The search for synonyms among streptomycetes by using SDS-PAGE of whole-cell proteins. Emendation of the species *Streptomyces aurantiacus*, *Streptomyces cacaoi* subsp. *cacaoi*, *Streptomyces caeruleus* and *Streptomyces violaceus*

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A collection of 93 *Streptomyces* reference strains were investigated using SDS-PAGE of whole-cell proteins. Computer-assisted numerical analysis revealed 24 clusters encompassing strains with very similar protein profiles. Five of them grouped several type strains with visually identical patterns. DNA–DNA hybridizations revealed homology values higher than 70% among these type strains. According to the current species concept, it is proposed that *Streptomyces albosporeus* subsp. *albosporeus* LMG 19403T is considered as a subjective synonym of *Streptomyces aurantiacus* LMG 19358T, that *Streptomyces aminophilus* LMG 19319T is considered as a subjective synonym of *Streptomyces cacaoi* subsp. *cacaoi* LMG 19320T, that *Streptomyces niveus* LMG 19395T and *Streptomyces spheroides* LMG 19392T are considered as subjective synonyms of *Streptomyces caeruleus* LMG 19399T, and that *Streptomyces violatus* LMG 19397T is considered as a subjective synonym of *Streptomyces violaceus* LMG 19360T.

Keywords: *Streptomyces*, SDS-PAGE of whole-cell proteins, synonyms, taxonomy

INTRODUCTION

At the introduction of the genus in 1943 (Waksman & Henrici, 1943) classifications were based solely on morphology and pigmentation. The lack of standardized procedures for describing streptomycetes, together with the unavailability of type strains, led to species which were poorly described. Moreover, antibiotics producing streptomycetes were described on the basis of trivial differences in morphology, for patent purposes. This unsound classification system has been improved by the International *Streptomyces* Project (ISP) in 1964. Standard procedures for describing streptomycetes were developed and applied to 463 *Streptomyces* and (former) *Streptoverticillium* species. Type strains became publicly available when they were deposited in four collections.

No attempts were undertaken by the ISP to determine synonymies among morphologically defined species. With the introduction of the principles of numerical taxonomy by Locci et al. (1981) and Williams et al. (1983), another view on the taxonomy of this complex genus emerged. Numerical taxonomy of phenotypic features without heavy emphasis on morphology and pigmentation allowed a more reliable classification than those previously defined. The taxonomic study of Williams et al. (1983) is therefore considered to be a milestone in *Streptomyces* systematics. An extensive species reduction was proposed, and probability matrices were created to identify isolates (Williams et al., 1989). Kämper & Kroppenstedt (1991) updated the classification system of Williams et al. (1983) by extending the numbers of phenotypic traits and by including more taxa.

*Streptomyces* systematics is gradually evolving from a phenotypically dominated taxonomy to a more poly-
Fig. 1. Dendrogram derived from an unweighted pair group method with arithmetic averages (UPGMA) algorithm of $r$ values (expressed as percentages) of protein profiles. Clusters are delineated at a similarity level of 90%. Symbols: *, cultivated for 48 h; †, growth temperature 48 °C.
phasic taxonomy comprising chemotaxonomic and genomic information. The large number of validly described Streptomyces species (more than 500) remains a major obstacle in the setting up of large fundamental taxonomic studies, including DNA–DNA hybridizations, and in establishing the link between phenotypic and genomic information. Furthermore, because of the lack of minimal standards for defining Streptomyces species (Manfio et al., 1994), the polyphasic approach remains difficult.

The aim of this study was to screen for synonymous taxa in a representative subset of the genus Streptomyces, using SDS-PAGE of whole-cell proteins, and to compare the data with those of Williams et al. (1989) and Kämpfer & Kroppenstedt (1991). It has been shown that under highly standardized cultivation conditions, SDS-PAGE of whole-cell proteins is an excellent and generally standardized method for defining relationships at the species level among large numbers of strains (Vandamme et al., 1991). It has been shown that under highly standardized cultivation conditions, SDS-PAGE of whole-cell proteins is an excellent and generally applicable method for defining relationships at the species level among large numbers of strains (Vandamme et al., 1996; Descheemaeker et al., 1994). Manchester et al. (1990) has already demonstrated the usefulness of SDS-PAGE of whole-cell proteins in streptomycete systematics.

