ORIGINAL ARTICLE

# Degradation of residual lincomycin in fermentation dregs by yeast strain S9 identified as *Galactomyces geotrichum*

**Lin Zhang · Yanli Shen · Fengli Hui · Qiuhong Niu**

**Abstract** Lincomycin is one of the most poorly degradable antibiotics in solid wastes from the fermentation process. Discharging solid wastes without appropriate treatment can indirectly threaten human health. To treat the lincomycin residuals in solid wastes effectively, some yeast strains with high degradation capabilities against lincomycin were screened from the environment in this study. The degradation efficiency of the most highly active strain, S9, reached 37 %. This strain was identified as *Galactomyces geotrichum*. The significance of this study lies in the biotransformation of solid wastes.

**Keywords** Lincomycin · Degradation · Yeast · Biotransformation

## Introduction

Antibiotics are used to treat numerous bacterial infections, but the lack of antibiotic degradation can theoretically lead to the development of multidrug-resistant strains, which can indirectly infect humans, causing increased morbidity and mortality (Randhawa and Kullar 2011). The ever-increasing presence of antibiotic-resistant bacteria has raised substantial concerns about the future effectiveness of antibiotics. In response,

studies have increasingly focused on environmental reservoirs of antibiotic resistance in recent years.

Lincomycin, which is a naturally occurring member of the lincosamide group of antibiotics, inhibits protein synthesis in Gram-positive bacteria and, to a lower degree, in Gram-negative bacteria (Vazquez 1974; Pestka 1977). The semisynthetic derivative clindamycin (CLI) is prescribed for the treatment of some infections caused by anaerobic bacteria and is also applied against the causative agent of malaria, *Plasmodium falciparum* (Lell and Kremsner 2002; Spizek and Rezanka 2004a). The Nanyang Pukang Group Chemical Pharmaceutical Factory in Henan, China, produces lincomycin hydrochloride as its main product, with an annual output of more than 15,000 t of fermentation dregs. During the biosynthesis of lincomycin by *Streptomyces lincolnensis*, the fermentation residue contains rich organic matter, such as proteins, carbohydrates, fats, and micro-scale lincomycin residues. According to the test results reported by the company, the detailed components of the fermentation dregs are 38 % crude proteins, 8.4 % crude fats, 7.1 % crude fibers, 5.3 % calcium, 0.9 % phosphorus, 17.02 % ash content, and 2,000 mg/kg of lincomycin. As an antibiotic with a very stable structure, lincomycin has steady physiochemical properties and is hard-degradable. Therefore, the fermentation residues pose a potential health risk. As biologically hazardous wastes, the large amount of fermentation residues must be disposed of and decontaminated by incineration, according to international and Chinese laws and regulations (Kummerer 2003); this requirement is a major problem in the production enterprise. Moreover, these fermentation residues of lincomycin can be transformed into good resources if treated effectively; however, this possibility has received little attention due to the refractory characteristics of lincomycin. Therefore, the isolation and screening of lincomycin-degrading microbes for the biodegradation of fermentation dregs is urgently needed.

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Yeasts are unicellular eukaryotic micro-organisms. These organisms are a source of protein and vitamins, particularly the B-complex vitamins. Specifically, some yeast strains can produce single-cell protein with corn starch or brewer's grain as the raw material. These yeasts can be used as fodder. These fodder yeasts can balance and increase the efficiency of the employed feedstuffs, promote animal growth and breeding, and improve the survival rate, the egg yield, and the growth rate.

Therefore, the isolation and screening of lincomycin-degrading yeasts for the transformation of waste fermentation dregs into high quality animal feed additives is important. In this paper, a yeast strain with a comparatively high capability of degrading lincomycin in fermentation dregs was isolated from biological pharmacy wastewater and soil samples in Nanyang city in Henan Province in China and identified as *Galactomyces geotrichum* based on phenotypic and genotypic characteristics. This paper is the first report concerning the biological degradation of residual lincomycin in waste dregs during the *S. lincolnensis* fermentation process. This study lays a theoretical foundation for the bioconversion of wastes from fermentation dregs.

