



RESEARCH PAPER

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Biodegradation of 7-ketocholesterol (7-KC) by *Thermobifidafusca* IP1

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Abstract

7-ketocholesterol (7KC), an oxidized derivative of cholesterol, has been implicated in a variety of chronic diseases including atherosclerosis, Alzheimer's disease, Parkinson's disease, cancer and age-related macular degeneration. It is formed by the autooxidation of cholesterol and especially cholesterol-fatty acid esters found in lipoprotein deposits, its elevated concentrations are associated with disruption of cellular homeostasis, decreased cell viability, and increased cell death. Enzymatic cleavage of 7-KC can serve as a key solution for the cure of a number of chronic diseases directly associated with its accumulation. A bacterial strain isolated from manure piles was characterized taxonomically and identified as *Thermobifida fusca* IP1 on the basis of amplification and sequencing of 16S rDNA. This isolate was tested for its ability to degrade 7-ketocholesterol in M9 liquid medium and showed to utilize 7-KC as the sole carbon and energy source. The degradation of 7-KC was hundred percent when tested in liquid culture. High Performance Liquid Chromatography (HPLC) analysis also showed complete removal of the compound from the sample after twelve days. This bacterium can effectively be used to remove 7-KC and can lead to the development of a single potential therapeutic enzyme preparation to target a number of above mentioned chronic diseases related to 7-KC.

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Introduction

7-Ketocholesterol (7-KC) is a naturally occurring oxysterol formed by the autooxidation of cholesterol and cholesterol-fatty acid esters (Dzeletovic *et al.*, 1995). It is commonly found in oxidized lipoprotein deposits associated with atheromatous plaques (Garcia-Cruset *et al.*, 2001; Ohtsuka *et al.*, 2006; van Reyk *et al.*, 2006) as well as in lipoprotein deposits in Bruch's membrane and choriocapillaris in the back of the retina (Moreira *et al.*, 2009). Cholesterol oxidation products, termed oxysterols, are increasingly considered of potential interest in the pathogenesis of atherosclerotic lesions, 7-Ketocholesterol is a major oxidation product of cholesterol found in human atherosclerotic plaque and is more atherogenic than cholesterol (Leonarduzzi *et al.*, 2002).

It has been shown to be the major cytotoxic component in oxidized LDL (Rodriguez *et al.*, 2004). This oxysterol is known to be highly inflammatory both *in vitro* (Brown and Jessup, 1999; Vejux and Lizard, 2009) and *in vivo* (Amaral *et al.*, 2013). Its inflammatory and cytotoxic properties have been implicated in the pathogenesis of numerous aging diseases (Vejux and Lizard, 2009), including atherosclerosis (Brown and Jessup, 1999; Reyk *et al.*, 2006), Alzheimer's disease (Vejux and Lizard, 2009; Poli *et al.*, 2013), cancer (Wang *et al.*, 2013), Parkinson's disease (Poli *et al.*, 2013) and age-related macular degeneration (Poli *et al.*, 2013; Rodri'guez and Larrayoz, 2010).

In vitro experiments have shown that 7-ketocholesterol, a major oxysterol in plaques, induces vascular Smooth Muscle Cell's (SMC's) death with features of apoptosis, such as nuclear condensation and internucleosomal DNA fragmentation (Lizard *et al.*, 1999). It has been well established that exposure of cells to 7-KC elicit a variety of defense responses, including inflammation, apoptosis, and the stimulation of vascular endothelial growth factor (Vejux *et al.*, 2008). The ability of 7KC to disrupt cellular Ca^{2+} homeostasis is likely an integral part of

its toxicity (Berthier *et al.*, 2004; Rimner *et al.*, 2005; Spyridopoulos *et al.*, 2001).

