Recent developments in the taxonomy of the genus Flavobacterium

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Abstract

The number of species in bacterial genera is constantly changing, but let's consider how many validly named Flavobacterium species exist as of this writing. The "official" lists (e.g. http://www.bacterio.cict.fr/) must be considered with great care because they also contain those species that have already been transferred to another or a new genus within the family Flavobacteriaceae (Chryseobacterium balustinum, С. gleum, С. indologenes, С. indoltheticum and C. scophthalmum; Elizabethkingia meningoseptica; Empedobacter brevis; Myroides odoratus; Psychroflexus gondwanensis; Salegentibacter salegens; and Zobellia uliginosa) or in other bacterial groups (Curtobacterium, Halomonas, Microbacterium, Novosphingobium, Pedobacter, Planomicrobium, Sphingobacterium and Terrimonas) as well as those that are still awaiting allocation to another or a new genus (F. acidificum Steinhaus 1941, F. acidurans Millar 1973 and F. thermophilum Loginova & Egorova 1982).

The graph below shows the number of new Flavobacterium species described per year.



The first bar represents the 10 species that were included in the genus following its extensive emendation [1]. Among those were [*Bacillus*] *aquatilis* Frankland & Frankland 1889 (brackets indicate generically misclassified species), the type species of the genus; the environmental species [*Cytophaga*] *johnsonae* Stanier 1947; and the three fish pathogens [*Bacillus*] *columnaris* Davis 1922, [*Cytophaga*] *psychrophila* Borg 1960 and *Flavobacterium branchiophilum* Wakabayashi *et al.* 1989.

The graph shows that the number of new *Flavobacterium* species described each year has increased steadily. There were 40 *Flavobacterium* species at the time of the *Flavobacterium* 2007 conference; since then, 41 new species have been published and 5 more are currently in

press in the International Journal of Systematic and Evolutionary Microbiology. Interestingly, a new bacterial species may subsequently be retracted; for instance, *F. sasangense* Yoon *et al.* 2009 has been retracted one year later as evidence had not been provided that the type strain had been deposited in two culture collections in different countries, as required for valid publication of a species name under the Bacteriological Code. Hence, 44 new *Flavobacterium* species have been published since the *Flavobacterium* 2007 conference, bringing the total to 85, more than twice the number it was at that time.

The two following graphs are attempts at characterizing this extraordinary increase in the number of *Flavobacterium* species in terms of geographical area and habitat.



The first graph shows that the vast majority of species have been isolated in Asia, mostly in Korea and China (as well as Japan and India to a lesser extent); also remarkable is the fact that 15 Flavobacterium species originate from Antarctica. The second graph reveals that most Flavobacterium species were retrieved from freshwater and soil environments, with a significant number also recovered from microbial mats (multi-layered sheets of microorganisms, mainly cyanobacteria and archaea) in polar lakes. These basic statistics, however, are considerably biased because they result from studies performed by a very low number of scientific groups in a few countries who focus on the characterization of bacterial communities in highly specific ecosystems. For instance, the Korean government has launched several projects for the survey of Korean indigenous species that have resulted in the description of hundreds of new bacterial species, including 23 new Flavobacterium species. Such studies have also been performed in China; for instance, 7 new Flavobacterium species were described from a single Chinese glacier by the same group of scientists. Regarding Antarctica, 10 new Flavobacterium species were described in the Laboratory of Microbiology in Gent University, Belgium, among the 800 bacterial strains that were retrieved from microbial mats in several Antarctic lakes in 1999-2000 in the frame of the Biotec project "Biodiversity in microbial mats in Antarctica" of the UE. When researchers from the German Collection of Microorganisms and Cell Cultures (DSMZ) focused on bacterial communities in one hard water rivulet in Germany, they discovered a wealth of Flavobacterium strains from which they described 6 new species.

Among the new *Flavobacterium* species described since 2007, three were isolated from fish. *Flavobacterium oncorhynchi* [2] is represented by 18 strains isolated in 2008–2009 in Spain from the liver and gills of juvenile rainbow trout presenting clinical signs indicative of *F. psychrophilum* infection. *Flavobacterium chilense* and *F. araucananum* were recovered from

farmed salmonid fish in Chile [3]; the single strain of *F. chilense* was isolated in 2006 from external lesion of a diseased rainbow trout, while the two strains of *F. araucananum* were recovered in 2008 from the kidney and external lesion of two different diseased Atlantic salmon. Interestingly, the three strains were isolated from mixed cultures that also contained *F. psychrophilum*. The virulence of these three species has not been assessed yet by challenge experiments. In addition, *Flavobacterium tilapiae* [4] was isolated in Taiwan from a pond where apparently healthy tilapia (*Tilapia rendalli*) were cultured. The same group has also described *Flavobacterium macrobrachii* [5] from a culture pond for giant river shrimp (*Macrobrachium rosenbergii*); shrimps were also apparently healthy.

Some of the newly described *Flavobacterium* species have special features. *Flavobacterium ceti* Vela *et al.* 2007 is the first *Flavobacterium* strain isolated from a mammal; it was recovered from internal organs of two apparently healthy stranded beaked whales (*Ziphius cavirostris*) in the Canary islands, Spain. One strain of *F. lindanitolerans* Jit *et al.* 2008 (originally isolated from hexachlorocyclohexane-contaminated soil in India) was isolated from the ascites sample of a Chinese child with EV71 virus infection. The first endophytic *Flavobacterium* species is *F. phragmitis* Liu *et al.* 2011, isolated from within the roots of reeds (*Phragmites australis*) in China. Other species display special degradation abilities that may lead to industrial or biotechnological applications in the future: *F. haoranii* Zhang *et al.* 2010 (isolated from activated sludge in a wastewater treatment facility in China) is able to degrade the pesticide cypermethrin; *F. glycines* Madhaiyan *et al.* 2010 (isolated from the rhizosphere of soybean in India) is a facultative methylotroph that can turn over one-carbon compounds in the environment; and *F. algicola* Miyashita *et al.* 2010 (isolated from marine algae) is able to degrade fucoidan, a sulfated polysaccharide of brown macroalgae.

To conclude on a taxonomic touch, it should be noted that the serious issue that burdens the taxonomy of the genus *Flavobacterium* (already stressed in my presentation at *Flavobacterium* 2007) has not been solved, i.e. it has not been possible yet to propose new taxa for the species that are only remotely related to the type species *F. aquatile*. No chemotaxonomic feature (fatty acids, polar lipids, respiratory quinones, polyamines, pigments, etc.) has been able so far to distinguish them from the *bona fide Flavobacterium* species. Hence, there are still three groups of *Flavobacterium* species. The main one contains the type species of the genus, *F. aquatile*. The other distinct cluster groups species (including *F. columnare*) that are only remotely related to *F. aquatile* and that should become the core of a new genus or new genera. Finally, several other *Flavobacterium* species occupy independent branches at even lower positions on the phylogenetic tree for which separate new taxa should be proposed.

References

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