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Rapid Detection Method and Characterization of the Virulence Factors from Pathogenic *Aeromonas*

In-Young Nam

Departments of Bioscience and Biotechnology, Hankuk University of Foreign Studies

The detection of virulence factors of *Aeromonas* is a key in determination of potential pathogenicity because they act multifunctionally and multifactorially. Water samples were collected seasonally in a trout farm, diseased fish and *Aeromonas* was isolated and identified. To detect six virulence factors of isolated *Aeromonas* rapidly, hexaplex-polymerase chain reaction (hexaplex-PCR) assay was used. Detected virulence factors are aerolysin (*aer*), GCAT (*gcat*), serine protease (*ser*), nuclease (*nuc*) lipase (*lip*) and lateral flagella (*laf*). As the results, the dominant strain was *Aeromonas sobria* and the dominant virulence factors were *aer* and *nuc,* for all seasons. We confirmed that *A. sobria* and two virulence genes (*aer* and *nuc)* are related. We proposed a method by which one can identify *Aeromonas* major strain: *A. hydrophila, A. sobria, A. caviae,* and *A. veronii,* using hexaplex-PCR.

A. encheleia, a potential human intestinal pathogen, was shown to infect human intestinal epithelial cell (Caco-2) in a noninvasive manner. We analyzed the transcriptional profile of Caco-2 cells after infection with the bacteria. A notable feature was that the expression of genes involved in chloride secretion including phospholipase A2 related platelet activating factor (PAF) and was upregulated. It was confirmed by realtime RT-PCR analysis for those genes. PAF was shown to be present when Caco-2 cells were infected with the bacteria as expected. PAF was also produced when the cells were treated with bacterial culture supernatant including bacterial extracellular proteins but lacking lipopolysaccharides (LPS). We showed that bacterial aerolysin induced the production of PAF.