Phylogenetic analysis of the genera *Proteus*, *Morganella* and *Providencia* by comparison of *rpoB* gene sequences of type and clinical strains suggests the reclassification of *Proteus myxofaciens* in a new genus, *Cosenzaea* gen. nov., as *Cosenzaea myxofaciens* comb. nov.

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Phylogenetic analysis of partial *rpoB* gene sequences of type and clinical strains belonging to different 16S rRNA gene-fingerprinting ribogroups within 11 species of enterobacteria of the genera *Proteus*, *Morganella* and *Providencia* was performed and allowed the definition of *rpoB* clades, supported by high bootstrap values and confirmed by $\geq 2.5\%$ nucleotide divergence. None of the resulting clades included strains belonging to different species and the majority of the species were confirmed as discrete and homogeneous. However, more than one distinct *rpoB* clade could be defined among strains belonging to the species *Proteus vulgaris* (two clades), *Providencia alcalifaciens* (two clades) and *Providencia rettgeri* (three clades), suggesting that some strains represent novel species according to the genotypes outlined by *rpoB* gene sequence analysis. Percentage differences between the *rpoB* gene sequence of the type strain of *Proteus myxofaciens* and other members of the same genus (17.3–18.9%) were similar to those calculated amongst strains of the genus *Providencia* (16.4–18.7%), suggesting a genetic distance at the genus-level between *Proteus myxofaciens* and the rest of the *Proteus*–*Providencia* group. *Proteus myxofaciens* therefore represents a member of a new genus, for which the name *Cosenzaea* gen. nov., is proposed.

Members of the three genera *Proteus*, *Morganella* and *Providencia* are components of the normal bacterial flora of the intestinal tracts of humans and animals and are widespread in the environment. Some species belonging to these genera have been recognized as opportunistic pathogens, causing primary and secondary infections (O'Hara *et al.*, 2000); these are mainly hospital-acquired infections (Burke *et al.*, 1971; Krajden *et al.*, 1987) with a high mortality rate directly related to bacteraemia (Kim *et al.*, 2003). These bacteria are frequently involved in

urinary tract infections (UTI) and species of the genus *Proteus* account for approximately 6% of nosocomially acquired UTI (Johansen *et al.*, 2006).

DNA relatedness studies have shown that the members of the tribe *Proteeae*, containing the three genera *Proteus*, *Morganella* and *Providencia*, are only distantly related to other species in the family *Enterobacteriaceae* and their taxonomic position is at the periphery of this family (Brenner *et al.*, 1978). At the time of writing, the genus *Proteus* included five species: *Proteus mirabilis*, *Proteus vulgaris*, *Proteus penneri*, *Proteus myxofaciens* and *Proteus hauseri* (O'Hara *et al.*, 2000a, b; Penner, 1992). The genus was first described by Hauser in 1885 and was successively separated into two species, *Proteus vulgaris* and *Proteus mirabilis*, on the basis of their ability to ferment maltose. Strains of *Proteus vulgaris* formed three biogroups characterized by different biochemical reactions for indole

Abbreviation: UTI, urinary tract infections.

The GenBank/EMBL/DDBJ accession numbers for the *rpoB* gene sequences of the strains analysed in this study are DQ836265–DQ836296.

Two supplementary tables are available with the online version of this paper.

production, salicin fermentation and aesculin hydrolysis. Based on DNA–DNA hybridization studies, biogroup 1 was shown to be a separate genetic species and was named *Proteus penneri* (Hickman *et al.*, 1982), biogroup 2 retained the name *Proteus vulgaris* and biogroup 3 was separated into four distinct genomospecies (Brenner *et al.*, 1995; Penner, 2005a). The species name *Proteus hauseri* was proposed for *Proteus vulgaris* genomospecies 3, while genomospecies 4, 5 and 6 remained unnamed pending better phenotypic differentiation (O'Hara *et al.*, 2000b). *Proteus myxofaciens* was included in the genus based on hybridization studies, since labelled *Proteus myxofaciens* DNA showed relatedness values of 44–46 % to both *Proteus mirabilis* and *Proteus vulgaris* strain PR1 but only 12–26 % to DNA from strains of members of the genera *Morganella* and *Providencia* and only about 10 % to other members of the family Enterobacteriaceae (Brenner *et al.*, 1978).

