**Streptomyces staurosporininus** sp. nov., a staurosporine-producing actinomycete

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The taxonomic position of a staurosporine-producing actinomycete isolated from a hay meadow soil was determined using a polyphasic approach. The organism had chemical and morphological characteristics consistent with its classification in the genus *Streptomyces* and formed a distinct branch between the *Streptomyces lydicus* and *Streptomyces noursei* clades in the 16S rRNA *Streptomyces* gene tree. DNA–DNA relatedness values between the isolate and its nearest phylogenetic neighbours, namely *Streptomyces lydicus* NBRC 13058T and *Streptomyces chattanoogensis* NBRC 12754T, were 53% and 40%, respectively. The isolate was also readily distinguished from the type strains of these species using a combination of morphological and other phenotypic properties. On the basis of these results, it is proposed that isolate BK179T (=KACC 20912T =NRRL B-24850T) be classified as the type strain of *Streptomyces staurosporininus* sp. nov.

Members of the genus *Streptomyces* remain a unique source of natural products, including clinically significant antibiotics, antimitabolites and antitumour agents (Wavre et al., 2001; Fiedler et al., 2005; Olano et al., 2009), hence the continued interest in screening streptomycetes for new bioactive compounds (Bérty, 2005; Goodfellow & Fiedler, 2010). Another remarkable feature of the genus is the large number of described species it contains, nearly 600 at the time of writing (Euzéby, 2011). The subgeneric classification of the genus, although complex, is being clarified by the application of judiciously chosen genotypic and phenotypic procedures (Kim et al., 1996; Kämpfer et al., 2008; Kumar & Goodfellow, 2010; Rong & Huang, 2010). These procedures are also being used to detect novel and rare streptomycetes for screening programmes (Hohmann et al., 2009a, b) as it is becoming counterproductive to screen common members of the genus as this practice leads to the costly rediscovery of known antibiotics (Busti et al., 2006; Lam, 2007).

In a continuation of our screening programme, a presumptively novel *Streptomyces* strain, isolate BK179T, was isolated from a hay meadow soil. A polyphasic study based on genotypic and phenotypic procedures showed that the isolate belonged to a novel species of the genus *Streptomyces*. The novel species, *Streptomyces staurosporininus*, was most closely related to, but readily differentiated from, the type strain of *Streptomyces lydicus*. Isolate BK179T was recovered from a plate of starch-casein agar (Küster & Williams, 1964), supplemented with cycloheximide and nystatin (each at 25 μg ml−1), which had been inoculated with a pre-heated (55 °C for 20 min) soil suspension and incubated at 28 °C for 21 days. The soil sample was collected from Palace Leas meadow hay plot 6 (Atalan et al., 2000) at Cockle Park Experimental Farm, Northumberland, UK (national grid reference NZ 200913). The organism was maintained on oatmeal agar slopes (International *Streptomyces* Project (ISP) medium 3; Shirling & Gottlieb, 1966) at 4 °C and as a mixture of mycelial fragments and spores in 20% (v/v) glycerol at −20 °C. Biomass for chemotaxonomic and molecular systematic studies was grown in shake flasks of tryptone-yeast extract broth (Shirling & Gottlieb, 1966) for 7 days at 28 °C, harvested by centrifugation and washed twice in distilled water; cells for chemical analysis were freeze-dried.

The 16S rRNA gene of the isolate was analysed as described previously (Kim et al., 1996). The resultant, almost complete sequence (1457 nt) was aligned manually against corresponding sequences of representatives of the genus *Streptomyces* using MEGA 4 software (Tamura et al., 2007), and the complete sequence (1457 nt) was aligned manually against previously (Kim et al., 1996). The resultant, almost complete sequence (1457 nt) was aligned manually against corresponding sequences of representatives of the genus *Streptomyces* using MEGA 4 software (Tamura et al., 2007).
Phylogenetic trees were inferred by using the maximum-likelihood (Felsenstein, 1981), maximum-parsimony (Fitch, 1971) and neighbour-joining (Saitou & Nei, 1987) tree-making algorithms drawn from the MEGA 4 (Tamura et al., 2007) and PHYML (Guindon & Gascuel, 2003) software packages. The Jukes & Cantor (1969) model was used to generate an evolutionary distance matrix for the neighbour-joining algorithm. The topology of the neighbour-joining tree was evaluated by a bootstrap analysis (Felsenstein, 1985) based on 1000 resampled datasets. Streptomyces macrosporus DSM 41499^T (GenBank accession no. Z68099) and Streptomyces megasporus DSM 41476^T (Z68100) were used as outgroups.