### RESULTS AND DISCUSSION

#### SDS-PAGE of whole-cell proteins

Before routine application of SDS-PAGE of whole-cell proteins, the method was optimized using *Streptomyces* LMG 5974 and LMG 5984T. The extent to which factors such as cultivation time and medium (agar versus broth) influence the resolution of protein profiles was investigated. Our results indicated that high-resolution and reproducible protein patterns were obtained only from cultures grown in liquid medium, whereas cultures grown on solid media yielded a high background (due to proteinase activity) and consequently gave a lower resolution. It was also demonstrated that the growth phase of cells in liquid medium should preferably be within the exponential phase, which means approx. 36 h for fast-growing streptomycetes. Protein patterns of strains harvested at the early stationary phase (51 h), in conditions analogous to those used in the study of Manchester et al. (1990), clearly had a lower resolution. Duplicate protein extracts were prepared in order to verify the reproducibility of the growth conditions and preparation of extracts. A correlation value above 92% was observed between duplicate protein patterns loaded onto separate gels.

Using the above-mentioned growth conditions, protein patterns were generated from 93 *Streptomyces* strains (see Fig. 1) belonging to different phenotypically defined clusters. After processing of the data, a cluster analysis was performed (Fig. 1). A 90% similarity level was used as guideline for delineating 24 clusters (Fig. 1) encompassing strains with very similar protein profiles. A correlation level (r) of 0.90 or higher in protein patterns of bacterial strains has often been used as an indication of possible relatedness at the species level (Kersters, 1985; Manchester et al., 1990).
Table 1. DNA hybridization between several Streptomyces taxa

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<th>SDS-PAGE cluster</th>
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DNA–DNA hybridization experiments

In the present study, delineated clusters contain not strains of a single species, but several type strains of different validly described Streptomyces species. Five clusters (1, 5, 8, 12 and 19; Fig. 2) contain type strains with identical profiles (there were only small differences in the intensities of bands). Other type strains grouping in the respective clusters, and all members of the other clusters, show highly similar (though not identical) patterns (there were minor differences in the presence or absence of bands). DNA–DNA hybridization experiments were performed to investigate whether synonymous names might be found among the species in these clusters.

The DNA–DNA hybridization results among strains of the five selected clusters (sharing identical patterns) is presented in Table 1. Within cluster 1, Streptomyces albosporus subsp. albosporus LMG 19403T and Streptomyces aurantiacus LMG 19358T share a DNA homology of 74%. Within cluster 5, Streptomyces cacaoi subsp. cacaoi LMG 19320T and Streptomyces amnophilus LMG 19319T are 100% related. Within cluster 8, Streptomyces endus LMG 19393T shows a relatedness of 92% (data from Labeda & Lyons, 1991) with respect to Streptomyces hygroscopicus subsp. hygroscopicus LMG 19335T. Within cluster 12, Streptomyces violaceus LMG 19360T and Streptomyces violatus LMG 19397T show a DNA relatedness of 90%. Within cluster 19, Streptomyces spheroides LMG 19392T shares DNA relatedness of 77% and 84%, respectively, with Streptomyces niveus LMG 19395T and Streptomyces caerulescens LMG 19399T. S. caerulescens LMG 19399T is highly related to S. niveus LMG 19395T, as they show a DNA homology of 100%. These data confirm that streptomycetes possessing

**Fig. 2.** All strains found in this study possessing visually identical protein profiles, except for cluster 22, encompassing strains with similar protein profiles. A correlation is made with the numerical phenotypic studies of Williams et al. (1989) and Kampfer & Kroppenstedt (1991). Molecular mass markers (from left to right), in kDa: β-galactosidase (116), bovine albumin (66), egg albumin (45), glyceraldehyde-3-phosphate dehydrogenase (36), carbonic anhydrase (29), trypsin inhibitor (21-1) and lysozyme (14-2).
visually identical protein patterns are genomically more than 70% related and represent the same genomic species.

In a second step, we investigated the level of DNA homology among the strains showing minor differences in protein profiles (r > 0.90, but differentiated by the presence or the absence of a few bands). Three strains belonging to cluster 22 (r ≥ 0.93), i.e. S. anulatus LMG 19301T, S. griseus subsp. griseus LMG 19302T and S. microflavus LMG 19327T, were studied. As presented in Table 1, S. anulatus LMG 19301T shows genomic relatedness of 61 and 45%, respectively, to S. griseus subsp. griseus LMG 19302T and S. microflavus LMG 19327T. S. griseus subsp. griseus LMG 19302T and S. microflavus LMG 19327T show a genomic relatedness of 43%. These intermediate DNA homology values confirm that strains possessing highly similar protein patterns but showing minor qualitative differences may share DNA homologies below 70% and may be considered as distinct taxa. Numerical analysis of the SDS-PAGE patterns of soluble proteins seems to be a perfect method for screening for highly related strains. Visual identity is indispensable if the relationship at the species level is being determined.

