Phylogenetics & Evolutionary Biology

Research Article

Phylogenetic Analyses of the Genus *Hymenobacter* and Description of *Siccationidurans* gen. nov., *Parahymenobacter* gen. nov

Gundlapally Sathyarayana Reddy*

CSIR-Centre for Cellular and Molecular Biology, Uppal Road, Hyderabad-500 007, India

Abstract

Phylogenetic analyses of 26 species of the genus *Hymenobacter* based on the 16S rRNA gene sequences, resulted in polyphyletic clustering with three major groups, arbitrarily named as Clade1, Clade2 and Clade3. Delineation of Clade1 and Clade3 from Clade2 was supported by robust clustering and high bootstrap values of more than 90% and 100% in all the phylogenetic methods. 16S rRNA gene sequence similarity shared by Clade1 and Clade2 was 88 to 93%, Clade1 and Clade3 was 88 to 91% and Clade2 and Clade3 was 89 to 92%. Based on robust phylogenetic clustering, less than 93.0% sequence similarity, unique in silico restriction patterns, presence of distinct signature nucleotides and signature motifs in their 16S rRNA gene sequences, two more genera were carved to accommodate species of Clade1 and Clade3. The name *Hymenobacter, sensu stricto*, was retained to represent 17 species of Clade2. For members of Clade1 and Clade3, the names *Siccationidurans* gen. nov. and *Parahymenobacter* gen. nov. were proposed, respectively, and sequence belonging to Clade1 and Clade3 were transferred to their respective genera. The genera *Hymenobacter, sensu stricto*, *Siccationidurans* gen. nov. and *Parahymenobacter* gen. nov. contained the signature motifs AAGGGCTTTTGAGTCGTAAG (414-432), TGACGGATCGAGGAAAT (480-499) and ATTAATACCGCATAACACT (168-185) in their 16S rRNA gene sequences, respectively. Further, the genus *Hymenobacter* was emended and proposed a more acceptable genus description.

Keywords: Phylogeny; 16S rRNA gene sequence; *Siccationidurans* gen. nov.; *Parahymenobacter* gen. nov.; *Hymenobacter*

Introduction

Analysis and validation of 16S rRNA gene sequence based phylogeny is the basis for prokaryotic systematics [1,2]. In this context, it is worth mentioning that, based on 16S rRNA gene sequence analyses, five distinct phylogenetic groups within the genus *Bacillus* [3], two novel orders, *Soliribrobacterales* and *Thermoleophilaes* [4], and a new hierarchical classification structure for the actinomycete line of descent [5] were proposed and the phylogenetic affiliation of the genus pseudomonads was assessed [6]. In congruence with these, to take few examples, several novel genera, such as *Solibacillus* [7] and *Planomicrobium* [8], were created on the basis of their 16S rRNA gene sequences, present work is focused on evaluating the internal features of the 16S rRNA gene sequences of the genus *Hymenobacter*.

The genus *Hymenobacter*, which belongs to the phylum *Bacteroidetes*, order *Sphingobacterales* and family *Cytophagaceae*, was described by Hirsch et al. [9] and subsequently emended by Buczolits et al. [10]. The genus accommodates species that are strictly aerobic, Gram-negative, rod-shaped, non-motile, red-pigmented and contain menaquinone MK-7, fatty acids iso-C15:0 anteiso-C15:0, C16:1ω5c, summed feature 3 (C16:1ω7c/iso-C15:0 2-OH) and summed feature 4 (iso-C15:0 1vanteiso-C16:1 B) with high DNA G+C content of 55 to 65 (mol %). The genus presently contains 26 species, including recently described species [11,12], which were isolated from various ecological niches. Klassen and Foght [13] and Reddy and Garcia-Pichel [12], in their recent study, discussed the polyphyletic clustering of all species into three major clades, (Clade1, Clade2 and Clade3), based on 16S rRNA gene sequence. Clade1, Clade2 and Clade3 encompassed seven, seventeen and two species, respectively. Exploration of the internal features of the 16S rRNA gene sequences of 26 species of the genus *Hymenobacter* warrant the creation of two novel genera to accommodate species that belong to Clade1 and Clade3; for which the names *Siccationidurans* gen. nov. and *Parahymenobacter* gen. nov. are proposed. *Hymenobacter soli* PB17′=LMG 24240′=KCTC 12607′, the oldest species belonging to Clade1, was elevated to the status of type species of the genus *Siccationidurans* and named as *Siccationidurans* soli PB17′=LMG 24240′=KCTC 12607′. Similarly, *Hymenobacter ocellatus* Myx 2105′=Txo1′=DSM 11117′=LMG 21874′ was transferred to the genus *Parahymenobacter* as *Parahymenobacter ocellatus* Myx 2105′=Txo1′=DSM 11117′=LMG 21874′ and designated as the type species. Further, the genus *Hymenobacter* needs be emended as Hirsh et al. [9] and Buczolits et al. [10] had included strain specific characteristics, some of which were not characterized in all the species, as in the case of spermidines. With the identification of signature nucleotides and signature motifs, a more acceptable genus description is proposed.

