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Published

2010

Journal Title

Comparative Biochemistry and Physiology, Part D

DOI

[10.1016/j.cbd.2009.09.004](https://doi.org/10.1016/j.cbd.2009.09.004)

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COMPARATIVE GENOMICS AND PROTEOMICS OF VERTEBRATE DIACYLGLYCEROL
ACYLTRANSFERASE (*DGAT*), ACYL CoA WAX ALCOHOL ACYLTRANSFERASE (*AWAT*) AND
MONOACYLGLYCEROL ACYLTRANSFERASE (*MGAT*)

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Keywords: Diacylglycerol acyltransferase-Monoacylglycerol transferase-Human-
Mouse-Opossum-Zebrafish-Genetics-Evolution-X chromosome

Running Head: **Genomics and proteomics of vertebrate acylglycerol
acyltransferases**

ABSTRACT

BLAT (BLAST-Like Alignment Tool) analyses of the opossum (*Monodelphis domestica*) and zebrafish (*Danio rerio*) genomes were undertaken using amino acid sequences of the acylglycerol acyltransferase (AGAT) superfamily. Evidence is reported for 8 opossum monoacylglycerol acyltransferase-like (*MGAT*) (E.C. 2.3.1.22) and diacylglycerol acyltransferase-like (*DGAT*) (E.C. 2.3.1.20) genes and proteins, including *DGAT1*, *DGAT2*, *DGAT2L6* (*DGAT2*-like protein 6), *AWAT1* (acyl-CoA wax alcohol acyltransferase 1), *AWAT2*, *MGAT1*, *MGAT2* and *MGAT3*. Three of these genes (*AWAT1*, *AWAT2* and *DGAT2L6*) are closely

localized on the opossum X chromosome. Evidence is also reported for six zebrafish *MGAT*- and *DGAT*-like genes, including two *DGAT1*-like genes, as well as *DGAT2*-, *MGAT1*-, *MGAT2*- and *MGAT3*-like genes and proteins. Predicted primary, secondary and transmembrane structures for the opossum and zebrafish *MGAT*-, *AWAT*- and *DGAT*-like subunits and the intron-exon boundaries for genes encoding these enzymes showed a high degree of similarity with other members of the AGAT superfamily, which play major roles in triacylglyceride (*DGAT*), diacylglyceride (*MGAT*) and wax ester (*AWAT*) biosynthesis. Alignments of predicted opossum, zebrafish and other vertebrate *DGAT1*, *DGAT2*, other *DGAT2*-like and *MGAT*-like amino acid sequences with known human and mouse enzymes demonstrated conservation of residues which are likely to play key roles in catalysis, lipid binding or in maintaining structure. Phylogeny studies of the human, mouse, opossum, zebrafish and pufferfish *MGAT*- and *DGAT*-like enzymes indicated that the common ancestors for these genes predated the appearance of bony fish during vertebrate evolution whereas the *AWAT*- and *DGAT2L6*-like genes may have appeared more recently prior to the appearance of marsupial and eutherian mammals.

1. INTRODUCTION

Acylglycerol acyltransferases (AGATs) are predominantly responsible for triglyceride synthesis in the body, via two major pathways: the glycerol phosphate (GP) pathway (Kennedy, 1957) and the monoacylglycerol (MG) pathway (see Coleman and Lee, 2004; Yen et al, 2008). The final step of both pathways involves diacylglycerol and fatty acyl CoA being catalytically converted into triglyceride via two distinct *DGAT* (diacylglycerol O-acyltransferase, E.C.2.3.1.20) families, *DGAT1* and *DGAT2* (Cases et al., 1998; Oelkers et al, 1998). The two pathways differ in the mode of synthesis of diacylglycerols prior to catalysis by *DGAT1* and/or *DGAT2*, with the GP pathway involving de

novo synthesis from glycerol-3-phosphate and fatty acyl CoA, whereas the MG pathway uses partially hydrolyzed monoacylglycerols and fatty acyl CoA. This penultimate step in the MG pathway is catalyzed by enzymes encoded by the monoacylglycerol acyltransferase (*MGAT*; 2-acylglycerol O-acyltransferase; EC 2.3.1.22) gene sub-family, for which three *MGAT* (also designated as *MGOT* and *MOGAT*) genes have been reported in humans (Yen et al., 2002; 2003; Cheng et al., 2003). The human *DGAT2*-like gene family comprises at least seven members, including *DGAT2* (Cases et al., 2001), *MGAT1* (Yen et al., 2002), *MGAT2* (Yen and Farese, 2003), *MGAT3* (Cheng et al., 2003), and three genes located together on the X chromosome (*DGAT2L6*, *AWAT1* and *AWAT2*) (Turkish et al., 2005). The latter two genes encode enzymes with acyl CoA wax alcohol acyltransferase (*AWAT*) activity, and are specifically expressed in sebocytes (skin), and play a role in preventing surface desiccation by the formation of wax esters.

The triglyceride forming pathways are differentially distributed in the body with the GP pathway being widely distributed and responsible for triglyceride synthesis in most tissues of the body. The MG pathway however is predominantly localized in specific cell types, including enterocytes (intestine), hepatocytes (liver) and adipocytes (adipose tissue), where large amounts of triglycerides are synthesized or stored. In particular, MG is the major pathway of the small intestine, where partially hydrolyzed fats are used to synthesize triglycerides following lipid ingestion (see reviews in Coleman and Lee, 2004; Yen et al, 2008).

This study describes the predicted sequences, structures and phylogeny of diacylglycerol acyltransferase-like (*DGAT*) and monoacylglycerol acyltransferase-like (*MGAT*) genes and enzymes from eutherian (human and mouse) and marsupial (opossum) mammals and from a bony fish (zebrafish)

species. Computational methods were used to predict the primary, secondary and transmembrane structures for these enzymes, as well as gene locations, exonic structures and sequences for *MGAT*- and *DGAT*-like genes, using published data from genome sequences. Predictions of *MGAT*- and *DGAT*-like enzyme sequences from a wider range of vertebrates were also used to examine the phylogeny and evolution of these genes and to identify conserved amino acid residues, including likely candidates for the active sites and substrate binding regions for these enzymes.

2. MATERIALS AND METHODS

2.1 *DGAT* and *MGAT* Gene and Enzyme Identification.

BLAT (BLAST-Like Alignment Tool) studies were undertaken using the UC Santa Cruz web browser [<http://genome.ucsc.edu/cgi-bin/hgBlat>] (Altschul et al., 1990; Kent et al., 2002) with the default settings. UniProtKB/Swiss-Prot database derived amino acid sequences for human, mouse and zebrafish *DGAT*-like and *MGAT*-like enzymes [<http://au.expasy.org>], GenBank derived amino acid sequences for zebra fish *DGAT*-like and *MGAT*-like enzymes [<http://www.ncbi.nlm.nih.gov/Genbank/>], and predicted NCBI sequences for opossum genes and enzymes [<http://www.ncbi.nlm.nih.gov/>] (see Table 1) were used to interrogate vertebrate genome sequences, particularly human (*Homo sapiens*) and mouse (*Mus musculus*) (MGC Project Team, 2004), opossum (*Monodelphis domestica*) (Mikkelsen et al., 2007) and zebrafish (*Danio rerio*) genomes (http://www.ensembl.org/Danio_rerio/Info/Index). Several other vertebrate genomes were also interrogated to examine *DGAT*-like and *MGAT*-like amino acid sequences for conserved residues that may play key roles in catalysis, substrate binding and maintaining enzyme structure and function (see Supplementary Table). Gene locations, predicted gene structures and

protein subunit sequences were observed for each of the predicted *DGAT*-like and *MGAT*-like genes and proteins. Structures for the major human *DGAT*, *AWAT* and *MGAT* isoforms (splicing variants) were obtained using the AceView website to interrogate the database of human mRNA sequences (Thierry-Mieg and Thierry-Mieg, 2006):

(<http://www.ncbi.nlm.nih.gov/IEB/Research/Acembly/index.html?human>)

2.2 Predicted Structures and Properties for Vertebrate *DGAT*-like and *MGAT*-like Subunits.

Predicted secondary and transmembrane structures for mammalian *DGAT*-like and *MGAT*-like subunits were obtained using the SWISS MODEL web tools (Schwede et al., 2003) (<http://swissmodel.expasy.org/workspace>) and the transmembrane prediction server (<http://www.cbs.dtu.dk/services/TMHMM-2.0/>) provided by the Center for Biological Sequence Analysis of the Technical University of Denmark (von Heijne, 1992; Tusnady and Simon, 2001). Theoretical isoelectric points and molecular weights for *MGAT* and *DGAT* subunits were obtained using Expasy web tools: (http://au.expasy.org/tools/pi_tool.html).

