Amycolatopsis plumensis sp. nov., a novel bioactive actinomycete isolated from a New-Caledonian brown hypermagnesian ultramafic soil

Danielle Saintpierre-Bonaccio,¹ Hamid Amir,¹ René Pineau,¹
G. Y. Annie Tan² and Michael Goodfellow²

Correspondence

Michael Goodfellow
m.goodfellow@ncl.ac.uk

¹Laboratoire de Biologie et Physiologie Végétales Appliquées, Université de la Nouvelle-Calédonie, BP4477 98847, Nouméa, New Caledonia

²School of Biology, University of Newcastle, Newcastle upon Tyne NE1 7RU, UK

The taxonomic position of an actinomycete isolated from a brown hypermagnesian ultramafic soil was examined using a polyphasic approach. The organism, which was designated SBHS Strp1^T, was found to have chemical and morphological properties typical of *Amycolatopsis* strains. It was most closely associated with *Amycolatopsis kentuckyensis*, *Amycolatopsis lexingtonensis*, *Amycolatopsis rifamycinica*, *Amycolatopsis pretoriensis* and *Amycolatopsis tolypomycina* on the basis of 16S rRNA gene sequence data, and showed a unique pattern of phenotypic properties that distinguished it from the type strains of these taxa. The combined genotypic and phenotypic data show that the organism merits description as a novel species of *Amycolatopsis*. The name proposed for the novel species is *Amycolatopsis plumensis* sp. nov.; the type strain is SBHS Strp1^T (= DSM 44776^T = NRRL B-24324^T).

The genus *Amycolatopsis* contains 25 species with validly published names at the time of writing. These species form a distinct phyletic line within the evolutionary radiation encompassed by the family *Pseudonocardiaceae* Embley *et al.* 1988 (as circumscribed by Warwick *et al.*, 1994), a taxon that is closely related to the family *Actinosynnemataceae* Labeda and Kroppenstedt 2000. *Amycolatopsis* species can be assigned to two multimembered 16S rRNA gene groups, the *Amycolatopsis methanolica* and *Amycolatopsis orientalis* subclades (Kim *et al.*, 2002; Huang *et al.*, 2004); the type strain of *Amycolatopsis fastidiosa* forms a single-membered phyletic line at the base of the *Amycolatopsis* tree (Goodfellow *et al.*, 2001; Huang *et al.*, 2001, 2004). A combination of chemical and morphological properties are available to distinguish *Amycolatopsis* from other genera classified in the family *Pseudonocardiaceae* (Kim & Goodfellow, 1999). Similarly, *Amycolatopsis* species can be separated from one another using a range of phenotypic properties (Goodfellow *et al.*, 2001; Kim *et al.*, 2002; Labeda *et al.*, 2003). The genus *Amycolatopsis* is grossly underspeciated and is a source of novel bioactive compounds (Tan, 2002).

Ultramafic soils account for about one-third of the land mass in New Caledonia (Jaffré, 1976). These infertile soils have a high metal toxicity due to the presence of significant concentrations of chromium, cobalt, iron and nickel, and seem to provide habitats for unusual actinomycetes (Saintpierre, 2001; Saintpierre *et al.*, 2003; Saintpierre-Bonaccio *et al.*, 2004a, b). In the course of a screening programme designed to isolate novel actinomycetes from ultramafic soils, an actinomycete, SBHS Strp1^T, was isolated and shown to have properties typical of the genus *Amycolatopsis*. The aim of the present study was to determine the taxonomic status of this organism by using a polyphasic approach. It is evident from the resultant data that the organism represents a novel species in the genus *Amycolatopsis*.

Strain SBHS Strp1^T was isolated from a suspension of a brown hypermagnesian ultramafic soil, which was used to inoculate a yeast extract/malt extract agar plate (ISP 2 medium; Shirling & Gottlieb, 1966) supplemented with 10 µg streptomycin sulphate ml⁻¹ and 100 µg cycloheximide ml⁻¹ (Vobis, 1992) and incubated at 30 °C for 2 weeks. The soil sample had been collected from the 'Plum' region at the southern end of the main island of New Caledonia (see Institut National Géographique, map no. 4836, série orange [Mont Doré] 668.5 × 7535). The isolate was purified and maintained on modified Bennett's agar (Jones, 1949) and

Published online ahead of print on 27 May 2005 as DOI 10.1099/ijms.0.63630-0.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of *Amycolatopsis plumensis* SBHS Strp1^T is AY262825.

preserved as a mixture of hyphae and fragmentation spores in glycerol (20 %, v/v) at -20°C .

