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<tr>
<td>Citation</td>
<td>International Journal of Systematic and Evolutionary Microbiology, 54: 843-846</td>
</tr>
<tr>
<td>Issue Date</td>
<td>2004</td>
</tr>
<tr>
<td>Doc URL</td>
<td><a href="http://hdl.handle.net/2115/5802">http://hdl.handle.net/2115/5802</a></td>
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<td>Type</td>
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<td>File Information</td>
<td>IJSEM54.pdf</td>
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Vibrio gallicus sp. nov., isolated from the gut of the French abalone Haliotis tuberculata

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Five alginolytic, facultatively anaerobic, non-motile bacteria were isolated from the gut of the abalone Haliotis tuberculata. Phylogenetic analyses based on 16S rDNA data indicated that these strains are related to Vibrio wodanis, Vibrio salmonicida, Vibrio logei and Vibrio fischeri (but with < 97 % 16S rRNA gene sequence similarity). DNA–DNA hybridization and fluorescence amplified fragment length polymorphism fingerprinting demonstrated that the five strains constituted a single species that was different from all currently known vibrios. The name Vibrio gallicus sp. nov. (type strain, CIP 107863T = LMG 21878T = HT2-1T; DNA G+C content, 43.6–44.3 mol%) is proposed for this novel taxon. Several phenotypic features were disclosed that discriminated V. gallicus from other Vibrio species: V. gallicus can be differentiated from Vibrio halioticoli on the basis of four traits (β-galactosidase test and assimilation of three carbon compounds) and from Vibrio superstes by 16 traits.

Vibrio halioticoli and a phylogenetically related species (Vibrio superstes), which are alginolytic, non-motile, fermentative, marine bacteria, are commonly found in the gut of Haliotis abalones in Japan (Sawabe et al., 1995, 2002), South Africa (Sawabe et al., 2003) and Australia (Hayashi et al., 2003). The hypothesized roles of V. halioticoli include its contribution to the digestion of alginate, which is a major polysaccharide in Japanese and South African kelps that is ingested by these animals, and its conversion into volatile short-chained fatty acids via fermentation (Sawabe et al., 2003). On the other hand, V. superstes may play a minor role in Australian abalone, due to a small population in the gut of the abalone (Hayashi et al., 2003).

We have examined the presence of V. halioticoli-like bacteria in the gut of abalones; recently, we isolated a set of five strains, which were most similar phenotypically to V. halioticoli, from the gut of French abalones (Haliotis tuberculata). DNA–DNA hybridization experiments, phenotypic characterization and phylogenetic and genetic analyses demonstrated that these strains represent a so far unknown species of the genus Vibrio.

Five strains of Vibrio gallicus sp. nov. (CIP 107863T = LMG 21878T = HT2-1T, LMG 21329 = CIP 107864 = HT1-3, CIP 107865 = HT1-12, CIP 107866 = HT2-6 and CIP 107867 = HT3-3) were isolated from the gut of French abalones (H. tuberculata). These were collected at the coastal area of Brest (Brittany, France) by Scuba diving in February 2001. Strains were cultured on ZoBell 2216E agar (Oppenheimer & ZoBell, 1952) and stored at −80 °C in ZoBell broth that contained 10 % glycerol.

About 1400 bp of the 16S rRNA gene sequences for strains CIP 107863T, CIP 107864, CIP 107865, CIP 107866 and CIP 107867 was determined according to Sawabe et al. (1998), by using six sequence primers (24F, 530F, 1100F, 520R, 920R and 1540R). Sequences of V. gallicus CIP 107863T, CIP 107864, CIP 107865, CIP 107866 and CIP 107867 were used for phylogenetic analyses. The 16S rRNA gene sequences of V. gallicus were used in a BLAST search of GenBank/EMBL.
and NRupdate (28 July 2003), in order to retrieve the 50 most closely related sequences. New sequences were included and aligned in a local database of 85,000 already aligned bacterial 16S rRNA gene sequences. Selection of sequences for the final analysis was according to previous phylogenetic analyses of the entire database and the results of the BLAST query. Thirty-one sequences were retained, excluding unidentified species and non-type species. Phylogenetic trees were constructed by using three different methods [BIONJ (neighbour-joining), maximum-likelihood (ML) and maximum-parsimony (MP)]. For neighbour-joining (NJ) analysis, distance matrices were calculated by using the Kimura two-parameter correction. BIONJ was used for neighbour-joining, maximum-likelihood (ML) and maximum-parsimony (MP) analyses. Branches with percentages (<97%) are shown. The topology shown combines the results of three analyses, i.e. NJ, MP and ML. The topology shown indicates that the five new strains belong to the genus Vibrio and suggests that they should be assigned to a novel species, as they do not form a robust clade with any single recognized Vibrio species.

