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ORIGINAL PAPER

Streptomyces zhihengii sp. nov., isolated from rhizospheric soil of *Psammosilene tunicoides*

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Abstract An actinomycete strain, designated YIM T102^T, was isolated from the rhizospheric soil of *Psammosilene tunicoides* W. C. Wu et C. Y. Wu collected from Lijiang, Yunnan Province, China. The taxonomic position of the new isolate was investigated by a polyphasic approach. Phylogenetic analyses based on 16S rRNA gene sequences indicated that strain YIM T102^T belongs to the genus *Streptomyces*. Strain YIM T102^T was most closely related to *Streptomyces eurocidicus* NRRL B-1676^T with a pairwise 16S rRNA gene sequence similarity of 98.9 %. However, DNA–DNA relatedness value between strain YIM T102^T and *S. eurocidicus* NBRC 13491^T was found to be 37.8 ± 1.8 %. The menaquinone composition detected for strain YIM T102^T was MK-9 (H_6) and MK-9 (H_8), while the major fatty acids were summed feature 4 (38.0 %), anteiso-$C_{15:0}$ (13.1 %), iso-$C_{16:0}$ (10.1 %), summed feature 3 (9.8 %) and $C_{16:0}$ (9.0 %) and iso-$C_{15:0}$ (5.2 %). The whole-cell hydrolysates contained galactose, glucose, ribose and mannose, along with LL-diaminopimelic acid as the diagnostic diamino acid in the peptidoglycan. The DNA G+C content was 70.7 mol%. Strain YIM T102^T also exhibited antagonistic activity against *Alternaria alternata*, *Alternaria brassicae* and *Colletotrichum nicotianae* Averna, based on the findings from the comparative analyses of phenotypic and genotypic characteristics; it is proposed that strain YIM T102 represents a novel species of the genus *Streptomyces*, for which the name *Streptomyces zhihengii* sp. nov. is proposed. The type strain is YIM T102^T (=KCTC 39115^T = DSM 42176^T = CGMCC 4.7248^T).

Keywords *Streptomyces zhihengii* sp. nov. · Rhizosphere soil · Lijiang · *Psammosilene tunicoides*

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Introduction

The genus *Streptomyces* was first proposed by Waksman and Henrici (1943). Since then, more than 700 species with validly published names have been reported (http://www.bacterio.net/index.html, 2016). The genus *Streptomyces* remains a unique source for novel antibiotics, novel bioactive products and pharmacologically active compounds (Watve et al. 2001; Abdalla et al. 2010; Goodfellow and Fiedler 2010; Rateb et al. 2011a, b; Kim et al. 2012a; Hayakawa et al. 2015; Také et al. 2015). Till date, more researchers focused on isolating novel *Streptomyces* from

special habitats including hot springs, marine sediments, medicinal plants or their rhizospheric soil and speleothem, with the view for isolating new therapeutic compounds or secondary metabolites from novel strains (Liu et al. 2013; Carmona-Novillo et al. 2014; Han et al. 2015; Khieu et al. 2015; Marta et al. 2015). As part of a study focusing on isolation of actinomycetes from traditional and precious Chinese herbal and medicinal plants, roots and rhizospheric soil samples of *Psammosilene tunicoides* in Yunnan, China, were collected. More than 300 actinomycete strains were isolated during the process, of which many were found to belong to the genus *Streptomyces*. The isolate YIM T102^T was one such *Streptomyces* strain isolated from rhizospheric soil. The strain YIM T102^T was characterized by phenotypic, chemotaxonomic and phylogenetic analysis. Based on the findings of the polyphasic study, isolate YIM T102^T is characterized as a novel species of the genus *Streptomyces*.

Materials and methods

Isolation and culture conditions

For the isolation of actinobacteria from the rhizospheric soil of *P. tunicoides*, 2 g of soil sample collected from Lijiang was pretreated at 50 °C for 2 h and taken into a conical flask containing 18 mL sterile water and several glass beads. The mixture was kept incubated under shaken conditions (28 °C, 200 rpm, 2 h). The sample suspensions were then diluted 100-fold, and 200 μL of the diluted suspension spread on oatmeal agar (International *Streptomyces* Project medium 3 or ISP 3; Shirling and Gottlieb 1966) plate. The isolation media were supplemented with nalidixic acid (25 mg L^{-1}) and nystatin (50 mg L^{-1}) to inhibit growth of fastidious bacteria and fungi. The plates were incubated at 28 °C for 15 days. Purified strain YIM T102^T was routinely cultured on yeast extract–malt extract agar (ISP 2) medium (Shirling and Gottlieb 1966) at 28 °C and stored as a glycerol suspension (20 %, w/v) at −80 °C.

