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REVIEW

Reference genes for measuring mRNA expression

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Abstract The aim of this review is to find answers to some of the questions surrounding reference genes and their reliability for quantitative experiments. Reference genes are assumed to be at a constant expression level, over a range of conditions such as temperature. These genes, such as GADPH and beta-actin, are used extensively for gene expression studies using techniques like quantitative PCR. There have been several studies carried out on identifying reference genes. However, a lot of evidence indicates issues to the general suitability of these genes. Recent studies had shown that different factors, including the environment and methods, play an important role in changing the expression levels of the reference genes. Thus, we conclude that there is no reference gene that can deemed suitable for all the experimental conditions. In addition, we believe that every experiment will require the scientific evaluation and selection of the best candidate gene for use as a reference gene to obtain reliable scientific results.

Keywords Reliability · Beta-actin · Reference genes · Polymerase chain reactions

Abbreviations

GADPH	Glyceraldehyde-3-phosphate dehydrogenase
PCR	Polymerase chain reaction
MARK3	Microtubule affinity regulating kinase 3
B2M	β2 Microglobulin
CorNV	Corneal neovascularisation
ACTB	Beta-actin
TBP	TATA binding protein
qRT-PCR	Quantitative real-time polymerase chain reaction
ALG9	Asparagine-linked glycosylation 9
RPL13A	Ribosomal protein L13a
qRT-PCR	Quantitative real-time PCR
HMBS	Hydroxymethylbilane synthase
qRT – PCR	Quantitative reverse transcription-polymerase chain reaction
HKG	Housekeeping genes
HPRT1	Hypoxanthine phosphoribosyltransferase 1
RT-qPCR	Reverse transcription-quantitative polymerase chain reaction
RT-PCR	Real time polymerase chain reaction
SAGE	Sequential analysis of gene expression
SDPH	Succinate dehydrogenase
ANOVA	One way analysis of variance
RPA	Ribonuclease protection assays

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Introduction

Reference genes are assumed to be stably expressed and are used for many experiments (de Kok et al. 2005). Some of the examples of reference genes are *MARK3* (Chia et al. 2010), *B2M* (Rho et al. 2010), *GAPDH* (Barber et al. 2005) and *beta-actin* (Mori et al. 2008). These genes are known as reference genes due to their stable gene expression levels (Zhang et al. 2005) and their role in aiding important regulatory functions such as protein folding and ribosome synthesis. These genes have been widely used for

investigations into the patterns of diseases (Reverter et al. 2008) such as cancer (Janssens et al. 2004). Such studies can help us in finding much needed information about these diseases as well as in designing better treatment strategies. Reference genes are used extensively in experimental work as they are assumed to have a minimal variation in gene expression (Chari et al. 2010), allowing reliable results from them.

Currently, there have been studies that question the reliability of these genes as reference genes for experiments (Caradec et al. 2010). Though these genes are known to present in all cells, their gene expression levels may vary depending on the cellular functions and the corresponding environmental conditions (Greer et al. 2010). It is a well accepted fact that these reference genes are not very resistant to the changes in their environment. They are susceptible, sometimes very easily, to any variations in temperature, stress and other attributes that may be affecting the environment (Ke et al. 2000). Thus, the use and reliability of the experimental results involving these reference genes in the past must be validated with considerable interest. There is a need to validate these genes for the specific experiments as the behaviour of each gene may change based on the experiments, environment conditions and human accuracy (Aleksandar et al. 2004). Some methods, such as Bestkeeper (Pfaffl et al. 2004), geNorm (Vandesompele et al. 2002) and NormFinder (Andersen et al. 2004), have been developed for doing the verification and selection of the reference genes. We argue that these past experiments, which had not performed the process of selecting appropriate reference genes, need to be validated as they might give different behaviour due to a change in the environmental factors such as temperature.

Contradictions in using reference genes

Recent studies have shown that the reference genes tend to fluctuate in different conditions and may give unexpected results in the involved experiments. Some of these reference genes tend to decrease in stability in the corneal neovascularization (CorNV) condition (Ren et al. 2010), with *GAPDH* (Barber et al. 2005) and *ACTB* (beta-actin) (Mori et al. 2008) being the least stably expressed. Clearly, the results from the past research work, which were using these reference genes without validation, may not be reliable due to such unexpected behaviour.

