

See discussions, stats, and author profiles for this publication at: <https://www.researchgate.net/publication/7904231>

Basic principles of real-time quantitative PCR

Article in Expert Review of Molecular Diagnostics · April 2005

DOI: 10.1586/14737159.5.2.209 · Source: PubMed

CITATIONS

339

READS

17,350

6 authors, including:



Iqbal Shergill

Betsi Cadwaladr University Health Board

185 PUBLICATIONS 1,544 CITATIONS

[SEE PROFILE](#)



Magali Williamson

University College London

40 PUBLICATIONS 3,477 CITATIONS

[SEE PROFILE](#)

Some of the authors of this publication are also working on these related projects:



Project

North Wales and North West Urological Research Center (NW2URC) Cancer Research [View project](#)



Basic principles of real-time quantitative PCR

Manit Arya[†], Iqbal S Shergill, Magali Williamson, Lyndon Gommersall, Neehar Arya and Hitendra RH Patel

Real-time quantitative PCR allows the sensitive, specific and reproducible quantitation of nucleic acids. Since its introduction, real-time quantitative PCR has revolutionized the field of molecular diagnostics and the technique is being used in a rapidly expanding number of applications. This exciting technology has enabled the shift of molecular diagnostics toward a high-throughput, automated technology with lower turnaround times. This article reviews the basic principles of real-time PCR and describes the various chemistries available: the double-stranded DNA-intercalating agent SYBR[®] Green 1, hydrolysis probes, dual hybridization probes, molecular beacons and scorpion probes. Quantitation methods are discussed in addition to the competing instruments available on the market. Examples of applications of this important and versatile technique are provided throughout the review.

Expert Rev. Mol. Diagn. 5(2), 209–219 (2005)

Even one copy of a specific sequence can be amplified and detected in PCR. The PCR reaction generates copies of a DNA template exponentially. This results in a quantitative relationship between the amount of starting target sequence and amount of PCR product accumulated at any particular cycle. Due to inhibitors of the polymerase reaction found with the template, reagent limitation or accumulation of pyrophosphate molecules, the PCR reaction eventually ceases to generate template at an exponential rate (i.e., the plateau phase) making the end point quantitation of PCR products unreliable. Therefore, duplicate reactions may generate variable amounts of PCR product. Only during the exponential phase of the PCR reaction is it possible to extrapolate back in order to determine the starting quantity of template sequence. The measurement of PCR products as they accumulate (i.e., real-time quantitative PCR) allows quantitation in the exponential phase of the reaction and therefore removes the variability associated with conventional PCR.

Since the first documentation of real-time PCR [1], it has been used for an increasing and diverse number of applications including mRNA expression studies, DNA copy number measurements in genomic or viral

DNAs [2–7], allelic discrimination assays [8,9], expression analysis of specific splice variants of genes [10–13] and gene expression in paraffin-embedded tissues [14,15] and laser captured microdissected cells [13,16–19].

Background & methodology

Real-time quantitative PCR is the reliable detection and measurement of products generated during each cycle of the PCR process, which are directly proportional to the amount of template prior to the start of the PCR process. Holland and coworkers demonstrated that the thermostable enzyme *Thermus aquaticus* (i.e., Taq) DNA polymerase had 5' to 3' exonuclease activity. This group also showed that cleavage of a target probe during PCR by the 5' nuclease activity of Taq polymerase can be used to detect amplification of the target-specific product [20]. An oligonucleotide probe, which was designed to hybridize within the target sequence, was introduced into the PCR assay. This probe was labeled with ³²P at its 5' end and was nonextendable at its 3' end to ensure it could not act as a primer. Annealing of probe to one of the PCR product strands during the course of amplification generated a substrate suitable for exonuclease activity. Also, during amplification, the 5' to 3' exonuclease

CONTENTS

Background & methodology

Standard & absolute quantitation

Housekeeping genes & normalization

Amplicon detection

Primer, probe & amplicon design

Multiplex real-time PCR

Available equipment

Expert opinion

Five-year view

Key issues

References

Affiliations

[†]Author for correspondence
Prostate Cancer Research Centre,
Institute of Urology,
University College London,
London, UK
Tel.: +44 208 502 1762
Fax: +44 208 502 1762
manit_arya@hotmail.com

KEYWORDS:
real-time quantitative PCR

activity of Taq DNA polymerase (when the enzyme extended from an upstream primer into the region of the probe) degraded the probe into smaller fragments that could be differentiated from undegraded probe. This dependence on polymerization ensured that cleavage of the probe occurred only if the target sequence was being amplified. After PCR, cleavage of the probe was measured by using thin-layer chromatography to separate cleavage fragments from intact probe.

The introduction of dual-labeled oligonucleotide fluorogenic probes allowed the elimination of post-PCR processing for the analysis of probe degradation [21]. The probe has a reporter fluorescent dye at the 5' end and a quencher dye attached to the 3' end. Whilst the probe is intact, the close proximity of the quencher significantly decreases the fluorescence emitted by the reporter dye. A fluorescence signal is only emitted upon cleavage of the probe, based on the fluorescence resonance energy transfer (FRET) principle [22].

In the real-time quantitative TaqMan[®] assay a fluorogenic nonextendable 'TaqMan' probe is used (FIGURE 1) [23]. The probe has a fluorescent reporter dye attached to its 5' end and a quencher dye at its 3' terminus. If the target sequence is present, the fluorogenic probe anneals downstream from one of the primer sites and is cleaved by the 5' nuclease activity of the Taq polymerase enzyme during the extension phase of the PCR. Whilst the probe is intact, FRET occurs and the fluorescence emission of the reporter dye is absorbed by the quenching dye. Cleavage of the probe by Taq polymerase during PCR separates the reporter and quencher dyes, thereby increasing the fluorescence from the former. Additionally, cleavage removes

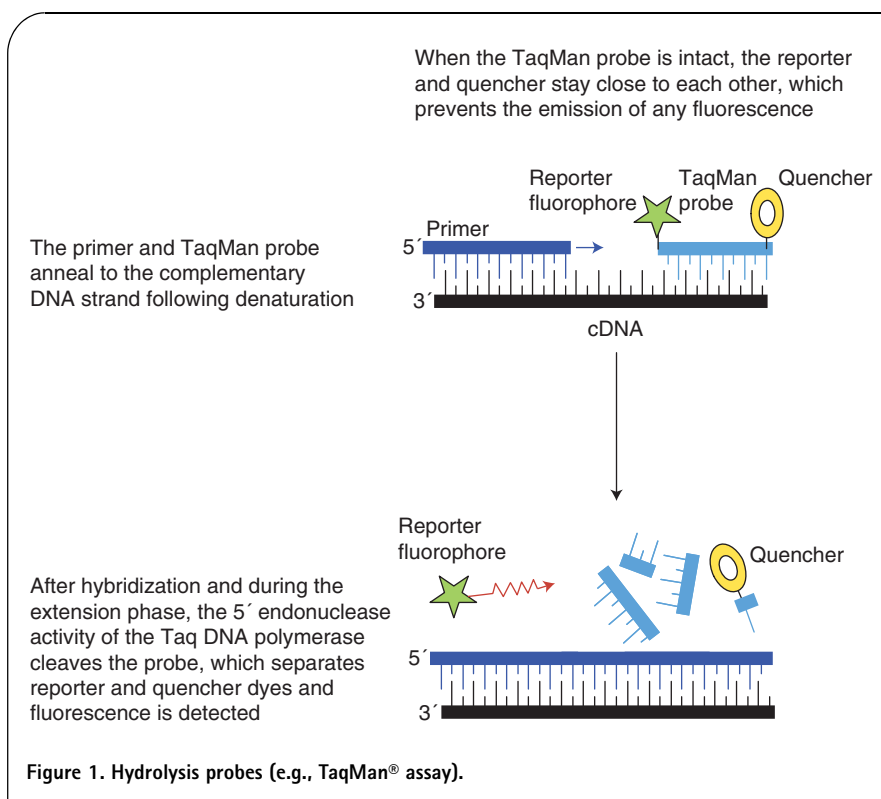
the probe from the target strand, allowing primer extension to continue to the end of template strand, thereby not interfering with the exponential accumulation of PCR product. Additional reporter dye molecules are cleaved from their respective probes with each cycle, leading to an increase in fluorescence intensity proportional to the amount of amplicon produced. The various available chemistries for real-time PCR are described later in this review.

