator variations and obtain consistent quantitative experimental result; yet the ideal mixing frequency is assay dependent, and should be determined prior to the reaction. Nevertheless, if a shaking condition is not available, Lillis et al. demonstrated that a decrease of the reaction volume (e.g. from 50 µL to 5 µL) could compensate for the shaking effect, as smaller volume increased interactions between the reagents and oligonucleotides required for the amplification.

2.6 Tolerability to mismatches, inhibitors and background DNA

Apart from temperature and agitation, tolerability to mismatches, inhibitors and background DNA are other vital factors for efficient and sensitive RPA reaction. RPA has the ability to tolerate mismatches, and the highest mismatch tolerability reported so far is nine nucleotide base pairs across the primer and probe binding sites. Studies also showed that the mismatches at the 5′-end or centre of primers only mildly affect the RPA reaction, but mismatches located at the 3′-end of primers significantly affect the reaction. This is consistent with the RPA reaction mechanism (see section 2.2), since the polymerase extends the primers and probe (once cleaved) from the 3′-terminus. A useful application for such mismatch sensitivity at the 3′-end is to distinguish single nucleotide polymorphism (SNP). Yamanaka et al. applied this property to differentiate polymorphisms for the tobacco use disorder genes; the DNA polymerase extension was efficient when the 3′-terminal base of a primer matched its target, whereas the DNA polymerase extension was inefficient or non-existent when the 3′-terminal base was mismatched. However, of the general RPA mismatch tolerability (outside of the 3′-end of the primer) can be advantageous, as it enables some flexibility in primer design for highly polymorphic targets, where long conserved target regions are hard to locate. Conversely, the drawback of such mismatch tolerability is a tendency towards non-specific detection of closely-related species. Indeed, non-specific detections have been observed by Patel et al., Moore et al. and Yang et al. when detecting chikungunya virus, epidemic human norviruses and porcine circovirus Type 2, respectively.

When testing clinical or field samples, numerous substances (e.g. inhibitors) are either present or could be introduced during sample preparation and processing steps, which can potentially interfere with nucleic acid amplification. RPA has been demonstrated to tolerate certain (PCR) inhibitors, including: (1) haemoglobin (20 g L⁻¹), heparin (0.5 U) and urine (1.25%) showed no effect on RPA reaction; and (2) haemoglobin (50 g L⁻¹), ethanol (4% v/v) and urine (up to 5%), which only slightly affected reactions. However, RPA reaction was totally inhibited in the presence of SDS (0.05% v/v) and urine (10%). It was also observed that RPA reactions were more susceptible to inhibitors when the DNA template concentration was close to the limit of detection.

However, it is also important to carefully consider the choice of extraction buffer or incubation medium for the sample preparation and processing steps, as these working solutions may also contain potential inhibitors. For example, Valasevich and Schneider found that Cetyltrimethyl ammonium bromide (CTAB) DNA extraction buffer strongly inhibited RPA reaction. Similarly, Liu et al. found that selenite cystine broth (bacterial enrichment medium) significantly affected RPA reactions, resulting in a large number of primer dimers that led to false positive results on the lateral flow strip detection.

In addition to tolerating inhibitors, RPA is capable of amplifying target nucleic acids in the presence of background DNA. However, similar to the tolerability for inhibitors, the tolerability for background DNA is also concentration dependent. Clancy et al. observed that the RPA reaction was significantly inhibited when 400 ng of background human DNA was present, but was much less inhibited when 200 ng of background human DNA was present. Rohrman and Richards-Kortum showed that RPA was completely inhibited by 0.5 µg of sheared salmon sperm DNA when 50 copies of human immunodeficiency virus-1 (HIV-1) target DNA were present, while only inhibited by 2 or 5 µg of sheared salmon sperm DNA when 10⁴ or 10⁵ copies of the target DNA were present respectively. In addition, Rohrman and Richards-Kortum also pointed out that the primer, probe and target sequences used in the assay could influence the maximum background DNA concentration tolerability. Both HIV-1 and Plasmodium falciparum RPA assays were completely inhibited by 2 µg of sheared salmon sperm DNA respectively when 10⁴ copies of HIV-1 and Plasmodium falciparum target DNAs were present. However, when the same amount of target DNA were present...
(10^3 copies), the Entamoeba histolytica and Giardia duodenalis assays were completely inhibited only by 1 and 0.5 µg of sheared salmon sperm DNA, respectively.\(^9\)

2.7 Nucleic acid labelling during RPA

One vital process for diverse down-stream RPA applications (e.g. lateral flow strip detection and enzyme-linked immuno-sorbent assay) is to incorporate labels into nucleic acid template during RPA reaction, so that the incorporated labels allow capture, detection and/or assist the signal generation of RPA assays. Such nucleic acid labelling can be achieved terminally using 5'-labelled primers or internally via labelled nucleotides.\(^9,40,98-104\) The labels used for nucleic acid labelling can be fluorescent entity (e.g. fluorescein), ligand (e.g. biotin) or even a short segment of nucleotides (overhang). Most terminal nucleic acid labelling using RPA employs both 5'-labelled forward and backward primers, such that the amplicons possess dual-labels that can be captured and detected by corresponding recognition molecules in down-stream assays. However, RPA only tolerates to certain labels via 5'-labelling process. Crannell et al.\(^10,5\) reported a failure of RPA incorporation of five different 5'-labels (Cy5, Cy3, bromodeoxyuridine, tetrachlorofluorescein and hexachlorofluorescein) compared to successful incorporation with three 5'-labels, Alexa Fluor488, fluorescein and digoxigenin.

For internal nucleic acid labelling during RPA, the reaction mixture can be supplemented with labelled nucleotides, mostly using digoxigenin-dUTPs, which randomly substitute dTTPs during polymerase extension to create labelled amplicons.\(^101-104\) In comparison to the terminal labelling, the internal labelling allows more labels to be incorporated into a single nucleic acid template, thus having more binding opportunities in down-stream assays. However, terminal labelling can be a better choice when the down-stream application is for a sandwich assay, as the two labels incorporated via terminal labelling are further apart (separated by the length of amplicon), which could prevent steric hindrance of binding if the labels were too close together.

