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# 1 Invited critical review

# 2 Real-time PCR detection chemistry

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Real-time PCR is the method of choice in many laboratories for diagnostic and food applications. This technology 19 merges the polymerase chain reaction chemistry with the use of fluorescent reporter molecules in order to 20 monitor the production of amplification products during each cycle of the PCR reaction. Thus, the combination 21 of excellent sensitivity and specificity, reproducible data, low contamination risk and reduced hand-on time, 22 which make it a post-PCR analysis unnecessary, has made real-time PCR technology an appealing alternative Q7 to conventional PCR. The present paper attempts to provide a rigorous overview of fluorescent-based methods 24 for nucleic acid analysis in real-time PCR described in the literature so far. Herein, different real-time PCR chem- 25 istries have been classified into two main groups; the first group comprises double-stranded DNA intercalating Q8 molecules, such as SYBR Green I and EvaGreen, whereas the second includes fluorophore-labeled oligonucleo- 27 tides. The latter, in turn, has been divided into three subgroups according to the type of fluorescent molecules 28 used in the PCR reaction: (i) primer-probes (Scorpions, Amplifluor®, LUX™, Cyclicons, Angler®); (ii) probes; 29 hydrolysis (TaqMan, MGB-TaqMan, Snake assay) and hybridization (Hybprobe or FRET, Molecular Beacons, 30 HyBeacon™, MGB-Pleiades, MGB-Eclipse, ResonSense®, Yin-Yang or displacing); and (iii) analogues of nucleic 31 acids (PNA, LNA®, ZNA™, non-natural bases: Plexor™ primer, Tiny-Molecular Beacon). In addition, structures, 32 mechanisms of action, advantages and applications of such real-time PCR probes and analogues are depicted in 33 34 this review.

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# 60Q9 1. Introduction

 Higuchi et al. [\[1,2\]](#page-15-0) pioneered the analysis of Polymerase Chain Reaction (PCR) kinetics by constructing a system that detected amplifi- cation products as they accumulated. This "real-time" system included intercalating ethidium bromide in each amplification reaction, an adapted thermal cycler to irradiate the samples with ultraviolet light and detection of the resulting fluorescence with a computer- controlled cooled CCD camera. The increase in fluorescence was due to the intercalation of ethidium bromide into the increasing amounts of double-stranded DNA (dsDNA) produced during each amplification cycle. By plotting this fluorescence increment versus cycle number, the system produced a graph that provided a more complete picture of the PCR process than analyzing the accumulation of products by electrophoresis after the reaction.

 Very quickly, this technology matured into a competitive market, becoming commercially widespread and scientifically influential. This is evidenced by the large number of companies offering real-time PCR instrumentation as well as the rapid growth rate of scientific publi- cations pertaining to quantitative real-time PCR (qPCR). Such instru- mentation was first made available by Applied Biosystems in 1996 [3]. At present, Applied Biosystems and other companies such as BioGene, Bioneer, Bio-Rad, Cepheid, Corbett Research, Idaho Technology, MJ Research, Roche Applied Science, and Stratagene all offer devices for qPCR [\[4](#page-15-0)–6].

ar agrepti that provides a interesting per particular and properties per the meater of the meater and the meater of the meat The deployment of this interesting methodology is growing expo- nentially in many molecular biology and clinical laboratories and, hence, it is replacing conventional PCR. The main advantage of qPCR over the traditional PCR assays is that the starting DNA concentration is determined with accuracy and high sensitivity. Thus, the obtained re- sults can be either qualitative (showing the presence or absence of the DNA sequence of interest) or quantitative. In contrast, conventional PCR is, at best, semiquantitative. Moreover, the amplification reactions are run and data are analyzed in a closed-tube system, eliminating the need for post-amplification manipulation and therefore reducing opportunities for contamination [7–9]. Real-time PCR technology has proven its versatility and usefulness in different research areas in- cluding biomedicine, microbiology, veterinary science, agriculture, pharmacology, biotechnology and toxicology. It also offers interesting new applications, such as for the quantification and genotyping of pathogens, gene expression, methylated DNA and microRNA analysis, validation of microarray data, allelic discrimination and genotyping (detection of mutations, analysis of SNPs and microsatellites, identifica- tion of chromosomal alterations), validation of drug therapy efficacy, forensic studies and quantification of genetically modified organisms 104 (GMOs).

 Basically, the qPCR instrument consists of a thermal cycler with an integrated excitation light source (a lamp, a laser or LED: light emitting diode), a fluorescence detection system or fluorimeter and software that displays the recorded fluorescence data as a DNA amplification curve, it being necessary to add a dsDNA intercalating dye or fluorophore-labeled probe to the reaction mixture.

 In the last 15 years, a large number of methods for DNA detection in qPCR have been described. This review offers a useful classification as well as a detailed description of such detection methods. They have been classified into two principal groups based on the fluorescent agent used and the specificity of the PCR detection. The first group uses dsDNA intercalating agents such as SYBRGreen I and EvaGreen, leading to the detection of both specific and non-specific amplification products. On the other hand, the other group employs fluorophores at-119 tached to oligonucleotides and only detects specific PCR products. It has been further divided into three subgroups according to the type of fluo- rescent molecules added to the reaction: (i) probes acting as primers, called primer-probes; (ii) hydrolysis probes emitting fluorescent light upon degradation during the extension phase, and hybridization probes that give a fluorescent signal when binding to the DNA target during the amplification reaction; and (iii) analogues of nucleic acids. In addition to 125 their structures and mechanisms of action, advantages and applications 126 of each DNA detection method are described in this review. 127

# 2. PCR chemistries for the detection and quantitation of nucleic acids 128

There are two main proceedings of DNA analysis in qPCR: methods 129 enabling both specific and non-specific detection of amplified products 130 using dsDNA binding dyes, and those that only detect specific PCR prod- 131 ucts via employing fluorophore-linked oligonucleotides (primer-probes 132 or probes). [Table 1](#page-3-0) summarizes the structures, mechanisms of action 133 and advantages of the different fluorescent molecules used in qPCR. 134



There is a wide variety of commercially available fluorescent DNA 136 dyes, including ethidium bromide [1], YO-PRO-1 [\[10,11\],](#page-15-0) SYBR® Green 137 I [12], SYBR® Gold [13], SYTO [14,15], BEBO and BOXTO [\[16\],](#page-15-0) and 138 EvaGreen [17]. The use of DNA binding dyes allows the detection of 139 specific products, nonspecific products and primer-dimers produced 140 during the qPCR reaction. 141

**2.1.1. Structure** 142 The most commonly used is SYBR® Green I [\[18\]](#page-15-0), an asymmetrical 143 cyanine dye (2-[N-(3-dimethylaminopropyl)-N-propylamino]-4-[2,3- 144 dihydro-3-methyl-(benzo-1,3-thiazol-2-yl)-methylidene]-1-phenyl- 145 quinolinium) with two positive charges under standard PCR reaction 146 conditions contributing to its high dsDNA binding affinity [18–[21\].](#page-15-0) The 147 resulting DNA-dye complex absorbs blue light ( $\lambda_{\text{max}} = 497 \text{ nm}$ ) and 148 emits green light ( $\lambda_{\text{max}} = 520$  nm). More recently, several authors 149 have described that EvaGreen and certain SYTO dyes (-9,-13 150 and −82) are more stable and sensitive than SYBR Green I for DNA 151 quantification by qPCR [14,15,17,22,23]. 152

2.1.2. Mechanism of action 153 When such a dye binds to the minor groove of dsDNA, its fluores- 154 cence is increased and can be measured in the extension phase of 155 each cycle of qPCR [19]. Given that nonspecific products and primer- 156 dimers can be formed during the PCR process [24], a melting curve anal- 157 ysis is highly recommended to check the specificity of the amplified 158 fragments. This analysis consists of applying heat to the sample 159 (from 50 °C to 95 °C) and monitoring the fluorescence emission during 160 the process. The temperature of DNA denaturation is shown as a 161 sharp drop in the fluorescence signal due to dissociation of the dye. 162 Nonspecific products and primer-dimers are denatured at lower 163 temperatures than the specific products [12]. In fact, PCR products of 164 different length and/or nucleotide content show distinct peaks 165 when the derivative of fluorescence is plotted with respect to tempera- 166 ture (-dT/dF), due to the fact that they are denatured at different 167 temperatures. 168

