

A comparison of PPAR signaling pathway genes in intramuscular adipose tissue of human beings and ruminants

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Abstract— Gene expression can be used to increase marbling. Of course, The PPARs are the important factors regarding gene expression in the adipose tissue. To characterize the main intramuscular fat, the present study compared the underlying genes in the human beings and ruminants. In doing so, the related genes PPAR signaling pathway were extracted and compared using KEGG and Ref seq RNA and the bioinformatics BLAST. The results indicated the cycle genes were, to a great extent, the same in the above -mentioned subjects and FABP1, UBC, CPT2, MMP1, UCP1, ILK, FABP3, OLR1, LPL genes were expressed in their intramuscular fat.

Keywords— PPAR, Marbling, Ruminants

I. INTRODUCTION

The meat quality is the most important factor in terms of meat marketing, sale and exportation, and of course, the main concern as for the meat livestock is their muscular growth maximization [19]. Also, meat tenderness mostly satisfies different consumers' preferences and tastes [16]. Moreover, intramuscular and subcutaneous fat is a contributing factor in the quality meat [4]. BMS intramuscular fat is a typical fat located in the muscle [6]. To maximize the intramuscular fat, we can apply gene expression which PPAR is involved in gene expression of the adipose tissue. Importantly, existing genes in the PPAR signaling pathway play a vital role in many species. Hence, the purpose of present study was to compare the afro-mentioned genes in both human beings and ruminants to characterize the intramuscular adipose tissue genes concerning PPAR signaling pathway.

Theoretical background

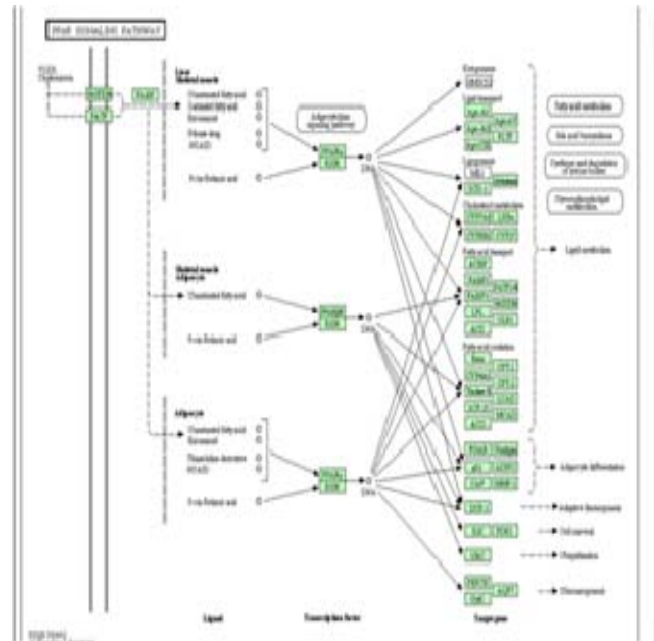
Intramuscular fat also known as marbling or marbling fat is characterized by streaks or sheets of white fat between muscle fibers in the meat. This characteristic can influence the quality

and quality of meat production obviously, the marbling maximization has been found as the quality meat index [5]. Since the marble meat is highly admired by the consumers, marble adipose tissue enjoys an advantage over other fat storages [7]. As discussed earlier, the gene expression in the fat tissue is used to maximize the marbling for which the PPARs are used most frequently. The PPARs are characterized as proxy zoom- induced receptors from ligand-dependent nuclear superfamily members and adjust the fat metabolism related genes. Additionally, they are attached to the lipid acid and its derivatives and adjust and determine the processes including genesis, cell cycle, apoptosis and lipid metabolism. The PPARs are activated through retinoid X receptors which function as partners for various nuclear receptors during transcriptional regulation. PPAR-RXR transcriptional complex contributes to energy balance triglycerides metabolism, fatty acid storage and glucose homeostasis in the ruminants and obesity as well as diabetes processes in the human beings [9]. There are three so called isotopes of PPARs known as PPAR α , PPAR β/δ and PPAR γ , with the varied distribution in the different tissues and each binds to specific ligands used to treat diabetes 2, hyperlipidemia and inflammation control in the human subjects [18]. PPAR α is highly expressed in tissues including liver, muscle, kidney and heart. It also stimulates the fatty acids beta oxidative degradation whereas PPAR β/δ has been rarely studied and is involved in the fatty acid oxidation. On the other hand, PPAR γ has been highly expressed in a wide range of tissues and cells with relatively higher levels of expression noted in brain, adipose and skin [1]. It is considerably engaged in signaling pathways of a biogenesis producing sufficient number of fat cells within muscles in the embryonic period [5]. In recent years, the biological role of PPARs has attracted many researchers. It can be analyzed through PPAR biological cycle [3]. The biological cycles facilitate the same genes identification in different tissues and species [10]. They are