2.8 Amplicon clean-up and post-amplification treatment

The above-mentioned issues have considered the conditions both before and during RPA reactions. In addition, post-reaction procedures are critical for successful RPA signal detections, and should be determined according to the intended use of RPA amplicons. The generation of RPA amplicons are RPA reaction kit dependent. Usage of the TwistAmp® Basic kit (also the Basic RT kits) produces a single amplicon from the forward and reverse primers. Conversely, usage of the TwistAmp® exo kit (also the exo RT kits) and the TwistAmp® fpg kits do not produce a single amplicon, the former is due to the exonuclease present in the reaction mixture digesting most of the amplicons during RPA reaction,\(^42\) and the latter is due to the glycosylase/lyase E. coli fpg cleavage generating a non-extensible 3'-phosphate group (also see section 2.3).\(^14\) For the TwistAmp® nfo kit, however, two types of amplicons are generated, due to the DNA polymerase displacement activity to the probe-primed template: a dual-labelled amplicon emerges as a short product from the probe and one of the primers, whereas a singly-labelled amplicon emerges as a longer product from the forward and reverse primers (Fig. 3C) (note that only the dual-labelled product will generate a positive signal in the test zone of a lateral flow strip detection based on a sandwich assay).\(^105-108\)

Nevertheless, the RPA amplicons are initially associated with proteins and crowding agents, and the resulting DNA-protein-crowding agent complexes prevent direct use of DNA molecules for gel electrophoresis detection.\(^109,110\) This is because these complexes affect the proper migration of the amplicons in gel electrophoresis, leading to a lump of smears on the gel pattern. Several methods have been reported in the literature to process RPA amplicons before gel electrophoresis detection, these include protein denaturation by heating (at 65 °C or 95 °C for 10 minutes) and detergent treatment (e.g. sodium dodecyl sulfate, SDS), enzymatic digestion (e.g. proteinase K), protein sedimentation via high-speed centrifugation and purification using commercial DNA clean-up kit.\(^7,109-113\) Among these methods, the heating method worked equivalently to the methods by proteinase K digestion or SDS treatment.\(^109,111\) However, heating at 65 °C for 10 minutes showed better result than that of heating at higher temperature (95 °C).\(^111\) SDS treatment (20% in loading buffer) generated brighter and thicker gel bands than the proteinase K digestion method (0.2 mg mL^-1 or 20 mg mL^-1);\(^109\) heating at 65 °C for 10 minutes generated equivalent brightness gel bands to the ones generated by SDS treatment method (5% or 10% in the loading buffer) in Londono and co-workers’ results, however, Kapoor and co-workers showed that the SDS treatment method (5% in the loading buffer) resulted in brighter gel bands than the heating method (65 °C for 10 minutes) but also resulted in a smear-like pattern above the target band.\(^111,112\) In comparison to the heating, proteinase K digestion and SDS treatment methods, usage of the commercial DNA clean-up kit produced only the target band but in a much lower band intensity.\(^7,109,111\) In addition, as an alternative method, centrifugation (3 minutes) to pellet RPA proteins showed equivalent performance to the heating method (65 °C for 10 minutes).\(^110\)

As with lateral flow strip detection, direct usage of RPA amplicons is possible, but it is recommended to dilute the amplicons with the running buffer (e.g. 1/100 dilution) before running on the strip to (1) improve its wicking performance\(^114\) and (2) avoid “ghost band” effects.\(^45,54,115-117\) Notably, Powell and co-workers pointed out that the viscous wicking problem on the lateral flow strip can be mitigated by replacing the high molecular weight PEG (5.5% 35 kDa; see also section 2.1) with the low molecular weight PEG (6.5% 3 kDa) in the RPA reagent formulae.\(^114\) Moreover, Powell and co-workers also developed methodology to alleviate the dilution step for lateral flow strip detection. They found that sometimes the RPA amplicons are being rendered unavailable in the “RPA globule” (the core of nucleic acid amplification which contains localised RPA reagents; Fig. 5A), the formation of which is highly associated...
2.9 Sensitivities and specificities

The sensitivities and specificities of RPA can be evaluated in two categories, namely analytical and clinical (or field). The analytical sensitivity indicates the lowest amount of analyte that an assay can detect (also known as limit of detection); the analytical specificity is the ability of an assay to measure one particular analyte rather than others in a sample. In comparison, the clinical sensitivity is the percentage of correct detection of positive clinical samples, while the clinical specificity is the percentage of correct detection of negative clinical samples.

From the analytical sensitivity and specificity perspective, RPA is very sensitive and can detect as little as a few molecules (copies) of the analyte, which approaches the analytical sensitivity of PCR (Table 5). Furthermore, ultra-sensitive detection down to even a single copy of the analyte can also be achieved in RPA (Table 4). In most cases, RPA is very specific for distinguishing one species from other non-closely related species, however, the natural function of these enzymes for performing homology directed repair becomes a disadvantage of RPA to discriminate towards closely-related species, especially when these species share high sequence similarity. Conversely, this indicates that RPA can tolerate to a certain degree of primers or probe mismatches to the target sequence (more details see section 2.6).

Apart from measuring the analytical sensitivity and analytical specificity, many researchers have applied RPA for testing clinical or field samples, and compared the results with a standard method (mostly PCR). From the summary Table 5, the clinical sensitivity of RPA is only half as sensitive as the benchmark method, whereas the clinical specificity of RPA is most of time as specific as the benchmark method. These results indicate that RPA may (in some cases only), mis-detect a positive sample (false negative), but is unlikely to show a false positive. In short, RPA is still at the beginning of undergoing clinical/field test evaluation, but not yet matured to be a routine test in the clinical/field settings.

3. Distinctive RPA detection methods

In the proceeding sections, we have discussed how RPA adapts to commonly used PCR detection methods, such as real-time fluorescent detection, gel electrophoresis and lateral flow strip detection. However, a myriad of different detection methods have been coupled with RPA, including flocculation assay, electrochemical, chemiluminescent, silicon microring resonator (SMR)-based photonic and surface-enhanced Raman scattering (SERS) detections. This section describes these distinctive RPA detection methods and discusses their advantages, which have enabled RPA assays to be more efficient and sensitive, yet sometimes simpler and faster.