Methods

Phylogenetic analyses

Almost full length 16S rRNA gene sequences belonging to species of the genera *Hymenobacter, Pontibacter, Adhaeribacter* and *Cytophaga*, were downloaded from the NCBI database (http://www.ncbi.nlm.nih.gov). For phylogenetic analyses, all the sequences were aligned using CLUSTAL-W, the multiple alignment program option of MEGA5 [14]. Evolutionary distances between all species were computed using Kimura 2-model [15], present in the distance option of MEGA5. Phylogenetic trees were constructed using four different tree-making algorithms (Neighbor-Joining, Minimum Evolution, Maximum Likelihood and Maximum parsimony analysis), using MEGA5. Bootstrap analyses in all the phylogenetic trees were performed employing 1000 replicate data sets in order to assess the stability among clades recovered in the phylogenetic tree.

*Corresponding author: Gundlapally Sathyarayana Reddy, CSIR-Centre for Cellular and Molecular Biology, Uppal Road, Hyderabad-500 007, India, Tel: 91-40-27192509; E-mail: rukmagari@gmail.com

Received September 04, 2013; Accepted October 17, 2013; Published October 25, 2013

Citation: Sathyarayana Reddy G (2013) Phylogenetic Analyses of the Genus *Hymenobacter* and Description of *Siccationidurans* gen. nov., *Parahymenobacter* gen. nov. J Phylogen Evolution Biol 1: 122. doi:10.4172/2329-9002.1000122

Copyright: © 2013 Sathyarayana Reddy G. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.
Restriction enzyme analysis

Fifteen Type II Restriction enzymes (Table S1) were considered for generating in silico restriction patterns. For this purpose, Restriction Mapper Version 3 (http://restrictionmapper.org) was used to map the restriction patterns of 26 Hymenobacter species (sequence length from 118 to 1460; with respect to E. coli 16S rRNA sequence with accession number J01695), employed for construction of phylogenetic framework. These restriction patterns were analyzed and a consensus pattern was determined for each species.

Cluster analysis for restriction profile

For cluster analyses NTSSYSpcs, Numerical Taxonomy System and multivariate statistical package, software version 2.2 [16] was used. Initially, data for restriction patterns generated in silico, using different type II restriction enzymes, was entered in the form of 1 (presence of a band) and 0 (absence of a band) in NTedt 1.1. The similarity matrix was generated using SimQual of similarity, the dendrogram was constructed with Shan of Clustering option and the trees were viewed with Graphics options present in NTSSYSp.

Signature nucleotides

Signature nucleotides that are highly conserved in every sequence or in a specific clade were identified in the alignment file that was generated using MEGAS5 [14]. Every single signature nucleotide found was then positioned on the secondary structure of 16S rRNA molecule of E. coli (accession number J01695; obtained from (http://www.rna.icmb.utexas.edu/SIM/4C/mfold_Eval/accuracy/16s.acc.detailed)). This analysis allowed interpretation of signatures found in terms of single or double compensatory mutations in helices of the secondary structure. Compensatory mutations are two nucleotides that stabilize a stem in the secondary structure (such as G–C or A–T), and are mutated (for example to C–G or T–A) in specific taxa.

Signatures motifs

Signatures motifs were identified in each of the species data set using the online MEME program [17]. Seven, seventeen and two sequence data sets of Clade1, Clade2 and Clade3, respectively, belonging to the genus Hymenobacter were submitted group wise in MEME program version 4.6.1 (http://meme.nbcr.net/meme/cgi-bin/meme.cgi). In order to obtain maximum number of motifs, the default setting was modified from 3 to 10 motifs. The default value of motif width was also modified and re-set between 10 and 20. Each of the 10 signatures was checked for its frequency of occurrence among a particular Hymenobacter species. The signatures which did not appear in other clades of the Hymenobacter species were considered as unique.

