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Identification and Characterization of Three Novel Lipases Belonging to Families II and V from *Anaerovibrio lipolyticus* 5ST

Florence Privé, Naheed N. Kaderbhai, Susan Girdwood, Hilary J. Worgan, Eric Pinloche, Nigel D. Scollan, Sharon A. Huws, C. Jamie Newbold*

Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Aberystwyth, Ceredigion, United Kingdom

**Abstract**

Following the isolation, cultivation and characterization of the rumen bacterium *Anaerovibrio lipolyticus* in the 1960s, it has been recognized as one of the major species involved in lipid hydrolysis in ruminant animals. However, there has been limited characterization of the lipases from the bacterium, despite the importance of understanding lipolysis and its impact on subsequent biohydrogenation of polyunsaturated fatty acids by rumen microbes. This study describes the draft genome of *Anaerovibrio lipolytica 5ST*, and the characterization of three lipolytic genes and their translated protein. The uncompleted draft genome was 2.83 Mbp and comprised of 2,673 coding sequences with a G+C content of 43.3%. Three putative lipase genes, *alipA*, *alipB* and *alipC*, encoding 492-, 438- and 248- amino acid peptides respectively, were identified using RAST. Phylogenetic analysis indicated that *alipA* and *alipB* clustered with the GDSL/SGNH family II, and *alipC* clustered with lipolytic enzymes from family V. Subsequent expression and purification of the enzymes showed that they were thermally unstable and had higher activities at neutral to alkaline pH. Substrate specificity assays indicated that the enzymes had higher hydrolytic activity against caprylate (C8), laurate (C12) and myristate (C14).


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* E-mail: cjn@aber.ac.uk

**Introduction**

Hobson and Mann [1] isolated a bacterium from the sheep rumen able to hydrolyze linseed oil triglycerides to glycerol and fatty acids, using anaerobic techniques and a combination of differential and selective media [2]. It was named *Anaerovibrio lipolytica* [3], since changed to *A. lipolyticus* [4]. The growth characteristics of strain 5ST were described in continuous culture. Ribose, fructose and D-lactate were used as growth substrates and glycerol was fermented to propionate, lactate and succinate [5,6,7]. Ruminal lipase activity in animals receiving mainly concentrate feeds is thought to be accomplished mainly by *A. lipolyticus*, although other lipolytic species might be expected to predominate in grazing animals as *A. lipolyticus* lacks the ability to hydrolyze galacto- and phospholipids [8]. These latter lipids are known to be hydrolyzed in vitro by *Butyrivibrio fibrisolvens* strains S2 and LM8/1B [9]. Culture studies have shown *A. lipolyticus* to be present at around 10^7/ml in rumen [10] and molecular studies based on the concentration 16S rDNA have tended to support this [11,12,13] suggesting that a major role for *A. lipolyticus* in the rumen. Despite the possible importance of *A. lipolyticus* in ruminal lipid metabolism its lipase activity remains relatively unstudied. *A. lipolyticus* extracellular lipase activity was characterized in cell free-medium and after purification by chromatography on Sephadex columns; the lipases were most active at pH 7.4 and 20 to 22°C, and diglycerides were hydrolyzed more rapidly than triglycerides [8,14,15]. However no recent studies have been undertaken to enhance our knowledge of the lipases in *A. lipolyticus*. This study describes a genomic analysis of *A. lipolyticus* 5ST using the 454 pyrosequencing technology (Roche, Life Sciences) and the identification of three lipolytic genes in this important rumen organism; their expression and the subsequent purification and characterization of the protein products from these genes.

**Materials and Methods**

**Preparation of Anaerovibrio lipolyticus 5ST genomic DNA**

Pure cultures of *A. lipolyticus* strain 5ST, as first isolated by Hobson and Mann [1] at the Rowett Research Institute (Aberdeen, Scotland), came from the Herbivore Gut Ecosystems group collection at IBERS. The genomic DNA was extracted using the BIO101 FastDNA® Spin Kit for Soil (Qbiogene, Cambridge, UK) from approximately 2 mg of cryopreserved freeze-dried culture. The manufacturer’s guidelines were followed, with the exception that the sample was processed for 3 x 30 s at speed 6.0 in the FastPrep instrument (QBiogene), with incubation for 30 s on ice between bead-beating.
De novo genome sequencing

The draft nucleotide sequence of the bacterium was established by a shotgun sequencing approach carried out on a Genome Sequencer FLX system (454 Life Sciences, Roche), following the supplier's protocol. Assembly of the reads was accomplished using gsAssembler v2.5.3 software (Roche, Life Sciences), using the default parameters.