The genus *Providencia* initially comprised five species, *Providencia alcalifaciens*, *Providencia stuartii*, *Providencia rettgeri*, *Providencia rustigianii* and *Providencia heimbachae*, as described by Penner (1992). More recently, three additional species of the genus *Providencia* have been described: *Providencia burhodogranariae*, *Providencia snee-bia* and *Providencia vermicola* (Juneja & Lazzaro, 2009; Somvanshi *et al.*, 2006). In biochemical characterization studies on *Providencia alcalifaciens*, four biogroups were initially recognized (Ewing *et al.*, 1972). After DNA relatedness tests, strains belonging to biogroup 3 were classified as a novel species, *Providencia rustigianii* (Hickman-Brenner *et al.*, 1983). Strains of biogroup 4 were found to be biochemically closer to *Providencia stuartii* and were therefore transferred to this species (Brenner *et al.*, 1978). Five biogroups were recognized in the biochemical characterization of *Providencia rettgeri* (Penner *et al.*, 1975). On the basis of DNA relatedness, biogroup 5 was found to be inseparable from *Providencia stuartii* (Brenner *et al.*, 1978) but not all biogroups of *Providencia rettgeri* have yet been examined for relatedness. Although DNA–DNA relatedness studies resolved the taxonomic position of many species and allowed the classification, without controversy, of most of the bacteria belonging to the *Proteus–Providencia* group, the present taxonomy of species with validly published names does not account for all the biogroups and genomospecies described within the group (Brenner *et al.*, 1978; Ewing *et al.*, 1972; O'Hara *et al.*, 2000b; Penner *et al.*, 1975). *Morganella morganii* is the sole species in the genus *Morganella* (Penner, 1992).

In a previous study, type and clinical strains of 11 different species of the genera *Proteus*, *Morganella* and *Providencia* were characterized by rRNA gene restriction pattern analysis after digestion by *EcoRV* and *HincII* (Pignato *et al.*, 1999). Clinical isolates of *Proteus mirabilis*, *Proteus penneri*, *M. morganii*, *Providencia rustigianii* and *Providencia heimbachae* had identical or very similar ribotyping patterns to those of the respective type strains; they could, therefore, be grouped into five homogeneous and discrete ribogroups corresponding to the five species.

On the other hand, distinct ribogroups were detected within clinical strains of the species *Proteus vulgaris* (two ribogroups), *Providencia alcalifaciens* (two ribogroups), *Providencia rettgeri* (four ribogroups) and *Providencia stuartii* (two ribogroups). These results raised concerns about how the current taxonomy corresponded with the genetic evolution of the respective genera.

16S rRNA gene sequence analysis is by far the most widely used method for the molecular identification and differentiation of bacterial species (Woese *et al.*, 1990). However, members of the family Enterobacteriaceae have not been subjected to extensive phylogenetic 16S rRNA gene sequence analysis because the high degree of conservation in closely related species leaves many taxonomic problems unresolved (Brenner, 1992; Spröer *et al.*, 1999). In particular, the genetic relationships between closely related species *Proteus vulgaris* and *Proteus penneri* could not be clearly resolved by this method (Cao *et al.*, 2009). In the family Enterobacteriaceae, the use of rRNA for bacterial typing has also been questioned because of its allelic heterogeneity. Sequence divergence between several gene copies (seven in *Escherichia coli* and species of the genus *Salmonella*) makes direct sequencing of PCR products seldom suitable for achieving a representative sequence (Cilia *et al.*, 1996; Hill & Harnish, 1981).

Among the core bacterial genes, the *rpoB* gene has been identified as one of the few potential candidates suitable for bacterial phylogenetic analyses and has been proposed as a powerful tool for universal bacterial genetic identification (Adékambi *et al.*, 2009; Mollet *et al.*, 1997). The *rpoB* gene, encoding the RNA polymerase β -subunit, is a highly conserved housekeeping gene and one copy is present in all bacteria because of its essential role in cellular metabolism. Primers and probes targeting the *rpoB* gene have been used for the specific detection and phylogenetic analysis of several bacterial groups belonging to the family Enterobacteriaceae (Drancourt *et al.*, 1998; Hoffmann & Roggenkamp, 2003; Kwon *et al.*, 2001; Merhej *et al.*, 2008; Stoop *et al.*, 2009). Partial *rpoB* gene sequencing and analysis has been proven to be more sensitive than using 16S rRNA gene sequences when used to differentiate type and clinical strains of 14 species of the family Enterobacteriaceae, including type strains of *Proteus mirabilis* and *Providencia stuartii* (Mollet *et al.*, 1997). However, members of the tribe Proteeae have not yet been subjected to extensive phylogenetic analysis based on *rpoB* gene sequences.