Results and Discussion

Twenty six, seven and four species of the genera Hymenobacter [9,10], Pontibacter [20] and Adhaeribacter [21], respectively, were aligned using CLUSTAL W option of MEGA5 [14]. The aligned 16S rRNA gene sequences exhibited two hyper variable regions spanning from 72 to 115 (33 nucleotides long) and 180 to 195 (15 nucleotides long) (with respect to E. coli 16S rRNA gene sequence; accession number J01695) and mapped V1 and V2 regions, respectively [22,23]. Most of the variation in 16S rRNA gene sequences of species of the genera was contributed by these two regions and rest of the variation is randomly distributed in the entire region of RNA gene sequences.

To avoid the ‘Felsenstein zone’ (i.e. retrieving a wrong tree even if it has high bootstrap values), phylogenetic analyses [24] were performed with different phylogenetic methods. For this purpose, Neighbor joining (NJ), Minimum evolution (ME), Maximum likelihood (ML) and Maximum parsimony (MP) options were used to generate the trees. Topology of Neighbor joining (NJ) and Minimum evolution (ME) trees indicated that species of the genera Pontibacter [20] and Adhaeribacter [21] formed coherent monophyletic clusters with bootstrap values above 85% (Figure 1 and S1). In case of Maximum likelihood (ML) and Maximum parsimony analyses, species of the genera Pontibacter appeared as a monophyletic clade, but Adhaeribacter showed a split in clustering, wherein Adhaeribacter terreus [25] emerged as a separate branch from the main cluster represented by rest of the species (Figure S2 and S3). Species of the genus Hymenobacter [9] were highly divergent, polyphyletic in all the methods and formed three major clusters, named arbitrarily as Clade1, Clade2 and Clade3 (Figures 1 and S1–S3), which are deeply rooted from each other and are sister clades emerging from a common ancestor. Further, delineation of Clade1 and Clade3 from Clade2 was supported by robust clustering and high bootstrap values of more than 90% and 100%, respectively in all the phylogenetic methods (Figures 1 and S1–S3), and the present clustering of species of the genus Hymenobacter is consistent with previous studies [12,13, 26–29].

Evolutionary distances, based on 16S rRNA gene sequence, as calculated using Kimura 2-parameter model [15], were found to be 90 to 97%, 92 to 99% and 95%, respectively, among species belonging to Clade1, Clade2 and Clade3 of the genus Hymenobacter. 16S rRNA gene
sequence similarity shared by Clade1 and Clade2 is 88 to 93%, Clade1 and Clade3 is 88 to 91% and Clade2 and Clade3 is 89 to 92% (Table S2), significantly larger than the ~95% threshold typically used to split genera [30]. The robust clustering of three clades belonging to the genus Hymenobacter with high bootstrap values (in all the four phylogenetic methods employed (Figures 1 and S1-S4), and aggregate sequence similarity of less than 93% among three clades (Clade1, Clade2 and Clade3), supported the proposal to assign species of Clade1 and Clade3 to a higher taxonomic rank [31]. The above proposal is significantly supported by the genera Adhaeribacter [21] and Pontibacter [20], as they also share a 16S rRNA gene sequence similarity of 88 to 92% and form a coherent cluster with high bootstrap values (Figures 1 and S1- S3).