Annotation and sequence analysis

The contigs were submitted for genome annotation to the RAST server at http://rast.nmpdr.org [16], tRNAscan-SE 1.23 [17] and RNAmmer 1.2 [18].

The predicted lipase genes and amino acid sequences were compared for similarity to known sequences using BLASTN and BLASTP search. Their signal sequences for peptide cleavage were predicted using SignalP 4.0 [19]. CD search [20], the Pfam database (version 25.0, available at http://pfam.sanger.ac.uk/) and ClustalW [21] were used to search for conserved domains in the predicted amino acid sequences and to execute multiple alignments to find potential gene products related to known families of lipolytic enzymes. The theoretical molecular mass and isoelectric point of the deduced lipolytic protein sequences were calculated using the Compute pI/Mw tool on the ExPASy proteomics server (available at http://expasy.org/tools/pi_tool.html, May 2011).

Expression and purification of recombinant lipases

Primers for the amplification of the lipase genes were designed with FastPCR 6.1 [22], with and without the N-terminal signal sequence where one could be identified (Table S2). The PCR reaction was set up in a total volume of 25 µl as follows: 2 µl of template (~100 ng), 1 µl of forward and reverse primer (10 µM), 8.5 µl of molecular water and 12.5 µl of PCR mastermix (ImmoMix™, Bioline UK Ltd., London, UK). Initial activation of the Taq was performed for 10 min at 95°C, followed by 25 cycles as follows: 95°C for 30 s, 50°C for 30 s, 72°C for 2 min, followed by a final extension at 72°C for 5 min and holding of samples at 4°C. After PCR, the products were verified by electrophoresis on a 1% agarose gel using 1 X TBE. The band of interest was cut out with a sterile razor blade and the DNA eluted using the MinElute Gel Extraction kit (Qiagen, Crawley, UK).

The expression of the lipolytic genes was then undertaken using the pTrcHis TOPO® TA Expression kit (Invitrogen, Carlsbad, CA, USA) following the supplier’s protocol. The PCR product was ligated to the pTrcHis TOPO vector and introduced into E. coli TOP10 cells. Twelve colonies for each transformation were picked for secondary screening and their insert was analyzed for size by growing and inducing 50 ml of cells as follows: 2 ml of LB containing 50 µg ml−1 ampicillin, 4% 2-propanol. After PCR, the products were verified by electrophoresis on a 1% agarose gel using 1 X TBE. The band of interest was cut out with a sterile razor blade and the DNA eluted using the MinElute Gel Extraction kit (Qiagen, Crawley, UK).

The specific activity of the enzyme was determined using the ProBond™ Purification System (Invitrogen, Carlsbad, CA, USA).

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Substrate specificity

The following β-nitrophenyl esters with different chain length were purchased from Sigma-Aldrich (Dorset, UK) or TCI Europe (Zwijndrecht, Belgium) and used at 1 mM final concentration for assaysing substrate specificities: β-nitrophenyl butyrate (C4), β-nitrophenyl caproate (C6), β-nitrophenyl caprylate (C8), β-nitrophenyl caprate (C10), β-nitrophenyl laurate (C12), β-nitrophenyl myristate (C14), β-nitrophenyl palmitate (C16) and β-nitrophenyl stearate (C18). The β-nitrophenyl ester substrates with C4 to C10 acyl chains were dissolved in acetonitrile at a concentration of 100 mM. β-nitrophenyl ester substrates with C12 to C18 acyl chains were dissolved in a 1:4 mixture of acetonitrile and 2-propanol in order to solubilise the substrate, and reactions were performed with final concentrations of 1% acetonitrile and 4% 2-propanol.
Figure 1. Maximum Parsimony tree of lipases. Protein sequences were aligned using the built-in ClustalW (default parameters), the tree was built using the Maximum Parsimony method with default parameters and 500 bootstrap replications.
doi:10.1371/journal.pone.0069076.g001