2.3 Alignment of Conserved Vertebrate *DGAT*-like and *MGAT*-like Residues.

Alignments of vertebrate *DGAT*-like and *MGAT*-like sequences were undertaken using a ClustalW-technique (<http://www.ebi.ac.uk/clustalw/>) (Chenna et al., 2004) and previously reported sequences for the human, mouse, zebrafish and other sequences obtained from BLAT and BLAST analyses following analyses of NCBI databases (<http://www.ncbi.nlm.nih.gov/>) (Table 1; see Supplementary Table). Predictions of key *DGAT*-like and *MGAT*-like amino acid residues were obtained from previous biochemical analyses of mammalian *DGAT1*

(Cases et al., 1998; Guo et al., 2001) and from the conserved sequences observed for the human, mouse, opossum, zebrafish and other vertebrate enzymes.

2.4 Phylogenetic Studies and Sequence Divergence.

Phylogenetic trees were constructed using a ClustalW-derived amino acid alignment of DGAT-like and MGAT-like protein sequences, obtained with default settings and corrected for multiple substitutions (<http://www.ebi.ac.uk/clustalw/>) (Chenna et al., 2003). Percentage sequence identities for the DGAT1 and DGAT2-like family subunits examined were determined using the SIM-Alignment tool for Protein Sequences (<http://au.expasy.org/tools/simprot.html>) (Schwede et al., 2003).

3. RESULTS AND DISCUSSION

3.1 Alignments of opossum and zebrafish DGAT1 amino acid sequences with human and mouse DGAT1. Evidence for two zebrafish *DGAT1*-like genes.

The deduced amino acid sequences of a predicted opossum DGAT1 subunit and two predicted forms of zebrafish DGAT1 subunits (designated as DGAT1A and DGAT1B) are shown in Figure 1 together with the previously reported sequences for human and mouse DGAT1 (Oelkers et al., 1998; Buhman et al., 2002) (see Table 1). The enzymes contained 488-505 amino acid residues in sequence and exhibited predicted MWs of ~ 55-58 kDa's and high theoretical isoelectric points (pI values of 9.4-9.6) (Table 1). The alignments showed high levels of sequence identities for human and mouse (85%) and for human and opossum (78%) DGAT1 but lower levels of identity for the mammalian sequences with zebrafish DGAT1A and DGAT1B sequences (59-61%) (Supplementary Table 2). Regions of high

sequence identity were observed for the mammalian and zebrafish DGAT1 sequences, with the exception of the N- and C-termini and residues 229-240 for the human DGAT1 sequence (Figure 1) where more diverse sequences were observed. All of the DGAT1 sequences examined were distinct from the DGAT2-like and MGAT-like sequences with <14% identity. This suggests that these enzymes are products of the same *DGAT* gene family (*DGAT1*) which is separate from the *DGAT2* family. The amino acid sequences observed for zebrafish DGAT1A and DGAT1B were ~63% identical (Figure 1; Supplementary Table 2), and the genes encoding these enzymes (*DGAT1A* and *DGAT1B*) were localized on different zebrafish chromosomes (16 and 19 respectively) (see Table 1). This supports the presence of two *DGAT1*-like genes in this species.

3.2 Alignments of opossum and zebrafish MGAT-like and DGAT2-like amino acid sequences with the corresponding human and mouse enzymes.

Predicted opossum DGAT2-like subunits were designated DGAT2, AWAT1, AWAT2, DGAT2L6, MGAT1, MGAT2 and MGAT3 following alignment of deduced amino acid sequences with the corresponding human enzymes (Figure 2). High levels of sequence identity with the human enzymes were observed in each case: DGAT2 (92%); AWAT1 (71%); AWAT2 (71%); DGAT2L6 (63%); MGAT1 (69%); MGAT2 (73%); and MGAT3 (72%) (Supplementary Table 2). A significant level of sequence identity was also observed between these opossum enzymes ($\geq 42\%$), and it is likely that they form part of a single gene family, previously designated as *DGAT2*-like (*DGAT2L*) proteins for the human enzymes (Turkish et al., 2005). Human and opossum DGAT2 sequences were longer (388 and 366 amino acid residues, respectively) than those for human and opossum AWAT1 (328 and 332), AWAT2 (333 and 335), DGAT2L6 (337 and 328), MGAT1 (334 and 335), MGAT2 (both 334 residues) and MGAT3 (341 and 327) sequences, as a result of extended N-termini for the human and opossum DGAT2 sequences (Figure 2). All of the

opossum DGAT2-like subunits exhibited high theoretical isoelectric points (pI values of 8.8-9.8) (see Table 1).

Predicted DGAT2-like subunit sequences are also reported for zebrafish, although only four enzymes were deduced from the BLAT analyses of the zebrafish genome: DGAT2 (69% identity with human DGAT2); MGAT1 (56% identity with human MGAT1); MGAT2 (63% identity with human MGAT2); and MGAT3 (50% identity with human MGAT3) (Table 1; Figure 2; Supplementary Table 2). Zebrafish DGAT2 also exhibited a longer amino acid sequence (361 residues) with an extended N-terminus, in comparison with the other zebrafish DGAT2-like enzymes: MGAT1, MGAT2 and MGAT3 (334, 330 and 336 residues, respectively). All of the zebrafish DGAT2-like subunits exhibited high isoelectric points (pI values of 8.5-9.6), which are similar to those reported for the human, mouse and opossum enzymes (Table 1).

3.3 Predicted secondary and transmembrane structures for human, mouse, opossum and zebrafish DGAT1 and DGAT2-like subunits.

Predicted secondary and transmembrane (TrM) structures for human, mouse, opossum and zebrafish DGAT1 subunits are compared in Figures 1 and 3. Similar α -helix and predicted TrM structures were observed for all of the vertebrate DGAT1 subunits examined, which were almost devoid of β -sheet structures. For each vertebrate DGAT1 subunit examined, nine high probability regions for TrM sequences were observed, each located in similar positions with those previously predicted for human DGAT1 (Oelkers et al., 1998). This supports the location of vertebrate DGAT1 subunits in the endoplasmic reticulum (ER), which has been previously reported for human DGAT1 (Stone et al., 2006). Figures 1 and 3 also compare the predicted topology of the DGAT1 TrM structures, showing an extended N-terminus located within the ER lumen (amino acid residues 1-103 for human DGAT1), as were residues 151-165

(between TrMs 2 and 3); an extended sequence located in the center of the subunit (residues 211-281) (between TrMs 4 and 5); and residues 353-406 between TrMs 6 and 7. This topology was retained for all of the vertebrate DGAT1 subunits examined and suggests major functional significance for the microlocalization of this enzyme within vertebrate ER membranes.

DGAT2-like subunits are also strongly membrane bound due to their highly hydrophobic character and have been difficult to purify and characterize (see Turkish et al., 2005; Yen et al, 2008). Transmembrane (TrM) predictions for the human, opossum and zebrafish DGAT2-like subunits (Figures 2 and 3) revealed distinct structures in comparison with those observed for the vertebrate DGAT1 subunits. All of the DGAT2-like subunits showed one or two (in proximal locations) predicted TrM(s) near the N-terminus, commencing within the lumen of the ER for the N-terminus and then extending into the cytosol following the transmembrane bound structure (human MGAT3 was an exception). These included the AWAT-like subunits (AWAT1 and AWAT2), for which human and opossum AWAT2 exhibited a second predicted TrM structure near the center of the subunit (residues 130-150 for human AWAT2). This second predicted TrM AWAT2 structure allows for an intermediate segment to extend into the cytosol (residues 58-129 for human AWAT2) prior to the location in the lumen following the second TrM structure. These differences in TrM structures may play major roles in contributing to the separate roles for these enzymes *in vivo*.

3.4 Identification of Key Residues for Vertebrate DGAT1 and DGAT2-like Enzyme Subunits

Comparisons of predicted mouse, opossum and zebrafish DGAT1 sequences with the human DGAT1 sequence enabled identification of key residues which

may contribute to catalysis and function (Figure 1; Table 2). Likely active site residues for human DGAT1, previously proposed by Oelkers and coworkers (1998), included Asn378 and His415 (catalytic residues) and a heptapeptide sequence (Phe360-Tyr361-Arg362-Asp363-Trp364-Trp365-Asn366), recognized as a potential fatty acyl CoA binding site. Evidence for identifying these residues was based on similarities with the active site residues for human acyl CoA cholesterol acyltransferase (ACAT) and other members of the membrane bound O-acyltransferase (MBOAT) superfamily (see Hoffmann, 2000; Guo et al., 2001; Chang et al., 2001). The putative catalytic His415 for vertebrate DGAT1 was also predicted within a transmembrane sequence (TrM 7), which is similar to the active site positioning for ACAT, which led Chang and coworkers (2001) to propose that the catalytic transfer of the acyl group takes place within the lipid bilayer of the ER. These 'putative' active site residues have been retained for all mammalian, amphibian and zebrafish DGAT1 subunits examined (Figure 1; Supplementary Table 1).