In addition, the number of nucleotides conserved in the 16S rRNA gene of Gram-negative bacteria is more than that of Gram-positive bacteria. Gram-negative and Gram-positive bacteria contain 713/1542 and 568/1542 nucleotides, respectively, in the highly conserved regions [30], and a total of 145/1542 (9.4%) more nucleotides are conserved in Gram-negative bacteria. Under these circumstances, the difference of 88 to 93% among species of Clade1, Clade2 and Clade3, being Gram-negative by virtue, belonging to the genus Hymenobacter, is huge and demands the creation of new genera [30], since earlier the genera were carved with >92% 16S rRNA gene sequence similarity [7,8,32-34]. The main impediment is the lack of diagnostic phenotypic differences. However, Stackebrandt et al. [5], Ash et al. [3], Reddy and García-Pichel [4] and Ivanova et al. [31] created the genera, families and orders based only on the presence of unique signatures in 16S rRNA gene sequences, further implicating that the phylogenetic evidence alone is sufficient to create a higher taxonomic rank. However, polyphasic taxonomy emphasizes the significance of consensus between phenotypic and genotypic characteristics [35-38], in delineation of taxa. But several phenotypic markers are variable and dependent on environmental cues. For instance, the expression of characteristics that serve in genus description, such as cell morphology [39-42], enzymes [43,44], fatty acids [45,46] menaquinones [47-49], lipids [50-53] and peptidoglycan [54-57], depend on the growth conditions. Further, discrepancies in the above traits were well documented among species of several genera [58,59], and thus hamper in drawing congruence between phylogeny and expressed characteristics. On the other hand, 16S rRNA sequence based phylogeny has been serving as a stable trait in delineation of several taxa, and is considered as the basis in creation of numerous taxonomic groups, as mentioned earlier [4,5]. However, the importance of other polyphasic characteristics cannot be discounted, but should be considered as significant ancillary and descriptive, rather than distinctive markers per se. In the present study, it is unambiguously established by phylogenetic analyses that the genera, Siccationidurans gen. nov. and Parahymenobacter gen. nov., are distinctly different from already described nearest genera. Therefore, phenotypic traits were considered in the description of genera (please refer to the genus description).

Because of the low 16S rRNA sequence similarity of less than 93%, it was assumed that the restriction patterns would be different for the three clades of the genus Hymenobacter. In the present study, fifteen type II restriction enzymes (Table S1) were used in silico and they revealed differences in the fragmentation patterns. Restriction sites for AluI, BfaI, BstUI, DpnI, HaeIII, Hhal, MboI, MseI, MspI, RsaI and Sau3AI (11 enzymes) occurred with a frequency of 2-10, resulting in 3-11 fragments. The enzyme SmaI gave 2 restriction fragments of length 1280 and 48 (positions are with respect to H. arizoneisis), restriction sites for the enzymes BamHI and EcoRI were not found in any of the 26 sequences studied and HindIII had a single cut in a single species; the Hymenobacter psychrophilus. Thus the enzymes, BamHI, EcoRI, HindIII and SmaI are less informative and serve no purpose. In spite of low frequency, HindIII can still be used to distinguish the species, Hymenobacter psychrophilus and SmaI can be combined with other enzymes to distinguish the members of Hymenobacter [9]. The enzymes, AluI, BfaI, BstUI, HaeIII, Hhal, MseI, MspI, RsaI and SmaI generated 31 out of 113 common fragments in all the 26 species and can serve as markers to identify the members of this group. Interestingly, the enzymes DpnI, MboI, Sau3A1, HaeIII and RsaI distinguish the species of Clade1 from other Clades in that DpnI, MboI, Sau3A1 generated a fragment size of 209 in 19 species of Clade2 and Clade3, but not in Clade1. Similarly, HaeIII created a fragment size of 321 in species of Clade2 and Clade3, but not in Clade1 and RsaI produced a fragment of 556 in 6/7 species of Clade1 and lacks the fragment size of 645. Clade3 can be differentiated from Clade1 and Clade2 using AluI, which generates a fragment size of 515 in all, but Clade1 and in Clade2, the fragment is produced only in 6/17 species. Thus, the enzymes, DpnI, MboI, HaeIII, Sau3A1 and RsaI can be used as markers to distinguish the species of the three clades. Approximately, 113 fragments generated among 26 species of the genus Hymenobacter were used in dendogram construction and the species of Clade1, Clade2 and Clade3 delineated at a similarity coefficient value of 80%, 81% and 86.5, respectively (Figure S4). Thus, the in silico restriction patterns resulted in the differentiation of three clades belonging to the genus Hymenobacter and their robust clustering into three Clades, congruent to the 16S rRNA gene sequence based phylogeny further strengthened the need to create two more genera to accommodate the species of Clade1 and Clade3.