Table 1. Putative lipase/esterase genes identified from *Anaerovibrio lipolyticus* 5ST using the RAST annotation and features of the encoded proteins.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Length (bp)</th>
<th>Protein size (aa)</th>
<th>Protein molecular weight (kDa)</th>
<th>Theoretical isoelectric point</th>
</tr>
</thead>
<tbody>
<tr>
<td>alipA</td>
<td>1476</td>
<td>492</td>
<td>56.27</td>
<td>5.64</td>
</tr>
<tr>
<td>alipB</td>
<td>1314</td>
<td>438</td>
<td>48.79</td>
<td>4.94</td>
</tr>
<tr>
<td>alipC</td>
<td>744</td>
<td>248</td>
<td>27.75</td>
<td>6.17</td>
</tr>
</tbody>
</table>

doi:10.1371/journal.pone.0069076.t001
Table 2. Best matches obtained using BLASTN for the lipolytic genes identified in *Anaerovibrio lipolyticus* 5ST.

<table>
<thead>
<tr>
<th>Contig</th>
<th>Gene</th>
<th>Best hit (accession number)</th>
<th>Nucleotide identities (%)</th>
<th>E-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Contig00046</td>
<td>alipA</td>
<td>Lipolytic protein GDSL family (CP002637) from <em>Selenomonas sputigena</em> ATCC 35185</td>
<td>533/842 (63%)</td>
<td>2e-13</td>
</tr>
<tr>
<td>Contig00136</td>
<td>alipB</td>
<td>None</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Contig00239</td>
<td>alipC</td>
<td>None</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

doi:10.1371/journal.pone.0069076.t002

Effect of temperature on enzyme stability and thermostability

The effect of temperature on the activity of enzyme activity was examined across the range 25–70°C under standard assay conditions. The pH of the MES buffer was adjusted to 6.5 at respecitive temperatures. The thermostability of the enzymes was analysed by measuring the residual activity after incubating the enzyme (2 µl in 50 mM MES, pH 6.5) for 1 h at 50, 60 and 70°C.

Effect of metal ions

The effect of metal ions on the activity of the enzymes were investigated by incubating the enzymes with various metal chloride salts (Na⁺, K⁺, NH₄⁺, Mg²⁺, Ca²⁺, Mn²⁺, Zn²⁺, Co²⁺) at final concentrations of 5 mM in 50 mM MES (pH 6.5) for 30 min at room temperature. The remaining activity was then measured under standard assay conditions.

Nucleotide sequence accession numbers

The draft genome was deposited with NCBI BioProject Accession: PRJNA187036 The nucleotide sequences of the genes reported here are available in the GenBank database under accession numbers KC579357–KC579359.

Results

Pyrosequencing results and identification of three lipolytic genes in the draft genome

Pyrosequencing generated 340,862 high quality reads with an average length of 425 bp, representing 144,706,594 bp of total information. These data represented 36× coverage for an estimated bacterial genome size of 4 Mbp. The assembly of the uncompleted draft genome resulted in 285 contigs with 2,830,874 bp total sequence information, comprising 247 large contigs (>5000 bp) with a total size of 2,816,384 bases. The RAST annotation identified 2,673 coding sequences and the G+C content was 43.3%. Copies of the 5ST and 23S rRNA genes (6 and 1 respectively) and 60 predicted tRNA genes were identified within the genome. There were 268 subsystems represented in the genome, however 63% of the predicted genes could not be assigned to a subsystem. Two genes annotated as “GDSL family lipolytic enzyme” and one gene annotated as “carboxylesterase” were named alipA, alipB and alipC respectively. Phylogenetic analysis indicated that alipA and alipB clustered with the GDSL/SGNH family II, and alipC clustered with lipolytic enzymes from family V (Figure 1).

