

Sequence of a lipase gene from the Antarctic psychrotroph *Moraxella* TA144

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Many bacteria and fungi excrete lipases (triacylglycerol acyl hydrolase, EC 3.1.1.3) heavily used in various industrial applications (1). These enzymes display unusual catalytic properties as they act at the oil-water interface of insoluble substrates and are activated by the binding to lipid micelles (2).

We recently described the isolation and the characterization of antarctic *Moraxella* strains excreting lipases and showed that these enzymes are able to efficiently catalyse lipolysis at temperatures close to 0°C (3). As part of a study devoted to cold active enzymes, a lipase gene from the psychrotrophic strain *Moraxella* TA144 was cloned and sequenced; it confers lipolytic activity to *E. coli* clones growing on plates containing an emulsified lipid.

The nucleotide sequence, 1469 bp in length, is shown in Fig. 1 along with the region coding for the cold active lipase and the flanking sequences. The deduced primary structure of the preprotein is composed of 319 amino acids with a predicted Mr of 34 662. Boxed is an hydrophobic peptide containing the G-X₁-S-X₂-G consensus sequence around the potential active serine residue. Interestingly, the psychrotrophic lipase displays a tryptophan residue at the X₁ position in contrast with all other lipases investigated so far (4).

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GATATCTGTTATTGGCTTGGATGAAAGACGAGTGATACAGCTAAGGGCTAAAA	53
ATATTACGTAGTAAATCTATAGTCAATATTATATAAGATGAGACCATATCTTTAATAAATATC	116
TATCATAAAGACAAGCAAGTTATATTATCACATCAAAGTGCCCTACTCAGTTTTAGATGTGTTA	179
TTGGCGCTACACTAAAGCATGTCCTCAATAGCCCTGTTATACATGTAGTCCATTTATACATG	242
CGCTTTCTTTAAATTTTCTACTACAGTCCAGTTGCATTTCGATACCGTGCAAGGTATTATGACT	305
TTGACAATGAAAAGATTAAATGCTACTATTATTGGCTTATCAGGCATACAGTCTGAAATAG	368
- 35	
- 10	
GCTAAACAACATAAATAGCTCATTAAAGACAATCATAGCCACAGACTCTCACATAAAAAAGA	431
ATG TTT ATC ATG ATA AAA AAG TCT GAG CTT GCA AAA GCT ATT ATC GTC	479
Met Phe Ile Met Ile Lys Lys Ser Glu Leu Ala Lys Ala Ile Ile Val	16
ACG GGC GCG TTG GTT TTT TCT ATA CCG ACT TTA GCT GAA GTT ACC TTA	527
Thr Gly Ala Leu Val Phe Ser Ile Pro Thr Leu Ala Glu Val Thr Leu	32
TCT GAA ACC ACG GTT AGC TCA ATA AAA TCT GAA GCT ACG GTT AGC TCA	575
Ser Glu Thr Thr Val Ser Ser Ile Lys Ser Glu Ala Thr Val Ser Ser	48
ACA AAA AAA GCA TTA CCA GCA ACG CCG TCA GAT TGT ATT GCT GAT AGC	623
Thr Lys Lys Ala Leu Pro Ala Thr Pro Ser Asp Cys Ile Ala Asp Ser	64