Using any of the developed chemistries, the increase in fluorescence emission during the PCR reaction can be detected in real time by a modified thermocycler. The computer software constructs amplification plots using the fluorescence emission data that are collected during the PCR amplification (FIGURE 2). FIGURE 2 demonstrates a representative amplification plot and defines the important terms associated with it.

- **Baseline:** the baseline is defined as the PCR cycles in which a reporter fluorescent signal is accumulating but is beneath the limits of detection of the instrument. By default, the computer software sets the baseline from cycles three to 15; however, this often needs to be changed manually.
- ΔR_n : a computer software program calculates a ΔR_n using the equation $R_n = R_{nf} - R_{nb}$, where R_{nf} is the fluorescence emission of the product at each time point and R_{nb} is the fluorescence emission of the baseline [23,24]. The ΔR_n values are plotted versus the cycle number. During the early cycles of PCR amplification, ΔR_n values do not exceed the baseline.
- **Threshold:** an arbitrary threshold is chosen by the computers, based on the variability of the baseline. It is calculated as

ten-times the standard deviation of the average signal of the baseline fluorescent signal between cycles three to 15. A fluorescent signal that is detected above the threshold is considered a real signal that can be used to define the threshold cycle (C_t) for a sample. If required, the threshold can be manually changed for each experiment so that it is in the region of exponential amplification across all amplification plots.

- **C_t :** this is defined as the fractional PCR cycle number at which the reporter fluorescence is greater than the minimal detection level (i.e., the threshold). The C_t is a basic principle of real-time PCR and is an essential component in producing accurate and reproducible data [1]. The presence of more template at the start of the reaction leads to a fewer number of cycles reaching the point at which the fluorescent signal is recorded as statistically significant above background [24]. This C_t value will always occur during the exponential phase of target amplification, which occurs during the early cycles of



PCR. As reaction components become limiting, the rate of target amplification decreases until the PCR reaction is no longer generating template at an exponential rate (plateau phase) and there is little or no increase in PCR product. This is the main reason why C_t is a more reliable measure of starting copy number than an endpoint measurement of the amount of accumulated PCR product. During the exponential phase, none of the reaction components is limiting and therefore C_t values are very reproducible for replicate reactions with the same starting copy number.

Standard & absolute quantitation

Two methods are available to quantify real-time PCR results, standard-curve or absolute quantitation and relative quantitation.

Standard-curve or absolute quantitation

As shown by Higuchi and coworkers, the plot of the log of initial target copy number for a set of known standards (five- or tenfold serial dilution) versus C_t is a straight line (the standard curve) [1]. Quantitation of the amount of target in the 'unknown' samples of interest is accomplished by measuring C_t and using the standard curve to determine starting copy number. The most common source of a known sample is a plasmid for the gene of interest and the standard curve is generated based on a serial dilution of a starting amount. Another option, and easier to generate if a plasmid is unavailable, is the use of a synthetic single-stranded sense oligonucleotide for the entire amplicon. The advantage of this approach is that it significantly simplifies the process of obtaining a standard curve for amplicons up to 100 bp, which encompasses most real-time PCR amplicons. Furthermore, it is also less susceptible to bias when quantified by a spectrophotometer due to the relative purity of the oligonucleotide. Together with the greater precision of measurement of the standard and the possibility of calculating the moles of oligonucleotide (hence, number of copies), it is possible to approximate the number of copies of a template in an unknown sample, although not in terms of absolute copy number. One final option for a standard curve is to use a cell line with a known copy number or expression level of the gene of interest. The standard curve method is used in circumstances when absolute quantitation is critical for the investigator (e.g., when measuring a small number of genes in either a few or many samples [25,26]) and in quantitation of viral load [27–29].

Relative quantitation

Relative quantitation is also known as the comparative threshold method ($2^{-\Delta\Delta C_t}$ method). This method eliminates the need for standard curves and mathematical equations are used to calculate the relative expression levels of a target relative to a reference control or calibrator such as a nontreated sample or RNA from normal tissue or a sample at time zero in a time-course study. The amount of target gene in the sample, normalized to an endogenous housekeeping gene and relative to the normalized calibrator, is then given by $2^{-\Delta\Delta C_t}$, where $\Delta\Delta C_t = \Delta C_t(\text{sample}) - \Delta C_t(\text{calibrator})$, and ΔC_t is the C_t of the target

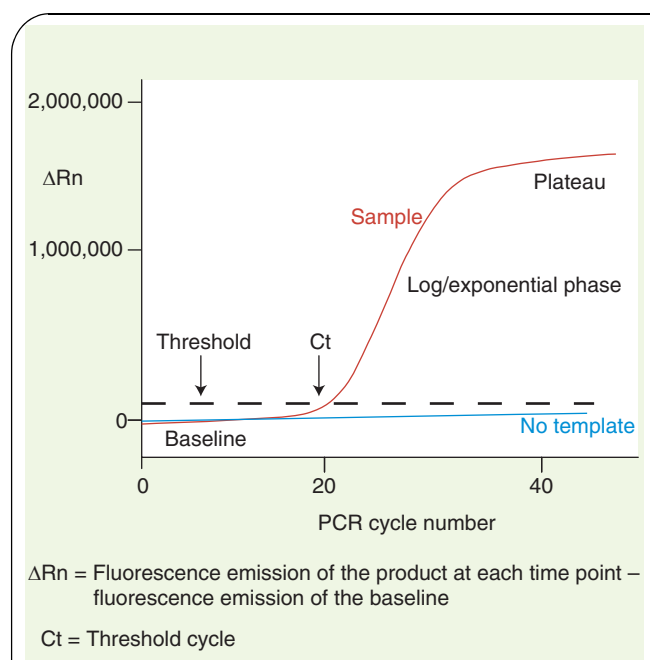


Figure 2. Model of a single amplification plot illustrating the nomenclature commonly used in real-time quantitative PCR.

gene subtracted from the C_t of the housekeeping gene. For this calculation to be valid and in order to obtain reliable results, it is imperative that the amplification efficiencies of the housekeeping and target gene are approximately equal and at or above 90%. This can be established by looking at how ΔC_t (of both sample and calibrator) varies with template dilution. If the plot of complementary DNA (cDNA) dilution versus ΔC_t is close to zero, it implies that the efficiencies of the target and housekeeping genes are very similar. If a housekeeping gene cannot be found whose amplification efficiency is similar to the target, the standard curve method is then preferable. Alternatively, new primers can be designed and/or optimized to achieve a similar efficiency for the target and housekeeping gene amplicons.