## Materials and methods

### Isolation, screening, and culture conditions

Soil and water samples were collected from the waste fermentation residue storage locations, diluted, inoculated onto solid agar plates with lincomycin (1.2 g/ml) as the sole carbon and energy source, and cultured for 3 days at 28 °C. Some yeast strains that could grow on inorganic salt and lincomycin solid agar plates (100 ml of medium composed of 0.1 g of $KH_2PO_4$, 0.05 g of $KNO_3$, 0.01 g of $MgSO_4$, 0.01 g of $FeSO_4$, 0.6 g of lincomycin and 1.5 g of agar) were obtained. Among these yeasts, some may use agar as a carbon and energy source, and others may be the expected strains, which have the capability to degrade lincomycin.

### Biodegradation activity assay

For antibiotics, an agar plug method was successfully developed based on the sizes of the inhibition zones formed by an antibiotic against an indicator organism (Filtenborg and Frisvad 1980; Filtenborg et al. 1983; du Toit and Rautenbach 2000; Kumar et al. 2000; Bragulat et al. 2001). The advantage of the cylinder plate method lies in its low cost and its potential application in high-throughput screening procedures for determining the bioactivity of chemicals. Thus, the cylinder plate method was used to determine the lincomycin concentrations in the fermentation residues. The test organism used in the experiments was a strain of *Sarcina lutea* ATCC 93411, which was provided by the Nanyang Pukang Group Chemical Pharmaceutical Factory in Henan Province in China. The samples were prepared using the procedure described below. The fermentation dregs were collected from the Nanyang Pukang Group, and rice husk was added in accordance with the recommended ratio of approximately 3:1. The samples were homogeneously mixed and sterilized. The candidate yeast strains were initially cultured on yeast extract-mannitol (YM) medium plates at 28 °C for 3 days, and the strains were subsequently washed out using sterilized water from the plates. After washing three times using sterilized water, 1 ml of the suspension (approximately $10^6$ cells) was inoculated into the solid fermentation medium in an Erlenmeyer flask. After solid fermentation at 28 °C for 7–15 days, 50 ml of distilled water was added to the flask, stirred, and immersed for 24 h. The fermentation liquid was obtained by centrifugation at 12,000 rpm for 5 min, with subsequent filtration sterilization and assays for lincomycin concentration. Samples that were prepared using the same procedure without inoculation with microbes were used as controls.

To quantify the residual lincomycin further, the enzyme immunoassay method was used to perform a quantitative analysis of lincomycin in fermentation dregs using a lincomycin ELISA test kit (America, Beacon). The degradation efficiency was calculated using the formula $(C_0-C)/C_0 \times 100$ where $C_0$ and $C$ represents the lincomycin concentrations of the control and of the samples after fermentation with yeast strains, respectively.

### Identification of the strain

Morphological, physiological, and biochemical characteristics were examined using standard methods that are employed in yeast taxonomy (Yarrow 1998). All assimilation tests were performed three times, and the results were read after 5 and 21 days of incubation. The assimilation of nitrogen compounds was investigated in liquid media with starved inocula (Nakase and Suzuki 1986). The ability of the isolates to assimilate a variety of carbohydrate-source compounds was determined using the BIOLOG yeast identification system, according to the manufacturer's instructions. Total genomic DNA was isolated from stationary-phase cultures according to the method described by Makimura et al. (1994). The sequences of the D1/D2 domain of the LSU rRNA gene and the ITS region were determined using the methods of Kurtzman and Robnett (1998) and White et al. (1990), respectively. The primers NL1 (5′-GCATATCAATAAGCGGAGGAAAAG-3′) and NL4 (5′-GGTCCGTGTTTCAAGACGG-3′) were used to perform PCR, with the following cycling conditions: 5 min at 95 °C for the first denaturation, 35 cycles of 40 s at 95 °C, 40 s at 55 °C, and 30 s at 72 °C for amplification, and 10 min at 72 °C for extension. The PCR product was verified using