7-KC is a major intracellular oxysterol species. Sterols, including oxysterols, enter the cell via receptor mediated endocytosis of low density lipoproteins and traffic to the lysosomes, which are a major site of non-enzymatic oxysterol formation. Consequently, 7KC levels are the highest in the endosomal and lysosomal compartments (Brown *et al.*, 2000). 7KC is known to inhibit sphingomyelinase (Maor *et al.*, 1995) and facilitate the intralysosomal accumulation of both sphingomyelin and cholesterol, possibly leading to foam cell formation. Subsequent free cholesterol loading of lysosomes also promotes deacidification (Cox *et al.*, 2007), impairs organelle trafficking (Fraldi *et al.*, 2010), and inhibits chaperone mediated autophagy (Kaushik *et al.*, 2006). At micromolar concentrations, 7KC causes lysosomal membrane permeabilization (LMP). The cellular response to LMP depends on the degree of permeabilization, with mild LMP causing induction of apoptosis or apoptosis-like cell death and sustained LMP generally leading to necrosis (Mathieu *et al.*, 2012). The aim of the present study was to isolate and characterize bacteria from environmental sample (manure piles) capable of catabolizing 7-KC.

Materials and methods

Chemicals

The substrate 7KC was obtained from Sigma-Aldrich (97.1% pure). A modified M9 medium was used in all experiments as growth medium. The composition of M9 was, 6.0 g Na_2HPO_4 , 3.0 g KH_2PO_4 , 0.5 g NaCl, 1.0 g HN_4Cl , 0.185 mg $(NH_4)_6Mo_7O_{24} \cdot 4H_2O$, 1.0 ml of 24.6% (w/v) $MgSO_4 \cdot 7H_2O$ and 1.0 ml of 1.47% (w/v) $CaCl_2 \cdot 2H_2O$ in 1000 ml of distilled water (final pH 7).

Isolation of bacteria

Manure pile sample was collected from Rawalpindi, Pakistan in sterile falcon tubes. Samples were properly labelled and kept in refrigerator (4 °C) till the processing. Sample (10 g) was suspended into 100 ml of sterile distilled deionized water, which was further used for inoculation purpose. M9 medium (10

ml) amended with 7KC (1mg L⁻¹ or 0.0025 M) as only carbon and energy source was inoculated with 10 drops of environmental sample. To enhance the solubility of 7KC, the medium was sonicated for 20 min prior to inoculation in a bath sonicator. After inoculation, culture was incubated in shaking incubator at 30 °C and 250 rpm agitation speed. Aliquots (100 µL) were sampled after every 24 hours and analyzed for the decrease in the concentration of target compound by HPLC. Growth was monitored by taking absorbance at 600 nm by spectrophotometer. After indication of decrease in concentration of 7-KC from the samples, cultures were streaked on M9 agar plates prepared by adding 5.0 mg of 7KC in methanol and evaporated to dryness on the surface. Plates were incubated at 30 °C for 72 hours. From M9 agar surface morphologically different colonies were picked and streaked on the nutrient agar plates in order to get pure cultures. Pure cultures were further confirmed for 7KC biodegradation potential by inoculating in 1ml of M9 medium containing 1mg of 7KC as the only carbon and energy source. One pure bacterial strain giving positive results for 7KC degradation from the environmental samples was selected for the molecular identification.

Molecular identification of bacteria

Genomic DNA extraction

According to the method of Adye and Mateles, (1969) bacterial culture of 48-72 hour was harvested by centrifugation at 7000 rpm for 20 minutes. The cells were frozen in liquid N₂. The frozen pellets were ground with a mortar and pestle. The powder was suspended in STE (100mM Tris-Cl, pH = 8.0, 150 mM NaCl and 100 mM EDTA) and incubated with 1% SDS at 37 °C for 3 hours. The solution was then centrifuged at 7000 rpm for 20 minutes to remove any cell debris.

The resulting solution was then extracted with a solution of phenol : chloroform : Isoamyl alcohol (25:24:1) saturated with 10mM Tris, pH 8.0, 1mM EDTA two times. The genomic DNA was recovered by slowly adding cold ethanol to the aqueous solution such that the ethanol remained on top of the aqueous

layer. At the interface a small glass rod was inserted and twirled around to spool the DNA onto the rod. The spooled DNA was resuspended in 1x TE (pH = 7.6) (1ml-1M Tris-HCl, 0.2 ml-0.5M EDTA at pH 8.0, 988 ml-ddH₂O).