Housekeeping genes & normalization

In real-time quantitative PCR experiments specific errors will be introduced due to minor differences in the starting amount of RNA, quality of RNA or differences in efficiency of cDNA synthesis and PCR amplification. In order to minimize these errors and correct for sample-to-sample variation, a cellular RNA is simultaneously amplified with the target, which serves as an internal reference against which other RNA values can be normalized. The most common genes used for normalization, termed housekeeping genes, are β -actin, a cytoskeletal protein, glyceraldehyde-3-phosphate dehydrogenase (GAPDH), a glycolytic enzyme [30], and ribosomal RNA (rRNA). These genes should theoretically be expressed at a constant level among different tissues of an organism, at all stages of development, and their expression levels should also remain relatively constant in different experimental conditions. However, none of these

housekeeping genes are ideal. It has been shown that GAPDH expression levels are altered by glucose, insulin, heat shock and cellular proliferation and β -actin levels may also be modified by experimental treatments [31–35]. rRNA production is less likely to vary under conditions affecting mRNA transcription [36,37]. However, it is not always a good representative of total mRNA population in a cell as rRNA is expressed at a much higher level than mRNA. Other alternative housekeeping genes have been proposed but none have been entirely satisfactory and no single unequivocal reference gene has been identified as yet. Some authors have suggested the use of several housekeeping genes in a single experiment and that the mean expression of these multiple housekeeping genes can be used for normalization [38].

Importantly, selection of the housekeeping gene for each specific experiment should be made very carefully as the reliability of the results depends on the choice of the most relevant housekeeping gene according to the cells of interest and specific experimental treatments.

Amplicon detection

Two general chemistries are available. These include double-stranded (ds)DNA-intercalating agents (DNA-binding dyes) and fluorescent probes. The former includes SYBR[®] Green 1 or ethidium bromide and is the simplest and most cost-effective method as amplicon-specific labeled hybridization probes are not required. SYBR Green 1 only fluoresces when intercalated into dsDNA. The intensity of the fluorescence signal is therefore dependent on the quantity of dsDNA present in the reaction. The main disadvantage of this method is that it is not specific since the dye binds to all dsDNAs formed during the PCR reaction (i.e., nonspecific PCR products and primer-dimers).

With fluorogenic probes, nonspecific amplification due to mispriming or primer-dimer artifact does not generate signal as specific hybridization between probe and template is necessary for fluorescence emission. Also, fluorogenic probes can be labeled with different and distinguishable reporter dyes, thus allowing the detection of amplicons that may have been produced by one or several primer pairs in a single PCR reaction – termed multiplex real-time PCR. However, different probes must be developed to detect different sequences. The various chemistries are now described in more detail.

dsDNA-intercalating agents (DNA-binding dyes)

SYBR Green 1 is a nonsequence-specific fluorogenic minor groove DNA-binding dye that intercalates into dsDNA (it does not bind to single-stranded DNA) (FIGURE 3). SYBR Green 1 exhibits little fluorescence when unbound in solution but emits a strong fluorescent signal upon binding to dsDNA [39]. An increase in the fluorescence signal occurs during

polymerization and this decreases when DNA is denatured. Fluorescent measurements are performed at the end of the elongation step of each PCR cycle to monitor the increasing amount of amplified DNA. The advantage of this technique is that it is relatively cheap as it can be used with any pair of primers for any target. However, as the presence of any dsDNA generates fluorescence, specificity of this assay is greatly decreased due to amplification of nonspecific PCR products and primer-dimers [40]. Generating and comparing melting curves (plotting fluorescence as a function of temperature) using the LightCycler[™] (Roche Molecular Diagnostics; or RotorGene, Smart Cycler, iCycler, Mx4000) is one method of increasing the specificity of the reaction [40]. A characteristic melting peak at the melting temperature (T_m) of the amplicon will distinguish it from amplification artifacts that melt at lower temperatures at broader peaks. It is possible to set the software to acquire fluorescence above the primer-dimers' melting temperature but below that of the target. Another controllable problem is that longer amplicons create a stronger signal. Usually, SYBR Green is used in singleplex reactions; however, when coupled with melting point analysis, it can be used for multiplex reactions. The SYBR Green 1 reaction has been used for many applications (e.g., viral load detection [41] and cytokine quantification [42–44]).

Hydrolysis probes (e.g., TaqMan probes)

This chemistry has already been outlined earlier in this review (FIGURE 1). A forward and reverse primer and a probe are used. The efficiency of the assay is mainly dependent on 5' to 3' nuclease activity – the most commonly used enzyme is Taq polymerase [20] but any enzyme with 5' nuclease activity can be used [45]. The oligonucleotide probe has a covalently bonded fluorescent reporter dye and quencher dye at the 5' and 3' ends, respectively. Various fluorescent reporter dyes are in use including 6-carboxyfluorescein (FAM), tetrachloro-6-carboxyfluorescein (TET), hexachloro-6-carboxyfluorescein (HEX), or VIC. Quenchers include either 6-carboxytetramethylrhodamine (TAMRA) or 4-(dimethylamino)azobenzene-4-carboxylic acid (DABCYL). When the probe is intact the proximity of the reporter and quencher dyes permits FRET, and fluorescence

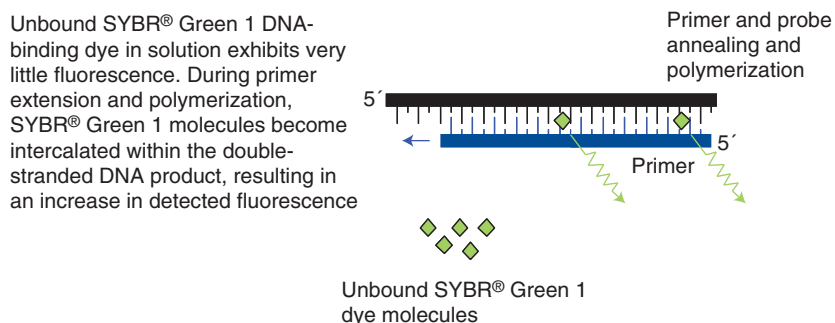


Figure 3. Double-stranded DNA-intercalating agents/DNA-binding dyes (e.g., SYBR[®] Green 1).

emission does not occur. During PCR amplification the probe anneals to the target and Taq polymerase cleaves the probe, allowing an increase in fluorescence emission. The increase in fluorescence intensity is directly proportional to the amount of amplicon produced. The TaqMan chemistry is the most widely used real-time PCR assay and has been used for multiple purposes [32,46,47].

TaqMan minor groove-binding probes have more recently been developed. In this chemistry, the standard TAMRA quencher at the 3' end is replaced by a nonfluorescent quencher and a minor groove-binder molecule is also incorporated at the 3' terminus. The latter stabilizes the probe–target complex by folding into the minor groove of the dsDNA. Additionally, the T_m of the probes is increased, allowing the use of very short oligoprobes (14 nucleotides in length) and providing more accurate allelic discrimination. Thus, TaqMan minor groove-binding probes are ideal for detecting single nucleotide polymorphisms [48,49] and for the quantitative analysis of methylated alleles [50].

Dual hybridization probes

This method has been convincingly validated in studies using the LightCycler instrument (FIGURE 4). Two hybridization probes are used – one carries a donor fluorophore at its 3' end and the other is labeled with an acceptor fluorophore at its 5' end. After the denaturation step, both probes hybridize to their target sequence in a head to tail arrangement during the annealing step. This brings the two dyes in close proximity allowing FRET. The donor dye in one of the probes transfers energy, allowing the other one to dissipate fluorescence at a different wavelength. The measured fluorescence is directly proportional to the amount of DNA synthesized during the PCR reaction. The specificity of this reaction is therefore increased as a fluorescent signal is only detected when two independent probes hybridize to their correct target sequence. This method has been widely used for detection of minimal residual disease after therapy [51,52] and viral load quantification [53,54].