In this study, partial *rpoB* gene sequences were obtained from type strains of 11 species of the genera *Proteus*, *Morganella* and *Providencia*: *Proteus hauseri* ATCC 13315^T, *Proteus mirabilis* ATCC 29906^T, *Proteus myxofaciens* ATCC 19692^T, *Proteus penneri* ATCC 33519^T, *Proteus vulgaris* ATCC 29905^T, *Morganella morganii* ATCC 25830^T, *Providencia alcalifaciens* ATCC 9886^T, *Providencia heimbachae* ATCC 35613^T, *Providencia rettgeri* ATCC 29944^T, *Providencia rustigianii* ATCC 33673^T and *Providencia*

stuartii ATCC 29914^T. The phylogenetic structure of the three genera was evaluated, including in this evaluation the analysis of conserved sequences of 21 clinical strains belonging to different 16S rRNA gene-fingerprinting ribogroups and biogroups previously determined for these species (Supplementary Table S1, available in IJSEM Online) (Pignato *et al.*, 1999). Genomic DNA was extracted using a commercial nucleic acid extraction kit (IsoQuick; InterBiotech ORCA Research, Othell, WA) according to the manufacturer's instructions. A portion of the coding region of the *rpoB* gene was amplified with primers CM7 (5'-AACCAGTTCCGCGTTGGCCTGG-3') and CM31b (5'-CCTGAACAACACGCTCGGA-3'), according to the technique described by Mollet *et al.* (1997). The PCR amplicons generated were sequenced with primers CM81 (5'-CAGTTCCGCGTTGGCCTG-3') and CM31b (seq) (5'-TGAACAACACGCTCGG-3') (Mollet *et al.*, 1997) to obtain partial *rpoB* gene sequences. Sequence alignment and phylogenetic analysis was carried out on 930 nt fragments using the CLUSTAL W algorithm (Thompson *et al.*, 1994) and MEGA software version 4.1 (Kumar *et al.*, 2004). To ensure the stability and reliability of phylogenetic relationships among strains used in this study, phylogenetic trees were reconstructed by using the neighbour-joining and maximum-parsimony methods in MEGA 4.1 package, with the option of complete deletion of gaps, and the maximum-likelihood method in the PHYLIP version 3.66 software package (Felsenstein, 2006). The Kimura two-parameter model was chosen as a substitution model for the neighbour-joining tree reconstruction. The statistical significance of the phylogenies inferred was estimated by bootstrap analysis with 1000 pseudoreplicate datasets. Accession numbers for the *rpoB* gene sequences of the strains used in this study are shown in Fig. 1.

The phylogenetic tree derived from partial *rpoB* gene sequences of type and clinical strains of 11 species of the genera *Proteus*, *Morganella* and *Providencia* (Fig. 1) showed genus-related branching patterns. The strains of the genus *Providencia* and almost all the strains of the genus *Proteus* grouped in two respective branches, while *Morganella morganii* was clearly separate in a third branch. However, *Proteus myxofaciens* constituted a well-defined fourth lineage. Bootstrap levels $\geq 57\%$ allowed the identification of *rpoB* clades that generally corresponded to the species level within the main genetic branches. No *rpoB* clade included strains belonging to different species and the majority of the species were confirmed as discrete and homogeneous, since they constituted a single monophyletic group. Within the *Proteus* branch, *Proteus penneri* and *Proteus vulgaris* strains were more closely related, while the type strain of *Proteus hauseri* stood apart as did the strains of *Proteus mirabilis*. Within the *Providencia* branch, two subclusters could be defined according to the phylogenetic relationships; one included the species *Providencia alcalifaciens*, *Providencia rustigianii* and *Providencia rettgeri*, while the second included *Providencia stuartii* and *Providencia heimbachae*. Clinical strains of the different

species generally clustered in close proximity to their respective type strains but distinct *rpoB* clades could be recognized in *Proteus vulgaris* (VurpoB1–2), *Providencia alcalifaciens* (AlrpoB1–2) and *Providencia rettgeri* (RerpoB1–3). As shown in Supplementary Table S1, when the phylogenetic tree obtained using *rpoB* gene sequences was compared with the results of previously obtained ribotyping studies from the same type and clinical strains after genomic DNA digestion by *EcoRV* or *HindIII* (Pignato *et al.*, 1999), the *rpoB* clades generally corresponded to the ribogroups.