The reference type strain *Streptomyces eurocidicus* NBRC 13491^T was obtained from NITE Biological Resource Center (NBRC), Japan. The strain was maintained routinely on ISP 2 medium (28 °C, 7 days). Biomass of strain YIM T102^T and the reference type strain for chemical and molecular tests was harvested from cultures grown on ISP 2 and/or tryptic soy broth (TSB, Difco) (28 °C, 6 days).

Phenotypic characteristics

Morphological and cultural characteristics were tested on ISP 2, ISP 3, inorganic salts-starch agar (ISP 4), glycerol–asparagine agar (ISP 5) (Shirling and Gottlieb 1966), potato dextrose agar (PDA), Czapek's agar and nutrient agar (Waksman 1967). The colors of the colony were determined by using the ISCC-NBS color charts (Kelly 1964). The morphological characteristics of strain YIM T102^T were observed by a light microscope (BH-2; Olympus, Tokyo, Japan) and scanning electron microscopy (ESEM-TMP) from the cultures grown on ISP 2 medium at 28 °C for 7 days. The spore chain morphology, spore size and surface ornamentation of isolate were observed. Growth at various NaCl concentrations (0–12 % w/v, at intervals of 1 % units) and different temperatures (10–60 °C, at intervals of 5 °C units) was examined by growing the strain on ISP 2 plates. The pH range for growth [4–12, at intervals of 1 pH unit prepared by using the buffer system as described by Xu et al. (2005)] was tested at 28 °C for 30 days by culturing the strains with ISP 2 broth. Activities of oxidase, catalase and urease, gelatin liquefaction, milk peptonization and coagulation, nitrate reduction, H_2S production, degradation of tweens 20, 40, 60 and 80, starch and cellulose were investigated according to the conventional procedures described by Williams et al. (1989) and Gordon et al. (1974). Carbon source utilization tests were performed according to the methods described by Shirling and Gottlieb (1966) and Athalye et al. (1985) using modified basal medium recommended by Pridham and Gottlieb (1948). Nitrogen sources utilization was observed according to Nie et al. (2012). Other physiological and biochemical characteristics were assessed by using the media and methods described by Gordon et al. (1974). Antibiotic susceptibility tests were performed by using antibiotic disks (μg per disk, unless indicated otherwise): amikacin (30), cefuroxime sodium (30), chloramphenicol (30), ciprofloxacin (5), erythromycin (15), ethylhydrocupreine (5), tetracycline (30), gentamicin (10), norfloxacin (10), novobiocin (30), oxacillin (1), penicillin (10 IU), piperacillin (100), polymyxin B (300 IU) sulfamethoxazole (300) and vancomycin (30). Disks were placed on ISP 2 agar plates spread with strain YIM T102, and the plates were incubated at 28 °C for 3 days.

Chemotaxonomy

Chemotaxonomic characteristics were determined following the standard procedures. The isomer of diaminopimelic acid of cell wall and sugars of whole-cell hydrolysates were analyzed as described by Hasegawa et al. (1983), Staneck and Roberts (1974) and Tang et al. (2009). Polar lipids were extracted, separated by two-dimensional thin-layer chromatography (TLC) and identified using the described procedures (Minnikin et al. 1979; Collins and Jones 1980). Menaquinones were extracted from lyophilized cells as described by Collins et al. (1977) and

Minnikin et al. (1984) and analyzed by HPLC (Kroppenstedt 1982; Hu et al. 2001). For analysis of cellular fatty acids, strains YIM T102^T and *S. eurocidicus* NBRC 13491^T were cultured under shaking condition using TSB medium (180 rpm, 7 days, 28 °C). The cellular fatty acids were extracted, methylated and analyzed by using the protocol of the Sherlock Microbial Identification System (MIDI) (Sherlock Version 6. 1; MIDI database: TSBA6) (Sasser 1990). The G+C content of the genomic DNA was determined by HPLC (Mesbah et al. 1989) using *Escherichia coli* JM-109 as the reference strain.