agarose gel electrophoresis, purified using the QIA Quick purification kit (Qiagen), and cycle-sequenced using the ABI BigDye Terminator Cycle sequencing kit, version 3.1 (Applied Biosystems). The sequences were determined using an ABI PRISM 3100 automated DNA sequencer (Applied Biosystems) according to the instructions of the manufacturer. The generated sequences were aligned with related species using the CLUSTAL_X version 1.8 software (Thompson et al. 1997). The phylogenetic trees were constructed from the evolutionary distance data calculated from Kimura's two-parameter model using the neighbor-joining method (Kimura 1980; Saitou and Nei 1987). Bootstrap analyses were performed based on 1,000 random resamplings (Felsenstein 1985). Reference sequences were retrieved from GenBank under the accession numbers indicated in the trees.

The GenBank accession numbers for the sequences of the D1/D2 domains of the large subunit rRNA gene and the ITS regions of the yeast strain S9 are JF701182 and JX291981, respectively.

## Results

### Screening results

Seven yeasts that used lincomycin as the sole source of carbon, nitrate, and energy were isolated from 12 soil samples and five water samples near the pharmaceutical factory in Nanyang, China. The strains were named S1, S9, W1, W3, W12, X5, and X8. After purification, the seven yeast strains were subjected to cylinder plate experiments to assess their degradation capabilities. The results are presented in Table 1. After fermentation for 7, 10, and 15 days, the inhibition zones of the negative cylinders on the plates filled with sterile water were 27.96, 29.97, and 29.99 mm, respectively, while the

**Table 1** Results of cylinder plate experiments after fermentation for different times

| Sample | Diameter of inhibition zone (mm) | | |
|---|---|---|---|
| | 7 days | 10 days | 15 days |
| S1 | 21.77 | 20 | 19.95 |
| S9 | 20.03 | 18.96 | 18.73 |
| W1 | 23.35 | 21.66 | 21.58 |
| W3 | 22.18 | 20.11 | 20.07 |
| W12 | 24.25 | 21.9 | 21.85 |
| X5 | 22.26 | 20.52 | 20.43 |
| X8 | 24.12 | 21.74 | 21.69 |
| ddH$_2$O | 27.96 | 29.97 | 29.99 |

diameters of the inhibition zones of the seven yeast strains ranged from 18.73 to 24.25 mm. These results are presented in Table 1, which suggests that the seven yeast strains had different lincomycin-degrading capabilities. Figure 1 presents the inhibition zones observed after different sample treatments during the cylinder plate experiments after fermentation for 15 days. According to Fig. 1, the plates with control cylinders developed pronounced and large inhibition zones. The test yeast strains on the plates exhibited comparatively small inhibition zones. The strains S9 and S1 exerted the weakest inhibitory effects, and the strains W12, X8, and W1 exerted the strongest inhibitory effects. These findings indicate that the yeast strains S1 and S9 had the greatest capabilities to degrade lincomycin. Yeast strain S9 was also grown in liquid inorganic salt medium (Sigma) containing 1.2 g/ml of lincomycin for 5 days at 28 °C, and growth was detected using a spectrophotometer to measure turbidity. The OD$_{600}$ value of this strain reached 0.8, while the control strain failed to grow in the medium at all (Fig. 2). This finding verified that isolate S9 exhibited the strongest lincomycin-degrading activity among the seven strains, as indicated by the results of the cylinder plate experiment.

### Enzyme-linked immunosorbent assay (ELISA) results

The ELISA method was used to perform a quantitative analysis of the drugs and quantify their degradable capabilities. The standard curve obtained during ELISA is presented in supplementary material. The initial concentration of lincomycin in the fermentation dregs was 5.012 ppb. The seven yeast strains were individually inoculated into the dregs, and after fermentation for different times, the degradation efficiency was assessed, as summarized in Table 2. The data presented in Table 2 demonstrate that the degradation rates of strains S9 and S1 reached 37.35 and 35.55 %, respectively, after fermentation for 15 days. This result demonstrated that these two strains degraded lincomycin most effectively. The lincomycin-degrading rates of the other five strains ranged from 20.75 % for W12 to 30.01 % for X5, as shown in Table 2. These results were consistent with those obtained in the cylinder plate experiments.