### 2.1.3. Advantages 169

The costs of employing DNA binding dyes in qPCR are much lower 170 than those of methods requiring fluorescent probes. However, a melting 171 curve analysis is necessary after the completion of each qPCR assay for 172 selective detection of amplicons of multiplex PCRs. The most commonly 173 used is SYBR® Green I but, despite its popularity, it presents some 174 limitations, including limited dye stability and dye-dependent PCR 175 inhibition [\[14,22\]](#page-15-0). EvaGreen is a third generation dsDNA binding dye 176 that offers several advantages such as being less inhibitory to PCR 177 than SYBR® Green I, and it can be used under saturating conditions to 178 generate greater fluorescent signals. EvaGreen is also well suited for 179 HRM [high resolution melt] analysis [\[22\]](#page-15-0). 180

# 181 2.1.4. Applications

 These dyes can be used to detect either single or two or more different DNA sequences in a single PCR reaction (multiplex assays). SYBR® Green I is mainly employed for pathogen detection [\[25\]](#page-15-0), gene expression [\[26\],](#page-15-0) mutation detection, SNP detection and GMO (genetically modified organismos) detection [\[27\]](#page-15-0). Furthermore, EvaGreen is being used for pathogen detection [\[28,29\]](#page-15-0), gene expression [\[26\]](#page-15-0), mutation detection [\[30\]](#page-15-0), genotyping [\[31\]](#page-15-0), SNP detection [\[32,33\]](#page-15-0) and GMO detection [\[34\].](#page-15-0)

# 189 2.2. Fluorophore-labeled oligonucleotides

 Fluorophores are small fluorescent molecules that are attached to ol-191 igonucleotides in order to function as probes in qPCR technology. These fluorescent oligonucleotides are classified as either: (i) primer-probes, (ii) probes or (iii) analogues of nucleic acids.

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and multiplex (methods are classified as ether; (b) pinner-probes, 22.2.1.1.2. Applications, Scorpion prime-probe<br>
and particles are classified as ether; (b) pinner-probes, There are two types of fluorophores: donor or reporter and acceptor or quencher. When a donor fluorophore absorbs energy from light, it rises to an excited state. The process of returning to the ground state is driven by the emission of energy as fluorescence. This emitted light from the donor has a lower energy and frequency and a longer wave- length than the absorbed light and can be transferred to an acceptor fluorophore. If both fluorophores are within a specific distance, usually 10 to 100 Å [\[35](#page-15-0)–37], the transfer of excited-state energy from a reporter to a quencher is denoted as Fluorescence Resonance Energy Transfer (FRET) [\[38,39\]](#page-15-0). There are two different FRET mechanisms, based on how the energy transferred to the acceptor fluorophore is dissipated; (i) FRET-quenching [40] in which the electronic energy of the quencher (a non-fluorescent molecule) is dissipated as heat, and (ii) FRET in which the transferred energy is emitted as fluorescence because the acceptor molecule is fluorescent.

209 At present, there are a wide variety of donors and acceptors with 210 different excitation and emission spectra that can be used in qPCR [5].

#### 211 2.2.1. Primer-probes

 Primer-probes are oligonucleotides that combine a primer and probe in a single molecule. They can be classified into three groups: Harpins, Cyclicons and Angler® primer-probes. Fluorescence emitted from primer-probes is detected and measured during the denaturation or extension phase of the qPCR, depending on the type of primer-probe used. The use of these primer-probes can lead to amplification of unspe- cific products or dimer-primers during the PCR reaction; therefore, melting curve analysis to determine the efficiency of the reaction is recommended.

 2.2.1.1. Hairpin primer-probes. Hairpin primer-probes are single- stranded (ss) oligonucleotides that contain: (i) a hairpin secondary structure, in which the loop of the structure specifically binds to the tar-224 get DNA [\[7\]](#page-15-0); (ii) a short tail sequence of 6 nucleotides (CG) at the 5'-end of the probe complementary to the 3′-end region; (iii) one or two fluorophores attached at the ends [41]; and (iv) in some cases, the probe also contains a primer linked to the hairpin structure. Hairpin primer-probes include Scorpions, Amplifluor® and LUX™.

229 2.2.1.1.1. Scorpion primer-probes

**Q11** 2.2.1.1.1.1. Structure. Described in 1999 by Whitcombe et al.  $[42]$ , the hairpin structure has a reporter at the 5′-end and an internal quencher at the 3′-end. The 3′-end of the hairpin is attached to the 5′-end of the primer by a HEG (hexathylene glycol) blocker, which prevents primer extension by the polymerase [\[42\]](#page-15-0) [\(Fig. 1A](#page-5-0)).

 2.2.1.1.1.2. Mechanism of action. In solution, the reporter and quencher are in close proximity and energy transfer via FRET-quenching is produced. After binding of the primer-probe to the target DNA, the polymerase copies the sequence of nucleotides from the 3′-end of the primer. In the next denaturation step, the specific sequence of the probe binds to the complementary region within the same strand of newly amplified DNA. This hybridization opens the hairpin structure and, as a result, the reporter is separated from the quencher leading to a fluorescent signal proportional to the amount of amplified PCR 243 product [\[42\].](#page-15-0) 244

2.2.1.1.1.3. Advantages. The primer-probe combines the binding and de- 245 tection mechanisms in the same molecule, making it an inexpensive 246 system. Oligonucleotides with hairpin structures prevent the formation 247 of primer-dimers and non-specific PCR amplification products [\[43\]](#page-15-0) 248 because the intramolecular binding of such structures is kinetically fa- 249 vorable and highly effective. The use of stems offers additional benefits, 250 such as minimal background signals as the unincorporated primer- 251 probes are switched off [\[42\]](#page-15-0). Furthermore, in this system enzymatic 252 breakdown of the primer-probe is not necessary and the fluorescent 253 signals are stronger than those produced when other probes are used 254  $[44,45]$ . 255

2.2.1.1.1.4. Applications. Scorpion primer-probes can be used in single 256 and multiplex formats for pathogen detection [\[46\],](#page-15-0) viral/bacterial load 257 quantitation, genotyping, SNP allelic discrimination [\[47,48\]](#page-15-0) and muta- 258 tion detection [49,50]. It is important to note that the addition of a 259 nucleic acid analogue (LNA) to a Scorpion primer-probe containing 260 reaction is recommended in order to obtain greater accuracy in SNP 261 detection and allele discrimination, given that the thermal stability 262 and hybridization specificity of such probes are increased. 263

2.2.1.1.2. Amplifluor<sup>™</sup> primer-probes 264

2.2.1.1.2.1. Structure. Described by Nazarenko et al. [\[41\]](#page-15-0). This system was 265 later reported as the Sunrise system [51] and commercialized under the 266 name Amplifluor™ by Oncor/Intergen (Gaithersburg, MD; USA) [\[52\].](#page-16-0) 267 The reporter is located at the 5'-end and the internal quencher is linked 268 at the 3′-end of the hairpin. The 3′-end acts as a PCR primer [\[41\]](#page-15-0) 269 (Fig. 1B). 270

2.2.1.1.2.2. Mechanism of action. It is similar to that described for Scorpion 271 primer-probes. When the primer-probe is not bound, the hairpin struc- 272 ture is intact and the reporter transfers energy to the quencher via 273 FRET-quenching. DNA amplification occurs after binding of the 274 primer-probe to the target sequence. In the next step of denaturation, 275 reporter and quencher are separated and, as a result, the emitted fluo- 276 rescence of the donor is measured by the fluorimeter [\[41,53\].](#page-15-0) 277 2.2.1.1.2.3. Advantages. These probes display the same advantages as 278 those described previously for Scorpion primer-probes. 279

2.2.1.1.2.4. Applications. Amplifluor™ primer-probes can be used in 280 single and multiplex formats for pathogen detection, viral/bacterial 281 load quantitation [54], genotyping, allelic discrimination, mutation 282 detection, SNP detection [55] and GMO detection [\[27\]](#page-15-0). 283

2.2.1.1.3. LUX™ primer-probes 284

2.2.1.1.3.1. Structure. LUX<sup>™</sup> (Light-Upon-eXtension) primer-probes 285 were first described by Nazarenko et al. [43]. The 3′-end acts as a primer 286 and contains a single reporter located in the guanosine rich region of the 287 primary sequence [56]. Unlike Scorpion and Amplifluor primer-probes, 288 they do not require the presence of an internal quencher [\[43\]](#page-15-0) [\(Fig. 1C](#page-5-0)). 289 2.2.1.1.3.2. Mechanism of action. The hairpin structure confers the ability 290 to decrease the fluorescence signal when the primer-probe is free and 291 increases the signal exponentially when it binds to its target sequence. 292 The maximum fluorescence emission is generated after the incorpora- 293 tion of LUX™ primer-probes into dsDNA [43] [\(Fig. 1C](#page-5-0)). Fluorescence is 294 measured during the extension phase. The contract of the 295