3.1 Flocculation assay detection

Flocculation assay detection is based on a bridging flocculation phenomenon in colloid chemistry described by Ruehrwein and Ward (1952),158 and later explained by La Mer and Healy (in 1960s).159–161 The basic principle of bridging flocculation involves the use of long polymers to cross-link multiple particles and thus flocculate out of solution at a specific buffer condition (e.g. pH and salt concentration; Fig. 6). A RPA reaction in combination with a flocculation assay detection was first demonstrated by Wee and co-workers, where RPA amplicons greater than 100 bp (from a plant patho-
incurred no flocculation. Following from this first application, such RPA-flocculation assays were further applied to PCR. In comparison to the standard method reverse transcription-PCR, achieved 70% clinical sensitivity and 100% clinical specificity. The TMPRSS2:ERG biomarker underwent clinical sample test, and consequently the precipitated RPA amplicons on the magnetic bead surface cross-link multiple other RPA-magnetic bead conjugates, and thus flocculate out of solution, causing a sharp transition between solution phase and flocculate. RPA reactions with no or non-target template do not produce long “DNA polymer segments”, hence no flocculation takes place. Reprinted and reproduced with permission from ref. 163. Copyright 2015 Springer Nature.

Fig. 6 RPA in combination with flocculation assay detection. The RPA amplicons are incubated with magnetic beads at low pH buffer condition. Consequently, the precipitated RPA amplicons on the magnetic bead surfaces cross-link multiple other RPA-magnetic bead conjugates, and thus flocculate out of solution, causing a sharp transition between solution phase and flocculate. RPA reactions with no or non-target template do not produce long “DNA polymer segments”, hence no flocculation takes place. Reprinted and reproduced with permission from ref. 163. Copyright 2015 Springer Nature.

Fig. 7 RPA in combination with electrochemical detection. The example demonstrates electrochemical detection from a RPA-enzymatic assay. The RPA-enzymatic assay is performed in an asymmetric manner, where one of the RPA primers is pre-immobilised on the solid surface, and another RPA primer, together with the DNA template and RPA reagents are free in the solution. After the RPA reaction, streptavidin-conjugated horseradish peroxidase is added, and followed by addition of electrochemically active 3,3′,5,5′-tetramethylbenzidine (TMB). The generated electrochemical signal can be detected on a screen printed carbon electrode.

3.2 Electrochemical detection

Another alternative detection strategy for RPA is electrochemical detection, which employs electrochemically active compounds to produce a signal in relation to the amplified nucleic acids. Most electrochemical approaches for RPA detection measure amperometric signals from RPA-enzyme-linked immunosorbent (ELISA) assay or RPA-enzymatic assay (more details please refer to literature167) due to the electrochemically active property of 3,3′,5,5′-tetramethylbenzidine (TMB) (Fig. 7).68,101,102,165 Results suggest that electrochemical detection could be up to 105-fold more sensitive than optical detection (by ELISA). Alternatively, Ng et al. and Lau et al. have applied gold nanoparticles as signal transducers for RPA amplicons detection. The gold nanoparticles can selectively bind to the RPA amplicons via specific conjugation, and transfers concentration of RPA amplicons into a measurable electrochemical signal. Again, such electrochemical detection exhibited high analytical sensitivity; Ng et al. was able to detect as low as 1 CFU of Mycobacterium tuberculosis bacilli DNA, while Lau et al. could detect down to 214 pM of Pseudomonas syringae (pathogenic bacteria for crops) DNA, which is 100 times more sensitive than RPA-GE detection. Recently, Tsaloglou et al. applied [Ru(NH3)6]3+ as an electroactive mediator for RPA-electrochemical detection. The [Ru(NH3)6]3+ can bind to the double-stranded DNA analogous
to the intercalating fluorescent dye SYBR Green I, consequently causing a drop in the diffusion-controlled current as more double-stranded DNAs are synthesised during RPA. This ruthenium compound-based electrochemical detection achieved 11 CFU mL⁻¹ of Mycobacterium tuberculosis analytical sensitivity, which is even more sensitive than the GeneXpert MTB/RIF (Cepheid Inc.) detection (a World Health Organisation recommended tuberculosis diagnostic system that employs PCR real-time fluorescence detection; 131 CFU mL⁻¹).

It is obvious that the RPA-electrochemical detection is advantageous for high analytical sensitivity. In addition, RPA-electrochemical detection is fast, low cost and field amenable, as it can be implemented easily with small components manufactured by inexpensive materials (e.g. screen printed carbon electrodes) with signal measured using a portable device (e.g. µSTAT 400 bipotentiotstat/galvanostat).¹⁰¹

3.3 Chemiluminescent detection

As an alternative to the fluorescent probe-based detection that requires a light source, RPA reactions can also be detected via chemiluminescence. The chemiluminescent detection converts chemical energy into the emission of visible light (luminescence) as the result of an oxidation or hydrolysis reaction.¹⁶⁹ Seidel’s research group has been applying RPA coupled with chemiluminescent detection of water-borne microbes on flow-based microarrays.¹⁷⁰,¹⁷¹ Their chemiluminescent detection employs conversion of energy from oxidation between luminol and peroxide catalysed by horseradish peroxidase to give off luminescent signals detected by a charge-coupled device (CCD) camera (Fig. 8).¹⁷⁶,¹⁷⁷ Seidel and co-workers first demonstrated a triplex detection of Human adenovirus 41 (HAdV 41), Phi X 174 (a virus) and the bacterium Enterococcus faecalis on the chemiluminescent flow-based microarray, and achieved the limit of detections of 35 genomic units (GU) µL⁻¹, 1 GU µL⁻¹ and 5 × 10³ GU µL⁻¹, respectively.¹⁷⁶ The limit of detection of HAdV 41 was in the same range as the TaqMan-qPCR result reported by Heim et al. (15 GU µL⁻¹).¹⁷² The limit of detection of Enterococcus faecalis was one order of magnitude lower than the reported RPA-electrochemical detection (of a Francisella tularensis, 2 × 10⁴ GU µL⁻¹) by Del Rio et al.¹⁶⁶ Seidel and co-workers’ second demonstration was a duplex detection of Legionella spp. and Legionella pneumophila, and they achieved the limit of detection of 87 GU µL⁻¹ and 26 GU µL⁻¹, respectively.¹⁷¹ The Legionella spp. could be quantified over four log-steps while the Legionella pneumophila could be quantified over five log-steps.¹⁷¹ In short, the chemiluminescence detection is highly sensitive, having long and stable dynamic range, and is a good candidate for coupling with portable detection device (e.g. a smart phone) in comparison to the fluorescent probe-based detection.