In a neuropathological study to investigate the relationship between brain-weight and mRNAs, it was found that the latter affected the expression of the genes, *Beta2M* (Rho et al. 2010) and *TATA*-binding protein (TBP) (Harrison et al. 2010). Therefore, it would be a risk to believe that these results, in the absence of reliable test cases for the validation of the known fluctuations in reference genes, did not have any effect on the involved experiments indirectly or directly. The past studies which were based on PCR (polymerase chain reaction) experiments had assumed that the reference genes were stable and independent of any experimental conditions. In a separate study (Noriega et al. 2010), the reference genes were validated using qRT-PCR (quantitative real-time PCR) and the reference genes *GADPH* (Barber et al. 2005), *ALG9* (Teste et al. 2009) and *RPL13A* (de Jonge et al. 2007; Curtis et al. 2010). The stability of their gene expression was tested using geNorm (Vandesompele et al. 2002), NormFinder (Andersen et al. 2004), and BestKeeper (Pfaffl et al. 2004). The use of quantile-normalized microarray gene expression values has shown an improvement in the selection of genes as reference genes (Noriega et al. 2010).

In a study of *Daphnia pulex* specimens (that were induced with *Chaoborus midge larva*), six candidate reference genes were tested for normalization using qRT-PCR (quantitative real-time PCR) (Spanier et al. 2010) and later studied. Of these, Xbp1, Tbp, CAPON, and Stx16 were found to be suitably expressed. This study also stated that there was no need for verifying the expression level of reference genes. However, a study on mouse liver (Chia et al. 2010) found that Tbp was not stably expressed.

Quantitative real-time PCR (qRT-PCR) depends on the selection of appropriate and stable reference genes (Huis et al. 2010) for gene expression analysis. Thus, geNorm (Vandesompele et al. 2002) and NormFinder (Andersen et al. 2004) algorithms were used to identify different sets of reference genes for expression data normalization in the roots, flowers, stems, and leaves of flax. Differences (Huis et al. 2010) in the identification of reference genes were found due to the use of two separate algorithms, albeit without any effect on the needed analysis, in the expression of reference genes for flax (*Linum usitatissimum* L.) in their various organs. This study (Huis et al. 2010) further identified *GADPH* as the most stable reference gene for such studies. Using real time PCR (polymerase chain reaction) experiments for a rat model based study (Wan et al. 2010) of three genes namely *beta-actin* (*ACTB*), glyceraldehyde-3-phosphate dehydrogenase (*GADPH*), and hydroxymethylbilane synthase (*HMBS*), it was found that *ACTB* and not *GAPDH* were stably expressed.

In another study (Hong et al. 2010), several genes of *Arabidopsis thaliana* were found to have more stable expression levels than traditional reference genes, when subjected to different environmental conditions. It is clear that methods such as RNA gel-blot analysis or quantitative reverse transcription-polymerase chain reaction (qRT-PCR) are dependent on stable reference genes. Thus, we believe that there is a different suitable combination of reference genes for each experimental study (Hong et al. 2010), which

needs to be validated and selected, depending on the specimens and the related environmental conditions.

In a separate study (Turabelidze et al. 2010) for observing the stability of nine reference genes in wound healing using reverse transcription-quantitative polymerase chain reaction (RT-qPCR) analysis, it was found that the expression levels of these reference genes were varying depending on the controlled experimental conditions. Another study found *GADPH* to be a reliable reference gene for quantitative gene expression analysis in human diploid fibroblasts (HDFs) (Zainuddin et al. 2010). Unicellular photosynthetic algae (dinoflagellates) from the genus *Symbiodinium* live symbiotically with coral reefs. In another study (Rosic et al. 2010), cultured *Symbiodinium* species (*clade C virus*) was studied under different environmental conditions and nine housekeeping genes (HKGs) were analysed. Using five stable HKGs as reference genes for the experiment, the Hsp90 expression levels were studied for *Symbiodinium* in culture and in symbiotic relationship with coral host (*Acropora millepora*) at varying temperature levels. The results showed varying levels for Hsp90 expression levels and presented a first list of HKGs for symbiotic *dinoflagellates*. The validation of reference genes in *Symbiodinium*, in the presence of thermal and light stress, revealed a drop in the *Hsp90* expression of the reference genes (Rosic et al. 2010).