Percentage nucleotide identity and pairwise uncorrected (*p*-) distances were calculated for the *rpoB* gene sequences of type and clinical strains of the 11 different species examined (Supplementary Table S2). Sequence divergences of 2.3–18.9% were observed in the *rpoB* gene region analysed when comparing strains of different species. On the basis of *rpoB* gene sequences, strains of *M. morganii* diverged by 14.1–16.1% and 12.1–16.5% from strains of the genera *Providencia* and *Proteus*, respectively, while the strains of the latter genera differed by 13.0–18.7% from each other. The type strain of *Proteus myxofaciens*, however, was only distantly associated (12.1–12.2% sequence divergence) with the closest taxon, *M. morganii*. Divergences between the *rpoB* gene sequences of the type strain of *Proteus myxofaciens* and other members of the genus (17.3–18.9%) were similar to those calculated between *Proteus myxofaciens* and members of the genus *Providencia* (16.4–18.7%), suggesting that a genetic distance exists at the genus-level between *Proteus myxofaciens* and the rest of the *Proteus*–*Providencia* group. The DNA G+C content of *Proteus myxofaciens*, determined by HPLC according to the method of Mesbah *et al.* (1989), was 36.5 mol%, while the type strains of other members of the genus *Proteus* ranged from 38 to 39.3 mol% (Penner, 2005a). Interestingly, sequence divergences of 2.4–1.9% were observed when a 5' 978 nt 16S rRNA gene fragment from the type strain of *Proteus myxofaciens* was compared to that of other type strains belonging to the same genus and 16S rRNA phylogenetic analysis could not clearly separate it from the other species of the genus *Proteus* (Fig. 2). However, the low degree of divergence in the 16S rRNA gene sequence was similar to that reported between closely related members of other genera within the family Enterobacteriaceae, such as between *Escherichia coli* and members of the genera *Shigella* and *Salmonella* (95.3–99.6% similarity) or between members of the genera *Enterobacter* and *Klebsiella* (97.2–98.3% similarity) (Fukushima *et al.*, 2002). Among the other species of the genus *Proteus*, 5.1–7.6% *rpoB* gene sequence divergences were observed, except when strains of *Proteus penneri* were compared to strains of *Proteus vulgaris* (2.3–2.7% differences). The low *rpoB* gene sequence divergences between strains of *Proteus penneri* and *Proteus vulgaris*, being the two closest taxa among all those examined in this study, and the high sequence similarity observed among the *rpoB* gene sequences of *Proteus penneri* clinical strains suggests that this species, formerly *Proteus*

Fig. 1. Phylogenetic analysis of partial nucleotide sequences of the *rpoB* gene of type and clinical strains of the genera *Proteus*, *Providencia* and *Morganella*, including the type strain of *Cosenzaea myxofaciens* gen. nov., comb. nov. (previously *Proteus myxofaciens*). The tree was generated using the neighbour-joining method with the Kimura two-parameter model. Bootstrap values >50% (based on 1000 pseudoreplicate datasets) are indicated at nodes. Each *rpoB* clade was named by the first two letters of the species epithet followed by the *rpoB* acronym and a number differentiating clades within a species. Bar, 0.02 substitutions per nucleotide position.

vulgaris biogroup 1 (Hickman *et al.*, 1982), could be the species that most recently diverged from other species within the genus *Proteus*. Accordingly, a single homogeneous restriction pattern had previously been observed in the *EcoRV*-digested rRNA gene fragments of all the strains of *Proteus penneri* analysed (Pignato *et al.*, 1999). In the present study, the type strain of *Proteus hauseri* was confirmed as occupying a separate position with respect to *Proteus vulgaris* in the phylogenetic tree based on *rpoB* gene sequences; a sequence divergence of at least 5.1% with respect to the *rpoB* gene sequence of other members of the genus *Proteus* further supports its position as a separate species within this genus. In fact, the present type strain *Proteus hauseri* ATCC 13315^T was the former type strain of *Proteus vulgaris* but it resided in a separate genogroup (genogroup 3) within biogroup 3, which was composed of only two strains that were not biochemically representative of the majority of the isolates identified as *Proteus vulgaris* (Brenner *et al.*, 1995; O'Hara *et al.*, 2000b). In addition, the five species of the genus *Providencia* that were analysed could be easily distinguished from one another based on *rpoB* gene sequence divergences, generally differing by 6.0–10.6%, except for *Providencia alcalifaciens* and *Providencia rustigianii*, whose strains showed only 3.4–5.3% *rpoB* gene sequence divergence.