A good correlation exists between the data for SDS-PAGE of whole-cell proteins (the present study) and published DNA-hybridization data (e.g. Labeda & Lyons, 1991; Kim et al., 1999). In the study of Labeda & Lyons (1991), it was proposed that S. endus be considered as a subjective synonym of S. hygroscopicus. Both strains have identical protein profiles (cluster 8; Fig. 2), confirming their conclusions. In the same study, it was observed that the phenotypically similar species Streptomyces violaceusniger and S. hygroscopicus show an intermediate DNA hybridization level of 42%. In our study, both strains shared highly similar (r = 0.89), though not identical, protein profiles. Kim et al. (1999) recently clarified the taxonomic status of thermophilic streptomycetes. For instance, it was shown that Streptomyces thermoviolaceus and Streptomyces thermovulgaris are distinct taxa, as they share a low DNA hybridization value of 10%. This low value is confirmed by different protein patterns (r = 0.83).

**Comparison with phenotypic data**

A low correlation is observed between the protein profiles and the numerical phenotypic data provided by Williams et al. (1989) and Kämpfer & Kroppenstedt (1991). We expected that taxa sharing high DNA–DNA hybridization values would group within the same phenotypic cluster. Only for the type strains of S. aminophilus, LMG 19319T, and S. cacaoi subsp. cacaoi, LMG 19320T, do the observed high relatedness (100%, Table 1) correlate with their phenotypic cluster assignment (Fig. 2), as both strains are classified in speciesgroup Cat. I-sp. 9 according to Williams et al. (1989), and in cluster 31 according to Kämpfer & Kroppenstedt (1991). A partial correlation with former studies was observed in the following case: S. hygroscopicus subsp. hygroscopicus LMG 19335T and S. endus LMG 19393T (DNA hybridization of 92%) are both grouped in speciesgroup Cat. I-sp. 16 by Williams et al. (1989), but belong to cluster 56 and cluster 41, respectively, according to Kämpfer & Kroppenstedt (1991). S. niveus LMG 19395T and S. spheroides LMG 19392T (DNA hybridization of 77%) belong to the speciesgroup Cat. I-sp. 2 according to Williams et al. (1989), but are classified in cluster 43 and cluster 40, respectively, according to Kämpfer & Kroppenstedt (1991). S. caereusus LMG 19399T, which belongs to the same DNA hybridization group (showing 85 and 100% DNA hybridization, respectively, to S. spheroides LMG 19392T and S. niveus LMG 19395T), is grouped in Cat. IV-sp. 7 by Williams et al. (1989), and in cluster 58 by Kämpfer & Kroppenstedt (1991). S. violaceus LMG 19360T and S. violatus LMG 19397T (sharing 90% DNA hybridization) are classified in Cat. I-sp. 5 and Cat. I-sp. 11 according to Williams et al. (1989), and in clusters 9 and 50 according to Kämpfer & Kroppenstedt (1991). In one case, no correlation existed between our data and those of other authors, i.e. S. aurantiacus LMG 19358T and S. albosporeus subsp. albosporeus LMG 19403T (having DNA hybridization of 74%), are classified in Cat. II-sp. 13 and Cat. IV-sp. 1 according to Williams et al. (1989), and in clusters 12 and 63 by Kämpfer & Kroppenstedt (1991). These results clearly confirm that the phenotypic groupings provided by Williams et al. (1989) and Kämpfer & Kroppenstedt (1991) do not always reflect the genomic relationships.

In the genus *Streptomyces* (conventional) phenotypic data still dominate the classification system. In other genera containing fewer species (e.g. the genus *Helicobacter*; Dewhirst et al., 2000), this phenotypic classification system has already gradually evolved into a polyphasic approach (in which genomic data are most often used as a basis for delineation of taxa). It is logical that we should pursue an analogous polyphasic taxonomy for the genus *Streptomyces*, and that it is no longer acceptable to use different criteria for speciation in different groups of bacteria. Genotypy should preferably precede phenotypy. Only when genome-based groups are defined can the search for phenotypic traits (which may or may not be successful) begin.

From our study, it is clear that SDS-PAGE of whole-cell proteins, applied under highly standardized conditions, is a valuable phenotypic tool for screening for synonyms within the genus *Streptomyces*, provided that DNA–DNA hybridization experiments are performed to confirm genomic relatedness at the species level.

On the basis of the data from this paper, we propose the following synonyms in the genus *Streptomyces*: S. albosporeus subsp. albosporeus LMG 19403T is a subjective synonym of S. aurantiacus LMG 19358T; S. aminophilus LMG 19319T is a subjective synonym of S. cacaoi subsp. cacaoi LMG 19320T; S. niveus LMG
19395^T and *S. spheroides* LMG 19392^T are subjective synonyms of *S. caeruleus* LMG 19399^T; *S. violatus* LMG 19397^T is a subjective synonym of *S. violaceus* LMG 19360^T. Emended descriptions are given below and are based on the species descriptions, as given by Williams *et al.* (1989), and the original descriptions.