3.4 Silicon microring resonator (SMR)-based photonic detection

Detection of RPA reactions can also be performed using silicon microring resonator (SMR)-based photonic detection, which involves performing nucleic acid amplification in an asymmetric manner (pre-immobilised on one of the primers on the SMR, and all the other oligonucleotides and reagents are free in the solution, see also section 4.2) in the evanescent field of a resonator waveguide.¹⁷³–¹⁷⁵ The binding of nucleic acids to pre-immobilised primers induces changes in the refractive index proximal to the waveguide surface. As the nucleic acid amplification progresses, the wavelength shift due to binding can be monitored in real-time on the SMR (Fig. 9). The SMR-based photonic detection is an alternative detection method for fluorophore-based real-time detection, yet is label-free and much more sensitive. Shin et al.¹³⁰ achieved the limit of detection for a 10⁻¹-fold diluted sample for Mycobacterium tuberculosis detection using real-time PCR, while they could detect down to a 10⁻⁶-fold diluted sample when using RPA-SMR detection. Sabaté del Rio et al.¹⁷⁶ demonstrated that RPA-SMR (2 fg µL⁻¹) was 1000 times more sensitive than the real-time PCR (5 pg µL⁻¹) for the detection of Francisella tularensis. Jin et al.¹⁵¹ showed that real-time PCR could only detect greater than 30% of the mutant allele in wild-type KRAS (a mutant gene in colorectal cancer) populations, while the RPA-SMR detection could detect 1% to 100% of the mutant allele. Since several silicon microrings can be accommodated on the resonator surface, a multiplexed RPA assay is achievable simultaneously on multiple microrings in parallel (also see section 4.2). Liu et al.¹¹¹ demonstrated a duplex detection of IS6110 and IS1081 insertion sequences of Mycobacterium bovis Bulgarian BCG using RPA-SMR assay, and achieved 3.2 and 12 genomic DNA copies per reaction analytical sensitivity respectively. Dao et al.¹¹⁷ also demonstrated a duplex RPA-SMR assay for the detection of Salmonella Typhimurium and Brucella ovis, and they could identify 50 CFU (in 10 mL urine) and 100 CFU (in 10 mL urine) respectively. In comparison to the...
multiplex fluorophore-based real-time detection, the multiplex SMR-based photonic detection mitigates potential signal interferences due to fluorophore spectrum overlap, as the wavelength shifts are measured individually on each silicon microring.

3.5 Surface-enhanced Raman scattering (SERS) detection

The final method to be highlighted for RPA detection is surface-enhanced Raman scattering (SERS). This is the phenomenon of when a laser excites nanoscale roughened metal surfaces (e.g. gold or silver), which resonantly drives surface charges, creating a highly localised (plasmonic) light field. When a molecule is absorbed, or lies close to, the enhanced field at the surface, a large enhancement in the Raman signal can be observed.\(^{178}\) SERS is a highly sensitive spectroscopic detection technique, which shows narrow and distinct spectral peaks of the detection molecules, and is particularly prominent for multiple target molecules detection (Fig. 10). Wang et al.\(^ {179}\) demonstrated a duplex RPA-SERS assay for the detection of two prostate cancer biomarkers T1E4 and RN7SL1. The peaks assigned to the phosphate backbone (913 cm\(^{-1}\)), purines (560, 742 and 1334 cm\(^{-1}\)) and pyrimidines (1632 cm\(^{-1}\)) could readily be observed in the SERS spectral profiles of both T1E4 and RN7SL1 target amplicons. Lau et al.\(^ {98}\) demonstrated a triplex RPA-SERS detection of plant pathogens (Botrytis cinerea, Pseudomonas syringae and Fusarium oxysporum); distinct peaks corresponding to the three pathogens (due to the labelled Raman reporters) could be clearly displayed on the spectrum. Their results also showed that the RPA-SERS detection (2.3 DNA copies) was 100 and 10,000 times more sensitive than RPA-Gel electrophoresis (GE) (2.32 × 10\(^2\) DNA copies) and PCR-GE (2.3 × 10\(^4\) DNA copies) detections, respectively. Koo et al.\(^ {99}\) however, has demonstrated the up-to-date highest multiplexity of RPA-SERS assay, a penta-plex...
detection of prostate cancer biomarkers (T1E4, T1E5, PCA3, ARV7 and RN7SL1). Distinct peaks corresponding to each prostate cancer biomarker was well-separated and clearly observed at 1075 cm$^{-1}$ (T1E4), 1175 cm$^{-1}$ (T1E5), 1285 cm$^{-1}$ (PCA3), 1338 cm$^{-1}$ (ARV7) and 1380 cm$^{-1}$ (RN7SL1). In comparison to the SMR-based photonic detection, the SERS detection is also a better suited alternative to the fluorescent-based detection, especially for multiplexed detection. The multiplex ability of SMR-based photonic detection is limited by the number of silicon microrings that can be accommodated on the resonator surface, while the multiplex ability of SERS-based detection is limited by the number of Raman reporters (typically labelled to the target molecules) that produce sharp and unique peaks in the SERS detection.

4. Hot spots for RPA development

As demonstrated in the proceeding sections, RPA is a fast developing nucleic acid amplification technique with a growing number of applications and detection systems. In this section, we consider some of the upcoming “hot spots” for RPA development, and discuss their progress and limitations. In particular, we discuss critical advancements in moving RPA into an accurate quantitative technique through the use of digital RPA, as well as increasing the detection capacity through multiplexing. We also outline progress in realising the ability of RPA to break through the bounds of the laboratory for true field implementation, either through mobile laboratory setups (such as the “RPA in a suitcase”), microfluidic integration, or simple single-step RPA procedures.

4.1 Quantitative RPA – digital RPA

One of the most important developments of RPA is to quantify nucleic acid amplification, as quantitative nucleic acid amplification can be informative of gene expression levels, enabling better understanding of biological mechanisms, such as gene regulation during replication or pharmacological treatments, or distinguishing symptomatic from asymptomatic infection. However, unlike the classical real-time PCR (or quantitative PCR), real-time RPA is not considered to be robust for nucleic acid quantification. This is because the RPA reaction employs a chemical start (by adding the magnesium acetate) rather than a thermal start (by increasing reaction temperature to 95 °C), thus the reaction starting point cannot be precisely controlled. In addition, PCR is synchronised during each thermal cycle, as the annealing occurs only at low temperature, while there is no such synchronisation in RPA, as the annealing takes places all the time at the optimal reaction temperature range. Because of these reasons, RPA generates non-linear calibration curves for quantification.