In psychiatric gene expression studies (Rosic et al. 2010) involving human brain tissue, the reducing intersubject variability and not experimental error was the main advantage of normalization. There has been evidence against the classification of reference genes (Tunbridge et al. 2010) (in biological psychiatry) under the simple methods of classification. This meant that there was a need to look at a deeper and extensive approach, which included consideration of issues related to human brain studies. Using PCR (*polymerase chain reaction*) based techniques and normalization of reference genes [with geNorm (Vandesompele et al. 2002) and NormFinder (Andersen et al. 2004)], a study was undertaken to identify genes for flat oyster *Ostrea edulis*. The findings suggested using *GAPDH* (Barber Robert D 2005) and *EF1-α* (Ledet-Jensen and Ørntoft 2004) combined as reference genes when studying expression levels in haemocytes of *Oestrea edulis* (Ledet-Jensen and Ørntoft 2004). However, beta-actin was found to be the least stable (Morga et al. 2010) in the study of expression levels in this case. In a separate study (Caradec et al. 2010), an experiment was performed to evaluate the effect of hypoxia on expression levels of housekeeping genes. Here, the expression levels of ten reference genes were recorded for four cell lines treated with four oxygen concentrations (from 1 to 20 %). The experiment revealed large variations in their gene expressions in hypoxic conditions based on the choice of cell line, oxygen concentration, and the methods for statistical mean analysis. In another study (de Jonge et al. 2007) involving the meta-analysis of 13,629 human gene array samples, the gene expression levels (de Jonge et al. 2007) of the sample reference genes such as *ACTB* (Mori et al. 2008), *GAPDH* (Barber et al. 2005), *HPRT1* (Fujimori et al. 1988), and *B2M* (Rho et al. 2010) were used (de Jonge et al. 2007). The experiments recorded values of their CV (coefficient of variation), SD (standard deviation), and MFC (the proportion of the maximum and minimum values observed within the sample set) (de Jonge et al. 2007). It was found that the expression levels of these genes fluctuated dramatically (de Jonge et al. 2007). The MFC value was found to range from 1.91 for *ACTB* to 15.15 for *ALDOA* (de Jonge et al. 2007). Among all the genes, the CV value was found to be less than the 5 % level only for *ACTB* (de Jonge et al. 2007), indicating the high levels of variations in the genes (de Jonge et al. 2007). It is interesting to note that these genes are considered as reference genes and are assumed to be very stable for a wide range of conditions (de Jonge et al. 2007). Moreover, there was no gene identified from these commonly used reference genes (de Jonge et al. 2007), as a deserving candidate reference gene in the top 50 recorded candidate reference (de Jonge et al. 2007) genes of the dataset of this experiment.

The above literature clearly shows the contradictions in the findings on reference genes, implying the need for more thorough investigation to get more reliable and accurate results (Heng et al. 2011; Too and Ling 2011). There is a clear dependence of the reference genes on the environmental and other aspects of the scientific study, which make their classification methodology even more specific and complex.

Current methods for identification of reference genes

There are several methods in the identification of reference genes. Internal control genes (or reference genes) can be validated using regression analysis (Dhar et al. 2009).