Isolate BK179^T formed a distinct phylogenetic line between the Streptomyces lydicus and Streptomyces noursei clades, the taxonomic status of which was supported by high bootstrap values and by all of the tree-making algorithms (Fig. 1). The organism was most closely related to the type strains of S. lydicus and Streptomyces chattanoogensis, sharing sequence similarities of 99.2 and 99.1 %, respectively, values which corresponded to 11 and 13 nt differences across 1435 and 1430 locations. The corresponding similarities with members of the Streptomyces noursei clade fell within the range 98.4–98.9 %, values equivalent to 16 and 23 nt differences.

DNA–DNA relatedness values between isolate BK179^T and Streptomyces chattanoogensis NBRC 12754^T and Streptomyces lydicus NBRC 13058^T were determined using the nitrocellulose filter hybridization method as described by Seldin & Dubnau (1983). Probe DNA samples were labelled using the non-radioactive digoxigenin (DIG) High Prime System (Roche), hybridized DNA visualized using DIG luminescent detection kits (Roche) and DNA–DNA relatedness quantified using a densitometer (Bio-Rad). It was evident from the resultant data that isolate BK179^T belongs to a distinct genomic species as it shared DNA–DNA relatedness values of 40.0 (±5.2 %) and 53.0 (±3.5 %) with Streptomyces chattanoogensis and Streptomyces lydicus, respectively; values well below the 70 % cut-off point recommended for the assignment of strains to the same genomic species (Wayne et al., 1987).

Isolate BK179^T was examined for chemical markers considered to be characteristic of members of the genus Streptomyces. Standard procedures were used to determine the isomer of diaminopimelic acid (A2pm; Hasegawa et al., 1983), predominant menaquinones (Collins, 1985), muramic acid type (Uchida et al., 1999) and diagnostic whole-cell sugars (Hasegawa et al., 1983), using the type strain of Streptomyces lydicus as control. Fatty acids were extracted from the isolate, methylated and analysed by GC using the standard Sherlock Microbial Identification (MIDI) system, version 5 (MIDI, 1999; Sasser, 1990), and the DNA base composition of the isolate was determined using the thermal denaturation method of Marmur & Doty (1962) with Escherichia coli K-12 as a control.

The isolate contained major amounts of L-l-diaminopimelic acid but lacked diagnostic sugars in whole-organism hydrolysates (wall chemotype I sensu Lechevalier & Lechevalier, 1970), contained N-acetyl muramic acid moieties and hexa- and octahydrogenated menaquinones with nine isoprene units [MK-9(H8), H9] as predominant isoprenoid quinones. The cellular fatty acid profile consisted of major amounts of iso-C16:0 (19.5 %), C16:0 (17.0 %) and anteiso-C15:0 (16.8 %) components, lower amounts (<10 %) of iso-C15:0 (7.8 %), C17:0 cyclo (7.6 %), anteiso-C17:0 (6.1 %) and iso-C14:0 (5.7 %) and trace amounts of iso-C16:1o7c, C15:0 2-OH, iso-C17:0, iso-C16:1 H, iso-C17:1ω9c and anteiso-C17:1ω9c. The DNA G+C content of the isolate was 71.2 %. All of these properties are consistent with the classification of the strain in the genus Streptomyces (Williams et al., 1983; Manfio et al., 1995; Anderson & Wellington, 2001; Kämpfer, 2012).
The isolate was also examined for cultural and morphological features after growth on several standard nutrient media at 28 °C for 3 weeks. Cultural properties were sought using glucose-yeast extract-malt extract (GYM; DSMZ medium 65) and modified Bennett’s (Jones, 1949) agars and on tryptone-yeast extract, yeast-extract-malt extract, oatmeal, inorganic salts-starch, glycerol-asparagine and tyrosine agars, that is, on ISP media 1–5 and 7 (Shirling & Gottlieb, 1966). Spore arrangement and spore surface ornamentation were observed by examining a gold-coated, dehydrated preparation prepared from the ISP3 plate, using a scanning electron microscope (Cambridge Steroscan 240 instrument) and the procedure described by O’Donnell et al. (1993). The isolate formed an extensively branched white substrate mycelium and aerial hyphae which differentiated into spiral chains of ridged ornamented spores on oatmeal agar. It produced a pale yellow substrate mycelium on glucose-yeast extract-malt extract, modified Bennett’s, inorganic salts-starch, glycerol-asparagine and tyrosine agars, but did not grow on the remaining media.