In total, 78 phenotypic characteristics of V. gallicus, V. halioticoli, V. superstes and V. fischeri strains were determined as described previously (Leifson, 1963; Hidaka & Sakai, 1968; West et al., 1977; Ostle & Holt, 1982; Baumann & Schubert, 1984; Holt et al., 1994). Phenotypic characterization was done under the same conditions at 20°C. All available phenotypic traits of sister species (V. salmonicida, V. logei and V. wodanis) and V. agarivorans (Baumann & Schubert, 1984; Egidius et al., 1986; Lunder et al., 2000; Macián et al., 2001) were compared to those of V. gallicus.

The five French abalone strains have the main phenotypic features of the genus Vibrio (except for the absence of flagella). The strains are non-motile, Gram-negative and fermentative (Sawabe et al., 1998). No flagellated cells were observed by transmission electron microscopic observations. These strains require salt for their growth, do not accumulate poly-β-hydroxybutyrate and are oxidase-positive (see Supplementary Table, available in IJSEM Online). No peritrichous cells were observed when the strains were cultivated on solid media. Other phenotypic features of V. gallicus are shown in the Supplementary Table (available in IJSEM Online). The mesophilic growth temperature of V. gallicus is a key phenotypic trait that differentiates it from its psychrophilic sister species V. salmonicida, V. logei and V. wodanis. The five abalone

**Fig. 1.** Rooted phylogenetic tree based on 16S rRNA gene sequence data. This figure combines the results of three analyses, i.e. NJ, MP and ML. The topology shown was obtained by using NJ. Bootstrap values (percentages of 1000 replicates) are shown only for branches that were also obtained in ML analysis (P<0.01; in likelihood, -4700-67781; 3675 trees examined) and in the strict consensus tree of 39 most parsimonious trees. Branches with percentages can thus be considered as robust.
isolates were most similar phenotypically to *V. halioticoli* IAM 14596T, although the strains differed by four traits out of 78 tested (see Supplementary Table, available in IJSEM Online).

DNA of bacterial strains was prepared by using a Promega Wizard DNA extraction kit for fluorescence amplified fragment length polymorphism (FAFLP) analysis, and by the procedures of Marmur (1961) for measurement of G + C content and DNA hybridization experiments. FAFLP analysis was performed as described previously (Thompson et al., 2001; Sawabe et al., 2002). Clustering of the patterns was done by using the Dice coefficient (S₀) and the Ward algorithm (Sneath & Sokal, 1973). DNA G + C contents were determined by HPLC (Tamaoka & Komagata, 1984). DNA–DNA hybridization experiments were performed in microdilution wells by using a fluorometric direct binding method, as described by Ezaki et al. (1988, 1989). DNA homology values are indicated as means of triplicate measurements.

FAFLP patterns of *V. gallicus* CIP 107863T and CIP 107864 consisted respectively of 87 and 103 bands. The similarity between these two band patterns was 79% (Fig. 2). The FAFLP pattern similarity of *V. gallicus* to *V. halioticoli*, *Vibrio rumoensis* and *Vibrio harveyi* was 48, 47 and 44%, respectively. FAFLP pattern similarity of CIP 107863T and CIP 107864 to other *Vibrio* species, including the sister species of *V. gallicus* (*V. wodanis*, *V. logei* and *V. salmonicida*), was < 44%, indicating clearly that this novel species is different from other vibrios (Thompson et al., 2001). The FAFLP results are supported by our DNA–DNA hybridization experiments, which showed that the five strains of *V. gallicus*, CIP 107863T, CIP 107864, CIP 107865, CIP 107866 and CIP 107867, were conspecific strains that were clearly separate from *V. halioticoli*, *V. superstes*, *V. fischeri*, *V. agarivorans* and *V. logei* (See Supplementary Table in IJSEM Online).