Morphological and staining properties of strain SBHS Strp1^T were detected using growth from modified Bennett's agar plates that had been incubated for 2 weeks at 30°C . The same medium and growth conditions were used to establish the ability of the organism to grow at different temperature and pH values. Additional phenotypic properties were determined by using standard media and methods (Williams *et al.*, 1983; Goodfellow *et al.*, 1997). The ability of the test strain to grow in modified Bennett's agar supplemented with a range of antibiotics and chemical inhibitors was determined as described by Saintpierre

et al. (2003). A number of the phenotypic tests were also carried out on the type strains of *Amycolatopsis tolypomycina* and *Amycolatopsis vancoremycina*, as shown in Table 1.

Biomass for the chemotaxonomic and 16S rRNA gene sequencing studies was prepared by growing the strain in shake flasks of glucose/yeast extract broth (Gordon & Mihm, 1962) at 100 r.p.m. for 7 days at 30°C . Cultures were checked for purity, killed by shaking with formalin (1 %, v/v), harvested by centrifugation and freeze-dried. The isomeric form of diaminopimelic acid was determined by TLC of a whole-organism hydrolysate on cellulose acetate sheets according to Stanek & Roberts (1974) with a

Table 1. Characteristics that separate *Amycolatopsis plumensis* sp. nov. SBHS Strp1^T and its nearest neighbours

Strains: 1, *A. plumensis* SBHS Strp1^T; 2, *Amycolatopsis balhimycina* DSM 44591^T (data from Wink *et al.*, 2003); 3, *A. kentuckyensis* NRRL B-24129^T (Labeda *et al.*, 2003); 4, *A. lexingtonensis* NRRL B-24131^T (Labeda *et al.*, 2003); 5, *Amycolatopsis mediterranei* ATCC 13685^T (Goodfellow *et al.*, 2001); 6, *A. pretoriensis* NRRL B-24133^T (Labeda *et al.*, 2003); 7, *A. rifamycinica* DSM 46095^T (Bala *et al.*, 2004); 8, *A. tolypomycina* DSM 44544^T (Wink *et al.*, 2003); 9, *A. vancoremycina* DSM 44592^T (Wink *et al.*, 2003). Symbols: +, positive; w, weakly positive; −, negative; ND, not determined.

Characteristic	1	2	3	4	5	6	7	8	9
Colour of aerial mycelium*	PO	ND	YO/BO	OB/RB	WH	OR	WH/PO	WH	WH
Production of soluble pigment	+	−	+	+	−	+	+	−	+
Acid production from:									
Adonitol	+	ND	+	+	−	−	+	−†	−†
L(+)-Arabinose	+	+	+	+	+	+	+	+	+
D(+)-Cellobiose	+	ND	+	+	+	+	+	+	+
D(+)-Fructose	+	+	+	+	+	+	+	+	+
D(+)-Galactose	−	ND	+	+	+	+	+	+	+
D(+)-Lactose	−	ND	+	+	+	+	−	−†	−†
D(+)-Maltose	+	ND	+	+	+	+	−	−†	−†
D(+)-Mannitol	+	+	−	W	+	−	−	+	+
D(+)-Melibiose	−	+	+	+	+	+	−	−	−
D(+)-Raffinose	−	+	+	+	−	+	−	−	+
α-L(+)-Rhamnose	−	+	+	+	+	+	−	+	+
D(−)-Sorbitol	−	−	+	−	+	W	−	−†	−†
D(+)-Sucrose	−	+	+	+	+	+	+	+	+
D(+)-Trehalose	+	+	+	−	+	+	+	+	+
D(+)-Xylose	−	ND	+	+	+	+	+	−	−
Decomposition of:									
Casein	+	ND	+	+	+	+	+	+	−†
Gelatin	+	ND	+	+	+	+	+	+	−†
Hypoxanthine	−	+	+	+	+	+	+	−	−
Xanthine	−	−	−	−	−	−	−	+	−
Growth at:									
10 °C	−	+	−	−	+	−	+	−	−
45 °C	−	−	+	+	−	−	−	+	−
Growth in the presence of 5 % (w/v) NaCl	−	ND	+	+	W	+	W	+	+
Production of:									
Amylase	+	−	−	−	−	−	−	−	−
Urease	+	+	+	+	+	W	+	+	−

*BO, Brownish orange; OB, orange–brown; OR, orange–white; PO, pale orange; RB, reddish brown; WH, white; YO, yellow–orange.