2.2.1.1.3.3. Advantages. The advantages of this system are similar to 296 those methods that rely on Scorpions and Amplifluor primer-probes. 297 The employment of these primer-probes offers high sensitivity and 298 specificity despite their containing only a single fluorescent molecule 299 [\[57\].](#page-16-0) 300

2.2.1.1.3.4. Applications. They can be used in single and multiplex formats 301 for pathogen detection [\[58,59\]](#page-16-0), viral/bacterial load quantitation [\[57\],](#page-16-0) 302 genotyping, allelic discrimination, mutation detection, SNP detection 303 [\[43\]](#page-15-0) and gene expression analysis [\[56\]](#page-16-0) and GMO detection [\[27\]](#page-15-0). 304

### 2.2.1.2. Cyclicon primer-probes 305

2.2.1.2.1. Structure. Described by Kandimalla and Agrawal in 2000 306 [\[60\]](#page-16-0), cyclicons contain a long primer-probe (complementary to the 307

<span id="page-3-0"></span>

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ds: double stranded; 5": 5'end;  $\Omega$ : Hairpin probe; R: reporter; 3': 3'-end; Q: quencher; HEG: HEG (hexathylene glycol) blocker PCR; LUX: Light Upon Extension; FRET: Fluorescence Resonance Energy Transfer; Cy5: Acceptor m Croove Binders; Tm: melting temperature; FIUb: fluorophore-labeled uracil base; Ph: phosphate group; Cy5.5: Acceptor moiety (Cy5.5); PNAs: Peptide Nucleic Acids; ss: single stranded; NAs: locked Nucleic Acids; LNAs: Locked Nucleic Acids; idCTP: non-natural nucleotide; idGTP: non-natural nucleotide; MB: Molecular Beacon.

<sup>a</sup> qPCR phase in which the fluorescence is measured.

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 $\geq$  1

<span id="page-5-0"></span>

 target DNA sequence) and a short modified oligo attached through 5′–5′ ends, which binds to six-eight nucleotides at the 3′-end of the primer- probe forming a cyclic structure with two 3′-ends [\[61\]](#page-16-0) (Fig. 1D). Cyclicons have a reporter at the free 3′-end of the modified oligo and a quencher placed on a thymine base at the 5′-position in the primer-probe sequence [\[60\].](#page-16-0)

 2.2.1.2.2. Mechanism of action. In the absence of the target sequence, reporter and quencher molecules are in close proximity and energy transfer occurs via FRET-quenching (Fig. 1D). The binding of Cyclicon probes to DNA opens up the cyclic structure and leads to extension of the 3′-end primer-probe by DNA polymerase without any interference from the quencher. The 3′-end of the modified oligo is not extendible since it does not bind to the target DNA and because its 3′-end is blocked by a reporter. The separation between donor and acceptor molecules results in emission of fluorescence, which is measured during the exten-sion phase [\[60\].](#page-16-0)

324 2.2.1.2.3. Advantages. The integrated primer-probe structure of 325 cyclicons is an important benefit for DNA detection in qPCR systems. It 326 allows the use of shorter oligonucleotides, reducing the costs of the

assay, simplifies the reaction set up and avoids unnecessary carry-over 327 contaminations (Kandimalla and Agrawal, 2000) [\[60\].](#page-16-0) On the other 328 hand, the linkage between the long primer-probe and the short oligo 329 can also be through their 3′–3′-ends. In this case, Cyclicons would func- 330 tion as probes similar to TaqMan probes [\[44\]](#page-15-0) and Molecular Beacons 331 [\[45\]](#page-15-0) (see [Section 2.2.2](#page-6-0) Probes). Interestingly, it has been reported that 332 Cyclicons with a 5′–5′-attached structure give less fluorescence back- 333 ground in reactions with polymerases devoid of nuclease activity [\[60\].](#page-16-0) 334

2.2.1.2.4. Applications. They can be used in single and multiplex qPCR 335 for pathogen detection, viral/bacterial load quantitation, genotyping, 336 allelic discrimination, mutation detection and SNP detection. Cyclicons 337 can also be directly fixed to solid supports on chips for high-throughput 338 screening in solid-phase PCR [\[60\]](#page-16-0). 339

# 2.2.1.3. Angler® primer-probes 340

2.2.1.3.1. Structure. Described in 2002 by Lee et al. [\[62\].](#page-16-0) The probe 341 component is a DNA sequence identical to that of the target, which is 342 bound to a reverse primer through a hex-ethylene glycol (HEG) linker 343 [63]. It has an acceptor fluorescent moiety at its 5'-end. SYBR® Gold 344



Fig. 1. Structure and mechanism of action of primer-probes. (A) Scorpion; (B) Amplifluor®; (C) LUX™ and (D) Cyclicon; (E) Angler®.

<span id="page-6-0"></span>345 DNA intercalating dye is employed in the assay as the donor fluorescent 346 moiety [\[62\]](#page-16-0) [\(Fig. 1](#page-5-0)E).

 2.2.1.3.2. Mechanism of action. In solution, the primer-probe does not emit fluorescence since there is no donor fluorescent moiety close enough for FRET. When the Angler® primer-probe binds to its target DNA during the annealing step, DNA polymerase starts the extension of the 3′-end reverse primer. Subsequently, during the denaturation phase, the specific sequence of the probe binds to the complementary region of newly amplified DNA, producing a dsDNA fragment in which SYBR®Gold dye can be intercalated to generate fluorescence [\[39,64,](#page-15-0) [65\]](#page-15-0). Hence, the emitted fluorescence is measured during the denatur-ation step in each cycle.

 2.2.1.3.3. Advantages. The combination of a dsDNA intercalating agent and a primer-probe in qPCR allows non-specific (SYBR® Gold) and specific (Angler® primer-probe) amplified products to be distin- guished without performing melting curves. In the PCR instrument, the 520 channel of the optical detector is used to detect the fluorescent signal from non-specific intercalation of the SYBR® Gold dye while the 705 nm channel recognizes the signal generated by the specific binding of the Angler® primer-probe. This faster system offers better cost effec-tiveness than other methods [62].

 2.2.1.3.4. Applications. They can be used in single or multiplex formats for rapid detection of DNA, in studies of gene expression, allelic discrimination, genotyping, SNP detection, identification and quantita- tion of infectious organisms, and screening of environmental and biological samples.

### 371 2.2.2. Probes

372 The probes are oligonucleotides with an attached-donor and/or 373 -acceptor fluorophore. There are two types: hydrolysis and hybridiza-374 tion probes.

 2.2.2.1. Hydrolysis probes. Their mechanism of action relies on the 5′–3′ exonuclease activity of Taq polymerase, which degrades the bound probe during amplification. This also prevents performing a melting curve analysis. In this system, the fluorescence is measured at the end of the extension phase and is proportional to the amount of amplified specific product [\[66\]](#page-16-0).

381 2.2.2.1.1. TaqMan probes

 2.2.2.1.1.1. Structure. Described in 1991 by Holland et al. [44]. These probes are oligonucleotides containing a donor fluorescent moiety at the 5′-end and an acceptor fluorescent moiety at the 3′-end that quenches the fluorescence emitted from the donor molecule due to their close proximity [67]. The hydrolysis probe is designed to bind to a specific region of the target DNA [44] (Fig. 2A).

 2.2.2.1.1.2. Mechanism of action. In solution, the fluorescent signal from the donor fluorophore is suppressed by the acceptor fluorophore, although a residual fluorescence can be detected [68]. During the extension phase, the bound hydrolysis probe is degraded by the 5′–3′- exonuclease activity of DNA polymerase, generating fluorescence from the donor [\[67,69\].](#page-16-0) This process is repeated in each cycle without interfering with the exponential synthesis of the PCR products [67].

395 2.2.2.1.1.3. Advantages. The design and synthesis of TaqMan probes are 396 easy but if they are not well designed, primer-dimers might be formed 397 during qPCR assay.

 2.2.2.1.1.4. Applications. They can be used in single and multiplex formats for virus detection [\[70\]](#page-16-0), viral/bacterial load quantitation, gene expres- sion, microarray validation, allelic discrimination, mutation detection 401 [\[71\],](#page-16-0) SNP detection and GMO detection [\[27\].](#page-15-0)

402 2.2.2.1.2. MGB-TaqMan probes. Minor Groove Binding-TaqMan probes 403 are described in: MGB-conjugated DNA probes (see [Section 2.2.2.2.4\)](#page-8-0). 404 2.2.2.1.3. Snake assays

 2.2.2.1.3.1. Structure. This assay, described in 2010 by Kutyavin et al. [\[72\],](#page-16-0) combines Snake primers and TaqMan probes in order to amplify DNA regions with a high percentage of secondary structures [\[72\]](#page-16-0) [\(Fig. 2B](#page-7-0)).