Molecular analysis

Genomic DNA extraction and PCR amplification of the 16S rRNA gene sequences were performed as described by Li et al. (2007). The amplicon was purified using a Sangon PCR purification kit (China). Purified PCR amplicon was sequenced in Sangon Biotech, Shanghai, using the Sanger sequencing method. The full-length 16S rRNA gene sequence of strain YIM T102^T was compared with cultured species from NCBI database via BLAST search (Altschul et al. 1990) and EzTaxon-e server database (Kim et al. 2012b). Multiple sequence alignments were performed using the CLUSTAL_X software package (Thompson et al. 1997). The Kimura two-parameter model (Kimura 1980, 1983) was used to calculate evolutionary distance. Phylogenetic trees were constructed by the neighbor-joining (Saitou and Nei 1987), maximum-likelihood (Felsenstein 1981) and maximum-parsimony (Fitch 1971) tree-making algorithms using the software packages MEGA version 5.0 (Tamura et al. 2011). Bootstrap analysis with 1000 resamplings was used to evaluate the topology of each tree (Felsenstein 1985). DNA–DNA relatedness was studied by applying the fluorometric micro-well method (Ezaki et al. 1989; Christensen et al. 2000; He et al. 2005) at the optimal hybridization temperature (50 °C). The experiments were set with eight replications between strain YIM T102^T and the reference type strain *S. eurocidicus* NBRC 13491^T.

Antimicrobial assay

Strain YIM T102^T was evaluated for antimicrobial activities against seven test fungi and bacteria: *Alternaria alternata*, *Alternaria brassicae*, *Colletotrichum nicotianae* Averna, *Escherichia coli*, *Monilia albican*, *Pseudomonas aeruginosa* and *Staphylococcus aureus* Rosenbach, by dual-culture antagonistic bioassay method. The test organisms were obtained from Yunnan Institute of Microbiology, Yunnan University, China. Sterile disks (8 mm diameter) were impregnated with cultures of strain YIM T102^T grown on ISP 2 agar (5 days, 28 °C). The culture disks were then placed at the center of PDA agar plates previously spread with test organism, viz. *Alternaria alternata*, *Alternaria brassicae*, *Colletotrichum nicotianae* Averna, *Staphylococcus aureus* Rosenbach, and LB agar plates with *Escherichia coli*, *Monilia albican* and *Pseudomonas aeruginosa*. All plates were incubated at 28 °C for 5 days. All the assays were performed in triplicate.

Results and discussion

YIM T102^T grew well on ISP 2, ISP 3 and PDA, moderately on ISP 4, ISP 5 and Czapek's agar, and weakly on nutrient agar. Aerial mycelium was produced on all tested media. Colors of the substrate mycelium varied between white, yellow-white, yellow-green cream-white or yellow, while the aerial mycelium had cream-white, white, light gray, medium gray or deep gray colors on the tested media. No diffusible pigment was produced on all media (Supplementary Table S1). A week-old culture of strain YIM T102^T had morphological properties typical of the genus *Streptomyces* such as abundant aerial hyphae and vegetative mycelium, long spore chains with rhabditiform-shaped spores having smooth surfaces (Supplementary Fig. S1).

Growth was observed at 0–9 % (NaCl, w/v) (optimum 1–3 %), 10–40 °C (optimum 25–30 °C) and pH 6–9 (optimum pH 7). The strain was found to be positive for oxidase and catalase tests, but negative for urease activity. It gave positive results for coagulation and peptonization of milk, hydrolysis of starch, cellulose and gelatin, while negative results for nitrate reduction and H_2S production tests. The strain could degrade Tweens 20, 40, 60 and 80. The strain was susceptible to the following antibiotics: amikacin, cefuroxime sodium, chloramphenicol, ciprofloxacin, tetracycline, gentamicin, novobiocin, penicillin, piperacillin, polymyxin B, sulfamethoxazole and vancomycin, while resistant to erythromycin, ethylhydrocupreine, norfloxacin and oxacillin. Characteristics that differentiate strain YIM T102^T phenotypically from its closest related strain are listed in Table 1. The detailed physiological characteristics of strain YIM T102^T are given in species description.