The lipase genes alipA, alipB and alipC identified as novel members of family II and V lipases

Gene length varied from 744 to 1,476 bp; and features of the encoded proteins are presented in Table 1. Tables 2 and 3 present the results of the BLASTN and BLASTP analysis of the identified putative lipase genes. Gene alipA matched with a gene coding for a lipolytic protein from *Selenomonas sputigena*, with 63% identity, whereas no homologous sequences were found for genes alipB and alipC in the Genbank database. However, the proteins were found to match with proteins from various *Veillonellaceae*, and the best hits were with GDSL lipolytic proteins from *Selenomonas* species for the proteins alipA and alipB (56 and 41% identity respectively) and with a lipase/esterase from *Mitsuokella multicauda* for alipC (51% identity). AlipC also shared 42% amino acid identity (e-value 8e-50) with a lipase from a rumen metagenome RlipE2 [29].

Domain analysis (Table S1) revealed that alipA and alipC did not contain a signal peptide; alipB contained a putative 24-residual signal peptide at the N-terminus. AlipA and alipB contained a unique SGNH/GDSL hydrolase superfamily domain (c|01053) at amino acid residues 306–482 and 242–413 respectively. No conserved domain could be identified on half of the protein sequences, on the N side. AlipC contained a COG1647 domain (esterase/lipase function prediction) at amino acid residues 1–244 and an esterase/lipase superfamily domain (c|12031) at amino acid residues 85–227.

The proteins alipA and alipB contained, respectively, the lipase-conserved catalytic triad residues Asp466/Asp405 and His469/His406 and the catalytic nucleophile Ser309/Ser249 in a GDS(L) motif (Figure 2).

Table 3. Best matches using BLASTP for the predicted amino acid sequence of lipolytic genes identified in *Anaerovibrio lipolyticus* 5ST.

<table>
<thead>
<tr>
<th>Protein</th>
<th>Putative function (accession number)</th>
<th>Most similar homolog (e-value)</th>
<th>Identity (overlapped aa)</th>
</tr>
</thead>
<tbody>
<tr>
<td>alipA</td>
<td>Lipolytic protein GDSL family (AEC00120)</td>
<td><em>Selenomonas sputigena</em> ATCC 35185 (0.0)</td>
<td>278/495 (56%)</td>
</tr>
<tr>
<td>alipB</td>
<td>GDSL-like protein (EFR39963)</td>
<td><em>Selenomonas sp. oral taxon</em> 137 str. F0430 (3e-106)</td>
<td>169/411 (41%)</td>
</tr>
<tr>
<td>alipC</td>
<td>Putative esterase/lipase (EEX68534)</td>
<td><em>Mitsuokella multicauda</em> DSM 20544 (3e-105)</td>
<td>126/249 (51%)</td>
</tr>
</tbody>
</table>

doi:10.1371/journal.pone.0069076.t003

Figure 1. Anaerovibrio lipolyticus 5ST Lipases

Figure 2. Enzyme active site residues of alipA and alipB from Anaerovibrio lipolyticus 5ST
and Ser90 in the pentapeptide motif GQSMG, and multiple amino acid alignments indicated alipC would be a new member of family V (Figure 3).

**Expression and purification of alipA, alipB and alipC**

In order to investigate the biochemical properties of the enzymes, they were expressed in the pTrcHis TOPO vector in *Escherichia coli*. AlipB without its signal sequence (alipBss) was chosen as alipB was either not expressed, degraded or insoluble during expression as it could not be detected on SDS-PAGE (data not shown). Figure 4 illustrates the purification process, with the total lysates of *E. coli* TOP10 expressing the recombinant proteins before and after induction with 1 mM IPTG, and the purified fraction after elution from the nickel resin. The purification protocol routinely yielded 0.2 to 0.4 mg ml$^{-1}$ of purified protein from 50 ml cultures grown for 5 h after induction.