Strain BK179T was investigated by HPLC-diode array analysis for the production of secondary metabolites. The strain was cultivated in a 500 ml Erlenmeyer flask on a rotary shaker at 120 r.p.m. and 27 °C in a complex medium that consisted of 10 g soluble starch, 10 g glucose, 10 g glycerol, 2.5 g corn steep powder, 5 g Bacto peptone, 2 g yeast extract, 1 g NaCl, 3 g CaCO₃ and 1 litre tap water; the pH was adjusted to 7.3 prior to sterilization. Samples were taken between 48 and 144 h of cultivation, and extracts were prepared from the culture filtrate using ethyl acetate and from the mycelium using methanol/acetone (1:1). Aliquots of the extracts were analysed by reversed-phase HPLC and diode array monitoring using a standard protocol (Fiedler, 1993). The dominant peak in the HPLC chromatogram, which reached a maximal intensity at 144 h of cultivation, was identified as staurosporine by its characteristic UV-visible spectrum and retention time of 7.4 min; these results were identical to those of the reference compound staurosporine in the HPLC-UV-Vis database which contained data on 950 natural products, mainly antibiotics (Fiedler, 1993). Staurosporine was originally discovered from a culture broth of *Saccharothrix aerocolonigenes* subsp. *staurosporae* strain AM-2282 during a screening programme for microbial alkaloids using a TLC detection method (Ômura et al., 1977; Takahashi et al., 1995).

Strain BK179T and the type strains of *Streptomyces chattanoogensis* and *Streptomyces lydicus* were examined for a restricted range of phenotypic properties known to be of value in streptomycete systematics (Table 1). These tests and some additional ones carried out on the isolate were performed using the media and methods described by Williams et al. (1983). The isolate, unlike the type strain of *Streptomyces lydicus*, used rhamnose but not D-fructose as a sole carbon source.