2.2.2.1.3.2. Mechanism of action. Given that snake assays employ hydro- 409 lysis probes, the fluorescence signals are generated by the 5′-nuclease 410 activity of DNA polymerase over the probe [\[73\].](#page-16-0) In this system, target 411 DNA amplification and detection of fluorescence are two processes sep- 412 arated in time and space [\[72\].](#page-16-0) [Fig. 2](#page-7-0)B illustrates the mechanism of Snake 413 systems [\[72\].](#page-16-0) A forward primer containing a 5′-flap sequence binds to 414 the target DNA sequence site located downstream from the primer 415 binding site. Extension of this primer results in the synthesis of an anti- 416 sense strand, which provides a double stranded amplicon (stage A). 417 After strand separation (95 °C), a reverse primer hybridizes to the  $418$ antisense strand and DNA polymerase extends the complex (stage B), 419 resulting in another double stranded amplicon. Since the 5′-flap of 420 the forward primer functions as a template for DNA synthesis, a comple- 421 mentary sequence appears at the 3'-end of the sense amplicon strand 422 (stage C, linear form). After another round of strand separation, the 423 sense amplicon (synthesized in stage B) folds into a secondary structure 424 in which the 3′-terminal nucleotide remains mismatched (stage C, 425 folded form). The hydrolysis probe binds to the sense strand of the 426 amplicon creating an optimal cleavage structure for 5′-nuclease 427 (stage D). Then, this structure is subsequently cleaved in stage E, releasing 428 a detectable fluorescent signal, stage E [72]. 429

The Snake assay needs an asymmetric PCR format (reverse  $>$  forward 430 primer) because one DNA strand is preferentially amplified (sense 431 amplicon) [72,73]. 432

magnes: The combination of a stable method one interval parameter appear and controlled and the proposition of a stable method of a stable method in the magnet of the stable prior is a stable in the controlled proposition Fig. 2B also shows an alternative pathway which could be taken by 433 the sense amplicon during the PCR assay [72]. Briefly, there is a small 434 fraction of linear form (C) amplicon that might be accessible to a for- 435 ward 5'-flap primer (stage F). In this context, the strand DNA replication 436 would be accomplished through a passive hybridization (pathway 437  $C \rightarrow F$ ). In addition, the active hybridization of the forward Snake primer 438 in stage G might be followed by a strand displacement in stage H, which 439 substantially accelerates the replication process [\[73\]](#page-16-0). 440 2.2.2.1.3.3. Advantages. The Snake assay favors the use of short probes 441 with reduced fluorescence background [72]. Thus, the cost-effectiveness 442 ratio of such assays is less than that of TaqMan systems. However, special- 443 ized software is required for the primer design since the length and base 444

composition of the 5′-flap sequences in Snake primers determine the 445 stability of the secondary structures in the folded PCR amplicons [\[73\]](#page-16-0). 446 2.2.2.1.3.4. Applications. The assays can be used in single and multiplex 447 formats for pathogen detection, viral/bacterial load quantitation, gene 448 expression, microarray validation, allelic discrimination, mutation 449 detection and SNP detection [72]. 450

2.2.2.2. Hybridization probes. The fluorescence emitted by binding 451 hybridization probes can be measured either during the annealing or 452 the extension phase. The use of these probes allows amplified fragments 453 to be analyzed by performing melting curves, this being the main 454 advantage over hydrolysis probes. The amount of fluorescent signal 455 detected is directly proportional to the amount of the target amplified 456 during the qPCR reaction [66]. 457

2.2.2.2.1. Hybprobes or FRET probes 458

2.2.2.2.1.1. Structure. Hybprobes, also known as FRET probes, were first 459 described in 1985 by Heller and Morrison [74]. This system consists of 460 a pair of oligonucleotides binding to adjacent target DNA sequences 461 [\[75\]](#page-16-0). The first probe carries a reporter fluorophore at its 3'-end and 462 the second probe contains a quencher at its 5′-end and a phosphate 463 group attached to its 3′-end to prevent DNA amplification [\[39,75\]](#page-15-0) 464 [\(Fig. 3A](#page-8-0)). 465

2.2.2.2.1.2. Mechanism of action. The sequences of the probes are designed 466 to hybridize to the target DNA sequences in a head-to-tail orientation so 467 that the two fluorophores are in close proximity [\[76,77\]](#page-16-0). During the an- 468 nealing phase, in which the probes are adjacently bound, the quencher 469 emits fluorescence due to the fact that it has been previously excited by 470 the energy released from the reporter [\[78\]](#page-16-0) [\(Fig. 3](#page-8-0)A). 471

2.2.2.2.1.3. Advantages. It has been reported that the design and synthesis 472 of these probes as well as the optimization of the PCR reaction conditions 473

<span id="page-7-0"></span>

Fig. 2. Structure and mechanism of action of hydrolysis probes. TaqMan probe (A) and scheme of Snake system (B).

474 is quick and easy (http://www.fluoresentric.com/documents/HybProbe. 475 [pdf](http://www.fluoresentric.com/documents/HybProbe.pdf)).

 2.2.2.2.1.4. Applications. They can be used in the multiplex format for pathogen detection [\[79,80\]](#page-16-0), viral/bacterial load quantitation, microarray validation, genotyping [81], allelic discrimination, mutation detection and SNP detection.

## 480 2.2.2.2.2. Hairpin probes: Molecular Beacon Probes

 2.2.2.2.2.1. Structure. Molecular beacons were first described by Tyagi and Kramer [\[45\]](#page-15-0). They are single stranded hairpin shaped oligonucleo- tide probes divided into four parts: (i) a loop, a fragment of 18–30 bp complementary to the target DNA sequence; (ii) a stem, which is formed by two complementary sequences of 5–7 bp located at each end of the probe; (iii) a fluorescent reporter attached to the 5′-end and (iv) a non-fluorescent quencher attached to the 3′-end, which ab- sorbs the emitted fluorescence from the reporter when the Molecular Beacon probe is in closed form [\[82\]](#page-16-0) [\(Fig. 3](#page-8-0)B).

 2.2.2.2.2.2. Mechanism of action. During the annealing phase, this probe unfolds and binds to the target, emitting fluorescence since the reporter is not quenched any longer. This fluorescent signal is proportional to the amount of amplified PCR product. If the Molecular Beacon probe and target DNA sequences are not perfectly complementary, there will be no emission of fluorescence because the hairpin structure prevails over the hybridization [\[82\]](#page-16-0).

2.2.2.2.2.3. Advantages. The binding specificity of Molecular Beacon 497 probes is higher than that of fluorescent oligonucleotides because they 498 are able to form a hairpin stem. Hence, the use of such probes allows 499 discrimination between target DNA sequences which differ in a single 500 nucleotide [82]. However, employing Molecular Beacon probes requires 501 a thermodynamic study to ensure that the binding energy of the loop- 502 target is more stable than that of hairpin formation.  $503$ 2.2.2.2.2.4. Applications. They can be used in single and multiplex formats 504 for pathogen detection, viral/bacterial load quantitation, genotyping, 505 allelic discrimination, mutation detection [83], SNP detection, mRNA 506 analysis in living cells and GMO detection [\[27\]](#page-15-0).  $507$ 

2.2.2.2.3. Hybridization Beacon probes or HyBeacon™ probes 508 2.2.2.2.3.1. Structure. HyBeacon™ probes, described by French et al. [\[84\],](#page-16-0) 509 consist of ss-oligonucleotide sequences containing fluorophore moie- 510 ties attached to internal nucleotides, and a 3′-end blocker (3′-phosphate 511 or octanediol), which prevents their PCR extension [\[84\]](#page-16-0) [\(Fig. 3C](#page-8-0)). 512 2.2.2.2.3.2. Mechanism of action. The amount of fluorescence emitted from 513 hybridized HyBeacons when they bind to their target is considerably 514 greater than the emission of ss-probes in solution [\[84\]](#page-16-0). The fluorescence 515 is measured during the extension phase.  $516$ 2.2.2.2.3.3. Advantages. This system allows melting curve analysis to be 517

carried out to address the specificity of the amplified product and the 518 efficiency of the reaction. Other benefits displayed by the HyBeacon 519

<span id="page-8-0"></span>520 technology derive from their simple mode of action, ease of design and 521 relatively inexpensive synthesis [\[84\].](#page-16-0)

522 2.2.2.2.3.4. Applications. They can be used in single and multiplex analy-523 sis sequence for detection, DNA quantification, genotyping [\[85\],](#page-16-0) SNP

524 detection [\[86\]](#page-16-0) and allelic discrimination [\[87\]](#page-16-0).

