Optimization of semi-quantitative RT PCR analysis for CPT I gene expression in Rainbow trout (*Oncorhynchus mykiss*)

Jalali, S. A. H.¹; Nikbakht, G*²; Mahboobi Soofiani, N.³; Jalali, S. M. A.⁴

Received: October 2010

Accepted: January 2011

1- Department of Pathobiology, Faculty of Veterinary Medicine, University of Tehran, Tehran-Iran.

- 2- Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran- Iran.
- 3- Department of Natural Resources, Isfahan University of Technology (IUT), Isfahan, Iran.
- 4- Department of Animal Science, Faculty of Agriculture, Islamic Azad University- Shahrekord Branch, Shahrekord, Iran.
- * Corresponding author's email: nikbakht@ut.ac.ir

Keywords: Carnitine Palmitoyltransferase I, Rainbow Trout, RT PCR, Gene Expression.

A key enzyme in mitochondrial β oxidation, carnitine palmitoyltransferase (CPT) I, is transcriptionally regulated in mammals, but this enzyme also experiences allosteric modulations (Harano et al., 1985; Murthy and Pande, 1987; Bezaire et al., 2004). CPT I is located on the inner side of the outer mitochondrial membrane and catalyses the acyl-CoA to fatty conversion of acylcarnitine (Kerner and Hoppel, 2000; Price et al., 2000). Quantitative RT-PCR is a reliable technique for measuring transcripts in small amounts of tissue (Spriewald et al., 2000). With this technique, multiple mRNAs can be assayed simultaneously in a relatively short period of time. Here we describe the standard procedure, optimized in our laboratory, to assess CPT I levels with β actin as an internal control in rainbow trout, and all the necessary controls to ensure a quantitative analysis.

RNA Extraction and Reverse Transcription Total cellular RNA was isolated from liver of rainbow trout using RNX reagent (Cinnagen-Iran). To obtain cDNA, 1 µg of total RNA was subjected to reverse transcription polymerase chain reaction (RT-PCR) with MuLV reverse transcriptase using the RevertAidTM M-MuLV Reverse Transcriptase Kit (Fermentase Life Science, Germany) and primer. Reaction random hexamer conditions in the reverse transcription step are mostly dependent on the enzyme and the primers of choice. Whereas other protocols to require the use of specific primers, we prefer to reverse transcribe the total RNA population with random hexamers so that different PCR analyses could be performed on the same cDNA sample.

PCR

Five μ l of cDNA products were amplified with 1 unit of Taq polymerase (Cinnagen-Iran), and in the presence of the specific primers for CPT I gene together with the β -actin gene, used as an internal control as described below. The amount of dNTPs used was 0.1 mM that was sufficient for amplification. A first cycle of 3 minutes at 95 °C, was followed by 45 seconds at 95 °C, 60 seconds at 56 °C and 2 minutes at 72 °C for 35 cycles and continued with 5 minutes at 72 °C for one cycle. Each set of reactions always included a no-sample negative control. To determine specificity, all sequences were compared with the GenBank sequences using the program Blast available at the National Center for Biotechnology Information website (www.ncbi.nlm.nih.gov). The following primers were used: CPT I F-5'-TGAAGATGCTCTCTGGGCGC -3' (melting temperature $(Tm)=60.7^{\circ}C$), and R- 5'-GTGTGGGAGTCACGTACAGC-3' (Tm=59°C); β-actin,

F- 5'-GTACCCTGGCATTGCTGA -3' (Tm=57.4°C) and, R- 5'-

TTAGAAGCATTTGCGGTGGACA-3' (Tm=58°C).

PCR products were loaded on 1 % agarose gels in TAE buffer (1X) and pictures were captured by Sony XC-75 CE camera (Vilber Lourant Inc. Cedex, France) and quantification of the bands was performed by Photo-Capt v.99 Image software (Vilber Lourant Inc. Cedex, France). Length of CPT I gene was 335 bp, which was different from β -Actin (207 bp). Reliable internal quality control of cDNA essential. Controls synthesis is are generally performed by PCR amplification of reference genes, mostly common housekeeping genes (GAPDH, albumin, actins, Elongation factor-1- α (EF-1- α), tubulins, cyclophilin, microglobulins, 18S ribosomal RNA (rRNA) or 28S (rRNA). In our experiment before selecting β -actin as an internal control in liver samples of rainbow trout, we chose Elongation factor-1- α (EF-1- α) gene for internal control (Gutieres et al., 2003), but didn't see any band on the gel. This problem showed that the chosen reference genes used as well as expression levels the vary between

different laboratories, and only few of them have been critically evaluated. In our conditions B-Actin content did not vary significantly within the same type of sample (i.e. the same tissue type). In conventional PCR, each primer was used in a concentration range of 0.05 to 0.4 μ M. We optimized CPT I and β -actin with 0.2 µM of each of the two specific primers (Fig. 1). We usually tested the following $MgCl_2$ concentrations: 1, 2, 3, 4 and 5 mM. As shown in Fig. 2, CPT I worked best at 1, 2 mM MgCl₂ and β -Actin worked best at 1, 2 and 3 mM MgCl₂ (Fig. 2). Another parameter to be analyzed thoroughly is the number of amplification cycles to perform. It is not sufficient to visualize the amplification product on a gel. It is well known that amplification is initially exponential but reaches a plateau when the activity of the enzyme declines and when any of the reagents become limiting in the reaction. At the plateau, RNAs initial present at high levels may give products of equal intensity to low abundant RNAs. An appropriate number of cycles was determined by testing the different cycles of 20, 22, 24, 26, 28, 30, 32 and 34 for both CPT I and β -Actin amplifications in one tube, whereas CPT I and β -Actin intensity increased up to 30 cycles, no increase could be seen in both at more than 32 cycles, i.e. it had already reached a plateau (Fig. 3). To determine whether the selected conditions were suitable for semi quantitative RT PCR with both primer sets (CPT I and β -Actin) at the same time, we performed a competition control, by amplifying the same sample at the same time in the presence of the specific primers for CPT I, the internal control β -Actin, and both sets together. Furthermore, different MgCl₂ concentrations for each reaction were tested. We have shown in Fig. 4 how CPT I and β -Actin did not compete when combined at 30 cycles in three mM MgCl₂. Different cDNA of rainbow trout liver were co-amplified with CPT I and β -actin specific primers in one tube PCR reaction