Listed below are some of the methods used for identifying reference genes:

1) Real Time Polymerase Chain Reaction (or RT-PCR) has been used extensively for many years (Dheda et al. 2004; Ullmannová and Haskovec 2003; Wu et al. 2000; Gerard et al. 2000; Savli et al. 2003) for the identification of suitable reference genes. In this technique, which is a variant of polymerase chain reaction (PCR), RNA sequence is reverse transcribed into complementary DNA with the help of the reverse transcriptase enzyme. The cDNA is then amplified

using traditional or real-time PCR. In a recent study (Infante et al. 2008), *RPS4*, *UBQ*, and *eEF1A1* genes were found to be useful in larvae studies using quantitative PCR (polymerase chain reaction). In the past, this technique has been used without any normalization of the genes, which could indicate an increased risk of inaccurate experimental results. Thus, there is a need to focus on normalisation strategies and validate the reference genes which are used in experiments (Huggett et al. 2005).

2) SAGE (Sequential Analysis of Gene Expression) is a genetic sequence profiling technique (Hu 2006) used for obtaining high quality, accurate and quantitative analysis of gene sequences in the given datasets. One of the main methods requires data-mining the microarray datasets for highly expressed and relatively constant transcripts (Chari et al. 2010) as done in a study involving SAGE (Velculescu et al. 1995). SAGE is a technique used for getting a complete analysis of the gene expression patterns in the given gene datasets. This is done by isolating unique sequence tags from given mRNA sequences and then concatenating these sequences into long DNA sequences (Yamamoto et al. 2001).This technique has the following steps (Velculescu et al. 1995; Yamamoto et al. 2001):-

2.1. The mRNA of the observation sample is first extracted and isolated.
2.2. For each mRNA sequence, a section is removed at a pre-specified position.
2.3. All these obtained sections of mRNA sequences are then put together to form a lengthy chain like sequence.
2.4. These chains like sequences are then cloned into a vector. This is done so that the microorganisms (such as bacteria) can consume them.
2.5. These chains are then sequenced using automatic DNA sequencing technologies.
2.6. Next, the number of sequence tags are then counted using computer algorithms and software support.

In another study (Chari et al. 2010), SAGE (serial expression of gene expression) based records were analysed and then the specificity of reference genes was evaluated using quantitative PCR (polymerase chain reaction) and the results were analysed. This study suggested the usefulness of SAGE for the normalization of housekeeping genes.

3) Microarray data analysis is also another technique which is used to uniquely identify reference genes (Chia et al. 2010; Heng et al. 2011; Too and Ling 2011). In a separate study (Maccoux et al. 2007), normalisation of gene expression levels was used for microarray data analysis of the canine osteoarthritic joint tissue, and then the reference genes were identified using three different algorithms. New reference genes (Maccoux et al. 2007) were identified using the traditionally normalised microarray data and were found to be more stable than those found using reverse transcription-quantitative polymerase chain reaction (RT-qPCR). This method proved to be very effective as at least one gene *MRPS7*, was found to be most stable across multiple datasets. A similar method was used to identify reference genes for breast cancer studies (Gur-Dedeoglu et al. 2009) in which three microarray datasets of breast tumours were normalised and matched with their normal counterparts. *ACTP* (beta actin) and *SDPH* (succinate dehydrogenase) were found to be the most stable reference genes in this study involving quantitative real time polymerase chain reaction (qPCR).

4) Statistical algorithm based software such as geNorm (Vandesompele et al. 2002) and NormFinder (Andersen et al. 2004) are also used to normalize reference genes. In a separate study, while analysing the expression levels in haemocytes of *Oestrea edulis*, the reference genes for the same were identified by analysing the RNA sequences (Morga et al. 2010), using polymerase chain reaction (PCR), in pools of haemocytes that were in touch with the parasite and the haemocyte alone. The above mentioned software was used to normalise the gene expression levels in the study. This is just one of the several experiments in which the above mentioned algorithms have played an important role for improving the appropriateness of the housekeeping genes

5) In the study for ovarian tissues, twenty reference genes were identified from 52 samples (Fu et al. 2010) involving non-malignant and malignant carcinogenic cells. One way analysis of variance (ANOVA) method was used to study the gene changes. Next, geNorm (Vandesompele et al. 2002) and NormFinder (Andersen et al. 2004) were used for further validation.