 2.2.2.2.4. MGB-conjugated DNA probes. In the last years, several types of probes including TaqMan [\[88\]](#page-16-0), Pleiades [\[89\]](#page-16-0) and Eclipse [\[90\]](#page-16-0) have been attached through their 3′ or 5′ ends to Minor groove binding (MGB) ligands in order to improve target DNA-binding specificity and sensitivity.

 2.2.2.2.4.1. Structure. MGB ligands are small molecule tripeptides, including dihydrocyclopyrroloindole tripeptide (DIP) or 1, 2-dihydro-Q12 (3H)-pyrrolo [3.2-e] indole-7-carboxylate (CDPI) that form a non- covalent union with the minor groove of dsDNA [91–94]. This type of ligand selectively binds to AT-rich sequences, favoring the inclusion of aromatic rings by van der Waals and electrostatic interactions. This interaction produces very minimal distortion in the phosphodiester backbone but greatly stabilizes the DNA structure [92,95]. Some features of these MGB-probes are listed in Table 2.

2.2.2.2.4.2. Mechanism of action. As shown in [Fig. 4](#page-9-0), FRET-quenching 539 occurs when the random coiling form of the probe brings the non- 540 fluorescent quencher and the fluorophore reporter together. The 541 probe is straightened out when it binds to its target, causing an increase 542 in the fluorescent signal [\[90\]](#page-16-0).  $543$ 

2.2.2.2.4.3. Advantages. The highly stable interaction between the 544 MGB-probe and the target increases the  $T_m$  of the probe [\[96\]](#page-16-0) and pre- 545 vents the amplification of non-specific products [\[88\]](#page-16-0). Moreover, the 546 use of a non-fluorescent or dark quencher (NFQ) in the MGB-probe 547 greatly reduces the background fluorescence. This method enables 548 the use of shorter probes capable of detecting short conserved geno- 549 mic sequences. In addition, post-amplification melt-curve analysis 550 can be performed when MGB-Pleiades and MGB-Eclipse probes are 551 used. 552

2.2.2.2.4.4. Applications. They can be used in single and multiplex formats 553 for pathogen detection [97,98], viral/bacterial load quantitation [\[99,](#page-16-0) 554 100], gene expression, microarray validation, allelic discrimination, mu- 555 tation detection [101], SNP detection [72,102], GMO detection [\[27\]](#page-15-0) and 556 forensic analysis [103]. 557



Fig. 3. Chemistry of hybridization probes. (A) Hybprobes/FRET probe; (B) Molecular Beacon Probe and (C) HyBeacons™ probe.

<span id="page-9-0"></span>t1:1 Table 2

INIOD DIODCJ.					
MGB-probes	Reporter	NFO <sup>a</sup>	MGB	Probe type	Log fluorescence
MGB-TaqMan MGB-Pleiades MGB-Eclipse	$5'$ end $5'$ end $3'$ end	$3'$ end $3'$ end $5'$ end	$3'$ end $5'$ end $5'$ end	Hydrolysis Hybridization Hybridization	Extension phase Annealing phase Annealing phase

t1:7 MGB: Minor Groove Binding.

t1.8 a NFQ: non-fluorescent quencher.

# 558 2.2.2.2.5. ResonSense® probes

 2.2.2.2.5.1. Structure. ResonSense® probes and Angler® primer-probes have similar features. These probes, described by Lee et al. in 2002 [\[62\]](#page-16-0), have a Cy5.5 fluorescent-Fluor at the 5′-end as an acceptor fluores- cent moiety and a phosphate group at the 3′-end to prevent DNA polymeration. The real-time PCR reaction also contains the binding dye SYBR®Gold as fluorescence donor, which intercalates into the DNA duplex formed by the probe and its target [62,104] (Fig. 5A).

 2.2.2.2.5.2. Mechanism of action. In solution, fluorescence is not emitted from the probe due to the absence of a fluorescent donor close enough to the acceptor. During the annealing phase, energy transfer by FRET is produced as a result of simultaneous binding of the probe to the target and intercalation of the DNA dye into the probe-target duplex [39,64, [65\].](#page-15-0) The fluorescence signal is proportional to the concentration of target DNA sequences.

Fig. 4. Structure and mechanism of action of hybridization probes: MGB-probes. (A) MGB-

2.2.2.2.5.3. Advantages. The use of a DNA binding dye and a probe in the 573 same reaction allows the signal coming from both non-specific and spe- 574 cific amplified products to be monitored [\[46\]](#page-15-0). In addition, the synthesis 575

of this type of probe, which contains a unique fluor, significantly reduces 576 the assay costs  $[62]$ .  $577$ 2.2.2.2.5.4. Applications. They can be use in single and multiplex formats 578 for rapid detection, gene expression, allelic discrimination, genotyping 579 [\[105\]](#page-16-0), SNP detection, mutation detection [\[106\]](#page-17-0), identification and quan- 580 titation of infectious organisms (bacteria and viruses) and for analysis of 581 environmental and biological samples.  $582$ 

2.2.2.2.6. Yin-Yang probes or 'displacing probes' 583

2.2.2.2.6.1. Structure. These double-stranded probes are composed of 584 two complementary oligonucleotides of different lengths. The 5′-end 585 of the longer positive strand is labeled with a fluorophore reporter 586 and blocked with a phosphate group at its 3′-end, whereas the 3′-end 587 of the shorter negative strand contains a fluorophore quencher [\[107\]](#page-17-0) 588  $(Fig. 5B)$ . 589

2.2.2.2.6.2. Mechanism of action. In solution, the shorter negative oligo- 590 nucleotide, which acts as a competitor, forms a stable DNA duplex 591 with the longer probe. This interaction prevents the fluorescent 592 emission due to the fact that the reporter and quencher remain in 593 close proximity. During the annealing phase, the shorter strand is 594 displaced by the target leading to the emission of fluorescence. These 595 so-called 'displacing probes' were first reported in 2002 by Li et al. 596 [107]. In such a system, an ideal competitor must be competitive 597 enough to prevent non-specific hybridizations but not too much so, in 598 order to favor the formation of perfectly matched probe-target du- 599 plexes. The authors proposed that a single-stranded oligonucleotide 600 with the same nucleotide sequence but shorter than that of the target 601 would be a suitable competitor [107]. 602

2.2.2.2.6.3. Advantages. The binding of Yin-Yang probes to the target is 603 highly specific and their design is much easier than that of dual-dye-  $604$ labeled probes. In addition, their synthesis is cost effective because it 605 only involves a single-dye modification [107]. 606

2.2.2.2.6.4. Applications. They can be used in single and multiplex formats 607 for a wide-range of applications including pathogen detection or viral/ 608 bacterial load quantitation as well as mutations detection [\[108\],](#page-17-0) 609 analysis and genotyping SNPs  $[109]$ , in which discrimination single  $Q13$ nucleotide substitutes are required. Furthermore, the use of these 611 probes has been proposed for tracing mRNAs in living cells or for the 612 construction of biosensors and biochip detection devices [\[107\].](#page-17-0) 613

### 2.2.3. Nucleic acid analogues 614

Nucleic acid analogues are compounds that are analogous (structur- 615 ally similar) to naturally occurring RNA and DNA. An analogue may have 616 alterations in its phosphate backbone, pentose sugar (either ribose or 617 deoxyribose) or nucleobases [110]. Normally, the analogues incorporate 618 all of the advantages of native DNA but are more stable in biological 619 fluids and have increased affinity for complementary nucleic acid 620 targets [111]. 621

A variety of nucleic acid analogues have been described in the last 622 years (Fig. 6): 623



Some of these analogues, including PNAs, LNAs, ZNAs and non- 633 natural bases (iG and iC) are currently used for different real-time PCR 634 applications. 635

TaqMan hydrolysis probe; (B) MGB-Pleiades hybridization probe and (C) MGB-Eclipse hybridization probe.

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 $MCR$ -probe



<span id="page-10-0"></span>

Fig. 5. Structure and mechanism of action of hybridization probes. (A) ResonSense® probe and (B) Yin-Yang probe.

## 636 2.2.3.1. PNAs

 2.2.3.1.1. Structure. Peptide nucleic acids were first described by Nielsen et al. [\[113\]](#page-17-0). They are achiral and electrically neutral DNA ana- logues in which the sugar-phosphate backbone has been replaced by a peptide of N-(2-aminoethyl)-glycine units linked to the nitrogenous bases by metilencarbonilo [113,122]. PNA hybridizes to complementary oligonucleotides obeying the Watson–Crick hydrogen-bonding rules [\[123\]](#page-17-0) [\(Fig. 6A](#page-11-0)).