Molecular beacons

Molecular beacons also contain covalently bound fluorescent and quenching dyes at either end of a single-stranded DNA molecule. However, they are also designed to adopt a hairpin or stem-and-loop structure whilst free in solution to bring the fluorescent dye and the quencher in close proximity for FRET to occur (FIGURE 5) [55]. The loop portion of the molecule is complementary to the target nucleic acid molecule and the stem is formed by the annealing of complementary arm

One hybridization probe carries a donor fluorophore at its 3' end and the other is labeled with an acceptor fluorophore at its 5' end. During denaturation both hybridization probes remain separate in solution and any fluorescent emission from the donor fluorophore (e.g., green fluorescence, which occurs when excited by the LightCycler's light source) is disregarded by the detector

During annealing the probes hybridize in a head-to-tail conformation, bringing the two dyes next to each other. Excitation of the donor leads to fluorescence resonance energy transfer to the acceptor resulting in a change of the fluorescent signal and emission of fluorescent light at a longer wavelength (red)

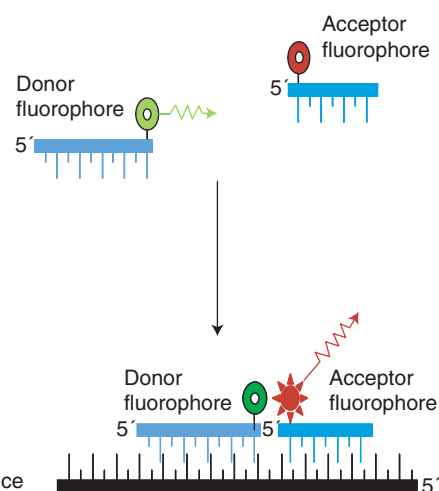


Figure 4. Dual hybridization probes.

sequences on the ends of the probe sequence. The close proximity of the fluorophore and the quencher in this hairpin configuration suppresses reporter fluorescence. When the probe sequence in the loop hybridizes to a complementary nucleic acid target sequence during the annealing step, a conformational change occurs that forces the stem apart. This results in a linear structure and thus separation of the fluorophore from the quencher dye (FRET does not occur) and an increase in fluorescence emission. A new hybridization takes place in the annealing step of each cycle, and the intensity of the resultant fluorescence indicates the amount of accumulated amplicon at the end of the previous cycle. Molecular beacons remain intact during PCR and they must rehybridize to the target sequence each cycle for fluorescence emission. Molecular beacons are particularly suitable for identifying point mutations [56–58].

Scorpions

Similar to molecular beacons, scorpions adopt a stem-and-loop configuration with a 5' fluorophore and 3' quencher (FIGURE 6). The specific probe sequence is held within the hairpin loop, which is attached to the 5' terminus of a PCR primer sequence by a nonamplifiable monomer (termed the PCR stopper). This chemical modification prevents PCR from copying the stem-loop sequence of the scorpion primer. During PCR, scorpion primers are extended to form amplicon. In the annealing phase, the specific probe sequence in the scorpion tail curls back to hybridize to the complementary target sequence in the amplicon, thus opening up the hairpin loop. This prevents the fluorescence from being quenched and a signal is observed [59]. As the tail of the scorpion and the amplicon are now part of the same strand of DNA, the interaction is intramolecular. The

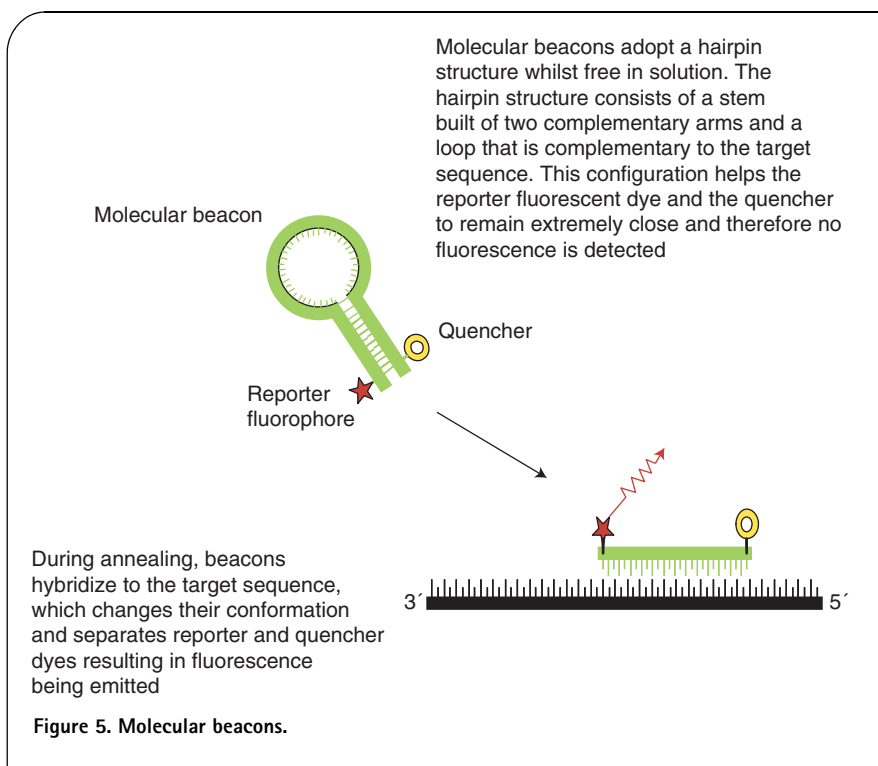


Figure 5. Molecular beacons.

benefits of Scorpions derive from the fact that the probe element is physically coupled to the primer element, which means that the reaction leading to signal generation is a unimolecular event. This contrasts with the bimolecular collisions required by other technologies such as TaqMan or molecular beacons. The benefits of a unimolecular rearrangement are significant in that the reaction is effectively instantaneous and the fluorescence signal much stronger. Also, better discrimination and specificity are achieved using scorpions. Scorpion probes have been used for viral load and mutation detection [60,61].

Duplex scorpions are a modification of scorpions. However, in contrast to scorpions (or molecular beacons), the fluorophore and quencher dye are separated onto different and complementary oligonucleotides. The advantage of duplex scorpions is the significantly greater separation between the quencher and reporter fluorophore, which decreases fluorophore quenching when the probe is bound to the target, resulting in improved signal intensity compared with conventional scorpions [62].

Primer, probe & amplicon design

Great care should go into the design of the assay. Primers, probes and amplicons are designed to very exacting specifications and the TaqMan system provides its own primer/probe design software from Applied Biosystems known as Primer Express, which is probably the most widely used oligonucleotide design program for developing real-time quantitative PCR assays. Primer3, a free program from Massachusetts Institute of Technology (MA, USA), can also be used to generate good real-time PCR assays, including designs incorporating an internal hybridization probe.

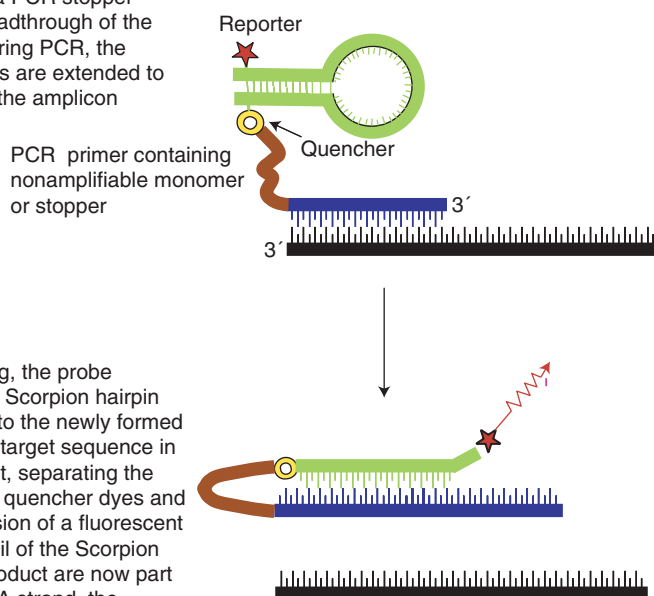
The amplicon for the PCR product should be as small as reasonably possible, usually 50–150 bp in length for designs using hybridization probes (and <300 bp for SYBR Green assays). Shorter amplicons amplify more efficiently and are more tolerant of reaction conditions. The optimal length for single-stranded primers is 15–20 bases with a G/C content of 20–80%. Their T_m should be in the range of 68–70°C for TaqMan primers. Molecular beacon and hybridization probe-associated primers can have a wider range of T_m , but the T_m of any one pair should be similar (i.e., not differ by >1–2°C). Nonspecific priming is minimized by selecting primers that have only one or two G/Cs within the last 5 nucleotides at the 3' end. If using a SYBR Green I approach, the PCR primers must not form an appreciable amount of primer-dimer bands. A melting curve analysis of each product is needed to ensure that the fluorescent signal observed is from the desired PCR product. In mRNA expression assays using a hybridization

probe, the probe sequence should span an exon/exon boundary if possible. Having the probe T_m 8–10°C higher than that of the primers ensures that the probe is fully hybridized during primer extension. TaqMan probes should not contain a G at their 5' ends due to the quenching effect of a G in this position on reporter fluorescence, even after probe cleavage.

