Transfer of the Type Species of the Genus *Thermobacteroides* to the Genus *Thermoanaerobacter* as *Thermoanaerobacter acetoethylicus* (Ben-Bassat and Zeikus 1981) comb. nov., Description of *Coprothermobacter* gen. nov., and Reclassification of *Thermobacteroides proteolyticus* as *Coprothermobacter proteolyticus* (Ollivier et al. 1985) comb. nov.

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Phylogenetic and phenotypic evidence demonstrates the taxonomic heterogeneity of the genus *Thermobacteroides* and indicates a close relationship between *Thermobacteroides acetoethylicus* and members of the genus *Thermoanaerobacter*. Since *T. acetoethylicus* is the type species of *Thermobacteroides*, its removal invalidates the genus. As a consequence, the remaining species *Thermobacteroides proteolyticus* is proposed as the type species of the new genus *Coprothermobacter* gen. nov., as *Coprothermobacter proteolyticus* comb. nov.

Recent phylogenetic studies (8, 9) of anaerobic thermophilic species demonstrated that the majority of strains fall within the phylogenetic confines of the *Clostridium-Bacillus* subphylum of gram-positive bacteria. In contrast to the phylogenetically coherent genera *Thermoanaerobacter* (6) and *Thermoanaerobacterium* (6), members of *Thermobacteroides* (1, 7) belonged to phylogenetically very diverse taxa (8). While the type species *Thermobacteroides acetoethylicus* (1) was closely related to members of *Thermoanaerobacter* (9), *Thermobacteroides proteolyticus* represented a deep root adjacent to members of the order *Thermotogales*, showing only 81.9% sequence similarity with *Thermobacteroides acetoethylicus* over the stretch of about 1,200 analyzed nucleotides (8). On the basis of these phylogenetic findings, supported by phenotypic characteristics, we put forward the evidence for the reclassification of the species investigated. The genus *Thermobacteroides* contains three validly described species, *Thermobacteroides acetoethylicus* (1, 9), *Thermobacteroides proteolyticus* (7), and *Thermobacteroides leptospartum* (4, 12). Attempts to obtain *Thermobacteroides leptospartum* IAM 13499 from the Institute of Applied Microbiology, University of Tokyo, Tokyo, Japan, failed.

This article is composed of two parts: (i) the transfer of the type species of *Thermobacteroides*, *Thermobacteroides acetoethylicus*, to the genus *Thermoanaerobacter*, with the consequence of invalidating the genus *Thermobacteroides*, and (ii) the description of the genus *Coprothermobacter* and the assignment of *Thermobacteroides proteolyticus* as the type species *Coprothermobacter proteolyticus*.

***Thermoanaerobacter acetoethylicus* comb. nov.** Genera *Thermobacteroides* and *Thermoanaerobacter* were both described in 1981 (1, 13), and the type strain of each was not available to the authors of the article on the other genus for direct comparison. It was not until recently that the close phylogenetic relatedness of the type strains of the type species of these two genera was demonstrated (9). *Thermobacteroides acetoethylicus* was never included in DNA

hybridization studies with all members of *Thermoanaerobacter* (6, 10) despite the fact that, like *Thermoanaerobacter* species, *Thermobacteroides acetoethylicus* is an anaerobic, thermophilic, glycolytic bacterium capable of growth above 70°C that has been isolated from geothermal environments. The reclassifications of the recent study of Lee et al. (6) increased the numbers of species of *Thermoanaerobacter* to now include *Thermoanaerobacter ethanolicus*, *Thermoanaerobacter brockii*, *Thermoanaerobacter finnii*, and *Thermoanaerobacter thermohydrosulfuricus*. *Thermobacteroides acetoethylicus* seems to have been overlooked in recent studies, possibly because of the differences previously reported to exist between *Thermobacteroides acetoethylicus* and *Thermoanaerobacter brockii* (1) in motility, Gram staining, fermentation end products, cell wall structure, and (detected later) spore formation (2). These organisms share as one of the main features used to define members of *Thermoanaerobacter* the reduction of thiosulfate, but not sulfate, to sulfide (1, 5). Other common features (for which data are available) are rod-shaped morphology of organisms from the logarithmic phase of growth, DNA base composition of 31 to 37 mol% (not considering the high values of 37 to 39 mol% determined for *Thermoanaerobacter ethanolicus* by the buoyant density method), high G+C composition (56 to 59 mol%) of genes coding for rRNA, lack of catalase and cytochromes, maximum growth temperature above 75°C, optimal growth temperature above 65°C, and a pH for growth between 5.5 and 8.5 (1, 5, 10, 13). In addition, Wiegel (14) pointed out that the only difference between *Thermoanaerobacter ethanolicus* and *Thermobacteroides acetoethylicus* is the inability of the latter species to form more than 1.5 mol of ethanol per mol of glucose utilized.

