Phylogenetic positions of *Aeromonas encheleia*, *Aeromonas popoffii*, *Aeromonas* DNA hybridization Group 11 and *Aeromonas* Group 501

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The 16S rDNA sequences of the recently described *Aeromonas encheleia* and *Aeromonas popoffii*, were determined and compared with data from all known *Aeromonas* sp. Diagnostic 16S rDNA regions were also sequenced for some strains previously considered as an extension of *A. encheleia* and a strain of *Aeromonas* Group 501 (formerly Enteric Group 501). Results indicated that *A. encheleia* and *A. popoffii* are phylogenetically separated species as originally described. A conclusion about HG11 taxonomic status is not recommended until previous discrepancies are clarified by further DNA–DNA hybridization and sequencing studies.

**Keywords:** *Aeromonas encheleia*, *Aeromonas popoffii*, *Aeromonas* sp. HG11, *Aeromonas* Group 501, rRNA

The taxonomy of the genus *Aeromonas* has undergone major changes since its description in *Bergey’s Manual of Systematic Bacteriology* (Popoff, 1984). Extensive DNA–DNA hybridization studies (Popoff et al., 1981; Hickman-Brenner et al., 1987, 1988; Kuijper et al., 1989; Carnahan et al., 1991b) have resulted in the recognition of fourteen so-called DNA homology groups (HG), *Aeromonas hydrophila* (HG1), *Aeromonas* sp. (unnamed HG2), *Aeromonas salmonicida* (HG3), *Aeromonas caviae* (HG4), *Aeromonas media* (HG5), *Aeromonas eucrenophila* (HG6), *Aeromonas sobria* (HG7), *Aeromonas veronii* biogroup sobria (HG8), *Aeromonas iandaei* (HG9), *Aeromonas veronii* biogroup veronii (HG10), *Aeromonas* sp. (unnamed; HG11), *Aeromonas schubertii* (HG12), *Aeromonas* Group 501 (HG13; formerly Enteric Group 501) and *Aeromonas trota* (HG14). The name *Aeromonas bestiarum* has been proposed for strains included in HG2 (Ali et al., 1996). Recently, three new descriptions of species include: *Aeromonas allosaccharophila* (Martínez-Murcia et al., 1992b), *Aeromonas encheleia* (Esteve et al., 1995) and *Aeromonas popoffii* (Huys et al., 1997b). Discrepancies remain between observed HGS and groups derived from phenotypic analysis. The species *Aeromonas ichthiosmia* (Schubert et al., 1990b) and *Aeromonas enteropelogenes* (Schubert et al., 1990a) are now considered to be synonyms of *A. veronii* and *A. trota*, respectively.

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**Keywords:** *Aeromonas encheleia*, *Aeromonas popoffii*, *Aeromonas* sp. HG11, *Aeromonas* Group 501, rRNA
A. popoffii were provided in 1995 by M. Altwegg (Institute of Valencia, Spain). All other strains, listed in Table 2, were conserved to all these known for strain CECT 4254 (ATCC 43946), from the Coleccion Medical Microbiology, Zurich, Switzerland. Strain \textit{A. encheleia}, \textit{A. popoffii} and \textit{Aeromonas sp.} DHG 11 were provided by P. Dominguez, Instituto de Microbiologia, Universidad de Valencia. Strain \textit{A. popoffii} (LG 17541T) was a gift from M. J. Figueras, Universidad Rovira i Virgili, Reus, Spain. Strains were cultivated in trypticase soy broth (Oxoid) at 30°C for 24 h. Cultures were harvested and washed in deionized sterile water. Total DNA was extracted and purified, PCR performed and 16S rDNA sequence (continuous stretch of 1502 nucleotides) of \textit{A. encheleia} CECT 4342T determined following the methods described in Martinez-Murcia et al. (1992a). The homologous sequence (1502 nucleotides) of \textit{A. popoffii} LGM 17541T and the diagnostic 16S rDNA nucleotides located at the V2 and V3 regions (ca a continuous stretch of 300 bp ranging from positions 230 to 530, approximately; Martinez-Murcia et al., 1992a) of the remaining strains (Table 2) were sequenced using the Cy5 AutoRead Sequencing Kit (Pharmacia) on the ALFexpress DNA sequencer (Pharmacia), according to the manufacturer's indications. After this work was completed, partial 16S rRNAs of \textit{A. encheleia} and \textit{A. popoffii} were submitted in the GenBank in February 1998 by Demarta and co-workers (accession numbers AJ224309 and AJ224308, respectively). Except for size, sequences were compared and no difference was found. Newly determined sequences at both ends (95 nucleotides) of the gene were found to be conserved to all these known for \textit{Aeromonas}. Sequences of \textit{A. encheleia}, \textit{A. popoffii} and \textit{Aeromonas Group 501}, were aligned to other previously published sequences of \textit{Aeromonas} (Martinez-Murcia et al., 1992a) and a phylogenetic tree produced by the neighbouring joining method (Saitou & Nei, 1987) using the MEGA Program version 1.01 (Fig. 1).