**Emended description of Streptomyces cacaoi subsp. cacaoi** Waksman in Bunting 1932, 515–517; Waksman and Henrici 1948, 951^AL

Spore chains are *spirales*. The spore surface is smooth. The aerial mass is yellow or grey. The reverse side of a colony has no distinctive pigments. Melanin pigment is not formed and soluble pigments are not produced. The following carbohydrates are utilized for growth: D-glucose, L-arabinose, D-xylene, D-mannitol and D-fructose. There is no growth, or only traces of growth, on iso-inositol and rhamnose. The G+C content of the DNA is 73 mol%. The type strain is IMRU 3082^T (= LMG 19320^T). Subjective synonym: *Streptomyces aminophillus* IJSB 30:371^AL ATCC 14961^T (= LMG 19319^T).

**Emended description of Streptomyces caeruleus** (based on the original descriptions of *S. caeruleus* and *S. spheroides*) (Baldacci 1944) Pridham, Hesseltinge and Benedict 1958, 60^AL (Actinomycyes caeruleus Baldacci 1944, 180)

Spore chains are *rectiflexibles* or *spirales*. The spore surface is smooth. The aerial mass is yellow or grey. The reverse side of a colony is dark blue-violet to black (for *S. caeruleus*) and is pale yellow to light yellowish brown (for *S. spheroides*). Melanoid pigments are not formed. Bluish-black to greenish-black diffusible pigments are produced on some media (for *S. caeruleus*). Carbon utilization in *S. caeruleus* occurs only on D-glucose. Very poor growth is observed on Pridham and Gottlieb carbon-utilization medium when other carbon sources are being used. *S. spheroides* utilizes D-glucose, L-arabinose, sucrose, D-xylene, D-mannitol, D-fructose and rhamnose. Growth is possible on iso-inositol and raffinose. The G+C content of the DNA is 71 mol%. The type strain is IPV 930^T (= ISP 5103^T = LMG 19399^T). Subjective synonyms: *Streptomyces niveus* Smith, Dietz, Sokolski and Savage 1956, IJSB 30:394^AL NRRRL 2466 (LMG 19397^T) and *Streptomyces spheroides* Wallick *et al.* 1956, IJSB 30:401^AL DSM 40292^T (LMG 19392^T).

**Emended description of Streptomyces aurantiacus** (Rossi-Doria 1891), Waksman in Waksman and Lechevalier 1953, 53^AL Streptothrix aurantiaca Rossi-Doria 1891, 417

Spore chains are *spirales*. The spore surface is smooth. Aerial mycelium (if developed) belongs to the red colour series. The reverse side of a colony is yellow, yellow-brown, red or red-brown. Melanoid pigments are not formed and soluble pigments are not produced. The following carbohydrates are utilized for growth: D-glucose, L-arabinose, rhamnose, D-xylene, raffinose, sucrose (only for *S. aurantiacus*), iso-inositol (only for *S. aurantiacus*), D-galactose (only for *S. albosporeus* subsp. *albosporeus*), and meso-inositol (only for *S. albosporeus* subsp. *albosporeus*). The G+C content of the DNA is 70 mol%. The type strain is INMI 1373^T (= LMG 19358^T). Subjective synonym: *Streptomyces albosporeus* subsp. *albosporeus* IJSB 30:370^AL DSM 40795^T (LMG 19403^T).

**Emended description of Streptomyces violaces** (Rossi-Doria) Waksman and Henrici = *Actinomyces violaceus* (Rossi-Doria) Gasperini 1894, emend. Krasilnikov 1941; *Streptomyces violaces* (Rossi-Doria) Waksman in Waksman and Lechevalier 1953, 43

Spore chains are *spirales*. Spore chains are moderately long, comprising 10–50 or more spores per chain. The spore surface is spiny. The aerial mass is in the white or red colour series. The reverse side of a colony is reddish or reddish-orange to purple. Reverse mycelium pigment is a pH indicator. Melanoid pigments are formed (sometimes slowly). A red to violet pigment is found in the medium in yeast-malt agar, oatmeal agar, salt-star and glycerol-asparagine agar. This pigment is pH-sensitive. The following carbohydrates are utilized for growth: D-glucose, L-arabinose, D-xylene, D-fructose, rhamnose, sucrose, raffinose, iso-inositol and D-mannitol. The G+C content of the DNA is 71 mol%. The type strain is INMI 1^T (= LMG 19360^T). Subjective synonym: *Streptomyces violatus* IJSB 30:404^AL INMI 1205^T (LMG 19397^T).

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