Multiplex real-time PCR

The term multiplex real-time PCR is used to describe the use of multiple fluorogenic probes for the discrimination of multiple amplicons in a single tube. The main advantages of multiplexing over single-target analysis are the ability to provide internal controls, lower reagent costs and preservation of precious samples. The main restrictions of this technique have been the limited number of available fluorophores, fluorescence emission from quenching dyes and the common use in real-time instruments of a monochromatic light source. The introduction of nonfluorescent quenchers, which have no inherent fluorescence, has been a breakthrough that has allowed an increase in the number of spectrally discernable fluorogenic probes used per reaction. Initial real-time instrumentation contained optimized filters to minimize overlap of the emission spectra from the fluorophores. Newer systems have used either multiple light-emitting diodes, which span the whole visible spectrum, or a tungsten lamp, which emits light over a broad range of wavelengths. However, despite these advancements, only four-color multiplex reactions are usually possible [63,64], of which one color may be used for an internal control. One recent advancement of note, which is the introduction of combinatorial fluorescence energy transfer tags [65,66], will help to boost the development of multiplex real-time PCR.

The Scorpion probe adopts a hairpin loop structure that is linked to the 5' end of a specific primer through a PCR stopper that prevents readthrough of the hairpin loop. During PCR, the Scorpion primers are extended to become part of the amplicon



During annealing, the probe sequence in the Scorpion hairpin loop hybridizes to the newly formed complementary target sequence in the PCR product, separating the fluorophore and quencher dyes and leading to emission of a fluorescent signal. As the tail of the Scorpion and the PCR product are now part of the same DNA strand, the interaction is intramolecular

Figure 6. Scorpion probes.

instruments is the collection of data from a passive reference signal to normalize each reaction for variances in the optics of the system. In addition, Applied Biosystems have launched the Applied Biosystems 7300 and 7500 Real Time PCR systems, which represent less expensive alternatives.

The low-priced LightCycler from Roche Molecular Biochemicals induces fluorescence excitation by a blue light-emitting diode that is read by three silicon photodiodes with different wavelength filters, allowing detection of spectrally distinct fluorophores. Therefore, multiplex PCR can be performed. A complete PCR run of 30–40 cycles is performed in 20–30 min; however, only a limited number of samples (maximum 32) can be analyzed simultaneously. As the LightCycler analyzes the specificity of the results by performing melting curves, it makes the use of dsDNA-binding dyes such as SYBR Green I more reliable. However, as samples must be placed in capillaries as opposed to tubes, it is less practical for the investigator.

Available equipment

There are a variety of instruments available on the market, each of which has its own individual characteristics (TABLE 1). Great care should be taken when choosing which instrument to buy and it is important to match the instrument's capabilities with laboratory needs. Cost should not be the only factor when making a choice; the cheaper models cannot compensate for the variance in the optics and therefore are not capable of detecting smaller differences. The higher throughput instrument may be more than is required.

The ABI Prism[®] 7700 Sequence Detection System (SDS) from Applied Biosystems was the first commercially available thermocycler for real-time PCR, but has now been discontinued. Continuous fluorescence wavelength laser light detection from 500–660 nm allowed multiplex PCR. The ABI Prism 7700 has more recently been replaced by the ABI Prism 7900HT, which has similar specifications to the 7700 SDS but is completely automated and designed especially for very high-throughput applications (384 samples per run). Another recent introduction is the less expensive ABI Prism 7000 SDS. It retains the Peltier-based 96-well block thermal cycling format of the ABI 7700, but replaces the laser with a tungsten–halogen lamp that simultaneously illuminates all sample wells. The software supplied with the instrument is much more user friendly and is Microsoft[®] Windows-based, which allows easy export of data and amplification plots. One of the major advantages of the ABI

The iCycler iQ from BioRad Instruments has a tungsten–halogen lamp allowing excitation of a wide range of fluorophores (400–700 nm). It is able to multiplex four different fluorophores per sample tube. Also, it has an optical module allowing fluorescence emission to be viewed during the course of PCR amplification. Furthermore, the 96 samples are tracked simultaneously, thereby providing a fast assay. A recently launched module allows it to amplify 384 samples at any one time.

The Mx4000[®] Multiplex (Stratagene) can detect multiple fluorescence PCR chemistries, including TaqMan, hybridization probes and molecular beacons. The light source for the Mx4000 system is a quartz tungsten–halogen lamp that generates a broad excitation range of 350–750 nm and there are four photomultiplier tubes with a detection range of 350–830 nm. The instrument is ideal for performing multiplex PCR. Importantly, the system contains an integrated personal computer that operates independently from the instrument's embedded microprocessor, which gives some protection against data loss.

The Smart Cycler (Cepheid) also detects multiple fluorescence PCR chemistries. With up to 96 independently programmable reaction sites, the Smart Cycler can simultaneously run multiple experiments with different protocols and at different times. This enables multiple users to use the Smart Cycler simultaneously. Up to four different fluorophores can be detected in each reaction.

Table 1. Instruments available for real-time PCR.

| Real-time PCR instrument | Light source | Number of samples/run | Run time | Detection | Miscellaneous |
|---|---|--------------------------|-----------|---|---|
| ABI Prism® 7900HT (Applied Biosystems) | Argon Laser (500–660nm) | 96 or 384 | 35 min | Spectrograph and CCD | Gold standard |
| ABI 7000® SDS (Applied Biosystems) | Tungsten–halogen | 96 | 2 h 7 min | Four-position filter wheel and CCD camera | User-friendly Microsoft® Windows-based software |
| Applied Biosystems 7300® Real Time PCR system | Single-excitation, four-emission filters and CCD camera | 96 | 2 h | CCD camera | Less expensive |
| Applied Biosystems 7500® Real Time PCR System | Five-excitation, five-emission filters and CCD camera | 96 | <2 h | CCD camera | Less expensive |
| LightCycler 2.0 (Roche) | Blue LED (470nm) | 30 in capillaries | 30 min | Six detection channels (530, 560, 610, 640, 670 and 710 nm) | |
| iCycler iQ (BioRad Instruments) | Tungsten–halogen lamp (400–700nm) | 96–384 | 2 h | CCD with proprietary intensifier technology | Data viewable during run |
| Mx3000®P Real Time PCR System (Stratagene) | Quartz–tungsten–halogen (350–750 nm) | 96 | 2 h | One scanning photomultiplier tube | |
| Mx4000® Multiplex (Stratagene) | Quartz–tungsten–halogen (350–750 nm) | 96 | 2 h | 350–830 nm | Detects multiple-fluorescence PCR chemistries |
| Smart Cycler Systems 1600 – 9600 (Cepheid) | Four channel (450–495, 500–550, 565–590 and 630–650) | 16–96 depending on model | 20–60 min | Four channel (510–527, 565–590, 606–650 and 670–750nm) | Expandable |
| Rotor Gene 3000 (Corbett Research) | (470, 530, 585 and 625 nm) | 36–72 | 2 h | (510, 555, 610 665, 570 and 610 nm) | Only centrifugal product |

CCD: Charge -coupled device.