The original description of \textit{A. schuberti} was based on seven highly related strains with the vernacular name Enteric Group 501 (Hickman-Brenner et al., 1988). This group included an eighth strain, CDC 2478-85 (ATCC 43946), which was less related to \textit{A. schuberti} than \textit{Aeromonas} hydorphila (ATCC 7966T), (X60404); \textit{A. bestiarum} CIP 7430T, (X60406); \textit{A. salmonicida} NCIMB 1102T, (X60405); \textit{A. caviae} NCIMB 13016T, (X60408); \textit{A. media} ATCC 33907T, (X60410); \textit{A. eucrenophila} NCIMB 741T, (X60411); \textit{A. sobria} NCIMB 12065T, (X60412); \textit{A. veronii} ATCC 35624T, (X60414); \textit{A. jandaei} ATCC 49568T, (X60413); \textit{Aeromonas} sp. DHG11 ATCC 35941T, (X604417); \textit{A. schuberti} ATCC 43700T, (X60416); \textit{A. trota} ATCC 49657T, (X60415); \textit{A. allosaccharophila} CECT 4199T, (539232); \textit{A. encheleia} CECT 4342T, (AJ224308); \textit{A. popoffii} LGM 17541T, (AJ224308); \textit{Aeromonas Group} 501 CECT 4254, (U88663).
Table 1. Number of nucleotide differences in the 16S rDNA sequences of A. encheleia, A. popoffii and Aeromonas Group 501 compared to those from all other Aeromonas species

<table>
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<td>30</td>
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schubertii only by six nucleotides. Present phylogenetic analysis indicated that this micro-organism may belong to a different Aeromonas sp., closely related to A. schubertii (Fig. 1), which is consistent with the relationship indicated by Hickman-Brenner et al. (1988) by DNA–DNA hybridization data.

Sequence comparison showed that the 16S rRNA of A. popoffii is species-specific with an inter-species range of 7–28 nucleotide differences (Table 1). Description of this species (Huys et al., 1997b) indicated some resemblances with A. hydrophila (HG1), A. bestiarum (HG2) and A. salmonicida (HG3) on the basis of genotype and phenotype. The highest DNA–DNA hybridization values were determined with A. bestiarum (51–63%; Huys et al., 1997b). The 16S rDNA of A. popoffii exhibited a significant number of differences with the sequences of these three species (9–12 nucleotides); instead, the closest relative was A. encheleia (7 nucleotides) and Aeromonas sp. HG11 (8 nucleotides). The phylogenetic analysis (Fig. 1) indicates that A. popoffii belongs to a new phylogenetic line of descent within this genus, which supports the original description.