The diagnostic cell wall diamino acid of the strain YIM T102^T was LL-diaminopimelic acid (LL-DAP), while glycine was also found in the peptidoglycan. The whole-cell sugars consisted of glucose, mannose, ribose and galactose. The polar lipids of strain YIM T102^T comprised of diphosphatidylglycerol, phosphatidyl methyl ethanolamine, phosphatidylglycerol, phosphatidylinositol, phosphatidylinositol mannosides and three unidentified phospholipids (Supplementary Fig. S2). The respiratory menaquinones of strain YIM T102^T were found to be MK-9 (H_6) and MK-9 (H_8). The fatty acids profile (>5 %) was summed feature 4 comprising iso-$C_{17:1}$ I and/or anteiso-$C_{17:1}$ B (38.0 %), anteiso-$C_{15:0}$ (13.1 %), iso-$C_{16:0}$ (10.1 %), summed feature 3

Table 1 Differential characteristics between strains YIM T102^T and *S. eurocidicus* NBRC 13491^T

Characteristics	1	2
Fatty acids		
Iso-$C_{14:0}$	3.6	1.13
Iso-$C_{15:0}$	5.16	11.34
Anteiso-$C_{15:0}$	13.06	19.32
Iso-$C_{16:0}$	10.12	5.38
$C_{16:0}$	8.97	5.17
Iso-$C_{17:0}$	1.84	3.96
Anteiso-$C_{17:0}$	3.27	9.47
Anteiso-$C_{17:1}$ $\omega 9c$	0	1.89
$C_{17:1}$ $\omega 8c$	0.63	0
Sum in feature 3[†]	9.82	3.07
Sum in feature 4[†]	37.96	31.09
Utilization of		
L-arabinose	−	+
Dulcitol	−	+
D-fructose	−	+
Lactose	−	+
D-maltose	−	+
Sorbinose	−	+
D-sucrose	−	+
D(+)-xylose	−	+
L-lysine	+	−
L-tryptophan	+	−
Biochemical tests		
Oxidase	+	−
Cellulose degradation	+	−
H_2S production	−	+
Growth conditions		
NaCl range (%, w/v)	0–9	0–6
pH range	4–9	4–10

Data obtained during this study were carried out under identical growth conditions

1, YIM T102^T; 2, *S. eurocidicus* NBRC 13491^T

+, Positive, utilized; −, negative, not utilized

[†] Summed features represent two or three fatty acids that cannot be separated by the Microbial Identification System. Summed feature 3 consisted of $C_{16:1}\omega 7c$ and/or $C_{16:1}\omega 6c$, while summed feature 4 comprised of iso-$C_{17:1}$ I and/or anteiso-$C_{17:1}$ B

comprising $C_{16:1}\omega 7c$ and/or $C_{16:1}\omega 6c$ (9.8 %), $C_{16:0}$ (9.0 %) and iso-$C_{15:0}$ (5.2 %). Detailed fatty acid profiles of strain YIM T102^T and the reference type strain are shown in Table 1. The DNA G+C content of strain YIM T102^T was determined to be 70.7 mol%, which is in accordance with the level for the genus *Streptomyces* (67–78 mol%).

To determine the phylogenetic position, full-length 16S rRNA gene sequence (1518 nt; accession number KU936048) of strain YIM T102^T was determined. Comparison of the sequence with the corresponding 16S rRNA gene sequences retrieved from GenBank/EMBL/DDBJ clearly demonstrated that strain YIM T102^T was a member of the genus *Streptomyces* with highest sequence similarity with *S. eurocidicus* NBRC 13491^T. In the neighbor-joining phylogenetic tree (Fig. 1), strain YIM T102^T formed a clade with five *Streptomyces* strains, but their 16S rRNA gene sequence similarities were less than 98.5 % except for *S. eurocidicus* NBRC 13491^T (98.9 % similarity). This phylogenetic relationship was also supported in the trees generated with maximum-parsimony phylogenetic tree and maximum-likelihood phylogenetic tree. Based on the phylogenetic analyses, sequence similarities profile and recommendation of Stackebrandt and Ebers (2006), the strain *S. eurocidicus* NBRC 13491^T was considered for DNA–DNA hybridization study with strain YIM T102^T. DNA–DNA relatedness value between strain YIM T102^T and the type strains *S. eurocidicus* NBRC 13491^T was determined to be 37.8 ± 1.8 %, which was notably lower than the threshold value (70 %) for the recognition of genomic species (Stackebrandt and Goebel 1994).

