PHYLOGENETIC AND VIRULENCE ANALYSIS OF *AEROMONAS VERONII* ISOLATED FROM FRESHWATER FISHES IN HUNGARY

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Bacterial infections, caused by motile members of the genus Aeromonas, are among the most common and troublesome diseases of fish raised in ponds and recirculating systems. These bacteria are widespread in the aquatic environment, since they are capable of utilizing nutrients present in water and surviving for long periods in the absence of the host, as well. Whether acting alone or in mixed infections with other organisms, they are responsible for the great variety of infections from the skin ulcer, superficial or invading deeply into the muscle, to the internal systemic disease (septicaemia). All species of fish, scaled and unscaled, are susceptible to infection.

Most frequently the *A. hydrophila*, *A. caviae* and *A. veronii* species induce disease in fishes. With great host and virulence ranges and with considerable zoonotic ability the A. veronii possesses. Moreover the increasing water temperature resulting from climate change enhances effectively its prevalence and infection intensity. For the delineation of presumed clonal subtypes with different pathogenicity is needed the exhaustive knowledge of the population.

Thus, the aim of our study was to detailed molecular analysis of *A. veronii* strains isolated from ulcerous skin, affected fins, and internal organs with lesions of wild and cultured freshwater fishes in Hungary. Following the genus-specific identification and species-specific classification carried out with PCRs, sequences of some housekeeping gene (16S ribosomal RNA, *cnp*60 - type I chaperonin, *gyr*A, *gyr*B - α, and β-subunit of DNA gyrase, *rpo*B - β-subunit of DNA-dependent RNA polymerase, and *dnaJ* - heat shock protein 40) were analysed for revealing their phylogenetic relations. In addition, the occurrences of the most prevalent virulence factors: lateral flagella, DNase, nuclease, serine protease, lipases involved the tissue invasion and toxins (entero-, haemolytic toxins) were detected. Comparison of generated different results indicated the existence of potential subgroups. Estimation of their virulence abilities required further in vitro pathogenicity assays.

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