Comparisons were also conducted of mammalian, opossum, amphibian (Xenopus) and zebrafish DGAT2-like sequences with the previously reported sequences for human and mouse DGAT2 and related family members, AWAT1, AWAT2 and DGAT2L6 (Cases et al., 1998; 2001; Oelkers et al., 1998; Turkish et al., 2005), together with MGAT1 (Yen et al., 2002), MGAT2 (Lardizibal et al., 2001; Yen and Farese, 2003; Lockwood et al., 2003; Cao et al., 2003) and MGAT3 (Cheng et al., 2003) (Figure 2; Table 2). A likely neutral lipid octapeptide binding domain was identified at residues 80-87 (human DGAT2 numbers used) [Phe-Leu-X-Leu-X-X-X-n], where n is a nonpolar amino acid (Table 4). This is consistent with a lipid binding domain previously described for human DGAT2 by Yen and coworkers (2008) and also reported for several enzymes which bind or metabolize neutral lipids, such as hormone-sensitive lipase, cholesterol ester transfer protein, lecithin:cholesterol

acyltransferase, cholesterol 7 α -hydroxylase, cholesterol esterase and triglyceride hydrolase (Au-Young and Fielding, 1992; Alam et al., 2006). This sequence is also similar to the consensus sequences described here for vertebrate DGAT2, mammalian DGAT2L6 and for two members of the MGAT-subfamily, MGAT1 and MGAT2 (Table 2). Mammalian AWAT1 and AWAT2 and vertebrate MGAT3 aligned octapeptide consensus sequences, however, do not match the neutral binding domain sequence, and these may reflect differences in lipid binding specificities for the AWAT and MGAT3 enzymes. A tetrapeptide sequence (His-Pro-His-Gly; residues 161-164 for human DGAT2) was conserved for all vertebrate DGAT2-like sequences examined (Figure 2; Table 2), which may serve as a catalytic site for this family of enzymes, as site-directed mutations for this region reduce DGAT2 activity (Stone et al., 2006). Several other vertebrate DGAT2-like amino acid residues have also been conserved for all family members, although their specific roles remain to be identified (Figure 2).

3.5 Predicted gene locations and exonic structures for human, mouse, opossum and zebrafish *DGAT1*-like and *DGAT2*-like genes.

Table 1 summarizes the predicted locations for human, mouse, opossum and zebrafish *DGAT1* and *DGAT2*-like genes examined, including three closely located mammalian *DGAT2*-like genes (*AWAT1*, *AWAT2* and *DGAT2L6*) on the X-chromosome; and two closely localized autosomal *DGAT2*-like genes (*DGAT2* and *MGAT2*) in humans (chromosome 11), mice (chromosome 7), opossum (chromosome 4) and zebrafish (chromosome 10). *DGAT1*, *MGAT1* and *MGAT3* (*MGAT3* not found in mice and rats) were also identified and localized elsewhere on the genomes examined (Table 1; see Supplementary Table 1). Two *DGAT1*-like zebrafish genes (designated *DGAT1A* and *DGAT1B*) were located on separate chromosomes (16 and 19, respectively) (Table 1). These BLAT interrogations of the respective

genomes used reported sequences for human *DGAT1* (Oelkers et al., 1998), *AWAT1*, *AWAT2* and *DGAT2L6* (Turkish et al., 2005) *DGAT2* (Cases et al., 2001), *MGAT1* (Yen et al., 2002), *MGAT2* (Yen and Farese, 2003) and *MGAT3* (Cheng et al., 2003) and the UC Santa Cruz Web Browser (Kent et al., 2002) (<http://genome.ucsc.edu/cgi-bin/hgBlat>). The human, mouse, opossum and zebrafish *DGAT1* and *MGAT3* genes, human and mouse *AWAT2* genes, mouse, opossum and zebrafish *DGAT2* genes, mouse, opossum and zebrafish *MGAT2* genes, as well as opossum *AWAT1* and *DGAT2L6* genes were all predicted for transcription on the negative strand, whereas others were transcribed on the positive strand (Table 1).

Predicted exonic start sites for the vertebrate *DGAT1* and *DGAT2-like* genes were examined with vertebrate *DGAT1* genes containing 17 exons, which are located in similar or identical positions to the 17 exons identified for human *DAGT1* (Oelkers et al., 1998) (Figure 1). Vertebrate *DGAT2-like* genes contained 8 exons for the vertebrate *DGAT2* gene; 6 exons for vertebrate *MGAT1* and *MGAT2* genes; and 7 exons for vertebrate *MGAT3* genes (Table 1; Figure 2). Mammalian *AWAT1*, *AWAT2* and *DGAT2L6* genes also exhibited 7 predicted exonic start sites in similar positions to the human, mouse and opossum genes examined (Table 1; Figure 2). Figure 4 summarizes the comparative exonic and intronic structures for the major human *DGAT1* and *DGAT2-like* isoforms, illustrating the distinctive nature and sizes for these genes and their transcripts for the human genome.

3.6 Phylogeny and divergence of vertebrate *DGAT1* and *DGAT2-like* sequences.

A phylogenetic tree (Figure 5) was calculated by the progressive alignment of human, mouse, opossum and zebrafish *DGAT1* and *DGAT2-like* amino acid sequences. The phylogram clustered into two major groups overall,

corresponding to DGAT1 and DGAT2-like proteins and genes. The latter group was further divided into 7 groups, including mammalian AWAT1, AWAT2 and DGAT2L6, and vertebrate DGAT2, MGAT1, MGAT2 and MGAT3, which is consistent with the nomenclature proposed for these enzymes. The tandem locations on the X-chromosome for the three mammalian *DGAT2*-like genes (*AWAT1*, *AWAT2* and *DGAT2L6*) and their apparent absence from chicken, frog and zebrafish genomes (Table 1; Supplementary Table 1) indicate that these genes may have arisen from successive duplications and translocations of an ancestral *DGAT2*-like gene to the X chromosome, prior to the common ancestor for marsupial and eutherian mammals. In addition, the tandem locations and levels of sequence identities observed for the vertebrate *DGAT2* and *MGAT2* genes (~45% identical) (Supplementary Table 2) is suggestive of an earlier common origin for these genes by tandem duplication of an ancestral *DGAT2*-like gene prior to the appearance of bony fish. The reasons for the retention of proximal locations of *DGAT2* and *MGAT2* genes over > 500 million years of vertebrate evolution remain to be established.

These studies of the comparative sequences of *DGAT1* and *DGAT2*-like genes and proteins derived from mammalian and bony fish genomes strongly suggest that these two gene families have evolved separately during vertebrate evolution. This conclusion is based on the low levels of sequence identity (<14%) and the distinct phylogenetic relationships observed (Table 2; Figure 5). A single *DGAT1*-like gene and protein was observed for most vertebrates, including representative mammals, birds (chicken) and amphibians (frog), whereas two distinct zebrafish and pufferfish *DGAT1*-like genes (with similar sequences (63% identical for zebrafish *DGAT1*-like proteins) with the genes located on separate chromosomes) (Table 1; Supplementary Table 1). This is suggestive of a gene duplication event giving rise to these genes within the ancestor for these bony fish species while other vertebrates have

apparently retained only one *DGAT1*-like gene (Table 1). The vertebrate *DGAT2*-like gene family, however, exists in at least 4 separate genes in both bony fish genomes examined, which have been provisionally designated as *DGAT2*, *MGAT1*, *MGAT2* and *MGAT3*, based on the clustering and higher percentages of identity of these sequences with the corresponding mammalian sequences (Figure 5; Supplementary Table 2). It is likely that these genes have appeared early in vertebrate evolution, certainly prior to the appearance of bonyfish, which occurred > 500 million years ago (Kumar and Hedges, 1998). The three mammalian X-linked genes (*AWAT1*; *AWAT2* and *DGAT2L6*), however, were observed only in mammals (Table 1; Supplementary Table 1) and these may have resulted from further gene duplication events prior to the appearance of the common ancestor for marsupial and eutherian mammals (~ 180 million years ago) (Woodburne et al., 2003).