also recognized as the biological systems main core due to empirical data and mathematical models systems integration [12]. The KEGG is a main internet source to interpret biological cycle components. It can interrelate the biological information including genes, proteins, chemical structures, molecular interactions, ligands and the cycles [9] and consider their biological function and the cycle management [10]. The KEGG pathways consist of 1300 different fat cycles and their related information [9]. Also, the expressed genes analysis of KEGG can be used for various tissues biological consideration. For example, the PPAR genes analyses could be applied to study the carbohydrate, amino acids and fat metabolism in the live species [3].

2-Materials and Methods

Display Differential Digital (DDD) is a web-based bio-informatics and a powerful tool for the identification of gene expression in different tissues. In the present study, human and animal genes were found to be highly expressed in adipose tissue by using DDD. Then, adipose tissue EST libraries were compared with EST libraries regarding liver, kidney, muscle and skin. Subsequently, PPAR signaling pathway gene was used from KEGG and its related genes were derived from ruminants and humans as can be seen in Figure1. [17]



After identifying genes associated with PPAR signaling pathway information such as DNA sequencing and Ref seq RNA genes in organisms were extracted from the NCBI. Finally, Ref seq RNA the PPAR signaling pathway genes related with organisms were compared with each other via BLAST bio-informatics tools.

3-Results and discussion

According to Digital Differential Display (DDD), it was found that LPL, FABP4 and SCD enjoyed the highest expression in the ruminants and human adipose tissue. Michal et al. [11] reported a significant between FABP4 relationship gene and obesity. In addition, several studies have reportedly confirmed the LPL, FABP4 and SCD role in fat metabolism [13], [14].

ISSN (Online): 2305-0225

Issue 19(2), January 2014, pp. 17-20

Table 1: The PPAR genes results in human beings and ruminants

	Total	Common Genes No.	Uncommon Genes No.
PPAR	72	60	12
Intramuscular Fat	34	10	24

83 percent of PPAR genes were similar among the human beings and the ruminants. Thus the results confirm theory of non-randomized and conserved expression of orthology genes. The theory implies that biological processes and the important genes are conserved among different species [15] such that FABP4, ACSL6, APOA5 and FABP1 genes may have 5 % (or more) adjustment. PPAR of intramuscular fat tissue (figure1) in the study animals revealed that OLR1, LPL, FABP3, FABP1, UBC, CPT2, MMP1,UCP1 and ILK genes were expressed in both groups such that OLR1, FABP3, CPT2, LPL were involved in the fat metabolism, while MMP1, UBC, UCP1 and PPAR contributed to adipose tissue differentiation, yobikinon, temperature control and fat metabolism ,respectively [3]. Most importantly, UPT2, MMP1, UCP1 and FABP3 are considered control points or hubs due to their underlying bound-genes confirming their excellence over other PPAR genes. Finally, FABP3 and FABP4 are adiposeness genes through primary adiposities differentiation [7].

Conclusion

Recently, experts have shown interest in breeding the livestock with the higher marbling, lower fat and most importantly, tender meat [8]. Hence, PPARs biological role-subject to PPAR biological cycle analyses -has gained much attention [3]. The cycles facilitate similar and common genes in different tissues of the species [10]. The present study revealed ruminants and human beings share most PPAR genes. Also, LPL, OLR1, FABP2, UBC, FABP1, CPT2, MMP1, ILK and UCP1 genes are expressed in both groups' intramuscular fat tissue. To sum up, due to intramuscular fat importance in people nutrition, it is suggested that other genes influencing intramuscular fat tissue be considered for quality meat production.

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ISSN (Online): 2305-0225

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