†Data from this work.

modified solvent system, namely methanol/water/HCl/10 M pyridine (85:15:5:10, by vol.). TLC of major whole-organism sugars was carried out according to the method described by Stanek & Roberts (1974). A standard procedure was used to establish the predominant menaquinones (Minnikin *et al.*, 1984).

Extraction of chromosomal DNA and PCR amplification of the 16S rRNA gene from strain SBHS Strp1^T were achieved using previously described procedures (Kim *et al.*, 1999). Similarly, a 16S rRNA gene from the isolate was amplified by PCR and sequenced directly using a Taq Dye Deoxy Terminator cycle sequencing kit (Applied Biosystems) and an automatic DNA sequencer (model 373A; Applied Biosystems). The resultant rRNA gene sequence was aligned manually using the PHYDIT program (available at <http://plaza.snu.ac.kr/~jchun/phydit/>) against corresponding sequences of representatives of the families Actinosynnemataceae and Pseudonocardiaceae retrieved from the EMBL and GenBank databases. Unrooted evolutionary trees were inferred by using the least-squares (Fitch & Margoliash, 1967), maximum-parsimony (Fitch, 1971) and neighbour-joining (Saitou & Nei, 1987) tree-making algorithms. An evolutionary distance matrix was generated using the distance model of Jukes & Cantor (1969). The topologies of the resultant trees were evaluated in bootstrap analyses of the neighbour-joining method, based on 1000 replicates, using the CONSENSE and SEQBOOT programs. All of the phylogenetic analyses were carried out using the PHYLIP suite of programs (Felsenstein, 1993).

An almost-complete 16S rRNA gene sequence (1488 nt) was generated for strain SBHS Strp1^T. Comparison of this sequence with corresponding nucleotide sequences of representatives of the genera classified in the families Actinosynnemataceae and Pseudonocardiaceae showed the organism to be a member of the genus *Amycolatopsis* (data not shown). This assignment is supported by the chemotaxonomic data, as the organism contains meso-diaminopimelic acid, arabinose and galactose (wall chemotype IV *sensu* Lechevalier & Lechevalier, 1970) and tetrahydrogenated menaquinones with nine isoprene units as the major isoprenologue. The organism is an aerobic, non-motile, Gram-positive, non-acid-alcohol-fast, catalase-positive actinomycete which produces an extensively branched substrate mycelium that fragments into squarish, rod-like elements when grown on modified Bennett's agar. The substrate mycelium carries abundant pale-orange aerial hyphae, which undergo fragmentation yielding squarish, rod-like elements. All of these phenotypic properties are consistent with the classification of the strain in the genus *Amycolatopsis* (Lechevalier *et al.*, 1986).

Strain SBHS Strp1^T belongs to the *A. orientalis* subclade and is most closely related to the type strain of *A. tolypomycina*. The relationship between these organisms is supported by the results from all of the tree-making algorithms and by a bootstrap value of 82 % (Fig. 1). The two strains share a 16S rRNA gene sequence similarity of 99.4 %, a value which corresponds to 8 nt differences at 1384 sites. The organism also shares high 16S rRNA gene sequence similarity values

Fig. 1. Neighbour-joining tree (Saitou & Nei, 1987), based on nearly-complete 16S rRNA gene sequences, showing relationships between SBHS Strp1^T and representatives of *Amycolatopsis* species. Asterisks indicate branches of the tree that were also found using the least-squares (Fitch & Margoliash, 1967) and maximum-parsimony (Fitch, 1971) treeing algorithms. P indicates a branch that was also recovered using the maximum-parsimony method. Numbers at nodes indicate levels of bootstrap support (%) based on a neighbour-joining analysis of 1000 resampled datasets; only values above 45 % are shown.