3.7 Functions of *DGAT1* and *DGAT2*-like Enzymes

Human and mouse *DGAT1* and *DGAT2* catalyze the final step in triglyceride biosynthesis by catalyzing the joining of diacylglycerol with fatty acyl CoA. The enzymes are differentially distributed in mammalian tissues with *DGAT1* occurring in most tissues, whereas *DGAT2* exhibits highest activity in the intestine, liver and adipose tissue, where triglycerides are required for major lipid biosynthesis for lipid digestion and transport, storage and lipoprotein synthesis (see Yen et al., 2008). Knock-out mice for both enzymes have shown that *DGAT1*-deficient mice are viable but show major reductions in tissue triglyceride content but have normal plasma triglyceride levels, whereas *DGAT2*-deficient mice die within hours of birth, and have severely reduced levels of triglycerides (Smith et al., 2000; Stone et al., 2004). In addition to the catalysis of triacylglycerol biosynthesis, *DGAT1* is also capable of synthesizing diacylglycerols, waxes and retinyl esters (Yen

et al., 2005). It is concluded however that DGAT2 has a more significant role in triglyceride biosynthesis in the body than DGAT1 although significant side effects were also observed for DGAT1-deficient mice, including an increased sensitivity to insulin and leptin, and atrophy of the skin sebaceous glands, resulting in hair loss and reduced formation of wax esters. The high levels of sequence identities for opossum and zebrafish DGAT1 and DGAT2 with the human and mouse sequences, (Figure 1; Supplementary Table 2), indicate that these enzymes serve similar metabolic functions reported for the human and mouse enzymes.

While there are no reports of knockout mice for the other DGAT2-like genes and enzymes, biochemical analyses and tissue expression studies provide clues as to their metabolic roles in the body. The human *AWAT1* and *AWAT2* genes, for example, are differentially expressed within the sebaceous glands of the skin and exhibit kinetic properties which are consistent with specific roles in the formation of wax esters (Turkish et al., 2005). *AWAT1* shows a preference for saturated fatty acyl CoAs, as compared with *AWAT2*, which prefers unsaturated fatty acyl CoAs, reflecting distinct but overlapping roles in the biosynthesis of wax esters, which protect the external surfaces of the body from desiccation.

The *MGAT* gene and enzyme subfamily have also been investigated in terms of their tissue expression profiles and substrate specificities. MGATs preferentially catalyze reactions involving monoacylglycerols and fatty acyl CoAs, forming diacylglycerols, which participate in triglyceride and phospholipid synthesis, which store energy, contribute to lipoprotein and membrane formation and serve as an intracellular signal for protein kinase activation (see Yen et al., 2008). MGAT2 is the major enzyme involved in fat digestion and absorption in the gut, where products of pancreatic lipase hydrolysis of triacylglycerols in the diet, *sn*-2-monacylglycerols and fatty

acids, are used in the resynthesis of triacylglycerols by the intestine (Yen and Farese, 2003). *MGAT2* is widely distributed in human and mouse tissues and exhibits high levels of expression within intestinal enterocytes and a preference for monoacylglycerols containing unsaturated fatty acyl CoAs. *MGAT1* is expressed at much lower levels in human tissues, but shows higher expression levels in mouse tissues. Mouse *MGAT1* is specific for catalyzing diacylglycerol synthesis and exhibits a preference towards monoacylglycerols containing unsaturated fatty acyl groups, and may play a role in recycling essential fatty acids in the body (Yen et al., 2002). Human *MGAT3* is specifically expressed in the digestive system, with high expression levels in the small intestine and colon, and may serve specific roles in lipid absorption by the digestive tract (Cheng et al., 2003).

4. Conclusions

BLAT analyses of the opossum and zebrafish genomes using the amino acid sequences reported for human and mouse *DGAT1* and *DGAT2*-like protein subunits were undertaken to interrogate these genomes. Evidence is reported for an opossum *DGAT1* gene and six *DGAT2*-like genes, including *DGAT2*, *AWAT1*, *AWAT2*, *DGAT2L6*, *MGAT1*, *MGAT2* and *MGAT3* genes. Evidence for two zebrafish and pufferfish *DGAT1*-like genes and four *DGAT2*-like genes (*DGAT2*, *MGAT1*, *MGAT2* and *MGAT3*) is also described. Three of the opossum genes (*AWAT1*, *AWAT2* and *DGAT2L6*) were closely localized on the X chromosome, which is comparable to the locations of these genes in human, mouse and several other mammalian genomes examined (see Supplementary Table). Two other opossum *DGAT2*-like genes (*DGAT2* and *MGAT2*) were also closely located on chromosome 4, for which tandem locations for these genes was observed for other mammalian, amphibian and zebrafish genomes examined (see Supplementary Table 1). The predicted amino acid sequences, secondary and transmembrane structures for the opossum

and zebrafish DGAT1 and DGAT2-like subunits showed a high degree of similarity with the corresponding human and mouse enzymes. Phylogenetic analyses undertaken with human, mouse, opossum, zebrafish and pufferfish DGAT1 and DGAT2-like proteins supported the designation of these enzymes with relevant families and sub-families previously described. It is likely that opossum and zebrafish enzymes perform similar functions to those reported for human and mouse in triacylglycerol (DGAT1, DGAT2 and DGAT2L6 subunits), wax (AWAT1 and AWAT2 for the opossum) and diacylglycerol (MGAT1, MGAT2 and MGAT3) biosynthesis.

ACKNOWLEDGEMENTS

I am grateful to Dr Laura Cox and Dr John VandeBerg of the Southwest Foundation for Biomedical Research in San Antonio Texas USA for helpful discussions and advice.

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Species	Gene	GenBank ID	UNIPROT ID	NCBI RefSeq ID ¹	Chromosome location (strand)	Gene Size (bps)	Coding Exons	Amino Acids	pI	Subunit MW	
Human	AWAT1	BC153034	Q58HT5	NM_001013579	X:69,371,271-69,376,865 (+ve)	5,595	7	328	9.1	37,759	DGT
	AWAT2	BC153070	Q6E213	NM_001002254	X:69,177,117-69,186,513 (-ve)	9,397	7	333	9.4	38,094	DGT
	DGT2L6	BC172336	Q6ZPD8	NM_198512	X:69,314,061-69,342,278 (+ve)	28,218	7	337	9.9	38,593	DG
	DGAT1	BC015762	O75907	NM_012079	8:145,511,028-145,521,107 (-ve)	10,080	17	488	9.4	55,278	
	DGAT2	BC015234	Q96PD7	NM_032564	11:75,157,685-75,189,198 (+ve)	31,514	8	388	9.5	43,831	
	MGAT1	BC146518	Q96PD6	NM_058165	2:223,244,749-223,282,850 (+ve)	38,102	6	334	9.5	38,630	MO
	MGAT2	BC103876	Q3SYC2	NM_025098	11:75,106,582-75,119,976 (+ve)	13,395	6	334	9.5	38,196	MO
	MGAT3	BC100953	Q86VF5	NM_178176	7:100,625,950-100,630,855 (-ve)	4,906	7	341	8.9	38,730	MO
Mouse	AWAT1	BC147680	A2ADU9	NP_001074605	X:97,767,586-97,773,545 (+ve)	5,549	7	328	8.9	37,573	Dgt
	AWAT2	BC138085	Q6E1M8	NP_808414	X:97,598,128-97,607,874 (-ve)	9,747	7	333	9.5	38,145	Dgt
	DGT2L6	AK079438	²	XM_001000486	X:97,720,262-97,740,936 (+ve)	20,675	7	337	9.8	38,362	Dgt
	DGAT1	BC003717	Q9Z2A7	NM_010046	15:76,332,669-76,342,211 (-ve)	9,543	17	498	9.5	56,790	DGT
	DGAT2	BC043447	Q9DCV3	NM_026384	7:106,303,059-106,331,022 (-ve)	27,964	8	388	9.5	43,770	DGT
	MGAT1	BC106135	Q91ZV4	NM_026713	1:78,508,537-78,534,670 (+ve)	26,134	6	335	8.9	38,803	Mo
	MGAT2	BC052831	Q80W94	NM_177448	7:106,368,318-106,387,075 (-ve)	18,758	6	334	9.7	38,591	Mo
Opossum	AWAT1	²	²	XP_001368551	X:59,097,964-59,104,042 (-ve)	6,079	7	332	9	38,599	DGT
	AWAT2	²	²	ENSMODP5771 ¹	X:59,181,618-59,199,570 (+ve)	17,953	7	335	9.8	38,536	DGT
	DGT2L6	²	²	XP_001368584	X:59,116,360-59,125,987 (-ve)	9,628	7	328	9.3	37,141	DG
	DGAT1	²	²	XP_001371565	3:435,794,358-435,825,910 (-ve)	31,553	17	505	9.4	56,590	
	DGAT2	²	²	XP_001364751	4:339,142,799-339,188,735 (-ve)	45,937	8	366	9.4	41,552	
	MGAT1	²	²	XP_001365685	7:228,853,668-228,886,321 (-ve)	32,654	6	335	8.9	39,134	MO
	MGAT2	²	²	XP_001364890	4:339,284,620-339,315,264 (-ve)	30,645	6	334	9.6	38,391	MO
MGAT3	²	²	XP_001371248	2:279,175,446-279,179,682 (-ve)	4,237	7	327	8.8	35,316	MO	
Zebrafish	DGAT1A	BC076012	²	NM_001002458	16:27,596,419-27,647,463 (-ve)	51,045	17	501	9.6	58,058	
	DGAT1B	BC063070	Q6P3J0	NP_956024	19:45,373,531-45,395,506 (-ve)	21,976	17	499	9.5	57,152	
	DGAT2	BC096927	²	NM_001030196	10:28,025,496-28,047,075 (-ve)	21,580	8	361	9.3	40,865	
	MGAT1	BC159110	²	NM_001122623	23:40,648,506-40,659,082 (+ve)	10,577	6	334	9.3	37,708	MO
	MGAT2	BC083237	²	NM_001006083	10:28,058,463-28,081,932 (-ve)	23,470	6	330	9	38,013	MO
	MGAT3	BC129046	²	NM_001008626	5:29,806,778-29,812,172 (-ve)	5,395	7	336	8.5	37,801	MO