The genomic DNA was run at 100 volts for 90 minutes on a 1% (w/v) agarose gel in 1x TAE (Tris Acetate EDTA) buffer containing 5 µL ethidium bromide solution (10mg/ml) to determine its relative size and concentration.

PCR Amplification of the 16S Ribosomal DNA

The extracted DNA was subjected to PCR (Gradient Cycler, MJ Research, PTC-200, Peltier Thermal Cycler) to amplify the 16S ribosomal DNA segments. One Taq®2x master mix with GC buffer (New England BioLabs® Inc.) was used. It was an optimized blend of Taq and Deep Vent® DNA polymerases. Master mix formulation contained NTPs, MgSO₄ and other buffer components. Primers sequences used were 16S-27F (5'-AGAGTTTGATCMTGGCTCAG-3'), (T_m=53.2 °C) and 16S-1492R (5'-TACGGYTACCTTGTACGACTT-3') (T_m=54.6 °C). The PCR mixture used had a final volume of 50 µL and contained 1 µL of each primer (100 µM), 25 µL of one Taq 2x Master Mix with GC Buffer, 22 µL of distilled deionized water and 1 µL of template (800 ng). The temperature cycle for the PCR was 1 min of denaturation at 94 °C, 1 min of annealing at 48 °C, and 3 min of primer extension at 72 °C. 25 additional cycles were used and a final primer extension for 10 min. The amplified DNA product was run on 1.5% agarose gel (1.5g agarose/100 ml of 1X TAE) at 100 Volts for 30 minutes along with 1kb DNA ladder (New England BioLabs® Inc.). The DNA fragment was excised from the agarose gel with a clean, sharp scalpel.

PCR product was purified by QIAquick® Gel Extraction Kit (250) (Qiagen Sciences Maryland, USA) according to the standard protocol recommended by the manufacturer. Automated Sequencing Reactions were performed with Perkin Elmer ABI Big Dye Reaction Mix. The sequences were matched against the NCBI GenBank Database

(<http://ncbi.nlm.nih.gov/Blast>) for phylogenetic identification of the bacteria.

Biotransformation experiment with purified culture

Purified culture was tested for its biodegradability for 7-KC. Three replicate batches (30 ml) were prepared in M9 medium, with 7-KC as only carbon source they were inoculated with bacterial culture of the isolate and incubated at 30 °C and 150 rpm. Samples (0.5 ml) were taken from each batch after 24 hours time intervals and were subjected to extraction. 7-KC was then extracted from the samples with a mixture of hexane/isopropanol (3:2), the solvent was evaporated using a rotary evaporator (BÜCHI rotavapor R-200), sample was redissolved in 50 µL of methanol, filtered and was analyzed by reverse phase HPLC (0.72 ml min⁻¹, 85:10:5 methanol/water/acetonitrile) using a

Waters Delta 600 Separation Module with a Waters 2487 dual λ absorbance detector, photodiode array (235 nm) and a Phenomenex LUNA C18 column (4.6 by 150 mm).

Results

Isolation and identification of 7KC degrading bacteria from environmental samples

Using enrichment technique several bacterial colonies were isolated for the sample of manure pile. These colonies were purified and tested for their growth on M9 media with 7-KC as sole carbon and energy source (unpublished data). One isolate having good positive activity on these plates was selected and purified. The bacterial isolate was growing in M9 media with 7-KC as sole carbon and energy source.