### Identification of the yeast strain

The strain S9, which had strong degradation capabilities, was subjected to polyphasic taxonomic analyses based on phenotypic characteristics and phylogenetic analysis. The colony morphology and microscopic structure of the strain are illustrated in Fig. 4. Colonies of strain S9 were white, flat, wrinkled, radial, and 4.0–5.0 cm in diameter after incubation for 2 weeks at 28 °C (Fig. 3a). The cells of strain S9 observed under the microscope were columnar,

**Fig 1** Inhibition zones observed after different sample treatments during cylinder plate experiments after fermentation for 15 days
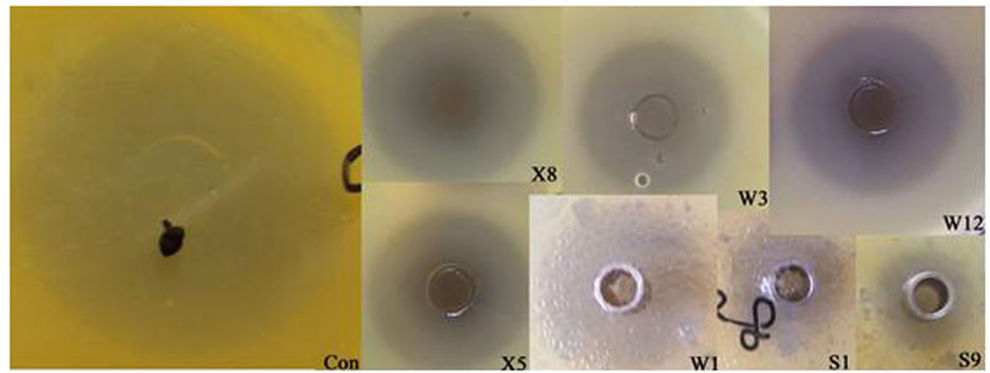


and the sizes of the cells were 1.6–2.4 μm wide by 1.6–4.9 μm long. In addition, random arthrospore fractures were easily observed (Fig. 3b).

The pH and temperature range for the growth of strain S9 were 2.0–8.0 and 4–36 °C, respectively. The optimum growth pH and temperature for the strain were 4.0 and 28 °C, respectively.

The following carbon compounds were fermented: D-glucose, D-galactose, L-sorbose, D-xylose, sucrose, methyl-D-glucoside, salicin, arbutin, ribitol, D-glucitol, D-mannitol, galactitol, D-glucono-1, 5-lactone, 2-keto-D-gluconate, D-gluconate, succinate, D-ribose, lactose, erythritol, 5-keto-D-gluconate, D-glucuronate, and ethanol. The other carbon compounds tested in this study, including D-glucosamine, L-arabinose, maltose, trehalose, melezitose, inulin, soluble starch, glycerol, xylitol, L-arabinitol, D-arabinose, L-rhamnose, cellobiose, melibiose, raffinose, myo-inositol, DL-lactate, citrate, and methanol, were not fermented.

A neighbor-joining tree based on the combined sequences of the D1/D2 domains of the LSU rRNA gene and the internal transcribed spacer (ITS) regions is presented in Fig. 4. Phylogenetic analysis revealed that the yeast strain S9 was located in the *Galactomyces* clade and included in a cluster with 24 strains of *G. geotrichum*, two strains of *Dipodascus australiensis*, two strains of undescribed *Galactomyces* species, and one strain of an undescribed *Dipodascaceae* species. The close relatives of three typical strains are *G. geotrichum* CBS 773.71[T], *Galactomyces citri-aurantii* CBS 175.89[T] and *Galactomyces reessii* CBS 179.60[T]. The ITS sequence of 773.71[T] differed from the S9 strain by two substitutions and two gaps.