 PNAs are able to interact with either dsDNA or RNA with higher affinity and greater specificity than conventional oligonucleotides. This is due to its electrically neutral character, which prevents the phenom- enon of repulsion between chains [113,124]. This binding takes place by strand displacement rather than by triple helix formation [125]. This nucleic acid analogue is attached to a molecule of thiazole orange or a fluorophore for qPCR reactions [\[126\].](#page-17-0)

 2.2.3.1.2. Mechanism of action. The mechanism of primer-probes or probes in which PNA molecules have been introduced is identical to the method of action of conventional probes. Noteworthy, the binding of PNAs to double-stranded DNA does not interfere with their proper-ties as probes.

656 2.2.3.1.3. Advantages. PNA containing probes are more resistant to 657 nucleases and proteases and can interact with DNA at lower salt concen-658 tration than standard probes/ primer-probes [\[123,127,128\].](#page-17-0)

 2.2.3.1.4. Applications. Their high affinity for DNA allows such probes to interact easily with target dsDNA sequences by strand invasion [129–[131\]](#page-17-0). It is highly recommended to employ these nucleic acid ana-logues in order to induce DNA recombination or block PCR amplification of specific genes [132]. Uniquely, allelic discrimination of single nucleo- 663 tide polymorphisms can be accomplished by using PNA-molecular 664 beacons [133]. Furthermore, they can also be used in mutation detection 665 [134,135], pathogen mutation [136] and for discriminating between 666 DNA and cDNA sequences in prokaryotes [\[137\]](#page-17-0). 667

### 2.2.3.2. LNA® 668

2.2.3.2.1. Structure. Locked Nucleic Acids, first described by Wengel 669 and co-workers in 1998 [118,138,139], are DNA or RNA sequences in 670 A conformation that contain one or more modified nucleotides [\[139\].](#page-17-0) 671 Specifically, they have a methylene bridge between atoms 2′-O and 672 4'-C in the ribose ring to form a bicyclic ring [\[139\]](#page-17-0) [\(Fig. 6B](#page-11-0)). 673

2.2.3.2.2. Mechanism of action. LNA containing primer-probes 674 or probes exhibit the same mode of action as that of conventional 675 primer-probes or probes. 676

2.2.3.2.3. Advantages. Like the PNA system, LNA probes are resistant 677 to degradation by nucleases [\[140\]](#page-17-0). LNA® nucleotides are often used in 678 combination with non-modified DNA/RNA nucleotides to increase the 679 thermal stability of the probe [\[141,142\]](#page-17-0), resulting in a high specificity 680 for their target sequences [\[143,144\]](#page-17-0). [Table 3](#page-12-0) shows an example of the 681 increment in  $T_m$  values based on the number of LNA® nucleotides intro- 682 duced into the oligonucleotide. 683

2.2.3.2.3.1. Applications. LNA® nucleotides can be introduced into most 684 primer-probes and probes described in this review [\[145\].](#page-17-0) For instance, 685 the use of LNA-Molecular Beacon and LNA TaqMan probes has been 686 reported for SNP detection of Mycobacterium tuberculosis [\[146,147\],](#page-17-0) 687 GMO detection [\[27\]](#page-15-0), determination of the presence of Helicobacter pylori 688

<span id="page-11-0"></span>

689 [\[148\]](#page-17-0), allele specific mutational analysis of KRAS and BRAF [\[149\]](#page-17-0) as well 690 as quantifying hepatitis B virus DNA in serum [\[150\]](#page-17-0).

# 691 2.2.3.3. ZNA™

 2.2.3.3.1. Structure. Zip nucleic acids, developed by the Polyplus- transfection company, are a novel type of synthetic modified oligo- nucleotide [\[119,120\].](#page-17-0) The introduction of ZNA™ molecules into oligonucleotides increases their affinity for the target by decreasing the electrostatic repulsion between the two nucleic acids [\[151,152\].](#page-17-0) This is achieved by conjugating cationic moieties (Z units), such as derivatives of spermine, to an oligonucleotide (Fig. 6D).

A number of Z units can be placed at the 5′ or 3′-ends or in the mid- 699 dle of primer-probes and probes [\[153\]](#page-17-0). The melting temperature of 700 ZNA-containing oligonucleotides is linearly dependent on the number 701 of cationic units grafted on this structure, providing a convenient 702 means to fine tune hybridization temperatures [\[151\]](#page-17-0). The  $T_m$  and global  $703$ charge of the ZNA™ are easily predictable using a simple mathematical 704 relation [\[119,153\]](#page-17-0). 705

2.2.3.3.2. Mechanism of action. During the annealing phase, ZNA™ 706 oligonucleotides are attracted towards the nucleic acid strands due to 707 their polycationic nature, starting their scanning of DNA sequences. 708



Fig. 6. Chemical structures of nucleic acid analogues. (A) PNA probe; (B) LNA® Monomer; (C) 2'-O-methyl RNA and (D) ZNA™. The global charge of ZNA™ is calculated by applying the following equation:  $(N_mS_n)^{3n-m+1}$ , where N: number of nucleotides and S: number of spermine cationic units.

<span id="page-12-0"></span>

 $t2.7 +$  symbol denotes the LNA® base.

709 Next, hybridization takes place by zipping up when the ZNA™ oligonu-710 cleotide meet its complementary sequence [\[119\]](#page-17-0) [\(Fig. 7A](#page-13-0)).

711 2.2.3.3.3. Advantages. ZNA™ oligonucleotides display an exceptionally 712 high affinity for their targets, mainly due to the presence of the Z units, 713 which enhance the interaction with the DNA target.

 2.2.3.3.4. Applications. ZNA™ represent a potent new tool for numer- ous nucleic-acid-based applications, including: real-time PCR, capture probes, Northern/Southern Blotting, microarrays and in situ hybridiza- tion. In PCR assays, these oligonucleotides can be used in single and multiplex formats for pathogen detection [154], gene expression, microarray validation, allelic discrimination, mutation/SNP detection, and viral/bacterial load quantitation [155]. In particular, LNA-based methods have been described to efficiently detect Hepatitis B virus re- sistance to drugs in patients [156]. Interestingly, it has been reported that the use of ZNA™ primers improves the synthesis of cDNA from total RNA, making them the best choice for the quantification of low-abundant transcripts [151].

 2.2.3.4. Non-natural bases: Plexor™ primers. The development of organic chemistry has made it possible to enlarge the number of standard nucle- otides beyond those known in nature [121,157,158]. Two modified bases, isoguanine (Iso-dG) and 5′-methylisocytosine (Iso-dC), which generate novel base pairings, have been successfully designed to allow protein recognition and site-specific enzymatic incorporation [158–[161\]](#page-17-0).

 2.2.3.4.1. Structure. Plexor™ primers, described by Sherrill et al. in 2004 [\[121\]](#page-17-0), take advantage of the highly specific interaction between two modified nucleotides: Iso-dG and Iso-dC. In Plexor™ reactions, one PCR primer contains an Iso-dC residue and a fluorescent reporter label at the 5′-end, whereas the second one is an unlabeled oligonucleo- tide that carries standard nucleotides. In this system, Iso-dG nucleotides, covalently coupled to a quencher, are added into the qPCR reaction [121] [\(Fig. 7](#page-13-0)B).

 2.2.3.4.2. Mechanism of action. During the amplification phase, the incorporation of Iso-dG nucleotides brings the quencher and reporter into close proximity, producing the quenching of the fluorescent signal released from the labeled primer [121]. In this system, the decrease in initial fluorescence is proportional to the starting amount of target [\(Fig. 7B](#page-13-0)).

 2.2.3.4.3. Advantages. Plexor-primer based-technology takes advan- tage of the highly specific interaction between Iso-dG and Iso-dC. These two modified nucleotides are not recognized either by nucleases nor proteases.

 2.2.3.4.4. Applications. Plexor™ primers can be used in single and multiplex formats for pathogen detection [\[162\]](#page-17-0), viral/bacterial load quantitation, gene expression, genotyping, SNP detection [\[163\]](#page-17-0) and GMO detection [\[27\].](#page-15-0)

### 755 2.2.3.5. Tiny-Molecular Beacon probes

 2.2.3.5.1. Structure. Molecular Beacon probes, described by Bratu et al. in 2011 [\[164\]](#page-17-0), are redesigned as small hairpins and synthesized from 2′-O-methyl RNA/LNA chimeric nucleic acid analogues [\[164,165\].](#page-17-0) 2.2.3.5.2. Mechanism of action. They display the same mode of action

760 as that of Molecular Beacon probes (see [Section 2.2.2.2.2\)](#page-7-0).