Nevertheless, the quantification of nucleic acids can be achieved using digital RPA that alleviates calibration curves by the ability of absolute quantification. Digital RPA involves fractionating a nucleic acid sample into thousands to hundred thousands of micro- to pico-litre volume compartments. Nucleic acid amplification subsequently occurs in each individual compartment. The amplification is usually detected via fluorescent probe, and compartments that encase nucleic acid from the sample will give rise to fluorescent signals. At the end of amplification, counting the positive and negative droplets gives precise, absolute quantification of the initial amount of nucleic acid template based on Poisson statistics (the targets end up in partitions independently and with a fixed rate). The published digital RPA reactions can be based on pre-fabricated partition and droplet partition of nucleic acid sample (Fig. 11).

The pre-fabricated partition employs a large amount of “mini-cavities” – wells that can hold a defined volume, which allows massively parallel nucleic acid amplifications. One demonstration of such pre-fabricated partition-based digital RPA is the slipchip. The slipchip contains two plates (top and bottom) containing wells and ducts which are pre-loaded with RPA reaction reagents respectively. The RPA reaction is initiated only when the top and bottom plates are aligned in a specific configuration by slipping. Tsaloglou et al. demonstrated a slipchip which allowed 8 parallel RPA reactions (each of the eight reactions comprises 500 nL of volume) for the detection of Clostridium difficile, and achieved a limit of detection of 1000 DNA copies. Shen et al. also demonstrated a slipchip that allowed 1550 parallel RPA reactions (each with 9 nL of volume) for methicillin-resistant Staphylococcus aureus (MRSA) detection, and achieved a limit of detection of 300 copies per mL of genomic DNA (Fig. 11A(i)). The other demonstration is on a “microcliff” structured microchip (Fig. 11A (ii), (iii)). Unlike the slipchip, the sample (nucleic acid and RPA reagents) delivery in this microchip is via passive polydimethylsiloxane (PDMS) degas pumping that alleviates external pumps and power source. RPA incubation starts once the sample is delivered into the wells. The “microcliff” structured microchip demonstrated by Yeh et al. encased 200 to 1500 wells (30–100 nL per well), which allowed detection of 10–10$^8$ copies per μL of MRSA DNA. Another demonstration of pre-fabricated partition-based digital RPA is on a pico-liter well array (PWA) chip (27 000 wells, with each well of 314 pico-litres, in a 6 cm$^2$ area; Fig. 11A(iii)). In this chip, the sample was evenly distributed into the wells using a scraping blade. The chip was sealed with oil to prevent evaporation before RPA incubation. The PWA chip could quantify serial dilutions of Listeria monocytogenes genomic DNA from 9 × 10$^{-1}$ to 4 × 10$^{-3}$ copies per well with an average error of less than 11% ($n = 15$).

The digital RPA by droplet partitions is based on water-in-oil emulsion and is generated by dispersing liquid within an oil phase. In this case, each generated droplet acts as an individual micro-reactor, which contains all the reagents for a miniaturised RPA reaction (Fig. 11B(i)). Schulier et al. is the first to demonstrate the RPA reaction in water emulsion-based droplets (also called digital droplet RPA, ddRPA), and they successfully quantified Listeria monocytogenes DNA (100, 215, 464 and 1000 copies) that was concordant to the number of copies measured with digital droplet PCR.
In summary, the digital RPA partitionates a RPA reaction into nano- or pico-litre sized cavities to allow absolute quantification of the starting nucleic acid. This provides an opportunity to reduce the quantitative variability associated with real-time fluorescent probe-based quantification, as it does not rely on calibration curves. In addition, the digital RPA quantification offers a robust and reliable method for nucleic acid detection and quantification.
cation is of significant value when testing samples that only contain negligible quantity (prospectively circulating tumour cells) in the original sample; the nucleic acid amplification from such samples can be overwhelmed in the tube (bulk) reaction, whereas, they become conspicuous in the digital RPA reaction.

4.2 Multiplex RPA

While quantitative RPA is critical to measure the amount of a single genetic marker in a system, multiplex testing is critical for assessing a series of different genetic markers, which can be equally important in gaining an improved understanding of a biological system, or for disease monitoring or detection. Multiplexing is highly preferred from a time and precision of understanding, as it greatly increases the result output per sample input in comparison to the single-plex detection within defined analytical turn-around time. Multiplex RPA reaction has been demonstrated either in a single tube (homogeneous) or in a parallel fashion (sometimes refers to heterogeneous). The single-tube multiplex RPA can be performed using single or multiple nucleic acid templates. For the former, Kim et al. performed a duplex detection of Campylobacter species: Campylobacter coli and Campylobacter jejuni [detection limits of each: 1 CFU mL\(^{-1}\) in pure culture and in chicken broth samples without enrichment; 3 log CFU g\(^{-1}\) in non-enriched egg and chicken meat samples; 1 CFU g\(^{-1}\) in enriched egg and chicken meat samples], and Wang et al. conducted a duplex assay to differentiate wild-type and gE-deleted vaccine pseudorabies [limit of detection of 100 viral DNA copies each]. However, the highest level of multiplexing is a triplex assay demonstrated by Piepenburg and co-workers for the detection of MRSA I, II and III genotypes (detection limits are 10 genomic copies each). For single-tube multiplex RPA using multiple different nucleic acid templates, a few duplex and triplex assays have been demonstrated for the detection of bacteria, parasites, fungus, genetic modified soybeans and prostate cancer biomarkers. In particular, Song and co-workers demonstrated the highest multiplexity via a 16-plex assay for pathogen detection by combing RPA reactions with LAMP on a microchip, which was termed a two-stage iso-thermal amplification [Fig. 12A]. In Song’s demonstration, a first-stage RPA reaction was applied to simultaneously amplify sixteen different DNA targets in the RPA reactor, while a second-stage LAMP reaction was performed in sixteen branching chambers that stemmed from the RPA reactor to amplify and detect the resultant RPA amplicons in parallel. Each of the branching chambers contained a specific set of primers and probe for amplifying a specific pathogen among a pool of sixteen RPA amplicons from the first stage reaction. The RPA-LAMP assay could detect down to 1 plaque-forming units (PFU) using Zika virus-American strain (mex 2-81, Mexico) as a demonstration (amplifying the DNA template with the present of 16 primer pairs), with a linear correlation between 5 PFU and 500 PFU.