with other organisms shown in Fig. 1, notably with the type strains of *Amycolatopsis pretoriensis* (99.2%), *Amycolatopsis lexicingtonensis* (99.0%), *Amycolatopsis kentuckyensis* (98.9%) and *Amycolatopsis rifamycinica* (98.9%). DNA–DNA relatedness studies were not carried out between isolate SBHS Strp1^T and these organisms, as some of the latter have almost identical 16S rRNA gene similarity values and have DNA–DNA relatedness values well below the cut-off point recommended by Wayne *et al.* (1987) for the delineation of strains that belong to the same genomic species. The type strains of *A. lexicingtonensis* and *A. pretoriensis*, for instance, share a 16S rRNA gene similarity of 99.9% and have a DNA–DNA relatedness value of 54.1% (Labeda *et al.*, 2003). In addition, the type strains of *A. methanolica* and *Amycolatopsis thermoflava* have almost identical 16S rRNA gene sequences but were found to have a DNA relatedness value of only 21% when DNA from the former was used as the probe (Chun *et al.*, 1999). The tested strain can be distinguished from the type strains of phylogenetically related *Amycolatopsis* species, including *A. tolypomycina*, using a range of phenotypic properties (Table 1).

The genotypic and phenotypic data show that strain SBHS Strp1^T represents a novel species of the genus *Amycolatopsis*. It is proposed that this organism be classified in this genus as *Amycolatopsis plumensis* sp. nov.

Description of *Amycolatopsis plumensis* sp. nov.

Amycolatopsis plumensis (plum.en'sis. N.L. fem. adj. *plumensis* referring to the Plum region of the main island of New Caledonia, the source of the soil from which the type strain was isolated).

Aerobic, Gram-positive, non-acid–alcohol-fast, non-motile, catalase-positive actinomycete which forms extensively branched substrate hyphae that fragment into squarish, rod-like elements. A pale-orange substrate mycelium, but no diffusible pigments, is formed on modified Bennett's agar. The substrate mycelium carries abundant pale-orange aerial hyphae. Chemotaxonomic characteristics are typical for *Amycolatopsis*. Grows at pH 4–12 and at 20–37 °C, but not at 10 or 45 °C. Hydrogen sulphide is formed, and elastin, L-tyrosine, Tween 80 and xylan are degraded. Growth occurs in the presence of erythromycin (4 µg ml⁻¹), gentamicin sulphate (10 µg ml⁻¹), rifampicin (6 µg ml⁻¹), streptomycin sulphate (5 µg ml⁻¹), crystal violet (0.0002%, w/v), phenol (0.01%, w/v) and potassium tellurite (0.005%, w/v), but the organism is susceptible to penicillin G (25 µg ml⁻¹), tetracycline hydrochloride (30 µg ml⁻¹), vancomycin hydrochloride (10 µg ml⁻¹) and sodium chloride (5%, w/v). Additional phenotypic properties are shown in Table 1. The organism shows activity against *Candida albicans*, *Corynebacterium* sp., *Fusarium oxysporum*, *Klebsiella pneumoniae* and *Staphylococcus aureus* strains but not against *Bacillus*, *Escherichia* or *Staphylococcus epidermidis* strains.

The type (and only) strain, SBHS Strp1^T (= DSM 44776^T = NRRL B-24324^T), was isolated from brown hyper-magnesian ultramafic soil at the southern end of the main island of New Caledonia.

Acknowledgements

The authors are indebted to Dr Pierre Cabalion (IRD, Institut pour la Recherche et le Développement, Nouméa, New Caledonia) for provision of the bacterial cultures from the Institut Pasteur de Nouméa. H. A., R. P. and D. S. would like to thank la Direction des Ressources Naturelles (DRN) de la Province Sud de la Nouvelle-Calédonie for financing the project. M. G. is grateful for support from the European Commission (grant QLK3-CT-2001-01783).