to confirm the conditions being optimized (Fig. 5). According to results obtained from different conditions 30 cycles and three mM $MgCl_2$ were selected for semiquantitative PCR.

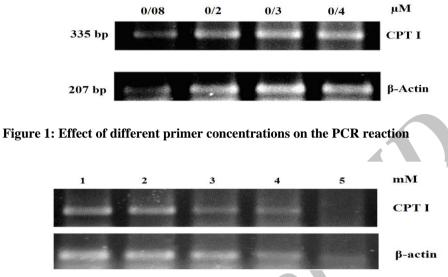


Figure 2: Effect of different MgCl₂ concentrations on PCR reaction

CPT I amplification was optimal at 1 and 2 mM $MgCl_2$ and decreased gradually at higher concentrations. Also, β -actin was optimal at 1, 2, and 3 mM $MgCl_2$ and decreased gradually at higher concentrations.

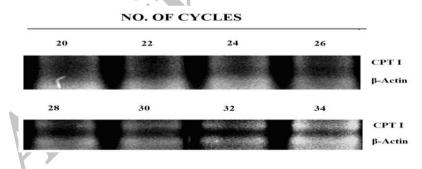


Figure 3: Determination of the exponential range of amplification for CPT I and β-Actin

The analysis was performed in 3 mM MgCl₂ at 63°C. The intensity of the CPT I amplification product increased up to 34 cycles, whereas β -Actin and CPT I reached a plateau at 32 cycles.

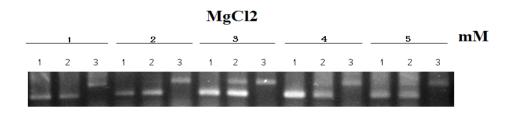


Figure 4: Control for competition between different primer sets

Reactions were performed in the same conditions for lanes 1, 2 and 3. Lane 1 contained the β -Actin primer set only, lane 3 the specific primers for the target RNA, and lane 2 both primer sets. In the selected conditions (3 mM MgCl₂, 63 °C, 30

cycles) CPT I and β -Actin did not compete (panel 3). The panel 1, 2, 4 and 5 show an example in which the specific primers for the CPT I competed with the β -Actin primers.

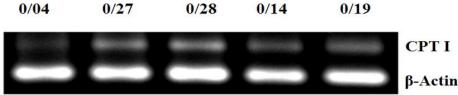


Figure 5: Representative of analyses performed on different concentration of CPT I relative to the β-Actin concentration.

(Above Numbers: The ratios of corresponding CPT I/β-actin absorption density of bands on a gel).

Our experiments confirmed that semiquantitative RT PCR provides reliable information as long as the proper controls are all performed correctly.We have described the protocols to have been reproduced on different types of rainbow trout samples.

References

Bezaire, V., Heigenhauser, G.J. and Spriet, L.L., 2004. Regulation of CPT I activity in intermyofibrillar and subsarcolemmal mitochondria from human and rat skeletal muscle. *American Journal* of *Physiology* - *Endocrinology* and *Metabolism.* 286:E85–E91.

Carding, S.R., Lu, D. and Bottomly, K .A., 1992. A polymerase chain reaction assay for the detection and quantification of cytokine gene expression in small number of cells. *Journal of Immunological Methods*, 151, 277-287.

Harano, Y., Kashiwagi, A., Kojima, H., Suzuki, M., Hashimoto, T. and Shigeta, Y., 1985. Phosphorylation of carnitine palmitoyltransferase and activation by glucagon in isolated rat hepatocytes. *FEBS Letters*. 188, 267–272. Kerner, J. and Hoppel, C., 2000. Fatty acid import into mitochondria. *Biochimica et Biophysica Acta*. 1486, 1–17.

Murthy, M.S. and Pande, S.V., 1987. Malonyl-CoA binding site and the overt carnitine palmitoyltransferase activity reside on the opposite sides of the outer mitochondrial membrane. *Proceedings of the National Academy of Sciences of the United States of America.* 84, 378–382.

Price, P .T., Nelson, C. M . and Clarke, S. D ., 2000. Omega-3 polyunsaturated fatty acid regulation of gene expression. *Current Opinion in Lipidology*, 11, 3–7.

Spriewald, B.M., Hara, M., Bushell, A., Jenkins, S., Morris, P.J. and Wood, K .J., 2000. Differential role for competitive reverse transcriptase–polymerase chain reaction and intracellular cytokine staining as diagnostic tools for the assessment of intragraft cytokine profiles in rejecting and nonrejecting heart allografts. *The American Journal of Pathology*. 157, 1453-1458.