The Rotor Gene™ 3000, designed by Corbett Research, is a centrifugal thermal cycler comparable with the Light-Cycler. It uses four separate light-emitting diode light sources that excite at 470, 530, 585 and 625 nm. Excitation is detected using six filters and photomultipliers at 510, 555, 610, 660, 580 and 610 nm. The design of this instrument is radically different to all other instruments: the real-time reactions are carried out in standard microfuge tubes inside a 36- or 72-well rotor that spins at 500 rpm. This is meant to remove any temperature equilibration time and nonuniformity, and sample-to-sample variation of less than 0.01°C is claimed.

Expert opinion

The introduction of real-time PCR technology has revolutionized the field of molecular diagnostics and has enabled the shift of molecular diagnostics toward a high-throughput, automated technology with lower turnaround times. It allows the sensitive, specific and reproducible quantification of mRNA.

Real-time PCR assays are characterized by a wide dynamic range of quantification of 7–8 logarithmic decades, a high technical sensitivity (<5 copies) and a high precision (<2% standard deviation) [32]. Also, no post-PCR steps are required, thus avoiding the possibility of crosscontamination due to PCR products. The disadvantages of real-time quantitative PCR when compared with conventional PCR include the fact that:

- Amplicon size cannot be monitored without opening the system
- Existing instruments have limited multiplexing capabilities
- Several systems are incompatible with some fluorogenic chemistries

Real-time PCR technology is only as reliable as the accompanying controls and associated quality assurance programs. This includes the quality of standards and choice of housekeeping gene (the search for the ideal housekeeping gene or protocol is ongoing), the use of suitably controlled standard curves and the need to fully optimize, validate and evaluate each and every new assay against previously standardized assays. Without such care, real-time PCR will provide an enormous amount of fast but inaccurate data.

Five-year view

Confirmation of expression levels of selected genes from microarray experiments will continue to be conducted using real-time PCR methods [67,68]. This is because current microarray technologies require a high amount of starting material and display only a limited dynamic range for quantification. Therefore, a combination of both technologies, in which the screening of the involved genes is performed by microarrays and the precise quantification and high-throughput screening is performed by real-time PCR is the ideal method. Similarly, real-time PCR technology will continue to be combined with advanced microdissection techniques [13,16–19] or nucleic acids obtained from paraffin-fixed archival samples [14,15]. The detection and analysis of minimal residual disease and viral loads will remain an important application [51,69]. Also, it will be possible to measure gene expression or DNA copy number

in specific cells that are isolated with difficulty and are present in only very small numbers. Real-time techniques will be used in the analysis of clinical samples to aid clinicians in prognosis and management of patients. Combining techniques for sorting fetal cells or DNA from the maternal circulation with real-time PCR will enable early prenatal diagnostics of numerous congenital disorders using minimally invasive procedures [70–72]. Improvements to the design of real-time instrumentation and the advancement of combinatorial FRET tags will greatly enhance the future of multiplex real-time PCR. Additionally, major biotechnology companies are currently working on projects in which allele-specific assays are automatically developed for all single nucleotide polymorphisms identified during sequencing programs. These assays are likely to become an important area of molecular diagnostics in the future.

Key issues

- The introduction of real-time quantitative PCR technology has revolutionized the field of molecular diagnostics and has enabled the shift of molecular diagnostics toward a high-throughput, automated technology with lower turnaround times.
- The introduction of dual-labeled oligonucleotide fluorogenic probes and the discovery that Taq DNA polymerase has 5' to 3' exonuclease activity has allowed the rapid advancement of real-time quantitative PCR.
- The threshold cycle (Ct) is defined as the fractional PCR cycle number at which the reporter fluorescence is greater than the minimal detection level (i.e., the threshold). The Ct is a basic principle of real-time PCR and is an essential component in producing accurate and reproducible data.
- Two different methods are commonly used to quantify the results obtained by real-time PCR – the standard-curve or absolute quantitation method and the relative quantitation also known as the comparative threshold method (2^{-Ct} method).
- Several detection chemistries are available: double-stranded DNA-intercalating agents (DNA-binding dyes [e.g., SYBR® Green 1]), hydrolysis probes (e.g., TaqMan® probes), dual hybridization probes, molecular beacons and Scorpion probes.
- In real-time quantitative PCR, normalization to a housekeeping gene is the accepted method to correct for intersample variations in different experiments (i.e., minor discrepancies in the amounts of input RNA and minor differences in PCR efficiency).
- Great care should be taken when choosing which real-time instrument to buy and it is important to match the instruments capabilities with laboratory needs.

References

- Higuchi R, Fockler C, Dollinger G, Watson R. Kinetic PCR analysis: real-time monitoring of DNA amplification reactions. *Biotechnology* 11, 1026–1030 (1993).
- Kariyazono H, Ohno T, Ihara K *et al.* Rapid detection of the 22q11.2 deletion with quantitative real-time PCR. *Mol. Cell. Probes* 15, 71–73 (2001).
- Nigro JM, Takahashi MA, Ginzinger DG *et al.* Detection of 1p and 19q loss in oligodendroglioma by quantitative microsatellite analysis, a real-time quantitative PCR assay. *Am. J. Pathol.* 4, 1253–1262 (2001).
- Ginzinger DG, Godfrey TE, Nigro J *et al.* Measurement of DNA copy number at microsatellite loci using quantitative PCR analysis. *Cancer Res.* 60, 5405–5409 (2000).
- Ingham DJ. The study of transgene copy number and organization. *Methods Mol Biol.* 286, 273–290 (2005).
- Bai RK, Perng CL, Hsu CH, Wong LJ. Quantitative PCR analysis of mitochondrial DNA content in patients with mitochondrial disease. *Ann. NY Acad. Sci.* 1011, 304–309 (2004).
- Desire N, Dehee A, Schneider V *et al.* Quantification of human immunodeficiency virus type 1 proviral load by a TaqMan real-time PCR assay. *J. Clin. Microbiol.* 39, 1303 (2001).
- Johnson VJ, Yucesoy B, Luster MI. Genotyping of single nucleotide polymorphisms in cytokine genes using real-time PCR allelic discrimination technology. *Cytokine* 27, 135–141 (2004).
- Petersen K, Vogel U, Rockenbauer E *et al.* Short PNA molecular beacons for real-time PCR allelic discrimination of single nucleotide polymorphisms. *Mol. Cell. Probes* 18, 117–122 (2004).
- Elson D, Thurston G, Huang E *et al.* Quiescent angiogenesis in transgenic mice expressing constitutively active hypoxia-inducible factor-1 α . *Genes Dev.* 15, 2520 (2001).
- Schmittgen TD, Teske S, Vessella RL, True LD, Zakrajsek BA. Expression of prostate specific membrane antigen and three alternatively spliced variants of PSMA in prostate cancer patients. *Int. J. Cancer* 107, 323–329 (2003).
- Caberlotto L, Hurd YL, Murdock P *et al.* Neurokinin 1 receptor and relative abundance of the short and long isoforms