Based on phenotypic characteristics and the sequences of the D1/D2 domain of the 26S rRNA gene and the ITS region, the strain S9 proved to be closely related to *G. geotrichum*. Therefore, this strain was identified as species *G. geotrichum* S9. The strain named S9 that mediated significant degradation of residual lincomycin in fermentation dregs was collected as No. CCTCC M 2012056 by the China Center for Type Culture Collection.

## Discussion

Lincomycin, which is a naturally occurring lincosamide, is active against many Gram-positive bacteria, such as *Streptococci* and *Staphylococci*. Most lincomycin is produced by fermentation. Many recent studies focused on improving the fermentation yield of lincomycin. Some major metabolic precursors have been isolated and identified (Kuo et al. 1992). The biosynthesis pathway and the genetic control of lincomycin fermentation were also described (Spizek and Rezanka 2004b). In addition, batch-type feeding of carbohydrates (Semenova et al. 1994), the use of olive oil as the sole carbon source (Choi et al. 2004), and phosphorus feeding (Li et al. 2007) individually improved the industrial fermentation of lincomycin. However, during the fermentation process, some residual lincomycin is present in the fermentation wastes, which causes the emergence of antibiotic-resistant strains and makes it difficult to use the fermentation wastes. Moreover, if the antibiotic is not degraded, it will eventually enter the environment, affecting microorganisms in the environment and disturbing natural elemental cycles. Watanabe et al. (2010) comprehensively evaluated the fate of antibiotics used in dairy operations under



**Fig 2** Growth in liquid, inorganic salt medium containing 1.2 g/ml of lincomycin for 5 days at 28 °C. *Left,* control; *Right,* S9 strain

**Table 2** Degradation efficiency results of different samples according to ELISA

| Sample | 10 days | | | 15 days | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | OD450 (%) | lgC | Degradation efficiency (%) | OD450 (%) | lgC | C (ppb) | Degradation efficiency (%) | OD450 (%) | lgC | C (ppb) | Degradation efficiency (%) |
| S1 | 0.1 | 0.564 | 26.9 | 0.126 | 0.515 | 3.273 | 34.7 | 0.129 | 0.509 | 3.23 | 35.55 |
| S9 | 0.12 | 0.526 | 33.02 | 0.131 | 0.512 | 3.25 | 35.16 | 0.1352 | 0.497 | 3.14 | 37.35 |
| W1 | 0.088 | 0.587 | 22.91 | 0.092 | 0.5796 | 3.798 | 24.22 | 0.098 | 0.568 | 3.698 | 26.21 |
| W3 | 0.098 | 0.568 | 26.22 | 0.101 | 0.562 | 3.648 | 27.21 | 0.107 | 0.551 | 3.556 | 29.05 |
| W12 | 0.071 | 0.62 | 16.82 | 0.079 | 0.605 | 4.03 | 19.59 | 0.082 | 0.599 | 3.972 | 20.75 |
| X5 | 0.093 | 0.5777 | 24.54 | 0.099 | 0.5662 | 3.683 | 26.52 | 0.11 | 0.545 | 3.508 | 30.01 |
| X8 | 0.082 | 0.5988 | 20.79 | 0.09 | 0.583 | 3.828 | 23.62 | 0.094 | 0.576 | 3.767 | 24.84 |
| Control | 0.0291 | 0.7 | | 0.0291 | 0.7 | 5.012 | | 0.0291 | 0.7 | 5.012 | |

relatively vulnerable groundwater conditions, and he detected lincomycin in shallow groundwater directly downgradient from the lagoons . The analysis of soil and water samples permitted the researchers to assess the potential for the off-site migration and degradation of antibiotics. Therefore, the biodegradation of the residual lincomycin and the biotransformation of these wastes are important topics of study.