Further evidence in support of awarding genus status to members of Clade1 and 3 comes from the analyses based on comparison of base-to-base 16S rRNA gene sequences. Species of Clade1 are characterized by the presence of nucleotides G-C (294-303), G (306), G-C (317-336), A (408), T-A (419-424), C (427), T (434), G-C/G-G (462-476), T (477), A (658), A (728), T (747), C-G/C-G (897-902), G (1285) and A (1286) (20 nucleotides), of which nucleotides at positions 306, 317-336, 408, 419-424, 427, 658, 728, 747 are unique (Table 1). Species of Clade2 contain C (256), C (268), C-G (294-303), T-A (317-336), C-G (419-424), C (441), G (493), C-G (897-902), A (903), A (1285) (14 positions), of which nucleotides at positions 294-303, 441, 493 are distinctive. Similarly Clade3 possesses G (127), G (128), T (131), T (140), T (165), A (206), A (215), C (219), A (231), C (233), C-G (294-303), C (304), T-A (317-336), G (490), T (492), C (594), T (833), C (854), G-C (897-902), G (1019), C (1174), A (1275), C (1364) (27 positions). Positions 127, 128, 131, 140, 1364 and the absence of nucleotide at 462 differentiate Clade3 from Clade1 and Clade2 (Table 1). Close to 48 signature nucleotides were identified at various positions (Table 1), of which 20, 14 and 27 were highly conserved among Clade1, Clade2 and Clade3, respectively. There is no limit to the number of signature nucleotides in carving new genera as Dai et al. [60], identified a difference of just 2 signature nucleotides between the genera Planococcus and Planomonibacter. Further, based on the difference of 13 unique nucleotides, the genus Sphingosinimella, without strong phenotypic support, was dissected from Sphingomonas [61]. Thus, the presence of above signature nucleotides not only distinguishes between the three Clades, but also serves as additional evidence in carving the genera.

Splitting of the genus Hymenobacter [9] into three genera was further substantiated by unique signature motifs. Out of 19 signatures motifs identified among the three clades of the genus Hymenobacter using MEME [17], only 1-2 unique signatures motifs were
| Species       | Position of the nucleotide |
|--------------|----------------------------|
| E. coli (J01695) | T A T A C C G T G T A C T A G T C C C A |
| S. arizonensis (JX294485) | T G G C A T A C T G G C C T G T |
| S. gluciae (GQ54806) | T G G C A T A C T G C C T G T |
| S. antarcticus (EU155012) | T G G C A T A C T G T G C C T G T |
| S. soli (AB251884) | T G G C A T A C T G T G C C T G T |
| S. metalli (HM032898) | T G G C A T A C T G T G C C T G T |
| S. flocculans (HM032897) | T G G C A T A C T G T G C C T G T |
| S. ginsengisoli (JN090860) | T G G C A T A C T G T G C C T G T |
| H. psychrophilus (GQ131579) | T G G C A T A C T G T G C C T G T |
| H. psychrotolerans (DQ177475) | T G G C A T A C T G C C T G T |
| H. perfusus (HM032896) | T G G C A T A C T G C C T G T |
| H. xingiensis (GQ888329) | T G G C A T A C T G T G C C T G T |
| H. yonginensis (EU382214) | T G G C A T A C T G T G C C T G T |
| H. rigui (DQ098697) | T G G C A T A C T G T G C C T G T |
| H. psychrophilus (GQ131579) | T G G C A T A C T G T G C C T G T |
| H. psychrotolerans (DQ177475) | T G G C A T A C T G C C T G T |
| H. perfusus (HM032896) | T G G C A T A C T G C C T G T |
| H. xingiensis (GQ888329) | T G G C A T A C T G T G C C T G T |
| H. yonginensis (EU382214) | T G G C A T A C T G T G C C T G T |
| H. rigui (DQ098697) | T G G C A T A C T G T G C C T G T |
| H. psychrophilus (GQ131579) | T G G C A T A C T G T G C C T G T |
| H. psychrotolerans (DQ177475) | T G G C A T A C T G C C T G T |
| H. perfusus (HM032896) | T G G C A T A C T G C C T G T |
| H. xingiensis (GQ888329) | T G G C A T A C T G T G C C T G T |
| H. yonginensis (EU382214) | T G G C A T A C T G T G C C T G T |
| H. rigui (DQ098697) | T G G C A T A C T G T G C C T G T |
| H. psychrophilus (GQ131579) | T G G C A T A C T G T G C C T G T |
| H. psychrotolerans (DQ177475) | T G G C A T A C T G C C T G T |
| H. perfusus (HM032896) | T G G C A T A C T G C C T G T |
| H. xingiensis (GQ888329) | T G G C A T A C T G T G C C T G T |
| H. yonginensis (EU382214) | T G G C A T A C T G T G C C T G T |
| H. rigui (DQ098697) | T G G C A T A C T G T G C C T G T |
Ph, Parahymenobacter; gen. nov.