The comparison of *rpoB* gene sequence divergences among clinical strains revealed that they were generally closely

related to their respective type strain (Supplementary Table S2). However, as already shown by the phylogenetic analysis, distinct *rpoB* gene sequence types could be recognized in *Proteus vulgaris*, *Providencia alcalifaciens* and *Providencia rettgeri*. In particular, two clades, corresponding to the *Proteus vulgaris* *rpoB* clades observed in the phylogenetic tree, VurpoB1 (type strain ATCC 29905^T and clinical strain 27) and VurpoB2 (clinical strains 23 and 26), showed sequence divergences of 3.1–3.6% from each other but both were equally distant from the other species of the genus *Proteus*. These two *Proteus vulgaris* *rpoB* clades, which diverged from each other more than they did from *Proteus penneri* sequences (2.3–2.7%), also belonged to separate ribogroups (Pignato *et al.*, 1999). Interestingly, strain 26, which belonged to the genetically heterogeneous biogroup 3, since it was positive for indole production and negative for salicin fermentation and aesculin hydrolysis, grouped with the same *rpoB* clade as the classical biogroup 2 *Proteus vulgaris* strain 23, further demonstrating the lack of accordance between biochemical types and genotypes, already demonstrated by the results of ribotyping. Of the two clinical strains of *Providencia alcalifaciens* analysed, one was identical to the type strain based on the *rpoB* gene fragment that was analysed (AlrpoB1 clade), while the other strain showed 3.9% sequence divergence (AlrpoB2 clade). Three *rpoB* clades could be defined for *Providencia rettgeri*; one clade comprised the type strain and a single clinical

Fig. 2. Neighbour-joining analysis of partial 16S rRNA gene sequences showing the relationship between *Cosenzaea myxofaciens* ATCC 19692^T and other members of the tribe Proteeeae. Bootstrap values >50% (based on 1000 pseudoreplicate datasets) are indicated at nodes. Bar, 0.005 substitutions per nucleotide position.

strain (RerpoB1 clade); the second included four clinical strains, whose sequence divergence from the type strain was between 2.5 and 2.7% of the fragment analysed (RerpoB2 clade), and the third was represented by a single clinical strain that differed from the first two sequence types by 5.9 and 5.7–5.8%, respectively (RerpoB3 clade). Genetic diversity had already been observed by DNA–DNA hybridization studies with species of the genus *Providencia*. In particular, *Providencia rettgeri* contained at least two relatedness groups and a variety of biogroups and atypical strains that have been described but have yet to be examined for DNA-relatedness (Brenner *et al.*, 1978). In fact, the *rpoB* clades observed in *Providencia rettgeri* and in *Providencia alcalifaciens* corresponded exactly to the ribogroups already described within these species (Pignato *et al.*, 1999). On the contrary, the two ribotypes of *Providencia stuartii* grouped within a single *rpoB* clade.

Attempts have been made to define a cut-off for *rpoB* gene sequence-based identification of bacteria. Mollet *et al.* (1997) found an intraspecies similarity range of 98–100% when they analysed a 512 bp fragment of the *rpoB* gene in clinical isolates of enteric strains. For 600–825 bp gene-fragments, a *rpoB* sequence similarity of at least 96–97% seems to be the threshold for correct species identification (Adékambi *et al.*, 2003; Khamis *et al.*, 2003; La Scola *et al.*, 2003). According to these limits, the $\geq 3.1\%$ sequence divergence detected between members of the two *rpoB* clades of *Proteus vulgaris* could be sufficient to suggest possible further taxonomic adjustments within this genus. Similarly, the detection of two *Providencia alcalifaciens* *rpoB* clades with 3.9% sequence divergence from each other and the sequence divergence of the type strain of *Providencia rettgeri* from members of the two additional RerpoB clades (2.5–2.7% and 5.9%) provide further evidence of the lack of genetic homogeneity in strains of the two species of the genus *Providencia*, as demonstrated by 16S rRNA gene-fingerprinting.