Collectively speaking, the single-tube multiplex RPA reaction saves both reaction space and volume. However, further increasing multiplexing levels is very challenging. In the case of using a single nucleic acid template, the multiplex capacity is mainly restricted by the capacity to accommodate multiple genes within a certain length of consensus sequence. However, the main restriction becomes the non-specific interactions among multiple oligonucleotides (primers, probes and nucleic acid templates) when using multiple nucleic acid templates. Although Song and co-workers’ methodology alleviates such restriction (as long as there were few correct RPA amplicons generated in the first-stage reaction, despite concurrently produced non-specific amplicons, these correct RPA amplicons would be specifically further amplified via a second-stage LAMP reaction), their methodology is still limited by the capacity of primer concentrations in the first-stage RPA reaction.

In contrast to single-tube multiplex RPA, performing multi-plex RPA in a parallel fashion omits the non-specific interactions among multiple oligonucleotides. This is because (1) each single-plex RPA reaction occurs next to each other but is independent of each other (performed as homogeneous assays) or (2) the RPA reaction is performed in an asymmetrical manner (heterogenous assay), where one of the RPA primer is pre-immobilised on a matrix while the other RPA primer remains in the solution together with the DNA template (and probe), in this way, only the RPA amplicons will be captured on the matrix for detection.

The in-parallel multiplex RPA that adopts homogeneous assay format can be performed either in solution or on a solid phase. For the former, multiple amplicons from collateral single-plex RPA reactions (in tubes) are combined together and submitted to a subsequent multiplex detection method, exemplified by quantum dot beads-coated microwell detection (duplex), quantum dot-based flow cytometry detection (penta-plex) and SERS detection (penta-plex). For the latter, one demonstration is on the digital video disk (DVD) by Maquieira research group, and the resulting signals can be detected by a DVD player (Fig. 12B). The other demonstration is on an electrowetting-on-dielectric (EWOD) surface, where the EWOD-based RPA reaction droplets are controlled using electric current by varying electric energy across the thin dielectric film between the liquid and conducting substrate. Kalsi et al. demonstrated a triplex EWOD-based RPA reaction in a parallel format for the detection of three antibiotic resistant genes (CTX-M-15, KPC and NDM-1). Each single-plex droplet RPA reaction was independent of other single-plex droplet RPA reactions, and could perform a set of programmed operations including move, merge, split, dispense and mix in an automatic manner (Fig. 12C). The EWOD-based RPA reaction achieved the limit of detections of 1000 DNA copies of each antibiotic resistant gene, which is 100 times less sensitive than the bench-top RPA reactions. Another demonstration is on paper by Magro and co-workers, which they constructed a wax patterned five-layer paper device in three-dimensional (3D) origami configuration (Fig. 12D). Freeze-dried RPA reaction reagents were pre-stored on multiple individual wax patterned areas. Once the liquid sample
mixture was pipetted onto the sample inlet, the input liquid sample mixture could be distributed via capillary force between adjacent paper layers by folding, and ultimately reached specific areas that contained pre-stored reagents, to initiate RPA reactions.

Unlike the in-parallel multiplex RPA that adopts homogeneous assay format, the demonstrations of the in-parallel multiplex RPA that adopts heterogeneous assay format on solid surfaces. The majority of such assay performs multiplex RPA in an asymmetric manner on a microarray. Kersting et al. performed triplex RPA in a 4 × 6 microarray for the detection of Salmonella enterica, Neisseria gonorrhoeae and MRSA on the epoxy-silanised glass slides, and achieved detection limits of 10 CFU, 100 CFU and 10 CFU respectively.
Kunze et al.\textsuperscript{170} conducted triplex RPA in a 5 × 5 microarray for the detection of \textit{Enterococcus faecalis}, Human adenovirus 41 (HADV 41) and Phi X 174 virus on the poly(propylene glycol) diamine (DAPPG) coated glass slides (also see section 3.3), and achieved detection limits of 35 GU µL\textsuperscript{-1}, 1 GU µL\textsuperscript{-1} and 5 × 10\textsuperscript{3} GU µL\textsuperscript{-1} respectively. Another demonstration of such an assay is the performance of multiple single-plex RPA reactions on multiple silicon microrings fitted on a resonator surface, demonstrated by Liu \textit{et al.}\textsuperscript{113} and Dao \textit{et al.}\textsuperscript{177} (more details refer to section 3.4).

Taken together, the multiplex RPA in a parallel fashion has a much higher assay throughput, circumvents cross-reaction (among oligonucleotides) issues, and possesses higher multiplex capacity compared to the single-tube multiplex RPA. However, its degree of multiplexing is limited by (1) the number of available unique labels conjugated to multiple nucleic acid templates which permit distinctive detection; (2) the size of the reaction surface; and (3) EWOD-based RPA reaction is also limited by the minimum volume of the droplet that permits an effective reaction.

4.3 RPA in a suitcase for mobile laboratory

The ultimate purpose of isothermal amplification such as RPA is to take the nucleic acid testing away from the centralised lab to the field or resource-limited settings. Abd El Wahed and co-workers turned this thought into reality by miniaturising the RPA diagnostic into a standard suitcase (56 cm × 45.5 cm × 26.5 cm by size), dubbed diagnostics-in-a-suitcase (Dias; costs around 5000 Euro; Fig. 13A).\textsuperscript{197} The Dias contained all the reagents and equipment necessary for the real-time RPA assay to detect the emerging avian influenza A (H7N9) virus at the site of an outbreak. The reagents and the equipment were fixed in the foam at the base of the suitcase which acted as a shock absorber during transport; a solar panel and a power pack provided the power support; and the storage box was refillable whenever needed.\textsuperscript{197} The RPA-Dias detection of influenza A (H7N9) was successful, and achieved detection limits of 10 and 100 RNA copies for the detection of H gene and N gene, respectively.