Signature nucleotides of the 16S rRNA gene sequences that differentiate the genera
Table 1:

| Position of the nucleotide | Species | 594 | 658 | 728 | 833 | 854 | 896 | 897 | 902 | 903 | 1019 | 1275 | 1285 | 1286 | 1364 |
|----------------------------|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-------|-------|-------|-------|
| E. coli (J01695)           | T       | C   | A   | A   | G   | G   | T   | G   | G   | A     | A     | A     | G     | A     | T     |
| H. arizonicus (JX294485)   | T       | A   | A   | T   | C   | T   | C   | C   | G   | G   | A     | T     | T     | G     | A     | T     |
| H. saltans (GQ454806)      | T       | A   | A   | A   | G   | G   | T   | C   | G   | A   | A     | T     | C     | G     | A     | T     |
| S. ophiolycus (Y18835)     | T       | A   | A   | T   | G   | T   | C   | G   | G   | G   | A     | T     | T     | G     | A     | T     |

Based on the robust phylogenetic clustering of the genus Hymenobacter into three clades, Clade1, Clade2 and Clade3, 16S rRNA gene sequence similarity of less than 93.0%, unique in silico restriction fragmentation pattern, signature nucleotides and signature motifs, two more genera were created to accommodate species of Clade1 and Clade3, retaining the name Hymenobacter, sensu stricto, to represent 17 species of the Clade2. For members of Clade1 and Clade3, the names Siccationidurans gen. nov. and Parahymenobacter gen. nov. are proposed and species belonging to Clade1 and Clade3 are transferred to the respective genera. In addition, Clade1 species are different from Clade2 and Clade3 in that they are negative for nitrate reduction and do not contain the fatty acid iso-C17:3-OH (Table 2). The other diagnostic characteristics of the genera are listed in Table 2.

Table 1: Signature nucleotides of the 16S rRNA gene sequences that differentiate the genera Siccationidurans gen. nov., Hymenobacter [9] and Parahymenobacter gen. nov. The numbering of nucleotide position is with respect to Escherichia coli 16S rRNA gene sequence (Acc. No. J01695); S. Siccationidurans; H. Hymenobacter; Ph, Parahymenobacter; -absence of a nucleotide; Positions in bold are the signature nucleotides of the genera.

Seven species of Clade1, H. arizonicus [12], H. glaciire [13], H. antarcticus [13], H. soli [62], H. metalli, H. flocculans [63] and H. ginsengisoli [11] were transferred to the genus Siccationidurans gen. nov. as Siccationidurans arizonicus comb. nov., Siccationidurans glaciei comb. nov., Siccationidurans antarcticus comb. nov., Siccationidurans soli comb. nov., Siccationidurans metalli comb. nov., Siccationidurans flocculans comb. nov., and Siccationidurans ginsengisoli comb. nov. Siccationidurans soli PB17^T = LMG 24240^T = KCTC 12607^T was designated as the type species of the genus, first described species among Clade1. Clade2 contains 17 species: H. actinosclerus [64], H. aerophilus [65], H. algircola, H. elongatus and H. fastidious [13], H. chitinivorans, H. gelipurpurascens and H. norwichiensis [10], H. dachaeongensis [66], H. roseosalivarius [9], H. rigui [67], H. psychrophilus [68], H. psychrotolerans [69], H. perfusus [69], H. tibetensis [70], H. xinjiangensis [71] and H. yonginensis [72]. Clade3 containing two species, H. deserti [73] and
Siccationidurans, gen. nov.

Phenotypic characteristics that differentiate the genera Table 2: [9], emend. Buczolits et al. [10] consists of iso- and anteiso C15:0, C16:1ω5c, iso-C15:0 3-OH, iso-C17:0 (APL3), while the quinone system present is MK-7. Fatty acid profile but positive for leucine arylamidase. Major polar lipids present are pigmented, non-motile, non-spore forming and rod shaped. They of the genus Hymenobacter, a rod growing in thin layers).

