

# CHARACTERISATION AND ANTIBIOTIC RESISTANCE OF HUNGARIAN FRESHWATER *FLAVOBACTERIUM* ISOLATES

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The aim of this work was to study the changes induced by increasing water temperature resulting from climate change in the prevalence of *Flavobacterium columnare* in wild and cultured freshwater fishes.

Using selective cytophaga agar and a species-specific PCR designed by Bader et al. (2003), we identified as *F. columnare* 25 isolates collected from ulcerous skin, eyes, gills and inner organs with lesions and from the skin or gills of healthy fishes. The genotypes of isolates were determined using PCR-RFLP according to Darwish et al. (2005); however, the electrophoretic profiles obtained were different from those published earlier. Twenty isolates were identical with each other, further four strains varied from the former only in restriction fragment profile with one or the other enzyme, while one isolate produced a different fragment profile with both enzymes.

Sequencing of 1360 bp long fragments of the 16S rRNA gene confirmed the discrepancy. Twenty-three isolates showed 97–99% identity with *F. johnsoniae*, a species closely related to *F. columnare*. The remaining two isolates were identified as *Chryseobacterium piscium* and an unnamed *Chryseobacterium* genomospecies.

The antibiotic resistance patterns of the isolates were determined by Kirby-Bauer disc diffusion susceptibility test against 10 antibiotics. All isolates were multiresistant, i.e. they showed resistance against at least four antibiotics. The majority of resistant isolates presented complete resistance to some antimicrobial agents, which made the estimation simple. All 25 isolates showed resistance against ampicillin and polymyxin B, the 23 *F. johnsoniae* strains proved to be resistant to cotrimoxazole, while only one *F. johnsoniae* and one *Chryseobacterium* sp. strain each was sensitive to gentamicin. High rates of resistance were present within the isolates against chloramphenicol (19) and oxytetracycline (17), as well. In contrast with these results, erythromycin (22), enrofloxacin (21), furazolidone (19) and florfenicol (17) were highly effective against flavobacteria.

The high-level multiresistance demonstrated in this study hampers medical treatment and can play a major role in the transmission of resistance genes from environmental to pathogenic bacteria.

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