In conclusion, our polyphasic study demonstrates clearly that the five abalone isolates represent a so far undescribed species of the genus *Vibrio*, for which we propose the name *Vibrio gallicus* sp. nov. This study also reveals the fourth finding of the presence of *V. halioticoli*-related bacteria in the gut of abalones. As *V. gallicus* is a major component (> 50%) of the gut microflora of the French abalone, a symbiotic association between *V. gallicus* and French abalone is also hypothesized.

We have found three species of vibrios, *V. halioticoli*, *V. superstes* and *V. gallicus*, that are associated with abalone. These species are related phylogenetically (Fig. 1), but are different phenotypically (see Supplementary Table, available in IJSEM Online). The ecological niches of these species are similar (Sawabe et al., 1998, 2003; Hayashi et al., 2003). A recent phylogenetic study that used internal transcribed spacer region sequences of 19 species of the genus *Haliotis* (Coleman & Vacquier, 2002) revealed three subclades in the genus, each encompassing low variation. North Pacific species group together, whereas Australian and European species are different subclades. A single species, *Haliotis iris* from New Zealand, is quite distant from the remaining species of *Haliotis. Haliotis midae* and *Haliotis diversicolor superstes* (Taiwan) both diverged basal to European and Australian species. Assuming co-evolution of the symbiotic relationships between vibrios and *Haliotis* species, the taxonomic status of *V. gallicus* and *V. superstes* as close relatives of *V. halioticoli* is in accordance with the phylogeny of *Haliotis* species. Comparative whole-genome analyses among these three species are needed to clarify the evolutionary history. Ecological studies of *V. gallicus* are also needed, in order to better understand its interactions in the gut of marine herbivores, particularly abalones.

**Description of *Vibrio gallicus* sp. nov.**


Gram-negative, facultatively anaerobic, non-motile and non-flagellated. Cells in ZoBell 2216E broth are rod-shaped with rounded ends (0.5–0.6 × 1.2–3.0 μm). No endospores or capsules are formed. Flagellation is not observed when the organism is cultivated on solidified media and/or in liquid media. Colonies on ZoBell 2216E agar are beige, circular, smooth and convex with an entire edge. Sodium ions are essential for growth. Mesophilic and neutrophilic chemo-organotroph that grows at temperatures between 15 and 30 °C. No growth occurs at
37 °C. Positive for acid production from glucose, nitrate reduction, hydrolysis of alginate, oxidase and catalase and assimilation of D-fructose, D-glucose, maltose, D-mannitol and alginate. The following tests are negative: gas production from glucose, acetoin production, lysine decarboxylase, ornithine decarboxylase, arginine dehydrodrolase, β-galactosidase test, luminescence, pigmentation, requirement for organic growth factors, hydrolysis of starch, gelatin, chitin, Tween 80 and agar, accumulation of poly-β-hydroxybutyrate, assimilation of D-mannose, sucrose, D-glucurate, D-sorbitol, 2-oxyglutarate, D-galactose, cellobiose, melibiose, lactose, D-glucuronate, trehalose, putrescine, ϑ-aminobutyrate, acetate, pyruvate, L-tartrate, propionate, D-glucosamine, fumarate, succinate, L-arabinose, citrate, DL-malate, δ-aminovarate and acetonate. DNA G+C content is 43.6–44.3 mol%.

The type strain is CIP 107863T = LMG 21878T. Isolated from the gut of the French abalone *Haliotis tuberculata*.

**Acknowledgements**

This work was supported by Grants-in-Aid for Scientific Research from the Ministry of Education, Science and Culture of Japan (nos 09460081 and 13760134) and F. L. T. has a PhD scholarship (no. 2008361/98-6) from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brazil. J. S. acknowledges grants from the Fund for Scientific Research (FWO), Belgium. We gratefully thank Dr Bernard Kloareg, Station Biologique (CNRS/Gemar), for helpful discussion and critical reading. This work was also supported by funds from the European Commission for the AQUA-CHIP project (OLK4-2000-00764). The authors are solely responsible for the content of this publication. It does not represent the opinion of the European Commission. The European Commission is not responsible for any use that might be made of data appearing therein.

**References**