Strain YIM T102^T exhibited antagonistic activity against the fungi *Alternaria alternata*, *Alternaria brassicae* and *Colletotrichum nicotianae* Averna, but not against *Escherichia coli*, *Monilia albican*, *Pseudomonas aeruginosa* or *Staphylococcus aureus* Rosenbach.

The phylogenetic analysis, morphological and chemotaxonomic characteristics support the characterization of strain YIM T102^T as a member of the genus *Streptomyces*. However, the differences in biochemical characteristics, DNA–DNA relatedness values and fatty acid compositions distinguish strain YIM T102^T from its closest related strain *S. eurocidicus* NBRC 13491^T. Therefore, based on these results, strain YIM T102^T is considered to represent a novel species of genus *Streptomyces*, for which the name *Streptomyces zhihengii* sp. nov is proposed.

Description of *Streptomyces zhihengii* sp. nov

Streptomyces zhihengii (zhi.hen'gi.i. N.L. gen. masc. n. *zhiheng* of Zhi-Heng, to Honor Zhi-heng Liu, a respected Chinese microbiologist, for his enormous contributions to the development of Streptomyces taxonomy in China).

Cells are Gram-staining positive and aerobic. Forms extensively branched substrate and aerial mycelia. Substrate mycelia range its colors from white, yellow-white, yellow-green, cream-white to yellow, while aerial mycelia are cream-white, white, light gray, medium gray or deep gray colors on tested media. No diffusible pigments are produced on the media tested. Growth occurs at 10–40 °C, pH 6.0–9.0 and in the presence of up to 9 % (w/v) NaCl. Utilizes cellobiose, D-galactose, D-glucose, maltose,

