NOTES

Bacillus galactophilus Is a Later Subjective Synonym of *Bacillus agri*

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We confirm that *Bacillus galactophilus* Takagi, Shida, Kadowaki, Komagata, and Uda 1993 is a later subjective synonym of *Bacillus agri* Nakamura 1993 on the basis of chemosystematic data and DNA relatedness data.

Recently, Nakamura (4) and Takagi et al. (5) published the results of taxonomic studies of *Bacillus brevis* and related bacilli independently and almost simultaneously. Nakamura separated the species *Bacillus agri* and *Bacillus centrosporus* from *B. brevis* on the basis of phenotypic characteristics and DNA relatedness data (4). *Bacillus migulanus*, *Bacillus choshinensis*, *Bacillus parabrevis*, and *Bacillus galactophilus* were separated from *B. brevis* on the basis of phenotypic characteristics, chemosystematic data, and DNA relatedness data by Takagi et al. (5). However, Nakamura and Takagi et al. did not exchange and compare the type strains designated by each other. In this study, we compared strains of *B. agri* and *B. centrosporus* with strains

of the four new species described by Takagi et al. on the basis of chemosystematic data and DNA relatedness data.

The organisms shown in Table 1 were cultured on T2 agar plates (6) for 24 h at 30°C and stored at room temperature. Preparation of chromosomal DNA, estimation of DNA base composition, analysis of cellular fatty acid composition and isoprenoid quinones, and immunological analysis of extracellular proteins by using the antiserum against the surface layer protein (protein HWP) of *B. choshinensis* HPD31 (1) were carried out by the methods described previously (5). DNA relatedness values were determined by using probes labeled with photobiotin (Vectra Laboratories, Inc., Burling-

TABLE 1. DNA base compositions and levels of DNA relatedness for *B. agri*, *B. galactophilus*, *B. centrosporus*, *B. migulanus*, *B. choshinensis*, *B. brevis*, and *B. parabrevis* strains

Strain ^a	G+C content (mol%) ^b	% Reassociation with DNA from ^c :						
		<i>B. agri</i> NRRL NRS-1219 ^{Td}	<i>B. galactophilus</i> NRRL NRS-616 ^T	<i>B. centrosporus</i> NRRL NRS-664 ^T	<i>B. migulanus</i> ATCC 9999 ^T	<i>B. choshinensis</i> HPD52 ^T	<i>B. brevis</i> JCM 2503 ^T	<i>B. parabrevis</i> IFO 12334 ^T
<i>B. agri</i> NRRL NRS-1219 ^T	53.2	100	99	NT ^e	18	22	19	20
<i>B. agri</i> NRRL NRS-874	52.2	100	100	NT	NT	NT	NT	NT
<i>B. agri</i> NRRL NRS-1060	52.1	74	87	NT	NT	NT	NT	NT
<i>B. galactophilus</i> NRRL NRS-616 ^T	52.5	80	100	37	NT	NT	NT	NT
<i>B. galactophilus</i> HP037	52.8	79	72	NT	NT	NT	NT	NT
<i>B. centrosporus</i> NRRL NRS-664 ^T	49.4	NT	42	100	43	31	21	20
<i>B. migulanus</i> ATCC 9999 ^T	43.1	1	NT	1	100	NT	NT	NT
<i>B. choshinensis</i> HPD52 ^T	48.2	13	NT	27	NT	100	NT	NT
<i>B. brevis</i> JCM 2503 ^T	47.0	8	NT	11	NT	NT	100	NT
<i>B. parabrevis</i> IFO 12334 ^T	51.8	20	NT	16	NT	NT	NT	100

^a Abbreviations for culture collections: NRRL, Microbial Properties Research, National Center for Agricultural Utilization Research, Peoria, Ill.; ATCC, American Type Culture Collection, Rockville, Md.; JCM, Japan Collection of Microorganisms, Saitama, Japan; IFO, Institute for Fermentation, Osaka, Osaka, Japan.

^b G+C contents are averages of the values from three determinations. The maximum variation observed was 0.2 mol%.

^c Reassociation values are the averages of the values from two determinations. The maximum variation observed was 8%.

^d T = type strain.

^e NT, not tested.

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game, Calif.) in microplate wells and a fluorometric method described by Ezaki et al. (2).

The major menaquinone of the type strains of *B. agri* and *B. centrosporus* was menaquinone 7 (more than 99% of the total menaquinones), and these strains contained anteiso-C_{15:0} acid (40% of the total cellular fatty acids in *B. agri* and 63% of the total cellular fatty acids in *B. centrosporus*) and iso-C_{15:0} acid (41 and 23% of the total cellular fatty acids in *B. agri* and *B. centrosporus*, respectively). The extracellular proteins produced by the type strains of *B. agri* and *B. centrosporus* cross-reacted with the antiserum against protein HWP (data not shown). These results were almost the same as the results obtained for the other species belonging to the *B. brevis* group (5).

The DNA base compositions and levels of DNA relatedness of the strains tested are shown in Table 1. The levels of DNA relatedness between the type strains of *B. centrosporus*, *B. migulanus*, *B. choshinensis*, and *B. parabrevis* were found to be low. Therefore, these taxa can be considered independent species. However, the DNA base compositions of the three strains of *B. agri* and two strains of *B. galactophilus* included in this study ranged from 52.1 to 53.2 mol% G+C. These strains exhibited DNA relatedness values of more than 72%. Therefore, these strains should be considered members of a single species on the basis of the criteria which were suggested by an ad hoc committee of the International Committee on Systematic Bacteriology (7). Since the name *B. agri* has nomenclatural priority over *B. galactophilus* according to the *International Code of Nomenclature of Bacteria* (3), *B. galactophilus* should be considered a later subjective synonym of *B. agri*. Therefore, we propose that the name *Bacillus agri* should be retained for this species; the type strain of this species is NRRL NRS-1219.

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