The currently available remediation methods for pharmaceutical wastes are usually expensive and may convert one toxic pollutant to another. Bioremediation methods use naturally occurring microorganisms to detoxify pollutants by converting pollutants to innocuous and useful products (Randhawa and Kullar 2011). Manure from different sources was reported to exhibit high activity for degrading antimicrobial agents, including chlortetracycline (Runsey et al. 1977), sulfadiazine (Ingerslev and Halling-Sorensen 2000), erythromycin, streptomycin, penicillin, bacitracin (Gavalchin and Katz 1994), enrofloxacin (Wetzstein et al. 1997), and cyclosporin A (Thiele-Bruhn 2003), due to the presence of known coprophilous basidiomycetes, such as strain NRRL 6464 and a strain identified as *Cyathus stercoreus* that was isolated from aged cattle dung by Wicklow and colleagues two decades ago (Wicklow et al. 1980; Wicklow 1992). The bacterium *Alcaligenes paradoxus* was demonstrated to degrade the pesticides 2,4-dichlorophenoxyacetic acid and 2-methyl-4-chlorophenoxyacetic acid due to its pJP1 plasmid (Fisher et al. 1978). A *Flavobacterium* sp. (strain 50001) could degrade 2, 4-dichlorophenoxyacetate (2, 4-D), 2-methyl-4-chlorophenoxyacetate, and 2-chlorobenzoate because the bacteria harbored the degradative plasmid pRC10 (Chaudhry and Huang 1988). Two plasmids of approximately 60 and 100 kilobases were potentially associated with the capability to degrade bromacil in strain 50235 of the Gram-negative bacterium *Pseudomonas* sp. (Chaudhry and Cortez 1988). From the researches above, we could see that the successful microorganisms degrading antibiotics mainly come from fungi and bacteria. However, very little information about yeast strains was reported to carry out bioremediation of antibiotics.