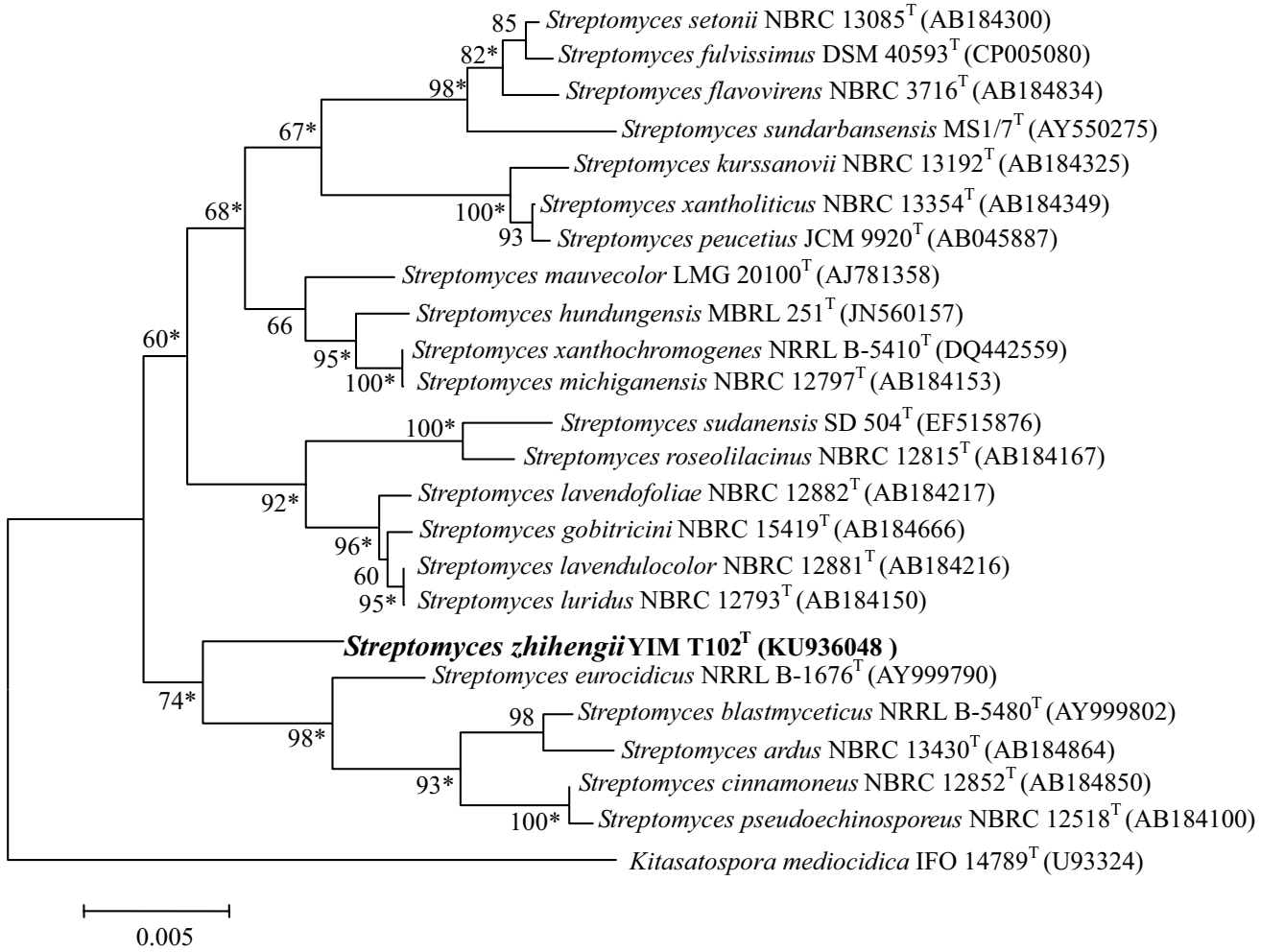

Fig. 1 Neighbor-joining phylogenetic tree showing the phylogenetic relationship of strain YIM T102^T and other closely related *Streptomyces* species based on 16S rRNA gene sequences. *Asterisks* indicate branches that were also recovered using the maximum-parsimony and maximum-likelihood methods. Bootstrap values (expressed as percentages of 1000 replications) of above 50 % are shown at branch points. *Bar* 0.005 substitutions per nucleotide position

D-mannose, D-xylitol as the sole carbon and energy sources, but not dulcitol, D-fructose, D-sucrose, sorbinose, L-arabinose, D-xylose and lactose. Utilizes L-alanine, L-arginine, L-asparagine, L-histidine, L-cystine, L-glutamic acid, hypoxanthine, L-lysine, L-phenylalanine, L-serine, L-threonine, L-tryptophan, L-tyrosine and L-valine as sole nitrogen sources. Positive for catalase and oxidase tests, milk coagulation and peptonization, hydrolysis of starch, cellulose and gelatin, but negative for of urease activity, nitrate reduction and H_2S production tests. Degrades Tweens 20, 40, 60 and 80. The diagnostic cell wall diamino acid is LL-diaminopimelic acid (LL-DAP). The whole-cell hydrolysates contain glucose, mannose, ribose and galactose. The polar lipids consist of diphosphatidylglycerol, phosphatidyl methyl ethanolamine, phosphatidylglycerol, phosphatidylinositol, phosphatidylinositol mannosides and three unidentified phospholipids. MK-9 (H_6) and MK-9 (H_8) are the menaquinones detected. The fatty acids profile (>5 %) is composed of iso-$C_{15:0}$, anteiso-$C_{15:0}$, iso-$C_{16:0}$, $C_{16:0}$, summed feature 3 and summed feature 4. The DNA G+C content is 70.7 mol%.

The type strain YIM T102^T (=KCTC 39115^T = DSM 42176^T = CGMCC 4.7248^T) was isolated from rhizospheric soil of *P. tunicoides* W. C. Wu et C. Y. Wu in Lijiang, Yunnan Province, southwest China.

The 16S rRNA gene sequence of strain YIM T102^T has been deposited in GenBank under the accession number KU936048.

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