References

- Bala, S., Khanna, R., Dadhwal, M., Prabakaran, S. R., Shivaji, S., Cullum, T. & Lal, R. (2004). Reclassification of *Amycolatopsis mediterranei* DSM 46095 as *Amycolatopsis rifamycinica* sp. nov. *Int J Syst Evol Microbiol* **54**, 1145–1149.
- Chun, J., Kim, S. B., Oh, Y. K. & 7 other authors (1999). *Amycolatopsis thermoflava* sp. nov., a novel soil actinomycete from Hainan Island, China. *Int J Syst Bacteriol* **49**, 1369–1373.
- Embley, T. M., Smida, J. & Stackebrandt, E. (1988). The phylogeny of mycolate-less wall chemotype IV actinomycetes and description of *Pseudonocardiaceae* fam. nov. *Syst Appl Microbiol* **11**, 16–19.
- Felsenstein, J. (1993). PHYLIP (phylogeny inference package), version 3.5c. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle, USA.
- Fitch, W. M. (1971). Towards defining the course of evolution: minimum change for a specific tree topology. *Syst Zool* **20**, 406–416.
- Fitch, W. M. & Margoliash, E. (1967). Construction of phylogenetic trees: a method based on mutation distances as estimated from cytochrome *c* sequences is of general applicability. *Science* **155**, 279–284.
- Goodfellow, M., Brown, A. B., Cai, J., Chun, J. & Collins, M. D. (1997). *Amycolatopsis japonicum* sp. nov., an actinomycete producing (S,S)-N,N'-ethylenediaminedisuccinic acid. *Syst Appl Microbiol* **20**, 78–84.
- Goodfellow, M., Kim, S. B., Minnikin, D. E., Whitehead, D., Zhou, Z.-H. & Mattinson-Rose, A. D. (2001). *Amycolatopsis sacchari* sp. nov., a moderately thermophilic actinomycete isolated from vegetable matter. *Int J Syst Evol Microbiol* **51**, 187–193.
- Gordon, R. E. & Mihm, J. M. (1962). Identification of *Nocardia caviae* (Erikson) nov. comb. *Ann N Y Acad Sci* **98**, 628–636.
- Huang, Y., Qi, W., Lu, Z., Liu, Z. & Goodfellow, M. (2001). *Amycolatopsis rubida* sp. nov., a new *Amycolatopsis* species from soil. *Int J Syst Evol Microbiol* **51**, 1093–1097.
- Huang, Y., Paściak, M., Liu, Z., Xie, Q. & Gamian, A. (2004). *Amycolatopsis palatopharyngis* sp. nov., a potentially pathogenic actinomycete isolated from a human clinical source. *Int J Syst Evol Microbiol* **54**, 359–363.
- Jaffré, T. (1976). Chemical composition and conditions of mineral supply for plants on ultrabasic rocks. In *ORSTROM Notebook, Biology Series II*, pp. 53–63. Paris: ORSTROM (in French).
- Jones, K. L. (1949). Fresh isolates of actinomycetes in which the presence of sporogenous aerial mycelia is a fluctuating characteristic. *J Bacteriol* **57**, 141–145.