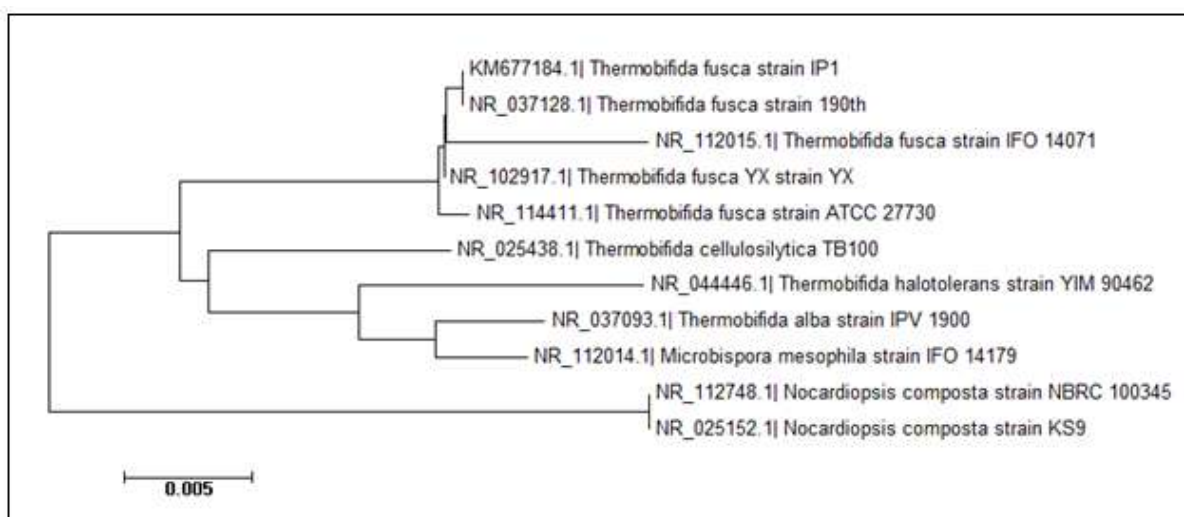


Fig. 1. Phylogenetic tree of *Thermobifidafusca* IP1 (accession number KM677184) isolated from manure piles.

Taxonomic characterization of the bacterial isolate IP1 was done. 16S rDNA gene was amplified and sequenced, sequences obtained were analysed by NCBI BLAST and phylogenetic tree was constructed (Fig. 1). The bacterial strain was identified as *Thermobifidafusca* (accession number KM677184).

Degradation of 7-KC by bacterial isolate Thermobifidafusca IP1

The growth of the bacterial isolate *Thermobifidafusca* IP1 was determined by increase in OD₆₀₀, results are shown in Fig. 2 there was a lag period of 3-6 hours after that gradual increase in

growth (Absorption at 600 nm) was observed. The OD₆₀₀ reached to a value of 0.8 in 30 hours. Degradation of 7-KC was monitored by HPLC. Within the set UV detection range of 190 to 400 nm, no accumulation of degradation metabolites was revealed. The absorption maximum for 7-KC is 233 nm, allowed accurate determination of 7-KC concentration.

On the basis of HPLC results, a rapid degradation was observed with *Thermobifidafusca* IP1 (Fig. 3, 4). There was gradual decrease in concentration of 7-KC from 1 g.L⁻¹ (initial concentration and reached to non

detectable concentration in 12 days). The strain IP1 cleared the 7KC 20% in 3 days, 85% in 6 days, 94% in 9 days and below detection levels in 12 days.

Discussion

Atherosclerosis, macular degeneration, and neurodegenerative diseases such as Alzheimer's disease, are associated with the intracellular

accumulation of recalcitrant substances that impair cellular function and viability (Rittmann and Schloendorn, 2007). Reversing this accumulation may be a valuable therapy, but the accumulating substances are refractory to normal cellular catabolism so there is need of an exogenous enzyme supply to clear these accumulated compounds (de Grey *et al.*, 2005).