**Substrate specificity**

To examine substrate specificity, activity was tested against various ρ-nitrophenyl esters with different acyl chain lengths. The results under standard assay conditions of pH 6.5 and 39°C are presented in Table 4. AlipA and alipBss showed a narrow chain length specificity, with the highest specific activity against ρ-nitrophenyl laurate (640 U·mg$^{-1}$) and myristate (157 U·mg$^{-1}$) respectively, and lower specific activity against ρ-nitrophenyl caproate (33 and 43 U·mg$^{-1}$ respectively). AlipC showed a broader range of activity with higher specific activities against short to medium acyl chain length: the activities were 187 U·mg$^{-1}$ against ρ-nitrophenyl butyrate, 270 U·mg$^{-1}$ against ρ-nitrophenyl caprylate, 118 and 242 U·mg$^{-1}$ against ρ-nitrophenyl laurate.

**Effect of pH and temperature on enzyme activity**

The effects of pH and temperature on the activity of the enzymes were determined (Figure 5). AlipA and alipC had maximal activity at pH 8.5 and 9.0 respectively, and presented >50% activity in alkaline pH ranges, respectively 7.5–9.5 and 9.0–10.0. AlipBss showed >50% of maximum activity in the pH range 6.0–8.0, with maximal activity at pH 7.5. The optimum temperatures were determined as 40°C (alipA, alipC) and 55°C (alipBss). The temperature range where the enzyme retained more than 50% activity was 40–50°C for alipA, 35–55°C for alipBss, and 35–50°C for alipC. The temperature stability of the proteins was examined by measuring its residual activity after incubating the purified enzymes for 1 h at 50, 60 or 70°C (Table 5) and thus represent both temperature stability including the protein unfolding and refolding potential of the proteins following thermal shock.
The proteins alipBss and alipC appeared to be temperature sensitive as less than 50% of activity was measured after 1 h incubation at 50°C. Activities ranged from 8 to 45% after incubating at 60 or 70°C. AlipA appeared to have some thermostability: it retained around 50% activity after incubation at 60 and 70°C.

Effect of ions on enzyme activity

The effects of different metal cations at a concentration of 5 mM on the activities of the enzyme was assayed, the results are presented in Table 6. Ca²⁺, Mn²⁺ and Co²⁺ inhibited alipA activity (<68% activity), K⁺ and NH₄⁺ did not modify the activity (98–99% activity), while Na⁺, Mg²⁺ and Zn²⁺ activated alipA. AlipBss activity was strongly inhibited by Ca²⁺ and Mg²⁺ (residual activities, 33 and 56% respectively) and moderately inhibited by Na⁺, K⁺ and NH₄⁺ (residual activities, 72, 67 and 69% respectively), whereas Mn²⁺, Zn²⁺ and Co²⁺ activated alipBss (residual activities, 130, 107, and 103% respectively). Zn²⁺ strongly inhibited alipC activity (17% residual activity); NH₄⁺, Mg²⁺ and Co²⁺ had more moderate inhibitory effects (residual activities from 74 to 81%). K⁺ had no effect, while Na⁺, Ca²⁺ and Mg²⁺ activated alipC (residual activities, 119, 185, and 141% respectively).

Discussion

Next-generation sequencing has provided scientists with quick and increasingly affordable methods to access genomic data. The 454 technology has been used successfully in a number of studies to establish draft and complete bacterial genomes and establish their gene catalogues, for example for the bacteria Anaerovibrio argentinus [31,32], Staphylococcus epidermidis A1487 [33], Acinetobacter baumannii [34]; and, combined with other sequencing platforms, the genomes of the rumen bacteria Megasphaera elsdenii [35], Ruminococcus albus [36] and Fibrobacter succinogenes [37].

The genus Anaerovibrio currently includes a single species, A. lipolyticus. The 454 technology was used in this study to establish the draft genome of A. lipolyticus SST, and to identify putative lipase genes. The draft genome was annotated using the Rapid Annotation Using Subsystem Technology (RAST) server [16]. However, the accuracy of the annotation also relies on the automated pipeline used [38], some predicted genes could be dissimilar to anything in the reference databases as they could have evolved extensively, represent uncharacterized sequences, or be misidentified [39]. Reference databases and computational methods constituting annotation pipelines are constantly developed, and there is hence a need to reprocess genome annotations on a regular basis to improve their quality and completeness [39,40]. As it was not the primary objective in this study, the genomic sequence of the bacterium remains as draft. However it would be valuable to complete the draft sequence, and subsequently annotate the complete genome, as the presence of other lipolytic genes may have been overlooked. In addition a closed genome would be useful to better understand A. lipolyticus’s role in the rumen and to share its genome in public databases for future use in molecular studies.