Description of *Thermoanaerobacter acetoethylicus* (Ben-Bassat and Zeikus) comb. nov. The description of the species has not been emended since its effective published description (1, 3). The transfer of the species to the genus *Thermoanaerobacter* does not change the description of this genus. The type strain of *Thermoanaerobacter acetoethylicus* is HTB2/W (ATCC 33265).

Description of the genus *Coprothermobacter*. The transfer of

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TABLE 1. Characteristics differentiating *C. proteolyticus* from phylogenetically related and phenotypically similar taxa

Bacterium(-a)	Morphology	Motility	mol% G+C	Optimum temp (°C)	Maximum temp (°C)	Fermentation end products ^a	S ⁰ metabolism
<i>Coprothermobacter proteolyticus</i>	Rods; pleomorph	—	45	63	75	A, CO ₂ , H ₂	NR ^b
<i>Aquifex pyrophilus</i>	Rods, aggregates	+	40	85	95	— ^c	H ₂ S from sulfur
<i>Thermotoga</i> spp.	Rods, toga	Var ^d	40–46	70–80	90	L, A, CO ₂ , H ₂	H ₂ S from sulfur
<i>Thermosipho</i> spp.	Rods, toga, chains	—	30	75	77	L, A, CO ₂ , H ₂	H ₂ S from sulfur
<i>Fervidobacterium</i> spp.	Rods, spheroids	Var	34–40	65	80	L, A, E, b, v, CO ₂ , H ₂	H ₂ S from sulfur
<i>Thermoanaerobacter</i> spp.	Rods	Var	31–37	64–69	75–78	A, E, L, CO ₂ , H ₂	H ₂ S from thiosulfate
<i>Thermoanaerobacterium</i> spp.	Rods	+	33–36	60	68–75	A, E, L, CO ₂ , H ₂	S ⁰ from thiosulfate

^a A, acetate; L, lactate; E, ethanol; b, *n*-butyrate; v, *n*-valerate.

^b NR, not reported.

^c —, *A. pyrophilus* is chemolithoautotrophic.

^d Var, variable.

the type species of the genus *Thermobacteroides* to the genus *Thermoanaerobacter* invalidates the genus *Thermobacteroides* (rule 37a [1]) (11). In order to find a place for the orphan *Thermobacteroides proteolyticus*, two options are available. One could revive the genus *Thermobacteroides*, or alternatively, a new genus could be proposed. The revival of *Thermobacteroides*, in our opinion, is unwise since the *-bacteroides* part of the name implies a relationship to the genus *Bacteroides*. As pointed out previously (8), *Thermobacteroides proteolyticus* is not a member of the *Bacteroides*-*Cytophaga* phylum but constitutes a deep-rooting phylum of the domain *Bacteria*. The origin of this species from a thermophilic digester fed with cattle manure and tannery waste led us to propose the genus name *Coprothermobacter*. This name appears to be appropriate, since the currently unavailable species *Thermobacteroides leptospartum* (12), which resembles *Thermobacteroides proteolyticus* in phenotypic properties and the base composition of DNA (Table 1), was also isolated from cattle manure. As long as *Thermobacteroides leptospartum* is unavailable, its phylogenetic position cannot be determined, and hence, this species cannot be reclassified at this time.

C. proteolyticus is proposed as the type species because its description (7) predates that of *Thermobacteroides leptospartum* (4, 12). Members of the genus *Coprothermobacter* can be distinguished from other anaerobic, thermophilic bacteria by a combination of characters (Table 1).

Description of *Coprothermobacter* Rainey and Stackebrandt
gen. nov. *Coprothermobacter* (co'pro.ther'mo.bac'ter) gen. nov. Gr. fem. n. *kopros* manure; Gr. adj. *thermos* warm; Gr. hyp. mas. n. *bakter* rod; N.L. mas. n. *Coprothermobacter*, because it is a thermophilic rod-shaped bacterium isolated from cattle manure. The cellular characteristics have been adopted from the descriptions of Ollivier et al. (7) for *Thermobacteroides proteolyticus*. Gram-negative, nonmotile, non-spore-forming rods. Obligately anaerobic. Chemoorganotrophs which metabolize peptone and are proteolytic. Glucose and lactose are fermented; other carbohydrates are used poorly unless yeast extract and either rumen fluid or Trypticase peptone are added. The principal fermentation end products are acetic acid, H₂, and CO₂ or acetic acid and ethanol. Thermophilic temperature range for growth, with optimum of 65°C. The G+C content of the DNA is 45 mol%. The type species *C. proteolyticus*, represents a novel line of descent within the radiation of deep-branching phyla of the domain *Bacteria*.

The description of *C. proteolyticus* comb. nov. is as published for *Thermobacteroides proteolyticus* by Ollivier et al. (7).

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