Our results indicate that *rpoB* gene sequence comparison seems to be an appropriate method for inferring genetic relationships within the *Proteus*–*Providencia* group and suggest the need for taxonomic adjustments. Differentiation of strains presently belonging to the species *Proteus vulgaris*, *Providencia alcalifaciens* and *Providencia rettgeri* and the introduction of novel species according to the groups outlined by *rpoB* gene sequence analysis should be

considered but larger studies, combining 16S rRNA gene sequence analysis with more discriminative methods like full *rpoB* gene sequence analysis and including the investigation of more than one gene (multi-locus sequence typing), are necessary in order to clarify the molecular relationships between strains of these species. The assignment of the type strain of *Proteus myxofaciens* to a separate genus was strongly supported by phylogenetic analysis based on *rpoB* gene sequences, showing low levels of sequence similarity to, and great evolutionary distances from, the other members of the tribe Proteeeae. This was further supported by differences in the DNA G+C contents, since the 1.5–2.8 mol% differences between strains of *Proteus myxofaciens* and other species of the genus *Proteus* is comparable to the 0.3–5 mol% differences observed between *Proteus myxofaciens* and members of the genus *Providencia*, the closest related taxon (Penner, 2005a, b). Based on the evidence presented in this study, it is proposed that *Proteus myxofaciens* be classified as a new genus, *Cosenzaea* gen. nov., as *Cosenzaea myxofaciens*, comb. nov.

Description of *Cosenzaea* gen. nov.

Cosenzaea (Co.sen.za'e.a. N.L. fem. n. *Cosenzaea* named after Benjamin J. Cosenza, the microbiologist who first described this micro-organism as *Proteus myxofaciens* in 1966).

A member of the family Enterobacteriaceae as defined by Penner (2005a). Cells are Gram-reaction-negative, straight rods, 0.4–0.8 × 1.0–3.0 µm and motile by means of peritrichous flagella. Grows on solid media producing a thin uniform film. Haemolysis occurs on blood agar. Optimal growth temperature is 37 °C. Based on 16S rRNA sequence data, the genus *Cosenzaea* belongs to the family Enterobacteriaceae within the tribe Proteeeae together with the genera *Proteus*, *Providencia* and *Morganella*. Conforming to the general definition of the family Enterobacteriaceae, *Cosenzaea* are facultatively anaerobic and chemo-organotrophic, having both respiratory and a fermentative metabolism. Oxidase-negative, catalase-positive. Urea is hydrolysed, indole is not produced. Voges–Proskauer and Simmons citrate tests are positive. Oxidatively deaminates phenylalanine and tryptophan. Lysine and ornithine decarboxylase and arginine dihydrolase are not produced. Tyrosine is not decomposed as is

Table 1. Phenotypic characteristics that differentiate members of the genus *Cosenzaea* from related genera within the tribe Proteae of the family Enterobacteriaceae

Genera: 1, *Cosenzaea* gen. nov.; 2, *Proteus*; 3, *Morganella*; 4, *Providencia*. +, Positive; –, negative.

Characteristic	1	2	3	4
Swarming	+	+	–	–
H ₂ S production	+*	+†	–	–
Slime production‡	+	–	–	–
Tyrosine clearing	–	+	+	+
Gelatin liquefaction 22 °C	+	+	–	–
Acid production from:				
D-Xylose	–	+	–	–
D-Mannose	–	–	+	+

*3–4 days required for positive result.

†One species of the genus *Proteus* (*P. penneri*) does not produce H₂S.

‡At 25 °C in trypticase soy broth.

demonstrated by the inability to produce a clearing in agar media supplemented with the insoluble amino acid. Slime is produced at 25 °C in trypticase soy broth. Hydrogen sulfide is produced but only after 3–4 days of incubation. Gelatin is hydrolysed at 22 °C. Grows on media containing KCN. Malonate is not utilized. Acid is produced from D-glucose, maltose, glycerol and α -methyl-glucoside. Phenotypic characteristics that distinguish the genus *Cosenzaea* from related genera within the tribe Proteae are listed in Table 1. The DNA G+C content of the type strain of the type species is 36.5 mol%. The type species is *Cosenzaea myxofaciens*.

Description of *Cosenzaea myxofaciens* (Cosenza & Podgwaite, 1966) comb. nov.

Cosenzaea myxofaciens (my.xo.fa.ci'ens. Gr. n. *muxa* mucus slime; L. part. adj. *faciens* producing; N.L. part. adj. *myxofaciens*, slime-producing [bacteria]).

Basonym: *Proteus myxofaciens* Cosenza & Podgwaite, 1966.

The genus *Cosenzaea* comprises only one species, *Cosenzaea myxofaciens*, the characteristics of which are given in the genus description and in the description given by Cosenza & Podgwaite (1966).

The type strain, ATCC 19692^T (=BCRC 12222^T =CCRC 12222^T =CCUG 18769^T =CIP 106872^T =DSM 4482^T =JCM 1670^T =LMG 7876^T =NCIMB 13273^T), was originally isolated from a larva of the gypsy moth *Porthetria dispar*.

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