A. encheleia was more related to A. salmonicida and A. eucrenophila than to any other species on the basis of 16S rDNA comparison (5 and 6 differences, respectively; Table 1). A close relationship to A. eucrenophila is supported by phenotype: most key phenotypic tests for the differentiation of all known Aeromonas spp. do not separate A. encheleia from A. eucrenophila (see Table 3 of Huys et al., 1997a, b). After alignment of all 16S rDNAs, the unnamed Aeromonas sp. HG11 exhibited a species-specific sequence including ‘unique’ nucleotides at two positions, i.e. a nucleotide composition at these sites only found in this species of the genus. The sequence of HG11 showed maximum similarity with that of A. sobria. Preliminarily, the tree of Fig. 1 and qualitative sequence analysis suggest the placement of HG11 as a single species phylogenetically separated from A. encheleia, according to previous data (Martinez-Murcia, 1993).

Diagnostic regions of the 16S rDNA (polymorphic sites at V2 and V3 regions; Martinez-Murcia et al., 1992a) of some A. eucrenophila and A. encheleia strains, considered to be a part of the A. encheleia extension (Huys et al., 1997a), were determined in the present work. The two known HG11 strains, A902 (a duplicate of ATCC 35941) and A926, showed the characteristic signature sequences of HG11, in agreement with published data (Martinez-Murcia et al., 1992a). In fact, both strains were peripheral to cluster II by AFLP (also called cluster A2: Huys et al., 1996a, b) and did not cluster to phenon 2 (Huys et al., 1997a), such a clustering considered as the A. encheleia extended-frame. Reported chromosomal DNA relatedness added more controversy: strain A902 (reference of HG11) shows 84% DNA–DNA similarity with the type strain of A. encheleia (Huys et al., 1997a), which is in marked disagreement to the 12% determined by Esteve et al. (1995). If the possibility of mislabelling or contamination of strains has been ruled out by performing experiments with duplicates from the original culture collections, this is one of the more serious discrepancies found in two sets of DNA–DNA hybridization values from different laboratories that used the same micro-organisms. Additional strains A9 and A1654, initially considered to be A. encheleia-like and A. eucrenophila, respectively, part of phenon 2 and grouped in cluster II of AFLP (Table 2), also showed the signature nucleotides of HG11. Relevant DNA–DNA hybridization values for strain A9, and the corresponding values for the pair A1654/HG11, were not reported (Huys et al., 1997a). Strain A1653 (A. eucrenophila), having shown a really high DNA–DNA hybridization value with HG11 (96%; Table 2), revealed the diagnostic nucleotides of A. encheleia. This result clearly represents a new case of conflict between these two approaches as these two taxa show separated phylogenetic lines. Two strains, A1655 and A1783, also showed the 16S rDNA nucleotides characteristic of A. encheleia, in agreement with the species assigned by Huys et al. (1997a). However, strains A1653, A1654 and A1655 were related to A. eucrenophila at a level of 80–82% DNA–DNA hybridization (Table 2; Schubert & Hegazi, 1988) and, therefore, they were included in the original description of this species. These data make present controversy deeper. The determined sequences...
of strains A1784 and A1786 were characteristic of *A. encheleia-like*. However, that of strain A1782 was characteristic of *A. eucvenophila*. These last two species are only distinguishable by two paired nucleotides at positions 1011 and 1018 (*A. eucvenophila*; Martinez-Murcia et al., 1992a), consistent with difficulties found in separating strains of HG2/HG3 by DNA–DNA pairing (Hanninen, 1994). Again, DNA–DNA hybridizations have not been reported for the last three versus reference strains (Table 2). As some DNA–DNA hybridization values are unknown and, worthy of note, the thermal stability of reassociated DNA was not determined (see recommendation of Wayne et al., 1987), it is better to consider these, and similar strains, in need of urgent investigation.

