小児難病、川崎病に合併する心臓病を予防し、安心・安全な子育て支援に資する研究

A Study to Identify Comprehensive Childcare by Protecting Patients from the Intractable Cardiac Complications Associated with Kawasaki Disease

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Summary

To determine the pathogenesis of Kawasaki disease, we attempted to develop novel tools for detecting the genomes of pathogens in upper gastrointestinal mucosa samples isolated from patients and their specific heat-shock proteins (HSPs) that induce coronary artery involvement in the disease.

We first developed specific primers for detecting the genomes by reverse transcription polymerase chain reaction. We successfully produced a specific primer (s-Aradi-F/s-Aradi-R2) as a superior detector of *Acinetobacter radioresistens*, which was a candidate pathogen. However, we only prepared a subgroup of *Nesseria* sp., another key candidate, because it was a molecular biological congenic strain to *N. subflava*, *N. perflava*, and *N. flavescens*. We managed to decode 16 of the 18 16s ribosomal RNA genes of neighboring *Neisseria* species by a sequence analysis.

In the second year of our study, we performed a molecular phylogenetic analysis for those *Neisseria* species after decoding all of the 16s ribosomal RNA genes. Finally, we developed specific primers for detecting five subgroups of the targeted *Neisseria* strain. We also tried to refine antibodies to specific HSPs associated with those pathogens. We were ultimately successful in determining the specific epitope of the HSPs for each species, as follows: *Nesseria* 419-432, *Acinetobacter* 125-138, and *Enterobacter* 426-439.