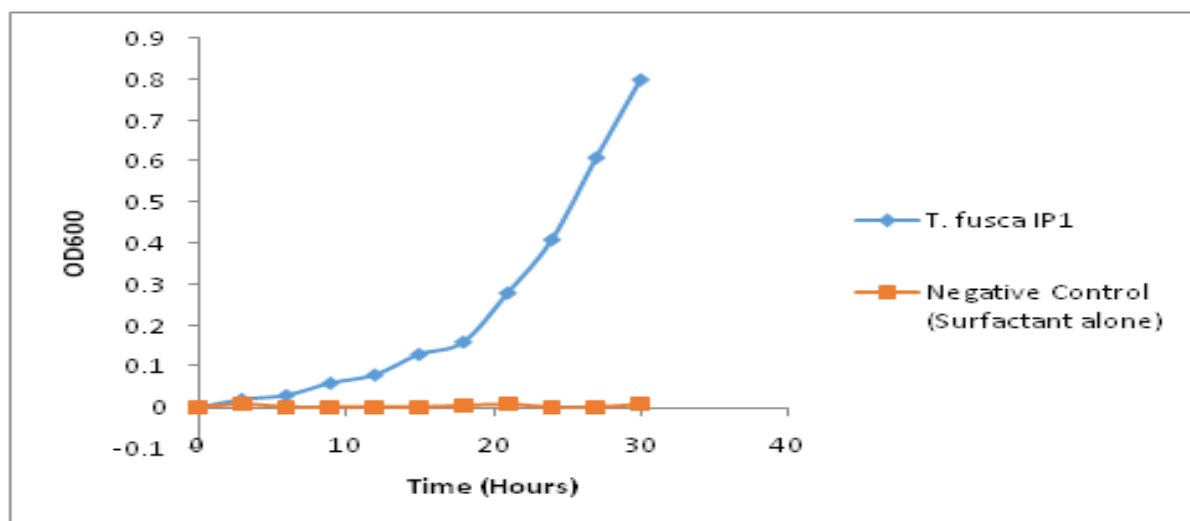


Fig. 2. Increase in OD600 of the isolate IP1 over a period of 30 hours. A negative control was run containing 7KC and surfactant only without IP1 inoculation.

On the other hand, these substances in ecosystem are naturally degraded in the soil and water by microorganisms. In environmental bioremediation, communities of microorganisms mineralize hydrophobic organics using a series of enzymes (Rittmann and Schloendorn, 2007). A radically new approach is augmenting humans' natural catabolic machinery with exogenous supply of microbial enzymes. Many recalcitrant organic molecules are naturally degraded in the soil. Since the soil in certain environments - graveyards, for example - is enriched in human remains but does not accumulate these substances, it presumably harbours microbes that successfully degrade and clear them up. The enzymes responsible could be identified and engineered to metabolise these substances *in vivo* (de Grey *et al.*, 2005).

