Identification and Genotyping of *Chryseobacterium aquaticum* Isolated from Farmed Salmonids Showing Clinical Disease Signs in Turkey

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Abstract

Flavobacterial diseases in fish are caused by multiple bacterial species within the family *Flavobacteriaceae* and are responsible for devastating losses in wild and farmed fish stocks around the world. With the recent advances in molecular biology, several novel genera within the family *Flavobacteriaceae* (e.g., *Chryseobacterium, Elizabethkingia and Tenacibaculum*) have emerged that encompass pathogens of fish, amphibians, reptiles, birds, and mammals, including humans[1]. Members of the genus *Chryseobacterium* have emerged as serious fish pathogens on multiple continents. During the last ten years alone, numerous novel *Chryseobacterium spp*., including *C. piscicola*[2], *C. chaponense*[3], *C. viscerum*[4], and *C. oncorhynchi*[5] were described and recovered from systemically infected fishes exhibiting clinical disease signs worldwide[1]. The objective of this study was to identify and genotyping of *C. aquaticum* isolates in rainbow trout. Herein, twenty-seven, *C. aquaticum* isolates recovered from farmed rainbow trout exhibiting clinical signs such as darkening of skin color, exophthalmia, and caudal fin root. The identification of the isolates was performed through biochemical tests and 16S rRNA sequence analysis with using 27F and 1387R universal primers. The isolates were compared through a phylogenetic analysis with *C. aquaticum* sequences accessed in GenBank which were isolated from rainbow trout in Iran and water isolates in New Zealand and South Korea[6]. We report that our *C. aquaticum* isolates were found to have close relationship between each other. Also, the isolates of Iran and South Korea showed 99.5% similarity with our isolates.

In conclusion, this is the first report of *C. aquaticum* recovered from rainbow trout in Turkey. Its pathogenicity was not assessed previously.[1] Further research is needed to determining the virulence mechanisms and pathogenesis of *C. aquaticum.*

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Literature Cited

1. Loch TP, Faisal M. 2015. Emerging flavobacterial infections in fish: A review. Journal of advanced research 6(3): 283-300.
2. Ilardi P, Fernandez J, Avendaño-Herrera R. 2009. *Chryseobacterium piscicola* sp. nov., isolated from diseased salmonid fish. International journal of systematic and evolutionary microbiology 59(12): 3001-3005.
3. Kämpfer P, Fallschissel K, Avendaño-Herrera R. 2011. *Chryseobacterium chaponense* sp. nov., isolated from farmed Atlantic salmon (*Salmo salar*). International journal of systematic and evolutionary microbiology *61*(3): 497-501.

4. Zamora L, Vela AI, Palacios MA, Sánchez-Porro C, Svensson-Stadler LA, Domínguez L, Fernández-Garayzábal JF. 2012. *Chryseobacterium viscerum* sp. nov., isolated from diseased fish. International journal of systematic and evolutionary microbiology, 62(12): 2934-2940.
5. Zamora L, Fernández-Garayzábal JF, Palacios MA, Sánchez-Porro C, Svensson-Stadler LA, Domínguez L,Vela AI. 2012. *Chryseobacterium oncorhynchi* sp. nov., isolated from rainbow trout (*Oncorhynchus mykiss*). Systematic and applied microbiology *35*(1): 24-29.
6. Akhlaghi M, Sharifiyazdi H, Fereidouni MS. 2012. Isolation and Identification of Chryseobacterium aquaticum from Caudal Fin Rot and Peduncle Erosion in Rainbow Trout (Oncorhynchus Mykiss). Iranian Journal of Veterinary Clinical Sciences 6(1): 19-27