- in the human brain. *Eur. J. Neurosci.* 17, 1736–1746 (2003).
- 13 Sethi N, Palefsky J. Transcriptional profiling of dysplastic lesions in K14-HPV16 transgenic mice using laser microdissection. *FASEB J.* 18, 1243–1245 (2004).
- 14 Godfrey TE, Kim SH, Chavira M *et al.* Quantitative mRNA expression analysis from formalin-fixed, paraffin-embedded tissues using 5' nuclease quantitative reverse transcription-polymerase chain reaction. *J. Mol. Diagn.* 2, 84–91 (2000).
- 15 Andreassen CN, Sorensen FB, Overgaard J, Alsner J. Optimization and validation of methods to assess single nucleotide polymorphisms (SNPs) in archival histological material. *Radiother. Oncol.* 72, 351–356 (2004).
- 16 Glockner S, Lehmann U, Wilke N, Kleeberger W, Langer F, Kreipe H. Detection of gene amplification in intraductal and infiltrating breast cancer by laser-assisted microdissection and quantitative real-time PCR. *Pathobiology* 68, 173–179 (2000).
- 17 Ehrig T, Abdulkadir SA, Dintzis SM, Milbrandt J, Watson MA. Quantitative amplification of genomic DNA from histological tissue sections after staining with nuclear dyes and laser capture microdissection. *J. Mol. Diagn.* 3, 22–25 (2001).
- 18 Fink L, Seeger W, Ermert L *et al.* Real-time quantitative RTPCR after laser-assisted cell picking. *Nature Med.* 4, 1329–1333 (1998).
- 19 Shieh DB, Chou WP, Wei YH, Wong TY, Jin YT. Mitochondrial DNA 4,977-bp deletion in paired oral cancer and precancerous lesions revealed by laser microdissection and real-time quantitative PCR. *Ann. NY Acad. Sci.* 1011, 154 (2004).
- 20 Holland PM, Abramson RD, Watson R, Gelfand DH. Detection of specific polymerase chain reaction product by utilizing the 5'–3' exonuclease activity of *Thermus aquaticus* DNA polymerase. *Proc. Natl Acad. Sci. USA* 88, 7276–7280 (1991).
- 21 Lee LG, Connell CR, Bloch W. Allelic discrimination by nick-translation PCR with fluorogenic probes. *Nucleic Acids Res.* 21, 3761–3766 (1993).
- 22 Cardullo RA, Agrawal S, Flores C, Zamecnick PC, Wolf DE. Detection of nucleic acid hybridization by non-radiative fluorescence resonance energy transfer. *Proc. Natl Acad. Sci. USA* 85, 8790 (1988).
- 23 Heid CA, Stevens J, Livak KJ, Williams PM. Real time quantitative PCR. *Genome Res.* 6, 986–994 (1996).
- 24 Gibson UE, Heid CA, Williams PM. A novel method for real time quantitative RT-PCR. *Genome Res.* 6, 995–1001 (1996).
- 25 Dumur CI, Dechsukhum C, Wilkinson DS, Garrett CT, Ware JL, Ferreira-Gonzalez A. Analytical validation of a real-time reverse transcription-polymerase chain reaction quantitation of different transcripts of the Wilms' tumor suppressor gene (WT1). *Anal. Biochem.* 309, 127–136 (2002).
- 26 Jurado J, Prieto-Alamo MJ, Madrid-Risquez J, Pueyo C. Absolute gene expression patterns of thioredoxin and glutaredoxin redox systems in mouse. *J. Biol. Chem.* 278, 45546–45554 (2003).
- 27 Borg I, Rohde G, Loseke S *et al.* Evaluation of a quantitative real-time PCR for the detection of respiratory syncytial virus in pulmonary diseases. *Eur. Respir. J.* 21, 944–951 (2003).
- 28 Lin JC, Wang WY, Chen KY *et al.* Quantification of plasma Epstein-Barr virus DNA in patients with advanced nasopharyngeal carcinoma. *N. Engl. J. Med.* 350, 2461–2470 (2004).
- 29 Castelain S, Descamps V, Thibault V *et al.* TaqMan amplification system with an internal positive control for HCV RNA quantitation. *J. Clin. Virol.* 31, 227–234 (2004).
- 30 Gilliland G, Perrin S, Bunn HF. Competitive PCR for quantitation of mRNA. In: *PCR Protocols: a Guide to Methods and Applications*. Innis MA (Ed.), Academic Press, CA, USA, 60–69 (1990).
- 31 Suzuki T, Higgins PJ, Crawford DR. Control selection for RNA quantitation. *BioTechniques* 29, 332–337 (2000).
- 32 Bustin SA. Absolute quantification of mRNA using real-time reverse transcription polymerase chain reaction assays. *J. Mol. Endocrinol.* 25, 169–193 (2000).
- 33 Rhoads RP, McManaman C, Ingvarsten KL, Boisclair YR. The housekeeping genes GAPDH and cyclophilin are regulated by metabolic state in the liver of dairy cows. *J. Dairy Sci.* 87, 248 (2004).
- 34 Steele BK, Meyers C, Ozbun MA. Variable expression of some "housekeeping" genes during human keratinocyte differentiation. *Anal. Biochem.* 307, 341–347 (2002).
- 35 Yperman J, De Visscher G, Holvoet P, Flameng W. β -actin cannot be used as a control for gene expression in ovine interstitial cells derived from heart valves. *J. Heart Valve Dis.* 13, 848 (2004).
- 36 Dheda K, Huggett JF, Bustin SA, Johnson MA, Rook G, Zumla A. Validation of housekeeping genes for normalizing RNA expression in real-time PCR. *BioTechniques* 37, 112, 116, 118 (2004).
- 37 BasA, Forsberg G, Hammarstrom S, Hammarstrom ML. Utility of the housekeeping genes 18S rRNA, β -actin and glyceraldehyde-3-phosphate-dehydrogenase for normalization in real-time quantitative reverse transcriptase-polymerase chain reaction analysis of gene expression in human T lymphocytes. *Scand. J. Immunol.* 59, 566–573 (2004).
- 38 Vandesompele J, De Preter K, Pattyn F *et al.* Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. *Genome Biol.* 3, 0034.I (2002).
- 39 Morrison TB, Weis JJ, Wittwer CT. Quantification of low-copy transcripts by continuous SYBR Green I monitoring during amplification. *BioTechniques* 24, 954–958, 960, 962 (1998).
- 40 Ririe KM, Rasmussen RP, Wittwer CT. Product differentiation by analysis of DNA melting curves during the polymerase chain reaction. *Anal. Biochem.* 245, 154–160 (1997).
- 41 Gibellini D, Vitone F, Schiavone P, Ponti C, La Placa M, Re MC. Quantitative detection of human immunodeficiency virus type 1 (HIV-1) proviral DNA in peripheral blood mononuclear cells by SYBR green real-time PCR technique. *J. Clin. Virol.* 29, 282–289 (2004).
- 42 Blaschke V, Reich K, Blaschke S, Zipprich S, Neumann CJ. Rapid quantitation of proinflammatory and chemoattractant cytokine expression in small tissue samples and monocyte-derived dendritic cells: validation of a new real-time RT-PCR technology. *Immunol. Methods* 246, 79–90 (2000).
- 43 Ramos-Payan R, Aguilar-Medina M, Estrada-Parra S *et al.* Quantification of cytokine gene expression using an economical real-time polymerase chain reaction method based on SYBR Green I. *Scand. J. Immunol.* 57, 439–445 (2003).
- 44 Nakamura T, Scorilas A, Stephan C *et al.* Quantitative analysis of macrophage inhibitory cytokine-1 (MIC-1) gene expression in human prostatic tissues. *Br. J. Cancer* 88, 1101–1104 (2003).
- 45 Gut M, Leutenegger CM, Huder JB, Pedersen NC, Lutz H. One-tube fluorogenic reverse transcription-polymerase chain reaction for the quantitation of feline coronaviruses. *J. Virol. Methods* 77, 37–46 (1999).