The species description is the same as that described by Klassen

Basonym: Hymenobacter solii [62].

The species description is the same as that described by Kim et al. [62].

H. arizonensis comb. nov.

The species description is the same as that described by Reddy and Garcia-Pichel [12].

Hymenobacter arizonensis: a.ri.zo.nen'sis.N.L. masc. adj. arizonensis, of or belonging to Arizona, one of the states of the United States of America).

Basonym: Hymenobacter arizonensis [12].

The species description is the same as that described by Reddy and Garcia-Pichel [12].

Description of Siccationidurans antarcticus comb. nov.

Siccationidurans antarcticus (antarcticus, southern, by extension pertaining to Antarctic, referring to its isolation source).

Basonym: Hymenobacter antarcticus [13].

The species description is the same as that described by Klassen and Foght [13].

Description of Siccationidurans glaciale comb. nov.

Siccationidurans glaciale (L. gen. n. glaciei, of ice, referring to its isolation from a glacier).

Basonym: Hymenobacter glaciei [13].

The species description is the same as that described by Klassen and Foght [13].

Description of Siccationidurans flocculans comb. nov.

Siccationidurans flocculans (N.L. part. adj. flocculans, flocculating,
referring to the organism's trait to flocculate in liquid cultures).

*Basonym: Hymenobacter flocculans* [63].

The species description is the same as that described by Chung et al. [63].

**Description of Siccationidurans metalli comb. nov.**

*Siccationidurans metallic* (L. gen. n. metalli, of a mine, from a mining area with metals).

*Basonym: Hymenobacter metalli* [63].

The species description is the same as that described by Chung et al. [63].

**Description of Siccationidurans Ginsengisoli comb. nov.**

*Siccationidurans ginsengisoli* (ginseng; L. n. ginseng; L. n. solum soil; ginseng field, the source of the type strain)

*Basonym: Hymenobacter ginsengisoli* [11].

The species description is the same as that described by Hoang et al. [11].

**Description of Parahymenobacter gen. nov.**

*Parahymenobacter: *Pa.*.ra.*hy.*me.*no.*ba*ct’er. Gr. prep. para, beside, near, like; N.L. masc. n. Hymenobacter, a bacterial genus name; N.L. masc. n. Parahymenobacter, beside Hymenobacter.

The genus *Parahymenobacter* gen. nov. contain the cells that are Gram-negative, strictly aerobic, pigmented, non-motile, non-spore forming and rod shaped. Catalase, oxidase leucine arylamidase and alkaline phosphatase positive, urease, arginine dihydrolase and indole forming and rod shaped. Catalase, oxidase leucine arylamidase and alkaline phosphatase positive, urease, arginine dihydrolase and indole production positive, hydrolyzes casein, gelatin and starch. MK-7 is the major menaquinone, while phosphatidylethanolamine (PE) and an unknown aminophospholipid (APL3) are the dominating lipids. Major fatty acids (above 5.0%) are iso-C₁₅:₀, anteiso-C₁₅:₀; C₁₆:₀ω₅c, iso-C₁₅:₀, 3-OH, iso-C₁₅:₀, 3-OH, summed feature 3 (C₁₆:₀ω7c/iso-C₁₅:₀, 2OH) and summed feature 4 (anteiso-C₁₇:₀, B/ anteiso-C₁₇:₁ I).

Signature nucleotides present are G (127), G (128), T (131), T (140), T (165), A (206), A (215), C (219), C (233), C (234), G-C (294-303), C (304), T-A (317-336), T (492), T (833), G-C (897-902), G (1019), C, A (1275), C (1364) and the signature motifs consists of the sequence ATTAATACCGCATAACACT (168-185) and TAGTTAAAGAATTT (205-218). Mole % G+C DNA content of the genus ranges from 58 to 65. *Parahymenobacter ocellatus* Myx 2105<sup>T</sup> = Txo1<sup>T</sup> = DSM 11117<sup>T</sup> = LMG 21874<sup>T</sup> is the type species of the genus.

**Description of Parahymenobacter ocellatus comb. nov.**

*Parahymenobacter ocellatus* (L. masc. adj. ocellatus, showing little eyes, referring to the bright granules at the cell poles).

*Basonym: Hymenobacter ocellatus* [10].

The species description is the same as that described by Buczolits et al. [10].