Only a small number of researchers have reported on the mechanism of biodegradation. The genome of the quinaldine-degrading bacterium *Arthrobacter* sp. Rue61a was completely sequenced and analyzed to identify the molecular mechanism of biodegradation (Niewerth et al. 2012). Bacteria capable of degrading a variety of aromatic compounds were identified, and the pathways involved in the degradation process were extensively characterized (Timmis et al. 1994; Diaz 2004). During degradation, peripheral enzymes, particularly
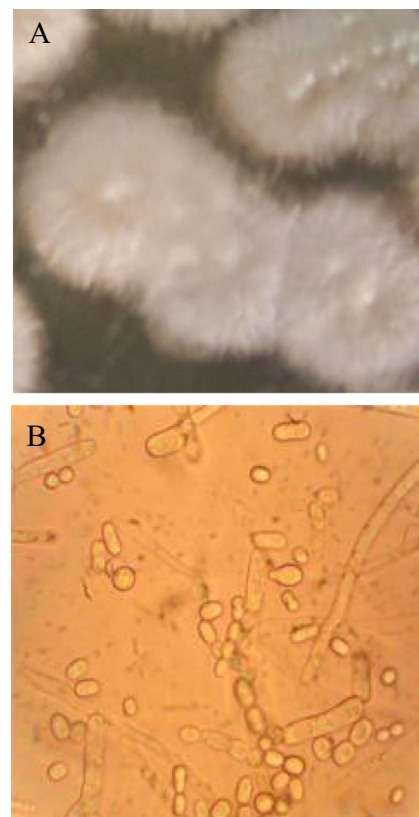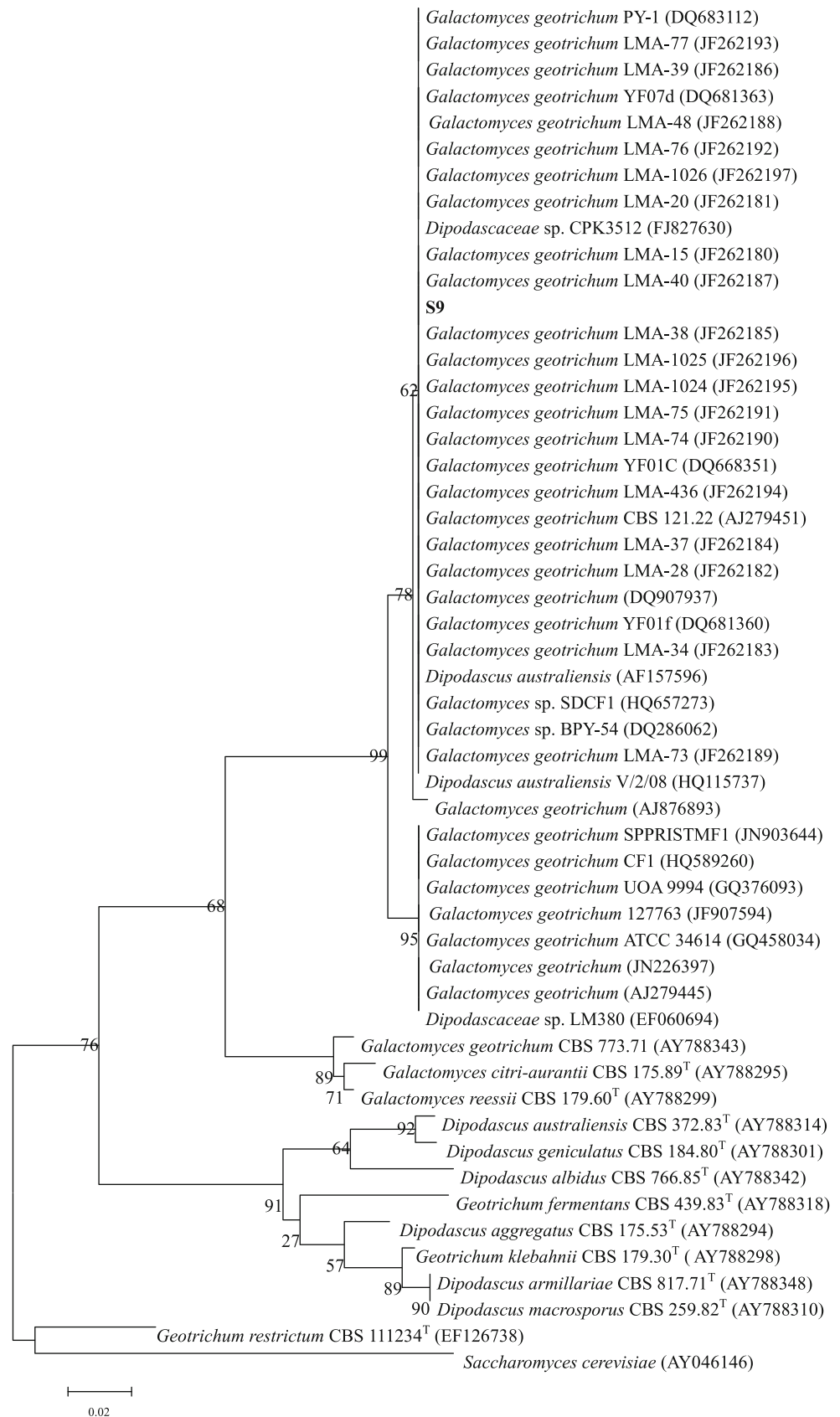


**Fig 3** Colony morphology and microscopic structure of the strain S9. **a** colony morphology; **b** microscopic structure. Image was taken at 400X

**Fig 4** Neighbor-joining tree
based on the combined sequences
of the D1/D2 domains of the LSU
rRNA gene and the ITS regions