Table 1: Diacylglycerol acyltransferase (DGAT) and monoacylglycerol acyltransferase (MGAT) genes and enzymes examined

GenBank mRNA (or cDNA) IDs identify previously reported sequences or predicted sequences (see <http://www.ncbi.nlm.nih.gov/Genbank/>); UNIPROT refers to UniprotKB/Swiss-Prot IDs for individual DGAT and MGAT enzymes (see <http://kr.expasy.org>); DGAT and MGAT sequences were provided by the above sources; opossum AWAT, DGAT2L6, DGAT1, DGAT2, MGAT1, MGAT2 and MGAT3 protein sequences were obtained from a blast of the opossum genome using web tools of the National Center for Biotechnology Information (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) and the corresponding human sequences. Predicted exon/intron locations and gene sizes were obtained by BLAT interrogations of the opossum genome using the predicted DGAT and MGAT sequences and the UC Santa Cruz web tools (<http://genome.ucsc.edu>); NCBI refers to database sources from the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/sites/entrez>); ¹ refers to the predicted Ensembl sequence observed from the BLAT analysis of opossum AWAT2; ² not observed; bps: base pairs; pI: theoretical isoelectric point.

DGAT2-like (Consensus)⁵	Putative Active Site¹	Neutral Lipid Binding Domain⁴ F L X L X X X n⁶
DGAT2 ²	H161-P162-H163-G164	F80-L81-V82-L83-G84-V85-A86-C87
DGAT2L6 ²	H107-P108-H109-G110	F27-L28-V29-L30-G31-V32-A33-C34
MGAT1 ²	H107-P108-H109-G110	F27-L28-L29-L30-A31-Q32-V33-C34
MGAT2 ²	H108-P109-H110-G111	F27-L28-A29-L30-A31-Q32-I33-C34
MGAT3 ²	H114-P115-H116-G117	F33-L34-F35-M36-G37-P38-F39-F40
AWAT1 ²	H103-P104-H105-G106	Y22-L23-A24-I25-F26-W27-I28-L29
AWAT2 ²	H104-P105-H106-G107	L26-L27-I28-V29-T30-T31-V32-I33

DGAT1	Putative Active Site¹	Fatty Acyl CoA Binding Site³
Human	N378 H415	F360-Y361-R362-E363-W364-W365-N366
Mouse	N389 H426	F371-Y372-R373-E374-W375-W376-N377
Opossum	N390 H427	F372-Y373-R374-E375-W376-W377-N378
Zebrafish (1A)	N388 H425	F370-Y371-R372-E373-W374-W375-N376
Zebrafish (1B)	N387 H424	F359-Y360-R361-E362-W363-W364-N365

Table 2: Key DGAT1 and DGAT2-like amino acid residues for vertebrate enzymes.

¹Identification of predicted active site residues for vertebrate DGAT1 is based on previous studies of Oelkers et al., 1998; prediction of active site residues for DGAT2-like sequences is based on a region containing a conserved tetrapeptide sequence with histidine residues (the active site residue for human DGAT1); ²DGAT2-like consensus sequences were obtained following alignment of vertebrate sequences for the particular sub-family of DGAT2-like enzymes (sequences used included human, mouse, opossum, zebrafish (see Figure 2) and 9 other vertebrate sequences (see supplementary list of species examined) using the ClustalW technique (see methods); ³identification of the fatty acyl CoA binding site sequences for vertebrate DGAT1 is based on a previous report (Oelkers et al., 1998); ⁴ identification of a potential neutral lipid binding domain for vertebrate DGAT2-like sub-families is based on a report from Yen and coworkers (2008).

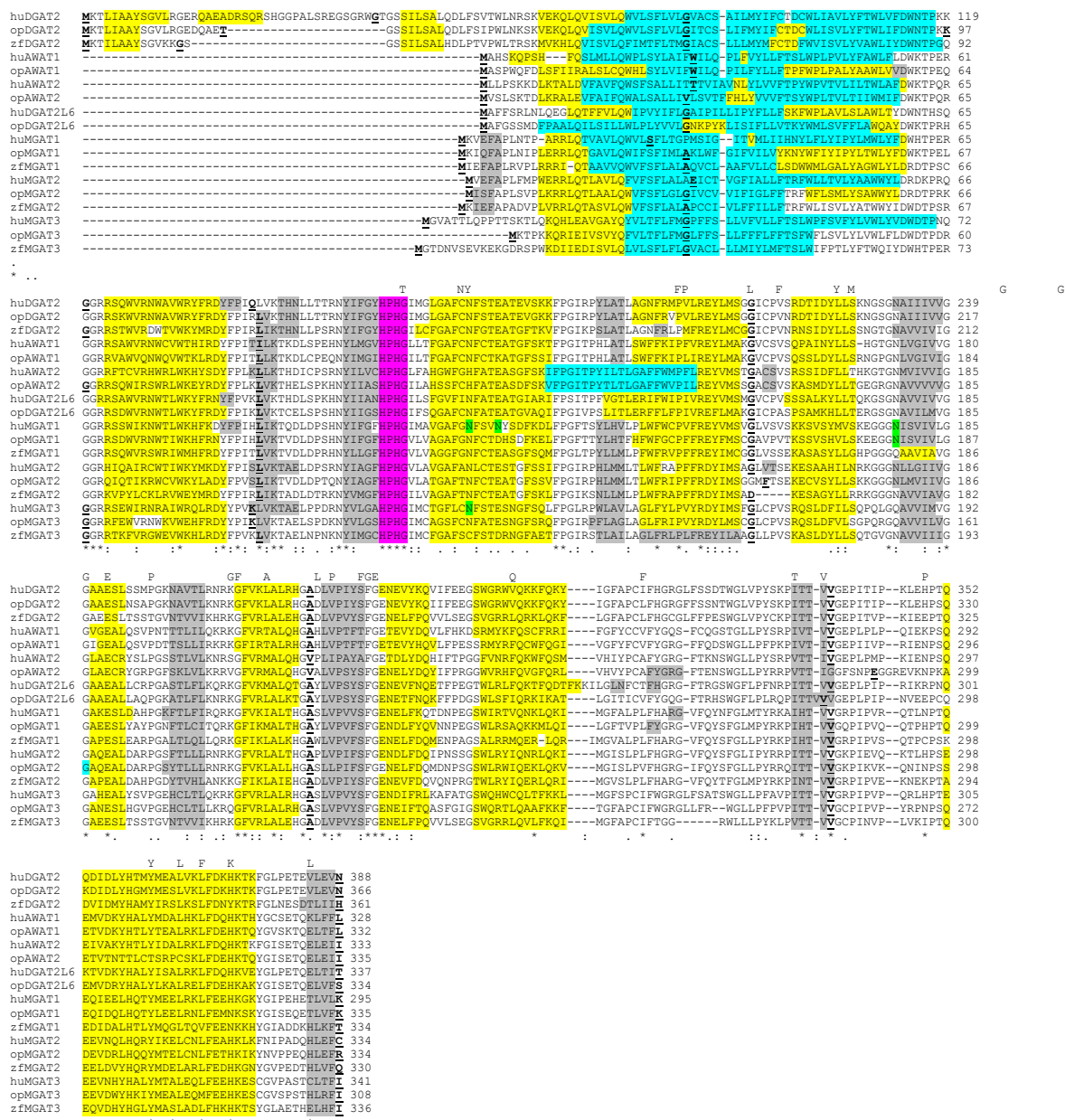


Figure 2: Amino acid sequence alignments for human, mouse, opossum and zebrafish DGAT2-like sequences.