761 2.2.3.5.3. Advantages. These probes have been reported to be very 762 resistant to nucleases and stable within a cellular environment. Further-763 more, they have high affinity and specificity for RNA sequences, due to the incorporation of LNA into RNA oligonucleotides in the probe 764 structure [\[165\].](#page-17-0) 765

2.2.3.5.4. Applications. The user-friendly synthesis protocol of these 766 probes as well as their ability to couple to a variety of fluorophores 767 make Tiny-Molecular Beacons the optimal technology to detect less 768 abundant, highly structured mRNAs and small RNAs such as microRNAs, 769 small nucleolar RNAs and nuclear RNAs. Recently, this technology has 770 also been used to visualize native mRNAs in living cells [\[164,165\].](#page-17-0)  $771$ 

# **3. Primer and probe design 772**

The design of primers and probes is a very important requirement 773 for most applications of qPCR [\[166\]](#page-17-0). The choice of specificity, length, 774 GC content, 3' end stability, sequence complexity, melting temperature, 775 and location in the target sequence of the primers determines amplicon 776 length, melting temperature and amplification efficiency [\[166,111\].](#page-17-0) The 777 choice of chemistry and probe design are a very personal matter and 778 there are, as always, numerous options that need to be considered 779 prior to sitting down and designing the probes [\[111\].](#page-17-0) We should con- 780 sider, (i) if we want to quantity DNA, profile mRNA or perform allelic 781 discrimination assays; (ii) which chemistry is most appropriate for 782 our experiment; (iii) if we wish to detect DNA, RNA or both; (iv) if it 783 is necessary to distinguish between closely related sequences, e.g., to 784 detect and quantify a determined pathogen that belongs to a family 785 with several species; (v) which fluorescent reporter/ quencher combi- 786 nations should be used; (vi) if our probe should contain DNA analogues, 787 MGB factors or any other modifications; and finally (vii) if the assay is 788 multiplex [111]. 789

er tragets, mannot que to me presence or me  $ZNAR$  from most approximate of me presence or me  $ZNAR$  represents a point of the presence of the Nowadays, numerous in silico tools have been developed to guide 790 the design of qPCR assays and analyze any resulting quantitative data 791 [167]. Many tools are freely available online, while others are bundled 792 with qPCR instruments or available from various software houses 793 [167]. Some in silico tools are Primer3 [\[168,169\]](#page-17-0), FastPCR software 794 [170,171], Java web tools [172], PerlPrimer [\[173\]](#page-18-0), IDTSciTools [\[174\],](#page-18-0) 795 UniPrime [175], and Primer-BLAST [176]; in addition, it is important to 796 analyze the secondary structure of primers using an additional software 797 program like mFold ([http://www.idtdna.com/Scitools/Applications/](http://www.idtdna.com/Scitools/Applications/mFold/) 798 mFold/). MPprimer is a program for multiplex PCR primer design 799 [177]. This program employs the program Primer3 [\[168\]](#page-17-0) for the primer 800 design and the program MFEprimer for assessing primer specificity 801 [178]. Recently, several authors have presented detailed descriptions, 802 step by step, of a qPCR assay design [\[167,179\].](#page-17-0) The MIQE guidelines 803 also provide clear guidance on the steps that are important for assay 804 design [180,181]. 805

Several research companies offer useful guidelines on their websites 806 for designing primers and probes: 807

- Qiagen's website: "Critical factors for successful real-time PCR" 808 [\(http://www.qiagen.com/resources/resourcedetail?id=f7efb4f4-](http://www.qiagen.com/resources/resourcedetail?id=f7efb4f4-fbcf-4b25-9315-c4702414e8d6&lang=en) 809 fbcf-4b25-9315-c4702414e8d6&lang=en). 810
- Cepheid's website [http://www.cepheid.com/us/component/](http://www.cepheid.com/us/component/phocadownload/%85/2-support?%85) 811 phocadownload/.../2-support?...). "Designing Real-Time Assays" 812 (SmartNote 6.1), "Optimizing and Analysing Real-Time Assays" 813 (SmartNote 6.2), "Dye-Quencher Considerations" (SmartNote 6.3)  $Q14$ and "Guidelines for the "Advance to Next Stage"" (SmartNote 6.5) 815 on the SmartCycler® II System. **816** 816
- Applied Biosystems' website: "Getting started guide: Designing 817 primers and probes for quantification assays and allelic discrim- 818 ination" ([http://www3.appliedbiosystems.com/cms/groups/](http://www3.appliedbiosystems.com/cms/groups/mcb_support/documents/generaldocuments/cms_041902.pdf) 819 [mcb\\_support/documents/generaldocuments/cms\\_041902.pdf](http://www3.appliedbiosystems.com/cms/groups/mcb_support/documents/generaldocuments/cms_041902.pdf)), 820 Designing MGB-TaqMan® probes design for allelic discrimina- 821 tion [\(http://www3.appliedbiosystems.com/cms/groups/mcb\\_](http://www3.appliedbiosystems.com/cms/groups/mcb_support/documents/general%20documents/cms_042997.pdf) 822 [support/documents/general documents/cms\\_042997.pdf\)](http://www3.appliedbiosystems.com/cms/groups/mcb_support/documents/general%20documents/cms_042997.pdf) or 823 Designing MGB-TaqMan® probe and primers sets for gene expres- 824 sion [\(http://www6.appliedbiosystems.com/support/tutorials/pdf/](http://www6.appliedbiosystems.com/support/tutorials/pdf/taqman_mgb_primersprobes_for_gene_expression.pdf) 825 [taqman\\_mgb\\_primersprobes\\_for\\_gene\\_expression.pdf\)](http://www6.appliedbiosystems.com/support/tutorials/pdf/taqman_mgb_primersprobes_for_gene_expression.pdf). 826

 - Roche Applied Science's website: "Designing Primers and Probes" [\(https://www.roche-applied-science.com/wcsstore/RASCatalog](https://www.roche-applied-science.com/wcsstore/RASCatalogAssetStore/Articles/Fast_and_Convenient_Primer_Probe_Design_for_Multiplex_Assays_with_the_LightCycler_Probe_Design_Software%202.0.pdf) [AssetStore/Articles/Fast\\_and\\_Convenient\\_Primer\\_Probe\\_Design\\_](https://www.roche-applied-science.com/wcsstore/RASCatalogAssetStore/Articles/Fast_and_Convenient_Primer_Probe_Design_for_Multiplex_Assays_with_the_LightCycler_Probe_Design_Software%202.0.pdf) [for\\_Multiplex\\_Assays\\_with\\_the\\_LightCycler\\_Probe\\_Design\\_](https://www.roche-applied-science.com/wcsstore/RASCatalogAssetStore/Articles/Fast_and_Convenient_Primer_Probe_Design_for_Multiplex_Assays_with_the_LightCycler_Probe_Design_Software%202.0.pdf) [Software%202.0.pdf](https://www.roche-applied-science.com/wcsstore/RASCatalogAssetStore/Articles/Fast_and_Convenient_Primer_Probe_Design_for_Multiplex_Assays_with_the_LightCycler_Probe_Design_Software%202.0.pdf))

832 - Invitrogen has developed the software called LUX™ Designer 833 [\(http://tools.lifetechnologies.com/content/sfs/manuals/luxprimers\\_](http://tools.lifetechnologies.com/content/sfs/manuals/luxprimers_man.pdf) 834 [man.pdf](http://tools.lifetechnologies.com/content/sfs/manuals/luxprimers_man.pdf)) for designing LUX™ primer-probes.

 It is noteworthy that, for DNA analysis of higher organisms, primers and probes should be designed to avoid complex regions contained in their genomes, such as repeat elements (LINEs, SINEs, alu), pseudogenes, and large duplications.

## **4. Real-time PCR instruments** 839

qPCR instruments basically consist of a thermal cycler with an 840 integrated excitation light source, a fluorescence detection system and 841 software, which performs the quantitative analysis of the detected fluo- 842 rescence during the assay. These instruments are able to simultaneously 843 detect different wavelengths [\[4\]](#page-15-0). 844

There are three basic devices: lamps, light emitting diodes (LED) and 845 lasers, which emit excitation energy. The lamps are instruments of the 846 emission spectrum, while LEDs and lasers are more restricted. These 847 devices containing lamps (usually tungsten halogen or quartz tungsten 848 halogen) include filters to limit excess excitation. Some examples 849 are the ABIPrism 7000 from Applied Biosystems, the MX4000 and 850



Fig. 7. Mode of action of nucleic acid analogues: ZNA™ (A) and Plexor™ probe (B).