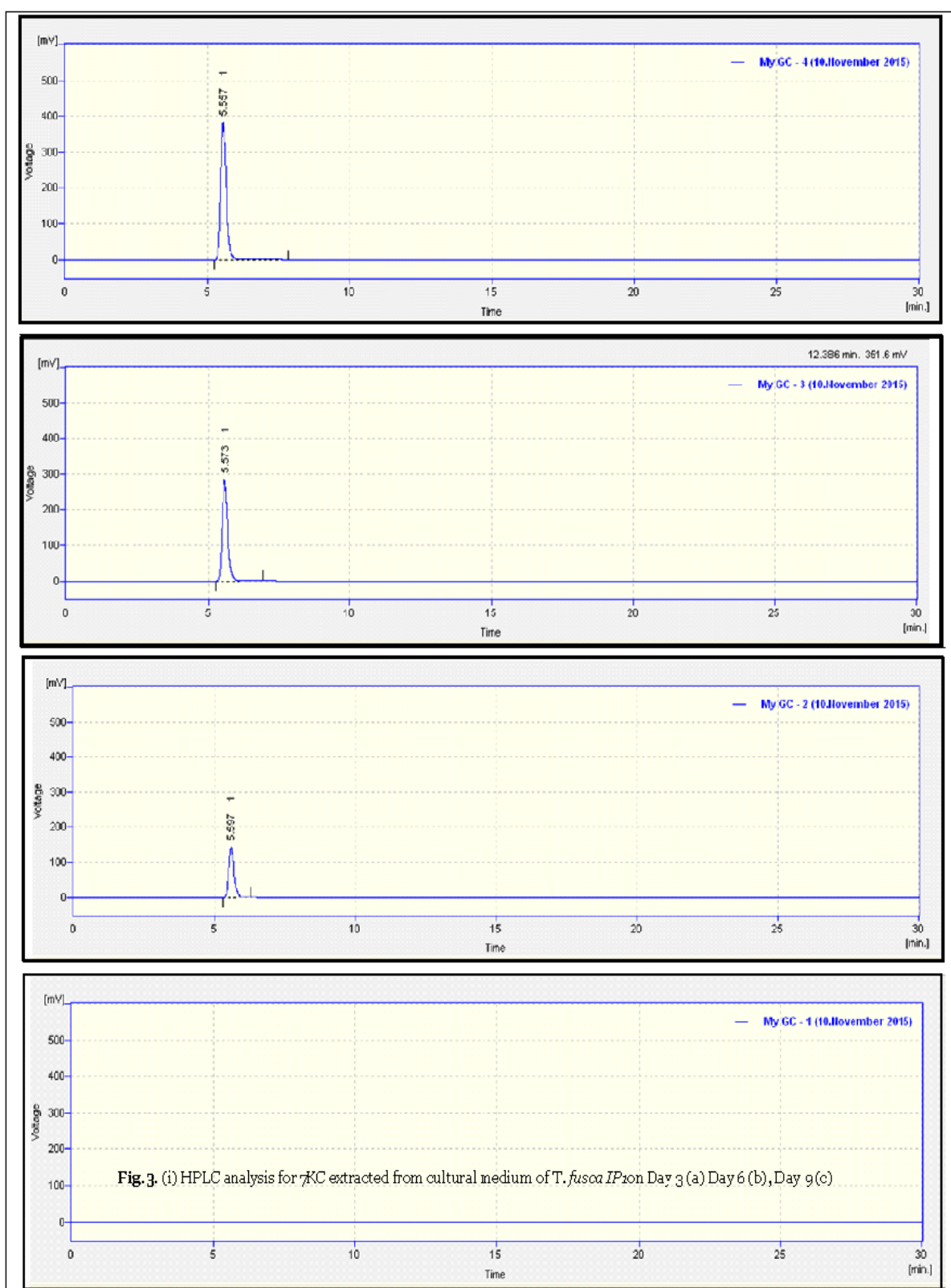
Due to its high concentration in atherosclerotic plaques (Garcia-Cruset *et al.*, 2001; Dreizen *et al.*,

1978), cytotoxicity, and other pro-atherogenic properties, 7KC is a prominent target for medical bioremediation. Contributing to the rationale for its elimination is that 7KC has also been associated with Alzheimer's disease by several studies (Vaya and Schipper, 2007; Casserly and Topol, 2004; Carter, 2007). The etiology of atherosclerosis is clearly a complex process, and 7KC certainly contributes. Thus reducing levels of 7KC may subsequently reduce the rate of LDL uptake and apoptosis, slowing atherosclerotic progression (Mathieu *et al.*, 2009).

In medical bioremediation, we hope to utilize single or a combination of microbial enzymes to degrade the intracellular recalcitrant compounds and convert them to innocuous products so that they can be cleared from the affected cells. Here, we present preliminary, but promising results for the bacterial biodegradation of 7-ketocholesterol, the main accumulator of foam cells associated with

atherosclerosis. In particular, we report on the isolation of bacterial strains found to effectively degrade 7-KC. All the isolates were capable of

utilizing 7KC as the sole organic substrate, resulting in its mineralisation, a key step towards identifying the key enzymes that may lead to a therapy.



We got several positive hits for 7KC biodegradation from environmental samples. One of isolate IP1 was further investigated for its 7KC biodegradation activity, and was identified as *Thermobifidafusca* on the basis of 16srDNA sequencing results. Several steroid degrading bacteria have been isolated from

soil samples previously (Merino *et al.*, 2013). On the basis of HPLC results, complete degradation was observed with isolate *Thermobifidafusca* IP1. The isolate removed the 7KC below detection levels within 12 days.