AAA ATT ACA GCA GTT GCT CTT TCA GAT ACT CGT GAT AAT GGC CCC TTT	671
Lys Ile Thr Ala Val Ala Leu Ser Asp Thr Arg Asp Asn Gly Pro Phe	80
TCT ATC CGT ACC AAA CCG ATT TCG CCG CAG TCG GCG AAG GGT TTC GGT	719
Ser Ile Arg Thr Lys Arg Ile Ser Arg Gln Ser Ala Lys Gly Phe Gly	96
GGT GGT ACG ATT CAC TAC CCA ACC AAC GCT ACG GGC TGC GGT CTG TTA	767
Gly Gly Thr Ile His Tyr Pro Thr Asn Ala Ser Gly Cys Gly Leu Leu	112
GCC GCT ATT GCC GTG GTT CCT GGT TAC GTT TCT TAC GAG AAC TCT ATC	815
Gly Ala Ile Ala Val Val Pro Gly Tyr Val Ser Tyr Glu Asn Ser Ile	128
AAG TGG TGG GGA CCG CGT CTG GCT TCT TGG GGC TTT GTC GTT ATC ACT	863
Lys Trp Trp Gly Pro Arg Leu Ala Ser Trp Gly Phe Val Val Ile Thr	144
ATC AAT ACC AAC TCT ATC TAT GAT GAT CCA GAT AGT AGA GCC GCA CAA	911
Ile Asn Thr Asn Ser Ile Tyr Asp Asp Pro Asp Ser Arg Glu Ala Gln	160
TTG AAT GCA GCA CTA GAT AAC ATG ATT GCT GAT GAC ACC GTC GGC AGT	959
Leu Asn Ala Ala Leu Asp Asn Met Ile Ala Asp Asp Thr Val Gly Ser	176
ATG ATA GAT CCT AAG CCG TTG GGC GCT ATT GGC TGG TCA ATG GGT GGC	1007
Met Ile Asp Pro Lys Arg Leu Gly Ala Ile Gly Trp Ser Met Gly Gly	192
GGC GGC GCG CTT AAA CTG GCA ACG GAG CCG AGC ACA GTA CGA GCC ATT	1055
Gly Gly Ala Leu Lys Leu Ala Thr Glu Arg Ser Thr Val Arg Ala Ile	208
ATG CCA CTA GCG CCC TAT CAT GAC AAA AGC TAT GGC GAG GTA AAA ACG	1103
Met Pro Leu Ala Pro Tyr His Asp Lys Ser Tyr Gly Glu Val Lys Thr	224
CCA ACC TTG GTC ATT GCC TGC GAG GAT GAC CCG ATT GCT GAG ACT AAG	1151
Pro Thr Leu Val Ile Ala Cys Glu Asp Asp Arg Ile Asn Glu Thr Lys	240
AAA TAT GCC AAC GCG TTT TAT AAA AAT GCC ATT GGC CCC AAG ATG AAG	1199
Lys Tyr Ala Asn Ala Phe Tyr Lys Asn Ala Ile Gly Pro Lys Met Lys	256
GTT GAA GTA AAC AAT GGC AGT CAC TTT TGT CCA AGC TAC CCG TTT AAC	1247
Val Glu Val Asn Asn Gly Ser His Phe Cys Pro Ser Tyr Arg Phe Asn	272
GAG ATA CTT TTA AGT AAG CCT GGC ATC GCG TGG ATG CAG CGT TAT ATT	1295
Glu Ile Leu Leu Ser Lys Pro Gly Ile Ala Trp Met Gln Arg Tyr Ile	288
AAT AAT GAT ACA CGC TTC GAT AAA TTC TTA TGT GCC AAC GAA AAC TAT	1343
Asn Asn Asp Thr Arg Phe Asp Lys Phe Leu Cys Ala Asn Glu Asn Tyr	304
AGC AAA AGC CCT CGT ATC TCA GCT TAT GAT TAT AAA GAT TGC CCA TAA	1391
Ser Lys Ser Pro Arg Ile Ser Ala Tyr Asp Tyr Lys Asp Cys Pro ***	
AGCGGTGTATAGGAATGGTGACATTCGCTTTAAGTATGCCTTTATTGGCTATATTAGATTTA	1454

AGTACATTCGAATTC	

Figure 1. *Moraxella* TA144 lipase 1 DNA sequence and predicted primary structure. The potential promoter regions (-35, -10), the Shine-Dalgarno sequence (SD), the in frame stop codons (***) and the inverted repeats (arrows) are indicated.