A comparison of the existing methods is essential for a making a better choice from them for different experiment scenarios. Real-time polymerase chain reaction (RT-PCR) can quantify for much smaller samples of mRNA (even from a single cell); thus, assures higher accuracy. This quantitative method can automate processes such as finding rare targets as well as abundant targets by measuring the reaction products in each cycle for every sample. This is because during the exponential phase of amplification (this is the phase in which the samples are analysed and quantitative data is collected from the given sample).

There are some drawbacks of using real-time polymerase chain reaction (RT-PCR) when compared to other

methods. It is time-consuming (Innis et al. 1990; Hunt 2006) and the results are not always reliable as ethidium bromide (which is used as a staining material for detection of PCR products) has low sensitivity. Real-time polymerase chain reaction (RT-PCR) has an increased cross contamination risk of the samples under consideration here. At the same time, there had been reported instances of contamination of cDNA transcripts with genomic pseudogenes (Smith et al. 2001) or degradation of RNA (Yang et al. 2011), which may arise from RNA preparation (Pinto et al. 2009). This will significantly increase the detection error as the detection of the polymerase chain reaction (PCR) products requires the post-amplification processing of the samples. However, there had been a sample processing steps to prevent genomic pseudogene contamination (Kreuzer et al. 1999; Lehmann et al. 2002) but these will increase the number of steps in sample preparation and validation using mitochondrial DNA (Malik et al. 2011). Moreover, the specificity of the assay is determined by the primers and which can give false-positive results. Another issue is that it is semi or even low quantitative technique, whereas the amplicon (it is a piece of DNA which is formed as the product of amplification events) can be can be visualized only after the amplification ends. Real-Time polymerase chain reaction (RT-PCR) is the most sensitive method and can discriminate closely related mRNAs. It is technically simple but it is difficult to get truly quantitative results using conventional polymerase chain reaction (PCR). Northern blotting and Ribonuclease Protection Assays (RPAs) require no amplification while in situ hybridization is qualitative in nature. Northern blotting and Ribonuclease Protection Assays (RPAs) provide good results, but consume more RNA than their counterparts. Polymerase chain reaction (PCR) considers amplification of the DNA; thus, more sensitive. Real-time PCR gives more quantitative results and is also easier and convenient to use (Hunt 2006; van Guilder et al. 2008).

SAGE and microarrays are different due to the need for prior knowledge (in the latter) of the gene sequences of the samples under consideration here (Patino et al. 2002). Microarrays need a uniform standard for platform fabrication, assay protocols, and analysis. They have large datasets and need complex statistical algorithms for processing them with high accuracy. A significant issue, besides normalization of data and the reduction of dimensionality of data, is the sequencing requirement in SAGE. It is comparatively easy and more reliable to search sequences from SAGE databases (which store experimental data using the SAGE technique) stored at different places and then perform northern blots on them. However, Microarrays have a higher degree of random and systematic errors, due to which a comparison of experimental data from different places (experimental sources) is difficult.

What reference genes had been identified?

We present a list (Table 1) showing each of the reference genes, the related parameters and the journal source referenced here. This is in addition to an extensive list presented in an earlier study on reference genes (Zhu et al. 2008).

Implications on experiments using unstable genes as reference genes

There is a growing assertion that the reference genes could be a wrong choice for experimentation if not properly validated for effective quantitative RNA analysis. A single reference gene cannot be a reliable reference gene for all experiments in all conditions (Janssens et al. 2004). Consider a scenario in which an existing gene, which is widely assumed to be a stable reference gene, is used in the traditional mode of experimentation (without any normalisation of the involved reference gene). The reference gene might have been stable for only a subset of the environmental conditions of the experiment. Could we think of the behaviour of the same reference gene if they were subjected to more extreme conditions? Based on the past studies that we reviewed in this paper, it is clear that the experimental results could be altered because of the changes in the experimental conditions. Thus, we argue based on the evidence, from the current scientific literature, that the past studies which did not perform the normalisation of the reference genes, could have issues in the accuracy of their results. This also means that the scientific results, obtained using invalid reference genes in the involved experiments, may not be acceptable as there will be certain extremes reached by the involved reference genes, which might not have been corrected. Thus, the entire experiment may have to be validated again using the corrected and normalised reference genes for a persuasive argument in favour of the obtained scientific results.