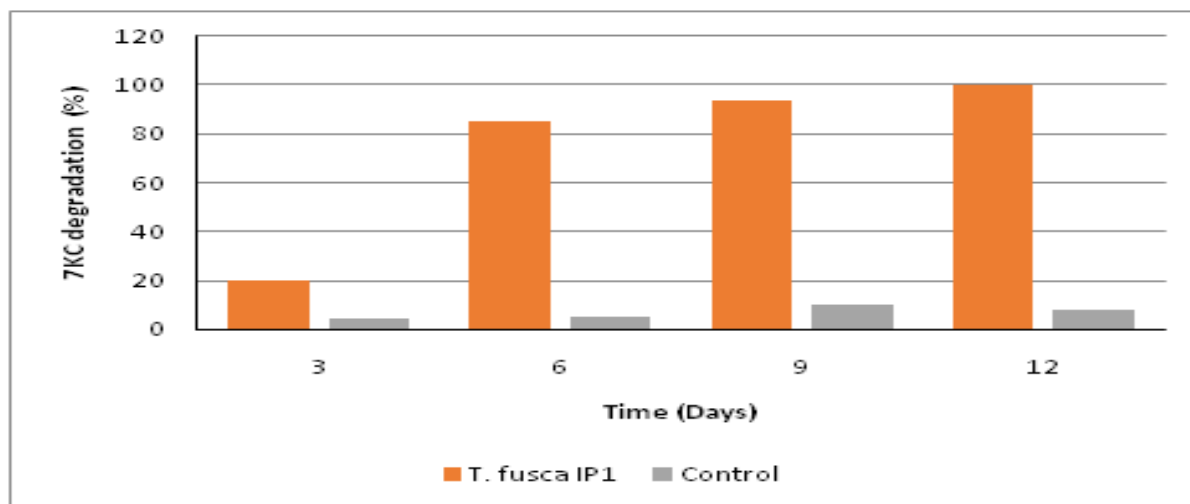


Fig. 4. HPLC analysis of 7KC degradation (experiment conducted at 30 °C, pH 7, 150 RPM) by environmental isolate, *Thermobifidafusca* IP1 in the 12-days incubation period. Three samples were run for isolate IP1 and the control.

7KC like Cholesterol is a steroid, i.e. a class of terpenoid lipids, an imbalance in their blood level causes serious diseases in humans. Bacterial degradation of steroids is widespread, many bacteria are capable of transforming steroids, and this property is used for the biotechnological production of steroid drugs (Bortolini *et al.*, 1997; Donova and Egorova, 2012; Mahato and Garai, 1997). In addition, bacteria from diverse phylogenetic groups can degrade naturally occurring steroids completely and use them as sources of carbon and energy (Holert *et al.*, 2013).

Bacteria belonging to the genera *Nocardia*, *Arthrobacter*, *Bacillus*, *Brevibacterium*, *Corynebacterium*, *Streptomyces*, *Microbacterium*, *Serratia*, *Achromobacter*, *Pseudomonas* or *Protaminobacter*, were reported to accomplish partial or complete cholesterol degradation (Whitmarsh, 1964; Brown and Peterson, 1966; Arima *et al.*, 1969; Ferreira and Tracey, 1984; Drzyzga *et al.*, 2009; 2011; Fernández de Las Heras *et*

al., 2009; Ge *et al.*, 2011).

Conclusion

In summary, we have found that isolated bacterial strain can degrade the oxysterol 7KC. The isolate demonstrated ability to utilize 7KC as sole carbon source. Overall, these results support the notion that oxysterol levels might be controlled by biodegradation processes, and further investigation of specific microbial enzymes involved in catabolism as well as the specific pathways involved in microbial 7KC degradation can be the next goals leading to come up with identifying enzymes capable of transforming oxysterols for potential environmental, industrial, pharmaceutical, and medical applications. This attempt at harnessing an exogenous enzyme to achieve the catabolic function of cells is in some ways similar to enzyme replacement therapies aimed at reversing lysosomal storage disease. 7-KC has been associated with numerous age-related and neurodegenerative diseases, and thus is an important therapeutic target. The biodegradation of 7KC and its

ultimate removal from body can serve as a mean to reverse disease conditions associated with its accumulation in body.

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