See Table 1 for the sources of DGAT2-like sequences: huDGAT2: human DGAT2; opDGAT2: opossum DGAT2; zFDGAT2: zebrafish DGAT2; huAWAT1: human AWAT1; opAWAT1: opossum AWAT1; huAWAT2: human AWAT2; opAWAT2: opossum AWAT2; huDGAT2L6: human DGAT2L6; opDGAT2L6: opossum DGAT2L6; huMGAT1: human MGAT1; opMGAT1: opossum MGAT1; zFMGAT1: zebrafish MGAT1; huMGAT2: human MGAT2; opMGAT2: opossum MGAT2; zFMGAT2: zebrafish MGAT2; huMGAT3: human MGAT3; opMGAT3: opossum MGAT3; zFMGAT3: zebrafish MGAT3; * shows identical residues; : shows one conservative amino acid substitution; . shows two conservative amino acid substitutions; **underlined bold font** shows known or predicted exon junctions; predicted β -sheet and α -helix secondary structures are shown; potential active site and neutral lipid binding domain residues are shown as **HPHG** (see Table 3); other fully conserved residues observed for all of the DGAT2-like sequences are also shown; predicted **transmembrane** structures are shown, note the additional transmembrane structure observed for the human and opossum sequences.

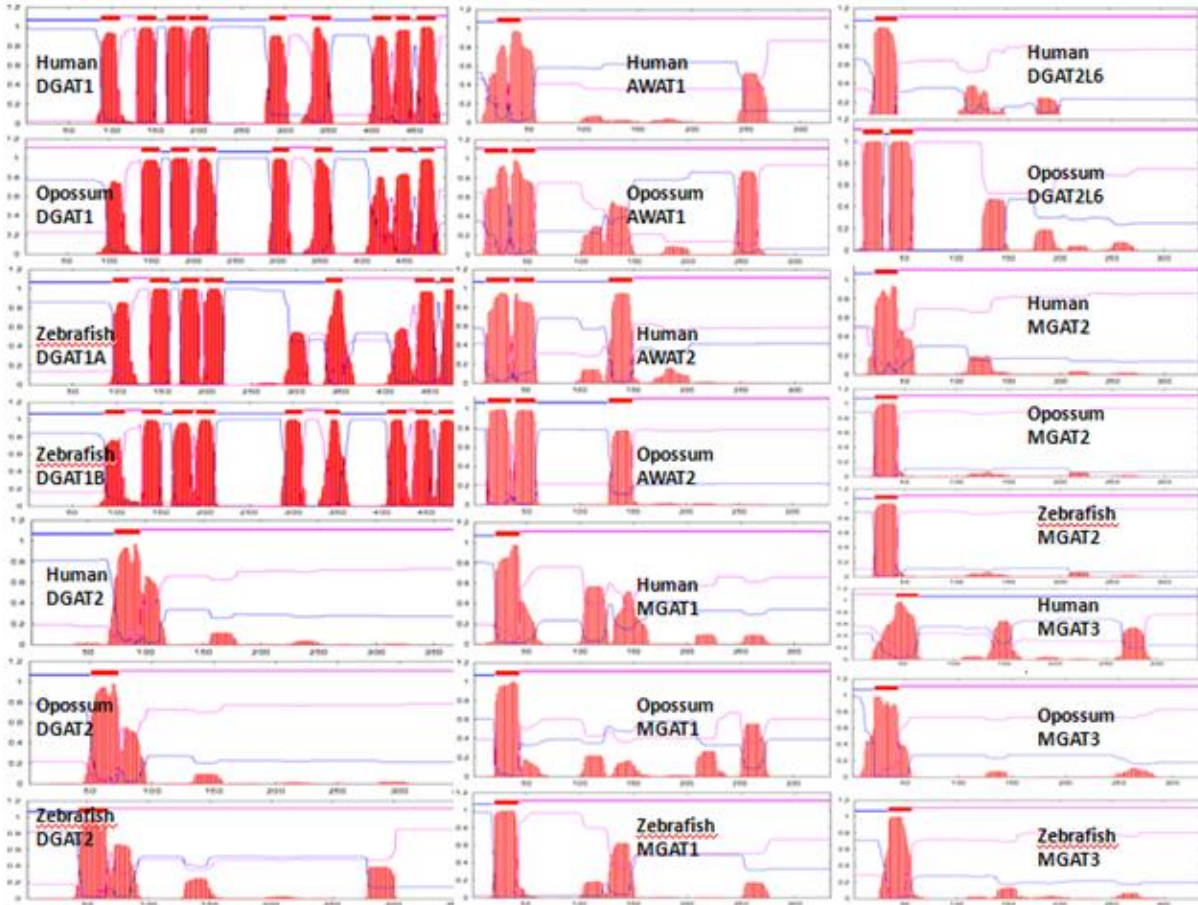


Figure 3: Predicted transmembrane helices for human, opossum and zebrafish DGAT1-like and DGAT2-like sequences.

See Table 1 for sources of DGAT1 and DGAT2-like sequences. The TMHMM web tools of the Center for Biological Sequence Analysis, Technical University of Denmark TMHMM Server plots the probability of the ALDH sequence forming a **transmembrane helix** (0-1) (shown in **red** for the relevant amino acid sequences) (<http://www.cbs.dtu.dk/services/TMHMM/>). Nine predicted transmembrane helices are identified for each of the DGAT1-like sequences; in contrast, only one major transmembrane helix (or helices) were observed for DGAT2-like sequences, with the exception of human and opossum AWAT2 sequences, which show a second major transmembrane region; regions of DGAT1 or DGAT2-like sequences predicted to be located inside or outside the membrane are shown in **blue** and **pink**, respectively.

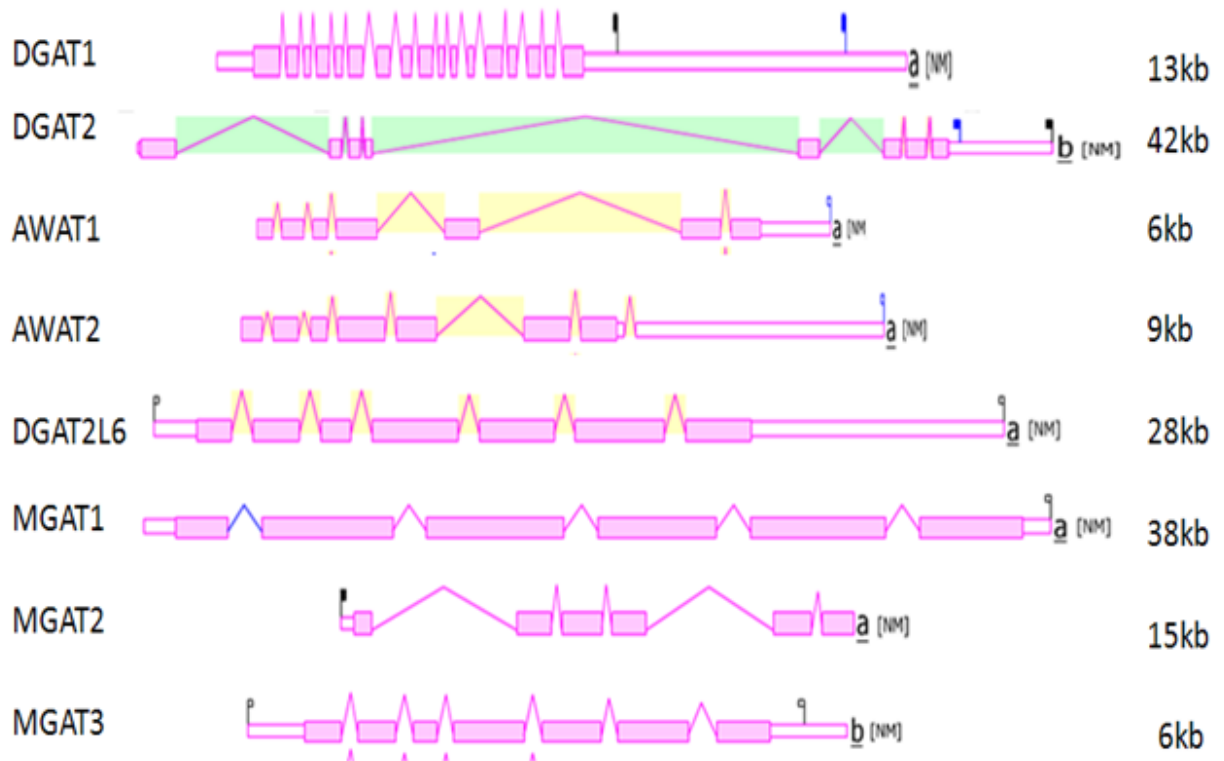


Figure 4: Gene structures and major transcript isoforms for human DGAT1 and DGAT2-like genes.

Derived from the AceView website (Thierry-Mieg and Thierry-Mieg, 2006); coding exons are shown as shaded boxes; untranslated exon regions are shown as blank boxes; introns are shown by the lines joining the exons; capped 5'- and validated 3'-ends are also shown. The genes are not drawn to scale but gene sizes are shown as kilobases of DNA. NM refers to validated sequences from NCBI database sources (National Center for Biotechnology Information).