- 46 Giulietti A, Overbergh L, Valckx D, Decallonne B, Bouillon R, Mathieu C. An overview of real-time quantitative PCR: applications to quantify cytokine gene expression. *Methods* 25, 386–401 (2001).
- 47 Ginzinger DG. Gene quantification using real-time quantitative PCR: an emerging technology hits the mainstream. *Exp. Hematol.* 30, 503–512 (2002).
- 48 van Hoeyveld E, Houtmeyers F, Massonet C *et al.* Detection of single nucleotide polymorphisms in the mannose-binding lectin gene using minor groove binder-DNA probes. *J. Immunol. Methods* 287, 227–230 (2004).
- 49 de Kok JB, Wiegerinck ET, Giesendorf BA, Swinkels DW. Rapid genotyping of single nucleotide polymorphisms using novel minor groove binding DNA oligonucleotides (MGB probes). *Hum. Mutat.* 19, 554–559 (2002).
- 50 Zeschnigk M, Bohringer S, Price EA, Onadim Z, Masshofer L, Lohmann DR. A novel real-time PCR assay for quantitative analysis of methylated alleles (QAMA): analysis of the retinoblastoma locus. *Nucleic Acids Res.* 32, E125 (2004).
- 51 Emig M, Saussele S, Wittor H *et al.* Accurate and rapid analysis of residual disease in patients with CML using specific fluorescent hybridization probes for real time quantitative RT-PCR. *Leukemia* 13, 1825–1832 (1999).
- 52 van der Velden VH, Hochhaus A, Cazzaniga G, Szczepanski T, Gabert J, van Dongen JJ. Detection of minimal residual disease in hematologic malignancies by real-time quantitative PCR: principles, approaches, and laboratory aspects. *Leukemia* 17, 1013–1034 (2003).
- 53 Schalasta G, Eggers M, Schmid M, Enders G. Analysis of human cytomegalovirus DNA in urines of newborns and infants by means of a new ultrarapid real-time PCR-system. *J. Clin. Virol.* 19, 175–185 (2000).
- 54 Aliyu SH, Aliyu MH, Salihu HM, Parmar S, Jalal H, Curran MD. Rapid detection and quantitation of hepatitis B virus DNA by real-time PCR using a new fluorescent (FRET) detection system. *J. Clin. Virol.* 30, 191–194 (2004).
- 55 Tyagi S, Kramer FR. Molecular beacons: probes that fluoresce upon hybridization. *Nature Biotechnol.* 14, 303–308 (1996).
- 56 Smit ML, Giesendorf BA, Vet JA, Trijbels FJ, Blom HJ. Semiautomated DNA mutation analysis using a robotic workstation and molecular beacons. *Clin. Chem.* 47, 739–744 (2001).
- 57 Abravaya K, Huff J, Marshall R *et al.* Molecular beacons as diagnostic tools: technology and applications. *Clin. Chem. Lab. Med.* 41, 468–474 (2003).
- 58 Wabuyele MB, Farquar H, Stryjewski W *et al.* Approaching real-time molecular diagnostics: single-pair fluorescence resonance energy transfer (spFRET) detection for the analysis of low abundant point mutations in K-ras oncogenes. *J. Am. Chem. Soc.* 125, 6937–6945 (2003).
- 59 Whitcombe D, Theaker J, Guy SP, Brown T, Little S. Detection of PCR products using self-probing amplicons and fluorescence. *Nature* 17, 804–807 (1999).
- 60 Hart KW, Williams OM, Thelwell N *et al.* Novel method for detection, typing, and quantification of human papillomaviruses in clinical samples. *J. Clin. Microbiol.* 39, 3204–3212 (2001).
- 61 Thelwell N, Millington S, Solinas A, Booth J, Brown T. Mode of action and application of Scorpion primers to mutation detection. *Nucleic Acids Res.* 28, 3752–3761 (2000).
- 62 Solinas A, Brown LJ, McKeen C *et al.* Duplex Scorpion primers in SNP analysis and FRET applications. *Nucleic Acids Res.* 29, E96 (2001).
- 63 Ugozzoli LA, Hamby K. Four-color multiplex 5' nuclease assay for the simultaneous detection of the factor V Leiden and the prothrombin G20210A mutations. *Mol. Cell. Probes* 18, 161–166 (2004).
- 64 Vet JA, Majithia AR, Marras SA *et al.* Multiplex detection of four pathogenic retroviruses using molecular beacons. *Proc. Natl Acad. Sci. USA* 96, 6394–6399 (1999).
- 65 Tong AK, Li Z, Jones GS, Russo JJ, Ju J. Combinatorial fluorescence energy transfer tags for multiplex biological assays. *Nature Biotechnol.* 19, 756–759 (2001).
- 66 Tong AK, Ju J. Single nucleotide polymorphism detection by combinatorial fluorescence energy transfer tags and biotinylated dideoxynucleotides. *Nucleic Acids Res.* 30, E19 (2002).
- 67 Rickman D, Bobek MP, Misek DE *et al.* Distinctive molecular profiles of high-grade and low-grade gliomas based on oligonucleotide microarray analysis. *Cancer Res.* 65, 6885–6891 (2001).
- 68 Miyazato A, Ueno S, Ohmine K *et al.* Identification of myelodysplastic syndrome-specific genes by DNA microarray analysis with purified hematopoietic stem cell fraction. *Blood* 98, 422–427 (2001).
- 69 Dolken G. Detection of minimal residual disease. *Adv. Cancer Res.* 82, 133 (2001).
- 70 Lo YM, Tein MS, Lau TK *et al.* Quantitative analysis of fetal DNA in maternal plasma and serum: implications for noninvasive prenatal diagnosis. *Am. J. Hum. Genet.* 62, 768–775 (1998).
- 71 Hu Y, Zheng M, Xu Z, Wang X, Cui H. Quantitative real-time PCR technique for rapid prenatal diagnosis of Down syndrome. *Prenat. Diagn.* 24, 704–707 (2004).
- 72 Costa C, Pissard S, Girodon E, Huot D, Goossens M. A one-step real-time PCR assay for rapid prenatal diagnosis of sickle cell disease and detection of maternal contamination. *Mol. Diagn.* 7, 45–48 (2003).

Affiliations

- Mani Arya, MBChB, FRCS
Research Fellow, Institute of Urology, Prostate Cancer Research Centre, University College London, UK
Tel.: +44 208 502 1762
Fax: +44 208 502 1762
mani_arya@hotmail.com
- Iqbal S Shergill, BSc Hons, MBBS, MRCS
Research Fellow, Institute of Urology, Prostate Cancer Research Centre, University College London, UK
Tel.: +44 208 502 1762
Fax: +44 208 502 1762
super_iqi@yahoo.co.uk
- Magali Williamson, PhD,
Research Supervisor, Institute of Urology, Prostate Cancer Research Centre, University College London, UK
Tel.: +44 208 502 1762
Fax: +44 208 502 1762
magali.williamson@ucl.ac.uk
- Lyndon Gommersall, BMedSci, BM, BS, MRCS,
Research Fellow, Division of Medical Sciences, University of Birmingham, UK
Tel.: +44 208 502 1762
Fax: +44 208 502 1762
don@hartledon.freemove.co.uk
- Neehar Arya, BSc, Hons, MBBS, MRCS,
Clinical Research Fellow and Specialist Registrar
Leicester Royal Infirmary, UK
Tel.: +44 208 502 1762
Fax: +44 208 502 1762
drna1@aol.com
- Hitendra RH Patel, BMSc, Hons, BM, BCh, MRCS, PhD, FRCS (Urol)
, Clinical Associate, Institute of Cancer Research, Department of Human Biomonitoring & Carcinogen Activation, Sutton, Surrey, UK;
Professor, Department of Urology, University of Rochester Medical Center, Rochester, NY 14642, USA; Consultant Uro-oncological Surgeon, Royal Free and University College Hospitals, Department of Urology, London, UK
Tel.: +44 207 794 0500
Fax: +44 207 830 2906
brhpatel@doctors.org.uk