Stenotrophomonas africana Drancourt *et al.* 1997 is a later synonym of *Stenotrophomonas maltophilia* (Hugh 1981) Palleroni and Bradbury 1993

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Type and reference strains of *Stenotrophomonas maltophilia* and *Stenotrophomonas africana* were compared with each other and with the type strains of other *Stenotrophomonas* species, using SDS-PAGE of whole-cell proteins, DNA–DNA hybridization and extensive biochemical characterization. *S. maltophilia* LMG 958^T and *S. africana* LMG 22072^T had very similar whole-cell-protein patterns and were also biochemically very similar. A DNA–DNA binding level of 70 % between both type strains confirmed that *S. africana* and *S. maltophilia* represent the same taxon. It is concluded that *S. africana* is a later synonym of *S. maltophilia*.

The genus *Stenotrophomonas* was created in 1993 to accommodate *Xanthomonas maltophilia* (formerly *Pseudomonas maltophilia*) (Palleroni & Bradbury, 1993). *Stenotrophomonas maltophilia* is an important cause of nosocomial infections and can be found in a wide range of environmental niches (Denton & Kerr, 1998). Several recent studies have shown that there is considerable genomic diversity within *S. maltophilia* and that this species consists of at least nine genomic groups (Hauben *et al.*, 1999; Coenye *et al.*, 2004). In addition, four novel *Stenotrophomonas* species have been described: *Stenotrophomonas africana* (Drancourt *et al.*, 1997), *Stenotrophomonas nitritireducens* (Finkmann *et al.*, 2000), *Stenotrophomonas acidaminiphila* (Assih *et al.*, 2002) and *Stenotrophomonas rhizophila* (Wolf *et al.*, 2002). The species *S. africana* was proposed for a single isolate recovered from cerebrospinal fluid. Phenotypically, this isolate was almost identical to the *S. maltophilia* type strain, the only difference being the absence of *cis*-aconitate assimilation in *S. africana*. However, DNA–DNA binding of only 35 % was observed between both strains (using the S1 nuclease/trichloroacetic acid method) (Drancourt *et al.*, 1997). In contrast, Assih *et al.* (2002) obtained a value of 65.9 %, using the initial renaturation method. To clarify the discussion regarding the taxonomic position of *S. africana*, we repeated the DNA–DNA hybridization experiment between the type strains of *S. africana* and *S. maltophilia*, determined biochemical and chemotaxonomic

characteristics for both taxa and re-evaluated previously published data.

The following strains were included in this study: *S. maltophilia* LMG 958^T, *S. africana* LMG 22072^T, *S. nitritireducens* LMG 22074^T, *S. acidaminiphila* LMG 22073^T and *S. rhizophila* LMG 22075^T, as well as seven additional *S. maltophilia* strains (LMG 3490, LMG 3491, LMG 3492, LMG 3495, LMG 3498, LMG 10875, LMG 10996) that belonged to the same genomic group as the type strain (Coenye *et al.*, 2004). A table with strain numbers is available as supplementary material in IJSEM Online.

Preparation of whole-cell proteins and SDS-PAGE were performed as described previously (Pot *et al.*, 1994). Densitometric analysis, normalization and interpolation of the protein profiles, and numerical analysis using the Pearson product-moment correlation coefficient were performed using the GelCompar 4.2 software package (Applied Maths). Computer-assisted and visual comparison of the protein profiles (Fig. 1) clearly showed that the profiles of *S. africana* and *S. maltophilia* reference strains were very similar.

High-molecular-mass DNA of the type strains of *S. africana* and *S. maltophilia* was prepared as described by Pitcher *et al.* (1989) and DNA–DNA hybridizations were performed with photobiotin-labelled probes in microplate wells as described by Ezaki *et al.* (1989), using an HTS7000 Bio Assay Reader (Perkin-Elmer) for the fluorescence measurements. The hybridization temperature was 50 °C. Reciprocal experiments were performed for every pair of strains. DNA from *S. africana* LMG 22072^T showed a high

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Supplementary material showing the strains used in the present study is available in IJSEM Online.

Fig. 1. Dendrogram derived from the unweighted pair-group average linkage of correlation coefficients between the protein patterns of the strains studied. The correlation coefficient is expressed as percentage similarity for convenience.