<span id="page-13-0"></span>

 Mx3000P from Stratagene, and the iCycler iQ Bio-Rad. The LED system is represented by the Roche LightCycler, the Cepheid SmartCycler, the Corbett Rotor-Gene and DNA Engine Opticon 2 from MJ Research. The ABI Prism 7900HT is the only device using a laser that excites in the range of 350–750 nm (Valasek and Repa, 2005) [\[4\].](#page-15-0)

 The number of channels available for reading fluorescence is also im- portant in qPCR experiments, given that it allows researchers to identify different targets in the same reaction (Multiplex PCR) and the presence of PCR inhibitors (Costa J, 2004) [\[8\].](#page-15-0)

 To record data, the energy emitted at discrete wavelengths by fluorophores is monitored in detectors, including chambers loaded with coupled devices, photomultiplier tubes or other photodetectors. Generally, filters or channels are used to detect short wavelength 864 ranges.

 On the one hand, a common and unaccounted for source of error in qPCR data is the PCR instrument itself. PCR instruments are subjected to vast and sudden changes in temperature (cycles of expansion and con- traction), leading to material fatigue. Thus, the device must be in perfect operating condition to guarantee temperature homogeneity for every well position [182–184]. So, there is a dispute about whether the PCR ef- ficiency is constant [185], which has led to the development of different methods to analyze amplification curves. For example, Ruijter et al. have evaluated the bias, resolution and precision as well as implications of qPCR curve analysis methods for reliable biomarker discovery [185].

 The instrumentation of qPCR is not complete without hardware and software for data analysis. The software simplifies analysis of the data and presents the results in graphs. In particular, amplification curves allow one to quantify the starting DNA, whereas dissociation curves show the purity of the final DNA product.

 The first qPCR thermocycler, the ABI 7700, was produced and marketed by Applied Biosystems in 1996 [3]. At present, large companies (Applied Biosystems, Roche, Stratagene, Cepheid, Corbett, Eppendorf and BioRad) are offering different models of qPCR platforms. Logan and Edwards have accurately described the device features of numerous brands of PCR apparatus, including company, model, laser/lamp, detec- tor, thermocycling, filters/detection channels, format (96-well plates, 0.2 ml tubes, 8-strips tubes among others), time (40 cycles), reaction volume, fluorescence chemistry, supports multiplexing, passive refer- ence, dimensions (H  $\times$  W  $\times$  D), weight and also software for primer and probes design [6,186].

### 891 5. MIQE guidelines

 Currently, a lack of consensus exists on how best to perform and interpret qPCR experiments. The problem is exacerbated by the lack of information that characterizes most reports of studies that have used this technology, with many publications not providing sufficient exper- imental detail to permit the reader to critically evaluate the quality of the results presented or to repeat the experiments [180], which makes it very difficult to compare results between several studies.

 To promote consistency between laboratories, increase experimen- tal transparency, and ensure the integrity of the scientific literature, guidelines for the Minimum Information required for the publication of qPCR Experiments (MIQE) were formulated by Bustin et al. in 2009 [\[180,181\].](#page-18-0) MIQE is a set of guidelines that describe the minimum infor- mation necessary for evaluating qPCR experiments [\[187\],](#page-18-0) which are sep- arated into nine major components (Experimental design, Sample, Nucleic acid extraction, Reverse transcription, qPCR target information, qPCR oligonucleotides, qPCR protocol, qPCR validation and Data analysis) that contain detailed information on pre- and post-assay parameters as well as comprehensive documentation of the experimental protocol 910 [\[180\]](#page-18-0).

911 By providing all relevant experimental conditions and assay character-912 istics, reviewers can assess the validity of the protocols used; in addition, 913 it can enable other investigators to reproduce the results [\[180\].](#page-18-0) MIQE details should be published either in abbreviated form or as an online 914 supplement [\[180,188\].](#page-18-0) 915

Today, the rationale underlying the MIQE guidelines has become 916 widely accepted [\[180\]](#page-18-0) and used [\[189](#page-18-0)–193], with more than 2200 cita- 917 tions by March 2014 and editorials in Nature and related publications 918 acknowledging the enormity of the problem [\[187\].](#page-18-0) However, it will be 919 some time before the many contradictions apparent in every area of 920 the life sciences are corrected [\[187\]](#page-18-0). 921

## **6. Concluding remarks** 922

The aim of the current review is to bring together, classify and 923 display available information and knowledge published on detection 924 chemistries for qPCR in the last years, approaching PCR-based DNA 925 analysis in a comprehensive way. Although several authors have also 926 described this information previously [194–198], this review offers a 927 useful classification as well as a detailed description of all such detection 928 methods. They have been classified into two groups based on the fluo- 929 rescent agent used and the specificity of PCR detection: dsDNA interca- 930 lating agents and fluorophores attached to oligonucleotides. The latter 931 have been further divided into three subgroups according to the type 932 of fluorescent molecules added to the reaction: primer-probes, probes 933 and analogues of nucleic acids. In addition to their structure and mech- 934 anism of action, advantages and applications of each DNA detection 935 method are described in this review. 936

or channels are used to detect snort wavelength<br>
dehenvisties for qPCR in the last years, approximated and amount and the comparison and the mathematic state of the mathematic way Athrones and the mathematic increase in em Several novel methods for DNA detection in real-time PCR have 937 recently been described, but the tendency in this field has been to intro- 938 duce new molecules such as MGB ligands or to combine distinct PCR 939 systems in order to improve target DNA-binding specificity and sensi- 940 tivity. As shown in the paper, the incorporation of MGB ligands 941 increases the melting curve of the primer/probe in order to enhance 942 its specificity of interaction with the target DNA sequence. This makes 943 MGB probes quite attractive for use in SNP detection and allelic discrim- 944 ination. Interestingly, combinations of dsDNA intercalating agents 945 (SYBR® Gold) with fluorescent primer-probes (Angler®) or fluorescent 946 probes (ResonSense®) in the same real-time PCR reaction are rapidly 947 becoming popular within studies to detect non-specific and specific 948 amplified products. On the other hand, nucleic acid analogues (PNA, 949 LNA, ZNAs) exhibit very high affinity and excellent DNA and RNA bind- 950 ing specificity. Furthermore, primers and probes containing modified 951 nucleotides display novel attractive features, such as resistance to the 952 action of nucleases or proteases and to changes in pH or ionic strength. 953

When we design a qPCR assay, it must take into account the MIQE 954 guidelines [180] for correct design, implementation and publication of 955 our study. Therefore, this study will provide sufficient experimental 956 detail to permit the reader to critically evaluate the quality of the results 957 presented or to repeat such experiments [180]. Since 2009, when Bustin 958 described the MIQE guidelines, many authors have applied these MIQE 959 guidelines [180] in their qPCR assays [189–193]. In addition, new arti- 960 cles have been published on how to improve the design, qPCR protocol, 961 qPCR validation and data analysis of qPCR assays. For example, Tuomi 962 et al. observed a bias in the threshold cycle (Ct) or quantification cycle 963 (Cq) with hydrolysis probes that can be corrected with the estimated 964 PCR efficiency value [\[199\]](#page-18-0), and Ruijter et al. evaluated this bias in differ- 965 ent chemistries (DNA-binding dyes, hybridization probes, hydrolysis 966 probes, LUX primers, hairpin primers and the QZyme system) and 967 have described how it requires a correction of the observed Cq [\[200\].](#page-18-0) Al- 968 though it will be some time before the many contradictions apparent in 969 every area of the life sciences are corrected [\[187\]](#page-18-0), we must be aware 970 that adherence to the MIQE guidelines by the scientific community 971 is vital, because basic studies may be reversed in subsequent clinical 972 studies. Also, it is useless to simply publish studies if they cannot be 973 compared due to not having followed the MIQE guidelines. 974

The experience of our group on the use of real-time PCR is focused 975 on molecular diagnosis of human brucellosis. We developed a Taqman 976 probe-PCR method to detect and quantify Brucella melitensis DNA in 977

<span id="page-15-0"></span>

 the blood and serum of patients with acute brucellosis [\[201\]](#page-18-0). Despite this PCR assay being highly reproducible, sensitive and specific in acute patients, it failed to detect and quantify B. melitensis DNA in chron- ic patients [\[202\]](#page-18-0). This failure is likely due to lower DNA concentrations in blood and sera from chronic patients. At present time, we are testing other probes (TaqMan-MGB, probes with PNAs, LNA®, ZNA™ and Plexor 984 primers™) in order to increase the detection efficiency of Brucella DNA in such patients, which will extremely be useful for setting up a new qPCR-based diagnostic tool for chronic brucellosis.

987 Thus, given our prior knowledge of such technology and that reported 988 by other authors [27,72], we highly recommend prior evaluation, includ-989 ing determinations of sensitivity, cost-effectiveness and simplicity of 990 probe-design, of different PCR chemistries and conditions to determine 991 the most appropriate qPCR assay for a particular scientific/clinical appli-Q16 cation, as well as to follow the MIQE guidelines [180,181] for each qPCR 993 assay.

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