AlipA, alipB and alipC exhibited very low nucleotide as well as amino acid sequence similarity to previously available sequences, except for a rather low match with some amino acid sequences from the Veillonellaceae genera Selenomas, Mitauella and Centipeda. It is therefore proposed that they represent novel esterases/lipases, and that they have not been isolated yet from previous metagenomic studies in the rumen [29,41].

AlipA and alipB exhibited the distinct GDSL sequence motif located at the N-terminal part and Ser, Asp and His residues as part of the active site. They also contained a SGNH hydrolase superfamily domain, thus classifying them as belonging to the subfamily of GDSL/SGNH enzymes [42,43,44]. The GDSL family of enzymes was first identified by Upton and Buckley [42], these enzymes contain a GDSL motif located in the N-terminal part of the protein instead of the conserved lipase motif GXSGXG [30]. The SGNH hydrolase subfamily was proposed from the crystal structures of Aspergillus aculeatus rhamnogalacturonan acetyl esterase, Streptomyces scabies and influenza C virus esterases and an acetylhydrolase isolated from Bos taurus [45,46]; where four amino acids were found to be essential for catalysis, namely serine, glycine, asparagine, and histidine. The catalytic serine is located in a GDSL motif, while the Gly and Asn serve as proton donors to the oxyanion hole, and the His helps increasing the nucleophilicity of the Ser by deprotonating its hydroxyl group [45]. However sequence analysis showed that only the second half of alipA and alipB amino acid sequences were predicted for esterase/lipase function, as the conserved domains were present on amino acid residues 306–482 and 242–413 on the native sequence of alipA.

### Table 4. Activity of lipases isolated from Anaerovibrio lipolyticus SST against different substrates.

<table>
<thead>
<tr>
<th>Substrate</th>
<th>Specific activity (U mg⁻¹ protein)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>alipA</td>
</tr>
<tr>
<td>pNP-acylesters</td>
<td></td>
</tr>
<tr>
<td>Butyrate (C4)</td>
<td>139.4±17.4</td>
</tr>
<tr>
<td>Caproate (C6)</td>
<td>73.8±19.0</td>
</tr>
<tr>
<td>Caprylate (C8)</td>
<td>98.4±17.4</td>
</tr>
<tr>
<td>Caprate (C10)</td>
<td>32.8±9.5</td>
</tr>
<tr>
<td>Laurate (C12)</td>
<td>639.6±24.0</td>
</tr>
<tr>
<td>Myristate (C14)</td>
<td>172.2±17.4</td>
</tr>
<tr>
<td>Palmitate (C16)</td>
<td>123.0±19.1</td>
</tr>
<tr>
<td>Stearate (C18)</td>
<td>73.8±17.3</td>
</tr>
</tbody>
</table>

ND. Not detected.

doi:10.1371/journal.pone.0069076.t004
and alipB (438 aa total) respectively. No conserved domain or homologies could be detected on the first part of the protein sequences; thus further studies would be needed to assess whether these parts of the proteins would contain other catalytic domains or serve protein structural functions such as autotransport. For example, GDSL hydrolases from *Pseudomonas aeruginosa*, *S. typhimurium* and *Photobacterium luminescens* harbour a C-terminus domain encompassing approximately one third of the entire protein. This domain is composed of 12 β-sheets which form a β-barrel inserted into the bacterial outer membrane and forms a structure similar to porines [47,48,49]. The N-terminal part of the protein carrying the catalytic activity is exported through the β-barrel and often cleaved off after translocation [50,51,52,53,54,55]. Enzymes belonging to the GDSL family were also described as exhibiting broad substrate specificity, due to a flexible active site that changes conformation with the binding of different substrates [43], and regioselectivity. In contrast, alipA had a very high specific activity against p-nitrophenyl laurate, and (492 aa total) and alipB (438 aa total) respectively. No conserved domain or homologies could be detected on the first part of the protein sequences; thus further studies would be needed to assess whether these parts of the proteins would contain other catalytic domains or serve protein structural functions such as autotransport. For example, GDSL hydrolases from *Pseudomonas aeruginosa*, *S. typhimurium* and *Photobacterium luminescens* harbour a C-terminus domain encompassing approximately one third of the entire protein. This domain is composed of 12 β-sheets which form a β-barrel inserted into the bacterial outer membrane and forms a structure similar to porines [47,48,49]. The N-terminal part of the protein carrying the catalytic activity is exported through the β-barrel and often cleaved off after translocation [50,51,52,53,54,55]. Enzymes belonging to the GDSL family were also described as exhibiting broad substrate specificity, due to a flexible active site that changes conformation with the binding of different substrates [43], and regioselectivity. In contrast, alipA had a very high specific activity against p-nitrophenyl laurate, and