### Table 1. Characteristics that separate strain BK179T from the type strains of phylogenetically closely related species of the genus *Streptomyces*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
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<th>3</th>
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<tbody>
<tr>
<td>Appearance on inorganic-salt starch agar</td>
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<tr>
<td>Aerial spore-mass colour</td>
<td>White</td>
<td>Yellow</td>
<td>Yellow</td>
</tr>
<tr>
<td>Reverse colour</td>
<td>White</td>
<td>White</td>
<td>Grey-yellow</td>
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<tr>
<td>Soluble pigment</td>
<td>–</td>
<td>Yellow</td>
<td>–</td>
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<tr>
<td>Spore surface</td>
<td>Rugose</td>
<td>Spiny</td>
<td>Smooth</td>
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<tr>
<td>Biochemical tests</td>
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<tr>
<td>Nitrate reduction</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<tr>
<td>Hydrogen sulphide production</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<td>Degradation of:</td>
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<tr>
<td>Adenine</td>
<td>–</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Casein</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<tr>
<td>Hypoxanthine</td>
<td>+</td>
<td>–</td>
<td>+</td>
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<tr>
<td>Xylan</td>
<td>+</td>
<td>–</td>
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<tr>
<td>Growth on sole carbon sources (1%, w/v)</td>
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<tr>
<td>L-Arabinose</td>
<td>+</td>
<td>–</td>
<td>+</td>
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<tr>
<td>Dextran</td>
<td>+</td>
<td>–</td>
<td>+</td>
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<tr>
<td>D-Fructose</td>
<td>–</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Rhamnose</td>
<td>+</td>
<td>–</td>
<td>–</td>
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<tr>
<td>D-Xylose</td>
<td>+</td>
<td>–</td>
<td>+</td>
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<tr>
<td>Growth at pH 4.0</td>
<td>+</td>
<td>–</td>
<td>–</td>
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<tr>
<td>Resistance to Gentamicin sulphate (8 µg ml⁻¹)</td>
<td>+</td>
<td>–</td>
<td>–</td>
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</table>
sole carbon source, degraded casein and xylan but not adenine, reduced nitrate, produced hydrogen sulphide and grew at pH 4.0. Similarly, unlike the type strain of *Streptomyces chattanoogensis*, it used L-arabinose, dextran, rhamnose and D-xylose, but not D-fructose, as sole sources of carbon, degraded hypoxanthine and xylan but not adenine and grew at pH 4.0. All three strains formed spiral spore chains but can be distinguished on the basis of spore ornamentation; the novel isolate formed ridged ornamented spores, and the type strains of *Streptomyces chattanoogensis* and *Streptomyces lydicus* formed smooth and smooth or spiny spores, respectively (Williams et al., 1983).

Strain BK179<sup>T</sup> can be distinguished from the type strains of its nearest neighbours, namely *Streptomyces chattanoogensis* and *Streptomyces lydicus*, based on 16S rRNA gene sequence, DNA–DNA relatedness, and phenotypic and morphological data. It is, therefore, proposed that the organism be recognized as a novel species, *Streptomyces staurosporininus* sp. nov.

**Description of Streptomyces staurosporininus**

*Streptomyces staurosporininus* (stau.ro.spo’ri.ni.nus. N.L. neut. n. *staurosporinum* staurosporine; L. masc. suff. -inus adjectival suffix used with the sense of belonging to or related to; N.L. masc. adj. *staurosporinus* related to staurosporine, producing the antibiotic staurosporine).

Aerobic, Gram-positive, non-acid–alcohol-fast actinomycete which forms an extensively branched substrate mycelium which carries aerial hyphae that differentiate into long spiral chains of ridged ornamented spores on oatmeal agar. Grows from 10 to 30 °C, from pH 4.0 to 10.0 and in the presence of NaCl (5.0%). Aesculin, allantoin and arbutin are hydrolysed. Degrades elastin and uric acid, but not cellulose, chitin, guanine or pectin. D-Arabitol, cellobiose, maltose, D-mannitol, melibiose, raffinose, *myo*-inositol and starch are used as sole carbon sources, but not adonitol, D-sorbitol or L-sorbose (1%, w/v). Susceptible to (μg ml<sup>−1</sup>): novobiocin (8), rifampicin (16) and vancomycin hydrochloride (2), but not to ampicillin (4), cephaloridine hydrochloride (2), kanamycin sulphate (8), penicillin G (2), streptomycin sulphate (4) or tetracycline hydrochloride (8). Resistant to lysozyme (0.05%, w/v). Additional properties are cited in the text and in Table 1. Contains LL-diaminopimelic acid, N-acetyl muramic acid moieties, and hexa- and octahydratedenogenied menaquinones with nine isoprene units [MK-9 (H<sub>6</sub>, H<sub>8</sub>)] as predominant menaquinones. The major cellular fatty acids are iso-C<sub>16:0</sub> C<sub>16:0</sub> and anteiso-C<sub>15:0</sub>. Produces staurosporine. The DNA G+C content is 71.2%.

The type and only strain, BK179<sup>T</sup> (=KACC 20912<sup>T</sup> =NRRL B-24850<sup>T</sup>), was isolated from hay meadow plot 6 at Cockle Park Experimental Farm, Northumberland, UK. The species description is based on a single strain and hence serves as a description of the type strain.

**Acknowledgements**

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**References**