**Description of Parahymenobacter deserti comb. nov.**

*Parahymenobacter deserti* (L. gen. n. deserti, of a desert).

*Basonym: Hymenobacter deserti* [73].

The species description is the same as that described by Zhang et al. [73].

**Acknowledgements**

The author acknowledges Jean P. Euzéby by for suggesting the genera names and their epithet and Gundlapalli Raga Reddy in preparing the manuscript.
Citation: Sathyanarayana Reddy G (2013) Phylogenetic Analyses of the Genus Hymenobacter and Description of Siccationidurans gen. nov., Parahymenobacter gen. nov. J Phylogen Evolution Biol 1: 122. doi:10.4172/2329-9002.1000122
62. Kim KH, Im WT, Lee ST (2008) Hymenobacter soli sp. nov., isolated from grass soil. Int J Syst Evol Microbiol 58: 941-945.

63. Chung AP, Lopes A, Nobis MF, Moraes PV (2010) Hymenobacter perfusus sp. nov., Hymenobacter flocculans sp. nov. and Hymenobacter metalli sp. nov. three new species isolated from an uranium mine waste water treatment system. Syst Appl Microbiol 33: 436-443.

64. Collins MD, Hutson RA, Grant IR, Patterson MF (2000) Phylogenetic characterization of a novel radiation-resistant bacterium from irradiated pork: Description of Hymenobacter actinocphinus sp. nov. Int J Syst Evol Microbiol 50: 731-734.

65. Buczolits S, Denner EB, Vybiral D, Wieser M, Kämpfer P, et al. (2002) Classification of three airborne bacteria and proposal of Hymenobacter aerophilus sp. nov. Int J Syst Evol Microbiol 52: 445-456.

66. Xu JL, Liu QM, Yu HS, Jin FX, Lee ST, et al. (2009) Hymenobacter diaecheongensis sp. nov., isolated from stream sediment. Int J Syst Evol Microbiol 59: 1183-1187.

67. Baik KS, Seong CN, Moon EY, Park YD, Yi H, et al. (2006) Hymenobacter rigui sp. nov., isolated from wetland freshwater. Int J Syst Evol Microbiol 56: 2189-2192.

68. Zhang DC, Busse HJ, Liu HC, Zhou YG, Schinner F, et al. (2011) Hymenobacter psychrophilus sp. nov., a psychrophilic bacterium isolated from soil. Int J Syst Evol Microbiol 61: 859-863.

69. Zhang G, Niu F, Busse HJ, Ma X, Liu W, et al. (2008) Hymenobacter psychrotolerans sp. nov., isolated from the Qinghai-Tibet Plateau permafrost region. Int J Syst Evol Microbiol 58: 1215-1220.

70. Dai J, Wang Y, Zhang L, Tang Y, Luo X, et al. (2009) Hymenobacter fubetensisp. nov., a UV-resistant bacterium isolated from Qinghai-Tibet plateau. Syst Appl Microbiol 32: 543-548.

71. Zhang Q, Liu C, Tang Y, Zhou G, Shen P, et al. (2007) Hymenobacter xinjiangensis sp. nov., a radiation-resistant bacterium isolated from the desert of Xinjiang, China. Int J Syst Evol Microbiol 57: 1752-1756.

72. Joung Y, Cho SH, Kim H, Kim SB, Joh K (2011) Hymenobacter yonginensis sp. nov., isolated from a mesotrophic artificial lake. Int J Syst Evol Microbiol 61: 1511-1514.

73. Zhang L, Dai J, Tang Y, Luo X, Wang Y, et.al. (2009) Hymenobacter deserti sp. nov., isolated from the desert of Xinjiang, China. Int. J Syst Evol Microbiol 59: 77-82.

Submit your next manuscript and get advantages of OMICS Group submissions

Unique features:
- User friendly/feasible website-translation of your paper to 50 world's leading languages
- Audio Version of published paper
- Digital articles to share and explore

Special features:
- 250 Open Access Journals
- 20,000 editorial team
- 21 days rapid review process
- Quality and quick editorial, review and publication processing
- Indexing on PubMed (partial), Scopus, BIOSIS, Index Copernicus and Google Scholar etc
- Sharing Options, Social Networking Enabled
- Authors, Reviewers and Editors rewarded with online Scientific Credits
- Better discount for your subsequent articles

Submit your manuscript at: www.omicsonline.org/submission/