- Jukes, T. H. & Cantor, C. R. (1969). Evolution of protein molecules. In *Mammalian Protein Metabolism*, vol. 3, pp. 21–132. Edited by H. N. Munro. New York: Academic Press.
- Kim, S. B. & Goodfellow, M. (1999). Reclassification of *Amycolatopsis rugosa* Lechevalier *et al.* 1986 as *Prauserella rugosa* gen. nov., comb. nov. *Int J Syst Bacteriol* **49**, 507–512.
- Kim, S. B., Brown, R., Oldfield, C., Gilbert, S. C. & Goodfellow, M. (1999). *Gordonia desulfuricans* sp. nov., a benzothiophene-desulphurizing actinomycete. *Int J Syst Bacteriol* **49**, 1845–1851.
- Kim, B., Sahin, N., Tan, G. Y. A., Zakrzewska-Czerwinska, J. & Goodfellow, M. (2002). *Amycolatopsis eurytherma* sp. nov., a thermophilic actinomycete isolated from soil. *Int J Syst Evol Microbiol* **52**, 889–894.
- Labeda, D. P. & Kroppenstedt, R. M. (2000). Phylogenetic analysis of *Saccharothrix* and related taxa: proposal for *Actinosynnemataceae* fam. nov. *Int J Syst Evol Microbiol* **50**, 331–336.
- Labeda, D. P., Donahue, J. M., Williams, N. M., Sells, S. F. & Henton, M. M. (2003). *Amycolatopsis kentuckyensis* sp. nov., *Amycolatopsis lexingtonensis* sp. nov. and *Amycolatopsis pretoriensis* sp. nov., isolated from equine placentas. *Int J Syst Evol Microbiol* **53**, 1601–1605.
- Lechevalier, M. P. & Lechevalier, H. A. (1970). Chemical composition as a criterion in the classification of aerobic actinomycetes. *Int J Syst Bacteriol* **20**, 435–443.
- Lechevalier, M. P., Prauser, H., Labeda, D. P. & Ruan, J. S. (1986). Two new genera of nocardioform actinomycetes – *Amycolata* gen. nov. and *Amycolatopsis* gen. nov. *Int J Syst Bacteriol* **36**, 29–37.
- Minnikin, D. E., O'Donnell, A. G., Goodfellow, M., Alderson, G., Athalye, M., Schaal, A. & Parlett, J. H. (1984). An integrated procedure for the extraction of isoprenoid quinones and polar lipids. *J Microbiol Methods* **2**, 233–241.
- Saintpierre, D. (2001). *Identification of novel actinomycete strains from New Caledonian ultramafic soils. Chemical characterization of some antibiotic products*. PhD thesis, Institut National Polytechnique de Toulouse, France (in French).
- Saintpierre, D., Amir, H., Pineau, R., Sembiring, L. & Goodfellow, M. (2003). *Streptomyces yatensis* sp. nov., a novel bioactive streptomycete isolated from a New-Caledonian ultramafic soil. *Antonie van Leeuwenhoek* **83**, 21–26.
- Saintpierre-Bonaccio, D., Maldonado, L. A., Amir, H., Pineau, R. & Goodfellow, M. (2004a). *Nocardia neocaledoniensis* sp. nov., a novel actinomycete isolated from a New-Caledonian brown hypermagnesian ultramafic soil. *Int J Syst Evol Microbiol* **54**, 599–603.
- Saintpierre-Bonaccio, D., Amir, H., Pineau, R., Lemriss, S. & Goodfellow, M. (2004b). *Streptomyces ferralitis* sp. nov., a novel streptomycete isolated from a New-Caledonian ultramafic soil. *Int J Syst Evol Microbiol* **54**, 2061–2065.
- Saitou, N. & Nei, M. (1987). The neighbor-joining method: a new method for constructing phylogenetic trees. *Mol Biol Evol* **4**, 406–425.
- Shirling, E. B. & Gottlieb, D. (1966). Methods for characterization of *Streptomyces* species. *Int J Syst Bacteriol* **16**, 313–340.
- Staneck, J. L. & Roberts, G. D. (1974). Simplified approach to identification of aerobic actinomycetes by thin-layer chromatography. *Appl Microbiol* **28**, 226–231.
- Tan, G. Y. A. (2002). *Selective isolation, characterisation and screening of novel species of Amycolatopsis*. PhD thesis, University of Newcastle, UK.
- Vobis, G. (1992). The genus *Actinoplanes* and related genera. In *The Prokaryotes, a Handbook of Habitats, Isolation and Identification of Bacteria*, pp. 1029–1060. Edited by A. Balows, H. G. Trüper, M. Dworkin, W. Harder & K. H. Schleifer. New York: Springer.
- Warwick, S., Bowen, T., McVeigh, H. & Embley, T. M. (1994). A phylogenetic analysis of the family *Pseudonocardiaceae* and the genera *Actinokineospira* and *Saccharothrix* with 16S rRNA sequences and a proposal to combine the genera *Amycolata* and *Pseudonocardia* in an emended genus *Pseudonocardia*. *Int J Syst Bacteriol* **44**, 293–299.
- Wayne, L. G., Brenner, D. J., Colwell, R. R. & 9 other authors (1987). International Committee on Systematic Bacteriology. Report of the ad hoc committee on reconciliation of approaches to bacterial systematics. *Int J Syst Bacteriol* **37**, 463–464.
- Williams, S. T., Goodfellow, M., Alderson, G., Wellington, E. M. H., Sneath, P. H. A. & Sackin, M. J. (1983). Numerical classification of *Streptomyces* and related genera. *J Gen Microbiol* **129**, 1743–1813.
- Wink, J. M., Kroppenstedt, R. M., Ganguli, B. N., Nadkarni, S. R., Schumann, P., Seibert, G. & Stackebrandt, E. (2003). Three new antibiotic producing species of the genus *Amycolatopsis*, *Amycolatopsis balhimycina* sp. nov., *A. tolypomycina* sp. nov., *A. vancoremycina* sp. nov., and description of *Amycolatopsis keratiniphila* subsp. *keratiniphila* subsp. nov. and *A. keratiniphila* subsp. *nogabecina* subsp. nov. *Syst Appl Microbiol* **26**, 38–46.