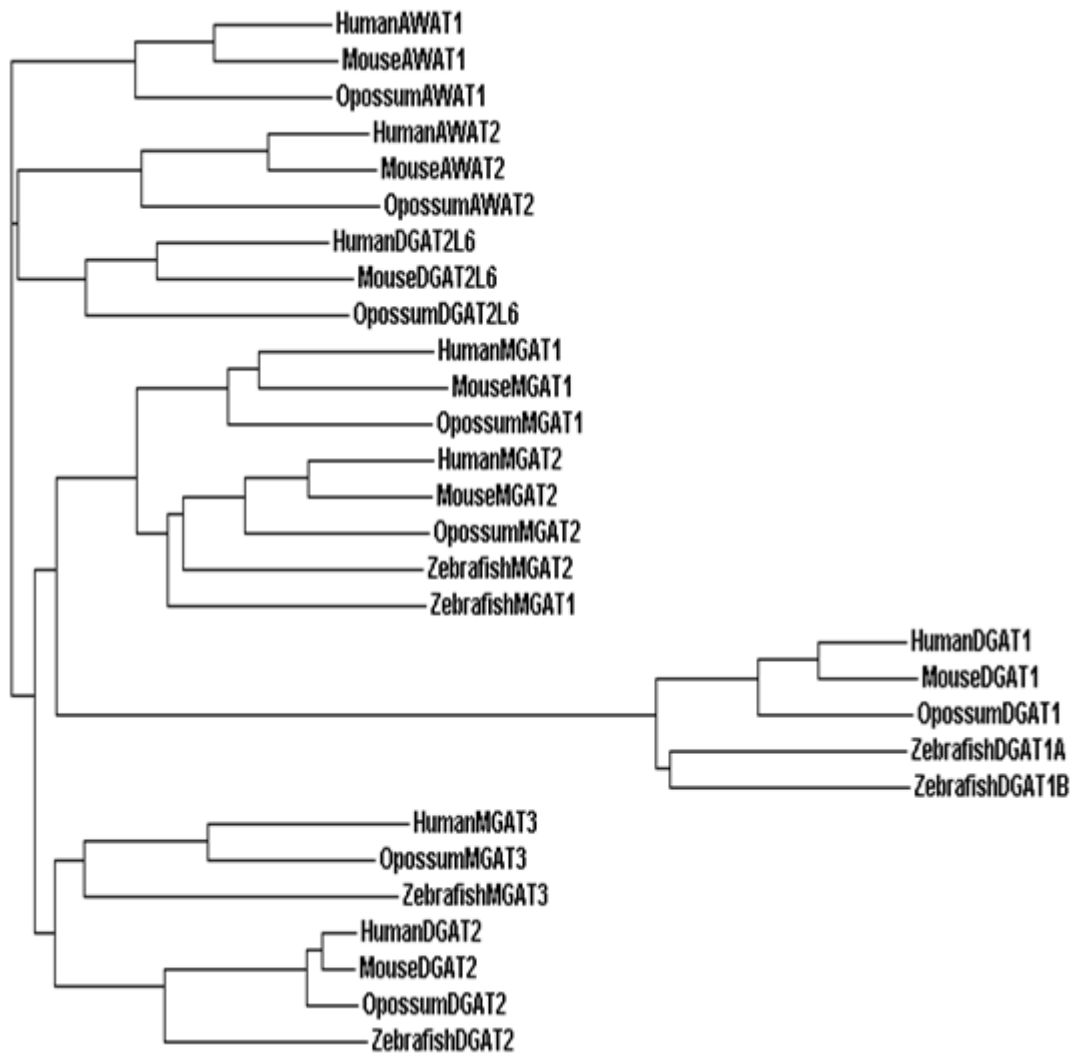


Figure 5: Phylogenetic tree of human, mouse, opossum, zebrafish and pufferfish DGAT1 and DGAT2-like sequences.

Each branch of the tree is labeled with the name of the vertebrate (human, mouse, opossum, zebrafish and pufferfish [Tetraodon]) followed by an abbreviation for the gene name: DGAT1; DGAT2; AWAT1; AWAT2; DGAT2L6; MGAT1; MGAT2; and MGAT3). Note the clustering into two groups: DGAT1 and DGAT2-like, and additional clustering of 7 groups for the DGAT2-like enzymes: DGAT2; AWAT1; AWAT2; DGAT2L6; MGAT1; MGAT2; and MGAT3.

Species	Gene	NCBI RefSeq ID ¹	Chromosome location (strand)	Gene Size (bps)	Coding Exons	Amino Acids
Orangutan	DGAT1	chr8.780.1 ²	8:152,680,375-152,690,672 (-ve)	10,298	17	476
	AWAT1 ¹	chrX.373.1 ²	X:67,880,885-67,886,778 (+ve)	6,133	6 ¹	328
	AWAT2	chrX.369.1 ²	X:67,699,769-67,708,297 (-ve)	8,529	7	333
	DGAT2L6	chrX.372.1 ²	X:67,820,883-67,851,887 (+ve)	31,005	7	336
	DGAT2	chr11.880.1 ²	11:71,216,741-71,248,907 (+ve)	32,167	8	388
	MGAT2	chr11.879.1 ²	11:71,168,993-71,183,490 (+ve)	14,498	6	334
	MGAT3 ¹	chr7.161.1 ²	7:10,267,219-10,270,493 (-ve)	3,275	4 ¹	220 ¹
Rhesus	DGAT1	XP_001090134	8:146,942,899-146,952,955 (-ve)	10,157	17	491
	AWAT1	XP_001083656	X:69,201,424-69,207,156 (+ve)	5,733	7	328
	AWAT2	XP_001085075	X:69,009,116-69,017,097 (-ve)	7,982	7	333
	DGAT2L6	XP_001083431	X:69,150,939-69,177,795 (+ve)	26,857	7	337
	DGAT2	chr14.74.017 ²	14:73,939,668-73,971,731 (+ve)	32,064	8	388
	MGAT1	XP_001107993	12:86,549,294-86,590,162 (+ve)	40,869	6	335
	MGAT2	XP_001086603	14:73,891,210-73,906,244 (+ve)	15,035	6	334
Marmoset	MGAT3	XP_001107764	3:48,480,648-48,485,922 (-ve)	5,275	7	341
	DGAT1	Contig6937.7 ²	Contig6937:123602-134361 (+ve)	10,760	16	515
	AWAT1	Contig7065.001 ²	Contig7065:4097-10,235 (-ve)	6,139	7	328
	AWAT2 ¹	contig4884.005 ²	Contig4884:169,128-171,732 (-ve)	2,605	5 ¹	303 ¹
	DGAT2L6 ¹	contig7065.001 ²	Contig7065:29,847-57,530 (-ve)	27,684	6 ¹	315 ¹
	DGAT2	contig1148.002 ²	Contig1148:150,614-182,017 (-ve)	31,404	8	388
	MGAT1	contig1051.003 ²	Contig1051:357,042-398,741 (+ve)	41,700	6	322
Dog	MGAT2	contig1148.003 ²	Contig1148:219,348-230,968 (-ve)	11,621	6	334
	MGAT3 ³	contig4929.008 ²	Contig4929:227,880-230,020 (+ve)	21,141 ³	4 ¹	198 ³
	MGAT3 ³	contig10131.5 ²	Contig10131:75,520-75,975 (-ve)	456 ³	2 ¹	118 ³
	DGAT1	XP_849176	13:40,777,205-40,786,043 (-ve)	8,839	17	498
	AWAT1	XP_549058	X:57,606,359-57,611,805 (+ve)	5,447	7	328
	AWAT2	XP_549056	X:57,445,045-57,459,716 (-ve)	14,672	7	333
	DGAT2L6	XP_849355	X:57,550,407-57,584,831 (+ve)	34,425	7	337
Rat	DGAT2	XP_542303	21:25,839,827-25,904,558 (-ve)	64,732	8	369
	MGAT1	XP_545667	37:31,731,937-31,763,738 (+ve)	31,802	6	335
	MGAT2	XP_542304	21:25,906,094-25,923,425 (-ve)	17,332	6	334
	MGAT3	XP_850305	6:11680127-11,683,533 (+ve)	3,407	7	345
	DGAT1	BC081742 ⁴	7:114,552,269-114,562,391 (-ve)	10,123	17	500
	AWAT1	NP_001102841	X:88,570,733-88,576,631 (+ve)	5,899	7	328
	AWAT2	XP_228583	X:88,395,932-88,404,189 (-ve)	8,258	7	333
Horse	DGAT2L6	XP_001053251	X:88,516,501-88,539,678 (+ve)	31,178	7	337
	DGAT2	BC089846 ⁴	1:156,448,541-156,478,563 (-ve)	30,023	8	388
	MGAT1	XP_001059515	9:77,875,371-77,908,608 (+ve)	33,328	6	340
	MGAT2	BC166995 ⁴	1:156,517,248-156,540,870 (-ve)	23,623	6	334
	DGAT1	XP_001917097	9:82,848,978-82,858,030 (-ve)	9,053	17	490