Conclusions

It is clear that the use of reference genes is appropriate only if they are normalised and considered on the basis of the environmental conditions and other factors such as method of gene expression. We believe that it is wrong to consider any reference gene without validating their suitability to the undertaken experiment. Thus, the past experiments, which may have made the mistake of ignoring the need to normalise the genes, may have to validate their results in corrected conditions, so as to get accurate details and remove the possible errors due to the wrong selection of reference genes. We conclude by considering genes (normalised using techniques such as geNorm (Vandesompele et al. 2002) and NormFinder

Table 1 List of housekeeping genes

S. no	Reference genes found	Organ/species/disease	Reference	Are they reliable?
1	NDUFA1, RPL19, RAB5C, and RPS18	Human lung samples—cancer affected	Chari et al. 2010	Yes
2	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	Human diploid fibroblasts	Zainuddin and Chua 2010	Yes
3	Beta-2 microglobulin and 18S rRNA	Serum-stimulated fibroblasts	Schmittgen et al. 2000	Yes
4	ATPsy6 (mATPsy6),GADPH, porphobilinogen deaminase (PBGD)	Human—number of cell lines and tumour versus matched normal tissue samples	Janssens et al. 2004	Yes
5	HMBS,GADPH	Human hepatocellular carcinoma(HCC)	Cicinnati et al. 2008	Yes
6	GADPH, 14-3-3 and rpl7	*Coffea arabica*	Barsalobres-Cavallari et al. 2009	Yes
7	Xbp1, Tbp, CAPON and Stx16	Chaoborus-induced *D. pulex* specimens	Spanier et al. 2010	Yes
8	LOC_Os06g11170.1	Rice	Narsai et al. 2010	Yes
9	eEF1A (s) and YT521-B	*Lolium perenne* L.	Lee et al. 2010	Yes
10	GhUBQ14 and GhPP2A1 for cotton plants; GhACT4 and GhUBQ14 for flower development, GhACT4 and GhFBX6 for the floral organs and GhMZA and GhPTB for fruit development	Cotton, flower and fruits (plants)	Artico et al. 2010	Yes
11	List of housekeeping genes	*Homo sapiens*	Zhu et al. 2008	Yes
12	ACTB	HKGs in human eESCs (embryonic stem cells)	Synnergren et al. 2007	Yes
13	AhR, p53, PCNA and β-actin	HKGs used in studying anticancer properties in *Polygela senega* organism species	Paul et al. 2010	Yes
14	TBP and HPRT	Human HBV-related hepatocellular carcinoma	Fu et al. 2009	Yes
15	ACTB and 18S	Human HBV-related hepatocellular carcinoma	Fu et al. 2009	No
16	List of expression data with list of several housekeeping genes	Housekeeping genes and cancer in humans	Khimani et al. 2005	Yes
17	PGBD	Housekeeping gene in ovarian tumour studies	Glaysher et al. 2010	Yes
18	ACTB, ALAS1, GAPDH, HPRT1, PBGD, PUM1, RPL29 and 18S rRNA	Housekeeping gene in human serous ovarian cancer	Li et al. 2009	No
19	GUSB, PPIA, and TBP	Housekeeping gene in human serous ovarian cancer	Li et al. 2009	Yes
20	S4 ribosomal protein (Rp-S4), calmodulin (Cal), and cytochrome oxidase subunit 1 (Cox),	Symbiodinium exposed to thermal and light stress	Rosic et al. 2010	Yes
21	List of 50 breast cancer control genes	Breast cancer control genes in humans in ranked format	Popovici et al. 2009—Table 3	Yes
22	List of HK genes used for *Arabidopsis* studies	*Arabidopsis*	Huis et al. 2010)—Fig. 1	Yes

(Andersen et al. 2004)) as good reference genes for PCR based experiments. These genes if used properly, especially for phylogenetic analysis, could increase our knowledge and provide useful information about related species.

Conflict of interest There are no competing interests cited by the authors of this paper.

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