Sequencing of 16S rRNA is today considered a robust way to achieve bacterial taxonomy (Woese, 1987; Olsen et al., 1994) and DNA–DNA hybridization has been recommended for defining species (Wayne et al., 1987). Although in *Aeromonas* most rDNA derived relationships correlate well with DNA–DNA data, identical rRNA sequences but different species by DNA–DNA pairing have previously been detected (Martinez-Murcia et al., 1992a). In view of these conflicts, the results of DNA reassocation have always been taken as definitive (Collins et al., 1993) as the high overall conservation of the 16S rRNA may preclude the splitting of very closely related genotypes. However, at present, *Aeromonas* strains showing a DNA–DNA similarity range as high as 84–94% have never shown a phylogenetic divergence based on 8 nucleotide positions, two of which were HG11-specific composition. Although these polymorphisms are noticeable considering the tight phylogenetic depth of this genus, the number of nucleotide differences is too low and the possibility of molecular clock ‘distortions’ (i.e. plesiomorphy, inter-cistronic and inter-strain diversity, etc.) has to be taken into account. Consequently, and according to the previously reported limitations of 16S rDNA analysis in the determination of relationships at the strain level (Stackebrandt & Goebel, 1994), a conclusion about the HG11 taxonomic status should be taken on the basis of DNA–DNA hybridization data.

Bacterial species definition based on chromosomal DNA hybridization (Wayne et al., 1987) was empirically derived from a wide range of taxa, but values should not be treated as absolute or fixed. Concerns about variation on the level of DNA–DNA below which organisms are considered to belong to different species have been previously reported (Zakrzewska-Czerwinska et al., 1988). DNA–DNA pairing may give a ‘too crude’ measure of DNA sequence homology or, at least, not fine enough to split highly similar species. Grimont et al. (1980) showed that a relative binding ratio (RBR) of 70% obtained with the hydroxyapatite method corresponds, at optimal temperature, to about 55–60% RBR obtained with the 5'-nuclease method and this correlation may vary with the temperature. Discrepancies may be important when many RBRs in *Aeromonas* are bor-
nderline to the recommended value (70%) to split species. The more pronounced lack of agreement so far reported is that for A. encheleia/HG11/ A. eucrenophila (Table 2) using the same reference strains but different hybridization methods: optical renaturation used by Huys et al. (1997a) and competitive nitrocellulose filter utilized by Esteve et al. (1995). Research on the correlation between several DNA-DNA procedures for these controversial strains is hereby suggested.

AFLP and ribotyping were added to support inclusion of HG11 in A. encheleia, commented in 'Letters to the Editor' of the International Journal of Systematic Bacteriology (Esteve, 1997). These grouping methods are based on fingerprints comprising chromosomal restriction fragments obtained from a limited (selected by availability) group of strains. Estimation of size-fingerprint resemblances and number of bona-fide strains included in each taxa might influence the final numerical analysis (Sneath & Sokal, 1973). Currently, difficulties caused by low intensity/background ratios are also a source of error for fingerprint scoring. As patterns are highly heterogeneous and strain-specific, there is no doubt about their usefulness for bacterial typing and epidemiological studies (Vos et al., 1995). To date, however, the taxonomic value of the 'AFLP concept' (Huys et al., 1996b) and similar methods (e.g. those yielding some selected information about genomic organization of unknown evolutionary nature) in a wide range of bacterial taxa, is still to be demonstrated. If a phylogenetic frame is desired, knowledge about mode and extent to which genomic organization interrelates with, and reveals final stages of, bacterial species evolution, should be required.

In view of the 16S rDNA results from the present study and all previously reported discrepancies between different sets of DNA–DNA hybridizations, a comprehensive study including all Aeromonas species (and HGs) is proposed by applying the same DNA–DNA hybridization method, sequencing of single 16S and 23S rDNA copies of all operons of each strain, but also presumably faster molecular clocks as the 16S-23S rDNA spacers or 'house-keeping' protein coding genes. A sequencing project with the above aim is under way.

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