*Galactomyces geotrichum* PY-1 (DQ683112)
*Galactomyces geotrichum* LMA-77 (JF262193)
*Galactomyces geotrichum* LMA-39 (JF262186)
*Galactomyces geotrichum* YF07d (DQ681363)
*Galactomyces geotrichum* LMA-48 (JF262188)
*Galactomyces geotrichum* LMA-76 (JF262192)
*Galactomyces geotrichum* LMA-1026 (JF262197)
*Galactomyces geotrichum* LMA-20 (JF262181)
*Dipodascaceae* sp. CPK3512 (FJ827630)
*Galactomyces geotrichum* LMA-15 (JF262180)
*Galactomyces geotrichum* LMA-40 (JF262187)
**S9**
*Galactomyces geotrichum* LMA-38 (JF262185)
*Galactomyces geotrichum* LMA-1025 (JF262196)
*Galactomyces geotrichum* LMA-1024 (JF262195)
*Galactomyces geotrichum* LMA-75 (JF262191)
*Galactomyces geotrichum* LMA-74 (JF262190)
*Galactomyces geotrichum* YF01C (DQ668351)
*Galactomyces geotrichum* LMA-436 (JF262194)
*Galactomyces geotrichum* CBS 121.22 (AJ279451)
*Galactomyces geotrichum* LMA-37 (JF262184)
*Galactomyces geotrichum* LMA-28 (JF262182)
*Galactomyces geotrichum* (DQ907937)
*Galactomyces geotrichum* YF01f (DQ681360)
*Galactomyces geotrichum* LMA-34 (JF262183)
*Dipodascus australiensis* (AF157596)
*Galactomyces* sp. SDCF1 (HQ657273)
*Galactomyces* sp. BPY-54 (DQ286062)
*Galactomyces geotrichum* LMA-73 (JF262189)
*Dipodascus australiensis* V/2/08 (HQ115737)
*Galactomyces geotrichum* (AJ876893)
*Galactomyces geotrichum* SPPRISTMF1 (JN903644)
*Galactomyces geotrichum* CF1 (HQ589260)
*Galactomyces geotrichum* UOA 9994 (GQ376093)
*Galactomyces geotrichum* 127763 (JF907594)
*Galactomyces geotrichum* ATCC 34614 (GQ458034)
*Galactomyces geotrichum* (JN226397)
*Galactomyces geotrichum* (AJ279445)
*Dipodascaceae* sp. LM380 (EF060694)
*Galactomyces geotrichum* CBS 773.71 (AY788343)
*Galactomyces citri-aurantii* CBS 175.89$^T$ (AY788295)
*Galactomyces reessii* CBS 179.60$^T$ (AY788299)
*Dipodascus australiensis* CBS 372.83$^T$ (AY788314)
*Dipodascus geniculatus* CBS 184.80$^T$ (AY788301)
*Dipodascus albidus* CBS 766.85$^T$ (AY788342)
*Geotrichum fermentans* CBS 439.83$^T$ (AY788318)
*Dipodascus aggregatus* CBS 175.53$^T$ (AY788294)
*Geotrichum klebahnii* CBS 179.30$^T$ (AY788298)
*Dipodascus armillariae* CBS 817.71$^T$ (AY788348)
*Dipodascus macrosporus* CBS 259.82$^T$ (AY788310)
*Geotrichum restrictum* CBS 111234$^T$ (EF126738)
*Saccharomyces cerevisiae* (AY046146)

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oxygenases and dehydrogenases, were found to transform structurally diverse aromatic compounds into one of these central intermediates by mediating the hydroxylation of the aromatic nucleus; thus, it is believed that bacteria developed these enzymes to extend their substrate range (van der Meer et al. 1992; Arora et al. 2009). However, little information is available concerning the effective biodegradation or bioremediation of fermentation residual lincomycin.

Actually, because of their rich nutrient and low virulence, yeasts can find potential application in the field of bioremediation. The aim of this paper was to screen yeast strains with high capabilities to degrade lincomycin in fermentation waste dregs. We obtained a yeast strain named S9, and this strain was identified as *G. geotrichum*, which uses lincomycin as single carbon source and degrades lincomycin efficiently. The proposed application of this strain is to use waste to produce yeast biomass as fodder. Given that residual lincomycin in fermentation dregs is a hard-biodegradable pollutant in aquatic and soil systems, and also facilitates the development of lincomycin-resistant strains, to select stains for lincomycin pollution control is meaningful. We are sure that our study can be useful for reducing residual lincomycin in fermentation dregs. The results of this study lay a solid foundation for the biological transformation of fermentation waste dregs. We are currently attempting to identify the enzymes that degrade lincomycin and the molecular mechanism of degradation, which will have important implications for antibiotic resistance and therapy.

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