This highly promising demonstration of the first RPA-Dias inspired Abd El Wahed and co-workers to perform further testing. They carried the Dias (a total weight of 23 kilograms including the aluminium case) to the field of both of Kedougou (Senegal) and Bangkok (Thailand), and set up a mobile laboratory for the real-time RPA detection of dengue virus (1–4 serotypes).\textsuperscript{121} The mobile lab was organised into 4 sites, including the RNA extraction, master mix, sample mix and detection (using a tubescanner, TwistDx, Cambridge, UK) in close proximity (Fig. 13B).\textsuperscript{131} All the reagents were cold-chain independent; the power was supplied either from a motor vehicle battery (via inverter) or from the solar panel. The real-time RPA assay performed successfully in such an open-air environment and observed no influence of dust on the assay quality. The clinical sensitivities and specificities tested in Kedougou (Senegal) and Bangkok (Thailand) were 98% and 100% and 72% and 100%, respectively.\textsuperscript{131} Later, Abd El Wahed and co-workers also carried the Dias to the local hospitals in Matoto (Guinea)\textsuperscript{134} and Mymensingh (Bangladesh)\textsuperscript{121} for the on-site detection of Ebola virus and \textit{Leishmania donovani}, respectively. The real-time RPA Ebola assay was able to correctly include positives (91% of clinical sensitivity) and exclude negatives (100% of clinical specificity);\textsuperscript{134} while the

![Fig. 13](image-url) Mobile RPA assay. (A): RPA in-a-suitcase. The standard suitcase (56 cm × 45.5 cm × 26.5 cm by size) contains all equipment and reagents for performing the real-time RPA assay. The equipment and reagents are imbedded into the foam or fixed for stable portability. Reprinted with permission from ref. 197. Copyright 2015 Abd El Wahed et al. Published by Elsevier B.V. (B): A mobile laboratory set up from the “RPA in-a-suitcase”. The mobile lab is arranged into 4 sites in close proximity, including the RNA extraction, master mix, sample mix and detection. The RNA extraction area encompasses magnetic separator stand, vortex, rotator, 1.5~2 mL Eppendorf tube rack, automatic 100~1000 µL micropipette, micropipette tips, digital timer, 1.5 mL disposable plastic Eppendorf tubes and a waste container with autoclavable plastic bags. Both the master mix and sample mix areas contain vortex, minicentrifuge, automatic 1~10 and 10~100 µL micropipettes, micropipette tips, scissor and 0.2 mL tubes rack. The detection was done using the tubescanner (Twista device, TwistDx, Cambridge, UK). Reprinted with permission from ref. 131. Copyright 2015 Abd El Wahed \textit{et al.}.
4.4 Microfluidic integration of RPA assays

Apart from multiplex RPA reactions and mobile RPA reactions that provide increasing diagnostic efficiency and portability respectively, a growing attention has been focused on developing RPA assays that encompass both of the two merits. The solution is to integrate RPA amplification with other chemical processes on a miniaturised device using microfluidics. The major chemical processes to combine with RPA amplification for an intact diagnosis are sample preparation, amplification and signal detection. There have been a few examples of integrating RPA amplification with signal detection, however, only a few demonstrations have been performed integrating all of the three processes. Branavan et al.198 developed a microfluidics that integrated RPA amplification and fluorescent signal detection for the detection of sexually transmitted infections; Renner et al.17 developed a degas-actuated microfluidics that integrated multiplex RPA amplification and fluorescent signal detection for the detection of ESKAPE (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa and Enterobacter spp.) bacterial pathogens; and Hu et al.199 developed thin film transistor-based microfluidics that integrated RPA amplification and electronic signal detection for the detection of anti-microbial resistance genes. We note that all these three examples require the input of manually pre-mixed RPA reaction reagents. For fully integrated assays, one demonstration is the self-powered integrated microfluidic by Yeh et al.183 The self-powered integrated microfluidic integrated sample preparation (plasma separation from blood cells), digital RPA amplification (preparation-based) and detection (fluorescent-probe based) in an automatic manner via a built-in vacuum battery system (that frees the chip from external pumps sources for pumping).183 The self-powered integrated microfluidic was able to detect 2 × 10^5 copies per µL of HIV-1 RNA spiked in human blood within 18 minutes, and was able to quantitatively detect 10 to 10^5 copies per µL of MRSA DNA in water or directly from spiked human whole blood.183 Another demonstration of fully integrated assays is the application of centrifugal microfluidics that perform all the required procedure for RPA reaction in an automatic manner governing by centrifugal forces. Zengerle’s research group was the first one to demonstrate such performance. They developed a foil disc (Fig. 14A) that performs metering of the RPA rehydration buffer to re-suspend RPA reaction pellet, and subsequently aliquot the resulting mixture into five parallel reaction chambers that were pre-stored with oligonucleotides (primers, probe and DNA template).200 The foil disc was fitted onto a modified Rotor-Genie 2000, which executed centrifugation to manipulate the liquid movement between different chambers on the foil disc and real-time fluorescent signal detection. Followed up this demonstration, they developed another foil disc that integrated sample preparation (DNA extraction from blood plasma), nucleic acid amplification and fluorescent detection of Bacillus anthracis and Francisella tularensis.201 And this time, they tailor-made a portable LabDisk Player (approximately 18 × 28×15 cm^2 and 2 kilograms by weight) which could process the integrated chemical processes on the foil disc in an automatic manner. The fully integrated microfluidic RPA assay detected 6 × 10^4 genome equivalents of Bacillus anthracis and 6 × 10^6 genome equivalents of Francisella tularensis in less than 45 minutes.201 Their centrifugal microfluidics is the first true example of fully integrated RPA assay device, with the entire procedure from DNA extraction through to detection, in a fully automated fashion. Later, Kim et al.202 also developed a centrifugal microfluidics that integrated sample lysis, RPA amplification, metering, dilution and lateral flow strip detection of food-borne pathogens (Salmonella enteritidis; Fig. 14B). The centrifugal microfluidics was fitted onto a computer-controlled unit that included a spinning motor, a laser for sample lysis and a local heating apparatus to support RPA assay procedure. Their demonstration achieved the limit of detections of 10 CFU mL^-1 and 100 CFU mL^-1 in phosphate-buffered saline (PBS) and milk respectively with a total analysis time of 30 minutes.202 The foil-based microfluidics described above are a compact and affordable platform for performing integrated RPA assays, but they require complicated and expensive design and fabrication. Nonetheless, paper-based microfluidics can be an alternative for performing integrated RPA assays, as they can also conduct many of the functions of the foil-based microfluidics. Cordray and Richards-Kortum106 developed a paper-based microfluidics that integrated RPA amplification, dilution and lateral flow strip detection. All the reagents for this three processes were pre-stored in different paper pads, and were mixed with each other sequentially by pulling the sliders (Fig. 14C).202 Their paper-based integrated RPA assay could detect as few as 50 synthetic Plasmodium DNA copies, which was equivalent to the analytical sensitivity of the bench-top RPA-GE assay. In comparison, Magro et al.193 developed a 3D origami paper-based device that integrated multiplex RPA amplification and fluorescent signal detection (refer to section 4.2). The pre-stored reagents and oligonucleotides in different wax-patterned areas were rehydrated once the device is folded and dipped into water. Although the integration of RPA amplification and signal detection showed successful paper-based microfluidics, it required human intervention to complete the integrated RPA assay, as opposed to a fully integrated RPA assay on foil-based microfluidics. Moreover, it is very challenging to integrate sample preparation with RPA amplification and signal detection on paper-based microfluidics, not to mention in an automated execution. The reason is that it is very difficult to manipulate liquid movement on paper merely via capillary force, which is a weak force, and thus results in a slow moving process (despite of the liquid has a high wettability and the matrix is very hydrophilic and porous).
Overall, developing a microfluidically integrated RPA assay is a transition towards the realisation of fully automated sample-in-answer-out RPA assay to increase the diagnostic efficiency and portability. Nevertheless, the sample preparation step is the bottleneck to achieve this ultimate goal. In particular, some samples (e.g. blood) require multiple processing steps before the extracted nucleic acids are ready for the subsequent amplification and detection. Zengerle’s research group and Kim and colleagues’ work by employing multiple sample preparation chambers together with the amplification chamber (and detection chamber) on a single foil-based microfluidics, demonstrates one feasible way, albeit with challenging and costly microfluidics design and fabrication.

