Oligonucleotide microarray-based molecular prediction of thirty pathogenic *Salmonella* serotypes

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Salmonella is the leading pathogenic bacterium which causes the foodborne infection in human and/or animals. *Salmonella* infection is occasionally fatal, resulting the morbidity and mortality. For *Salmonella* infection control, disease assessment, and epidemiological surveillance, it is important to determine the exact serotype among more than 2,500 types. In this study, we developed an oligonucleotide microarray-based system for molecular determination of the commonly isolated *Salmonella* serotypes in Korea. This microarray system employed a single gene as a novel marker, thiamine synthase H subunit (*thiH*) gene which was found by comparative genome analysis and have the definite ability of the serotype-level identification. Each target serotype of Salmonella can be identified and determined efficiently by the distinctive probe-signal patterns, which can discriminate even the highly closed (related) serotypes. ThiH-based oligonucleotide microarray system can be a useful, robust, and efficient molecular serotype determination tool for Salmonella compared to routine laboratory testing.