![Figure 5. The effect of pH (A) and temperature (B) on the activity of proteins alipA, alipBss and alipC.](http://www.plosone.org)

The pH assays were determined against p-nitrophenyl caprylate (C8) at a constant temperature of 39°C in a wide-range pH buffer set at the indicated pH values. Temperature assays were determined against the same substrate at a constant pH of 6.5 in 50 mM MES.

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<th>Table 5. Relative activity of lipases cloned from Anaerovibrio lipolyticus 5ST after incubation for one hour at 50, 60 or 70°C.</th>
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<td>Temperature of incubation</td>
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The enzymes were incubated 1 h at 50, 60 and 70°C in 50 mM MES buffer (pH 6.5); the residual activities were measured with a standard assay against p-nitrophenyl caprylate (C8). The activity of the enzyme at 40°C was defined as 100%. Control activities at 40°C were 794, 564 and 793 U·mg⁻¹ protein for alipA, alipBss and alipC respectively.

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alipBss against \( \rho \)-nitrophenyl myristate. Assessment of their activity towards a broader range of substrate would be needed to further characterize these enzymes.

Analysis of the alipC-encoded protein showed that the protein belongs to the serine hydrolase group and has common features to basic lipases [30], as well as the conserved sequence motifs of family V of lipases. The amino acid sequence of alipC showed significant homology with other bacterial enzymes such as epoxide hydrolases and haloperoxidases, which also possess the \textit{hydrolase fold} [30,44]. Only four enzymes from this family have been cloned and characterized to date: the carboxylesterase Est2 from \textit{Acetobacter pasteurianus}, showing maximum activity at 78°C and pH 7.8 [56,57], the carboxylesterase EstV from \textit{Helicobacter pylori} with an optimum temperature of 50°C and pH of 10 [58], the lipase Lip1 isolated from the thermophilic bacterium \textit{Fervidobacterium changbaicum} with an optimum activity at pH 10 [59], and the lipase Lip1p from \textit{Ruminococcus obeum} showing maximum activity at pH 9. Fay and colleagues [60] also observed that pure cultures of \textit{A. lipolyticus} 5ST could not efficiently catalyze \( \rho \)-nitrophenyl palmitate and concluded this substrate was more likely to indicate esterase activity rather than lipase activity.

So far, only six pure cultures of obligate anaerobic and lipolytic bacteria have been isolated from the rumen of sheep, cattle and deer [1,10,61,62,63,64]. It was estimated that \textit{A. lipolyticus} alone could account for the total rates of esterified fatty acid production in the rumen, based on lipid hydrolysis rates and population density studies [65]. Three lipase/esterase genes from the draft genome of \textit{A. lipolyticus} 5ST were isolated, and their characterization is an important step in increasing our knowledge on the lipase activity within the rumen.

**Supporting Information**

**Table S1 Conserved domains and predicted signal sequences in the proteins alipA, alipB and alipC.**

**Table S2 Primers used for amplification of the lipolytic genes in \textit{Anaerovibrio lipolytica} 5S.**

**Author Contributions**

Conceived and designed the experiments: FP NS SH CJN. Performed the experiments: FK NK SH HW EP. Analyzed the data: FK NK SG CJN. Contributed reagents/materials/analysis tools: NK SH EP. Wrote the paper: FP SH CJN.

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**References**