Table 1. Taxon-dependent phenotypic characteristics

1, *S. maltophilia* LMG 958^T; 2, *S. africana* LMG 22072^T; 3, *S. nitritireducens* LMG 22074^T; 4, *S. acidaminiphila* LMG 22073^T; 5, *S. rhizophila* LMG 22075^T.

Characteristic	1	2	3	4	5
Oxidase activity	–	–	+	+	–
β -Haemolysis	+	+	–	+	+
Growth at 42 °C	+	–	–	+	–
Growth in oxidation–fermentation medium with:					
Glucose	–	–	+	–	–
Maltose	+	+	–	+	+
D-Fructose	+	–	–	+	–
D-Xylose	–	–	+	–	–
Growth on cetrimide	+	–	–	–	+
Hydrolysis of Tween 80	+	+	–	–	+
Decarboxylation of lysine	+	+	–	–	+
Reduction of:					
Nitrate	+	–	–	+	+
Nitrite	–	–	+	+	–
β -Galactosidase activity	+	+	–	–	+
DNase activity	+	+	–	–	+
Growth in 4.5 % (w/v) NaCl	+	+	–	–	+
Assimilation of:					
D-Mannose	–	–	–	+	+
L-Malate	+	+	–	–	+
Citrate	+	+	+	–	+
Sucrose	+	+	–	–	–
DL-Lactate	–	–	+	+	–
Maltose	+	+	–	+	+
Activity of:					
Gelatinase	+	+	–	–	+
C-4 esterase	+	+	+	–	+
Valine arylamidase	–	+	+	–	+
Chymotrypsin	–	–	+	–	–
α -Galactosidase	–	+	–	–	–
α -Glucosidase	+	+	–	–	+
β -Glucosidase	+	+	–	–	+
N-Acetyl- β -glucosidase	–	–	+	+	–

binding level to DNA from *S. maltophilia* LMG 958^T (70 %), indicating that both strains belong to the same taxon.

The phenotypic characteristics of the type strains of all five *Stenotrophomonas* species were determined as described previously (Vandamme *et al.*, 1993). All strains investigated showed catalase, alkaline and acid phosphatase, C-8 esterase, leucine arylamidase and phosphoamidase activity and grew at 30 and 37 °C, on Drigalski agar (bioMérieux), in 0.5, 1.5 and 3.0 % (w/v) NaCl. None of the strains investigated showed amylase, tryptophanase, arginine dihydrolase, ornithine decarboxylase, arginine decarboxylase, urease, C-14 lipase, cysteine arylamidase, trypsin, β -glucuronidase, α -mannosidase or α -fucosidase activity or grew on fluorescein, 10 % lactose, acetamide or in 6.0 % (w/v) NaCl. All strains investigated hydrolysed aesculin and assimilated D-glucose and N-acetylglucosamine, whereas none of the strains investigated produced indole, produced acid or H₂S on triple-sugar-iron agar, or assimilated trehalose, L-arginine, DL-norleucine, L-arabinose, D-mannitol, D-glucuronate, caprate, adipate or phenylacetate. Taxon-dependent characteristics are shown in Table 1. The results of these tests clearly demonstrate that, although not identical, *S. africana* and *S. maltophilia* are phenotypically very similar. In addition, comparison of these phenotypic data with data obtained in previous studies (Van den Mooter & Swings, 1990; E. Falsen, unpublished data) showed that several of these phenotypic features (including growth at 42 °C, growth in oxidation-fermentation medium with D-fructose, growth in the presence of cetyltrimethylammonium bromide (Cetrimide; Sigma) and nitrate reduction) are variable within *S. maltophilia*.

The relationship between *S. africana* and *S. maltophilia* has been investigated previously. As mentioned above, Assih *et al.* (2002) had already noted a relatively high DNA-DNA binding value between the type strains of both species. The same authors also showed that the fatty acid composition of both type strains was virtually identical. We have recently shown that RFLP analysis of the PCR-amplified gyrase B gene is a convenient way to determine the genomic relationships between *Stenotrophomonas* sp. isolates, and we showed that the *Hae*III RFLP patterns of PCR-amplified *gyrB* of *S. maltophilia* LMG 958^T and *S. africana* LMG 22072^T were highly similar (Coenye *et al.*, 2004). The data from these studies, together with the novel data presented here, clearly show that *S. africana* LMG 22072^T is a strain of the species *S. maltophilia*. Consequently, *S. africana* Drancourt *et al.* 1997 is a later synonym of *S. maltophilia* (Hugh 1981) Palleroni & Bradbury 1993.

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