4.5 One-step RPA assays
A simple and feasible way to facilitate full automation of the RPA assay without introducing multiple sample preparation chambers is to perform a one-step RPA assay, or in other...
words, to perform RPA amplification directly from the crude sample (in the same tube). RPA has been able to amplify nucleic acids directly from crude samples, such as plant tissue extract,\textsuperscript{111,203} crude sap,\textsuperscript{79,112} soil and water samples,\textsuperscript{71} food samples (eggs and chicken meat)\textsuperscript{119} and vaginal swab lysate.\textsuperscript{137}

Nevertheless, Choi and co-workers were the first to demonstrate a fully integrated RPA assay on foil-based microfluidics that was facilitated by the one-step assay approach. Choi \textit{et al.} employed direct PCR buffer in RPA reaction for the detection of food poisoning bacteria (\textit{Salmonella enterica}, \textit{Escherichia coli} O157:H7 or \textit{Vibrio parahaemolyticus}).\textsuperscript{204,205} The direct PCR buffer was able to lyse the bacterial cells, inactivate amplification inhibitors from the lysed sample and was compatible to the RPA reaction system.\textsuperscript{204} The entire assay completed within 30 minutes, which was much shorter than the time required for a non-sample preparation integrated microfluidic or a sample preparation integrated microfluidic system (\textit{e.g.} at least 60 minutes). Although the direct RPA assay is a shortcut to assist full automation of foil-based microfluidics, there is no rule of thumb for the direct RPA assay buffer. This is because each sample has different lysis difficulty levels, and the effective lysis buffer may not be compatible with the RPA system and may also have potential impact on fluid movement within the microfluidics. Therefore, it is a trail-and-error process to identify such effective direct RPA buffers.

5. Conclusions and future perspectives

The PCR is a revolutionary watershed in nucleic acid test, however, isothermal nucleic acid amplification, as an alternative to PCR, has a lower requirement in heating conditions and performs nucleic acid replication more rapidly. RPA was a comparatively late introduced isothermal amplification method, however, it is one of the fastest developing methods. This is due to its true isothermal properties, simple reaction scheme, fast reaction time and excellent reports of sensitivity and specificity. In this review, we provide comprehensive knowledge of RPA technology: from its reaction components and mechanism, to the design of RPA assay and detection methods. In particular, we summarise many experimental tips from practical implementation, dispose clinical/field performance data and point out focused RPA development, to help researchers make better use of RPA and make contributions to boost its development.

RPA has just passed its first decade of development, and is now stepping into a next stage of evolution. We have considered some critical issues for future development. Firstly, more attention is needed for developing field-amenable sample preparation methods including concentration, extraction and purification, as this would largely facilitate a complete RPA assay for on-site or field application. Secondly, developing portable and fully automated RPA diagnostic devices is of paramount importance not only to further increase the diagnostic efficiency, but more importantly to bring RPA diagnostic closer to the layperson and people who live in places with poor healthcare infrastructure. Thirdly, RPA can be applied for developing wearable sensors by virtue of its close-to-body reaction temperature. Imagine if people can simply take some samples from their own body (\textit{e.g.} body fluid) and perform a fast RPA assay using their body temperature to detect potential pathogens, this could revolutionise RPA diagnostics to be a self-testing. Fourthly, unlike real-time PCR which is controlled by heat cycle, RPA employs continuous amplification after reaction initiation; it would be beneficial to develop a method or mechanism to precisely control the starting point of each RPA amplification cycle, so as to assist obtaining reliable quantitative RPA results (other than the absolute quantification by digital RPA). Fifthly, the current market share of RPA (7.08\%) is far less than that of PCR, and is less in comparison to other isothermal nucleic acid amplification methods (\textit{e.g.} SDA and LAMP). To boost its market share, more studies in comparative clinical validations between RPA and existing PCR assays can be performed. In addition, practical websites or software should be developed to ease and streamline the RPA primers and probe design, and screen for optimal oligonucleotide pairs for the reaction. Rationally speaking, RPA may not replace the status of PCR in years to come, but it can be a versatile complement of PCR. At this time point, RPA technology is maturing for application in the clinic, however, it is still at a transition period towards on-site or field application. With its continuous fast development, we foresee that RPA technology will ultimately become robust mobile and point-of-need applications in the future.

Conflicts of interest

There are no conflicts to declare.

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References

7 Isothermal nucleic acid amplification technology (INAAT) market analysis by product, by technology (NASBA, HDA, LAMP, SDA, SPIA, NEAR, TMA, RCA, RPA, SMAP2), and segment forecasts, 2018–2025, Report GVR-1-68038-588-5, Grand View Research, 2017.
91 A. Rosser, D. Rollinson, M. Forrest and B. L. Webster, *Parasites Vectors*, 2015, 8, 446.