	AWAT1	XP_001490162	X:52,206,564-52,212,113 (+ve)	5,550	7	328
	AWAT2	XP_001496780	X:51,957,754-51,965,116 (-ve)	3,263	7	327
	DGAT2L6	XP_001490853	X:52,164,937-52,183,186 (+ve)	18,350	7	337
	DGAT2	XP_001495352	7:68,414,190-68,443,579 (-ve)	29,390	8	383
	MGAT1	XP_001495519	6:11,748,405-11,768,285 (+ve)	19,981	6	335
	MGAT2	XP_001917405	7:68,477,526-68,493,887 (-ve)	16,362	7	355
	MGAT3 ¹	chr13.155.1 ²	13:9,131,363-9,133,483 (-ve)	2,121	7	266 ¹
Cow	DGAT1	BC118146 ⁴	14:444,097-446,531 ¹ (+ve)	2435 ¹	17	489
	AWAT1	XP_608355	X:50,032,716-50,038,781 (-ve)	6,066	7	328
	AWAT2	XP_599558	Un.004.31: 456,157-465,814 (-ve)	9,658	7	331
	DGAT2L6	NP_001095331	X:50,087,116-50,107,900 (-ve)	20,785	7	337
	DGAT2	NP_991362	15:54,717,587-54,748,692 (+ve)	31,106	8	361
	MGAT1	NP_001001153	2:115,337,770-115,367,035 (+ve)	29,266	6	335
	MGAT2	XP_001253431	Un.004.554:9,151-22,088 (+ve)	12,938	6	334
	MGAT3	XP_875499	25:37,644,824-37,647,942 (+ve)	3,119	7	395
Chicken	DGAT2	XP_419374 ¹	Un:45202148-45,211,195 (+ve)	9,036	8	352
	MGAT1	chr9.162.1 ²	9:9,089,059-9,109,902 (+ve)	20,844	6	326
	MGAT2	XP_424082	1:199,685,261-199,697,403 (-ve)	12,143	7	351
	MGAT3	XP_426251	4:1,199,365-1,202,827 (+ve)	3,463	8	361
Xenopus	DGAT1	scaffold_1631.3 ²	scaffold1631:25,368-41,663 (+ve)	16,296	14	413
	DGAT2	BC064191 ⁴	725:199,049-214,323 (+ve)	15,275	7	361
	MGAT1	CR942398 ⁴	224:1,013,476-1,018,678 (+ve)	5,203	6	335
	MGAT2	BC158509 ⁴	725:156,829-176,037 (+ve)	19,029	5	331
	MGAT3	BC088019 ⁴	738:466,628-473,346 (+ve)	6,719	6	335
Melanogaster	DGAT1	AF468650 ⁴	2L:16,820,210-16,826,713 (+ve)	6,504	9	536

Supplementary Table 1: Diacylglycerol acyltransferase (DGAT) and monoacylglycerol acyltransferase (MGAT) genes and enzymes examined

Orangutan, rhesus, marmoset, dog, rat, horse and cow AWAT, DGAT2L6, DGAT1, DGAT2, MGAT1, MGAT2 and MGAT3 protein sequences; chicken DGAT2, MGAT1, MGAT2 and MGAT3 sequences; frog DGAT1, DGAT2, MGAT1, MGAT2 and MGAT3 sequences; pufferfish DGAT1, DGAT2, MGAT1, MGAT2 and MGAT3 sequences; and the fruit fly DGAT1 sequence were obtained either from BLATs of the respective genomes using UC Santa Cruz web tools (<http://genome.ucsc.edu>) or from Blasts using the National Center for Biotechnology Information website (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) and the corresponding human sequences. Predicted chromosomal locations, gene sizes, numbers of coding exons and amino acids for the encoded proteins were obtained by BLAT interrogations of the respective genomes using the predicted human DGAT and MGAT sequences and the UC Santa Cruz web tools (<http://genome.ucsc.edu>); ¹ refers to NCBI database sources from the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/sites/entrez>); ² predictions of sequence using the N-SCAN gene structure prediction software provided by the Computational Genomics Lab at Washington University in St. Louis, MO, USA; ³ two partial sequences were observed; ⁴ GenBank IDs identified previously reported sequences (see <http://www.ncbi.nlm.nih.gov/Genbank/>); ⁵ predictions of protein sequences according to the GAZE program: Howe KL, Chothia T and Durbin R (2002), "GAZE: A Generic Framework for the Integration of Gene-Prediction Data by Dynamic Programming", *Genome Res.* 12:1418-1427; ⁶ unknown chromosomal location.

Gene	huDGAT1	opDGAT1	huDGAT2	opDGAT2	huAWAT1	opAWAT1	huAWAT2	opAWAT2	huDGAT2L6	opDGAT2L6	huMGAT1	opMGAT1
huDGAT1	100	78	5	6	6	8	8	6	4	13	9	6
opDGAT1	78	100	7	6	8	6	7	5	4	7	6	6
huDGAT2	5	7	100	92	50	51	48	45	50	49	48	46
opDGAT2	6	6	92	100	50	49	48	45	50	50	48	46
huAWAT1	6	8	50	50	100	71	51	46	52	51	40	43
opAWAT1	8	6	51	49	71	100	50	46	52	49	42	44
huAWAT2	8	7	48	48	51	50	100	66	51	47	40	41
opAWAT2	6	5	45	45	46	46	66	100	51	47	41	39
huDGAT2L6	4	4	50	50	52	52	51	51	100	63	44	45
opDGAT2L6	13	7	49	50	51	49	47	47	63	100	41	44
huMGAT1	9	6	48	48	40	42	40	41	44	41	100	69
opMGAT1	6	6	46	46	43	44	41	39	45	44	69	100
huMGAT2	7	8	45	43	43	41	41	38	42	44	53	53
opMGAT2	5	5	47	47	45	45	39	40	44	44	55	52
huMGAT3	12	12	48	48	44	45	39	41	45	44	43	40
opMGAT3	8	5	52	52	47	48	42	45	48	47	44	43

Gene	huDGAT1	moDGAT1	opDGAT1	zfdGAT1A	zfdGAT1B	Gene	huMGAT1	moMGAT1	opMGAT1	zfmGAT1	huMGAT2	moMGAT2
huDGAT1	100	85	78	61	62	huMGAT1	100	72	69	56	52	52
moDGAT1	85	100	74	59	60	moMGAT1	72	100	67	55	52	52
opDGAT1	78	74	100	60	61	opMGAT1	69	67	100	59	53	54
zfdGAT1A	61	59	60	100	63	zfmGAT1	56	55	59	100	58	59
zfdGAT1B	62	60	61	63	100	huMGAT2	52	52	53	58	100	81
						moMGAT2	52	52	54	59	81	100
Gene	huDGAT2	moDGAT2	opDGAT2	zfdGAT2		opMGAT2	54	52	52	59	72	69
huDGAT2	100	95	92	69		zfmGAT2	54	52	53	62	63	65
moDGAT2	95	100	92	70		huMGAT3	43	40	40	43	46	46
opDGAT2	92	92	100	70		opMGAT3	45	42	44	49	46	47
zfdGAT2	69	70	70	100		zfmGAT3	43	41	43	44	42	43

Supplementary Table 2: Percentage identities for human, rat, opossum and zebrafish DGAT1 and DGAT2-like amino acid sequences

Numbers show the percentage of amino acid sequence identities. Numbers in **bold** show enzymes of high sequence identity and identify members of the same family or sub-family; huDGAT1: human DGAT1; opDGAT1: opossum DGAT1; huDGAT2: human DGAT2; opDGAT2: opossum DGAT2; huAWAT1: human AWAT1; opAWAT1: opossum AWAT1; huAWAT2: human AWAT2; opAWAT2: opossum AWAT2; huDGAT2L6: human DGAT2L6; opDGAT2L6: opossum DGAT2L6; huMGAT1: human MGAT1; opMGAT1: opossum MGAT1; huMGAT2: human MGAT2; opMGAT2: opossum MGAT2; huMGAT3: human MGAT3; opMGAT3: opossum MGAT3; moDGAT1: mouse DGAT1; zfdGAT1A: zebrafish DGAT1A; zfdGAT1B: zebrafish DGAT1B; moDGAT2: mouse DGAT2; zfdGAT2: zebrafish DGAT2; moMGAT1: mouse MGAT1; moMGAT2: mouse MGAT2; moMGAT3: mouse MGAT3; zfmGAT1: zebrafish MGAT1; zfmGAT2: zebrafish MGAT2; zfmGAT3: zebrafish MGAT3.