One hundred and thirty five isolates (135/283; 47.7%) were confirmed to be *S. aureus* when the gene *nuc* and the target 16S rRNA were observed to be present simultaneously. The genotypic identification was totally in concordance with the results obtained for the phenotypic characterization namely, the Gram staining, fermentation of mannitol, Catalase and coagulase. Table 1 shows the analysis of the risk factors for *S. aureus* carriage. Since many of the MRSA strains exhibit a hetero-resistance phenotype, detection of the mecA gene by molecular methods has become the reference method for confirmation of MRSA strains (Becker et al., 2006; Hososaka et al., 2007). In the present study, the mecA gene was detected in 15% of the overall *S. aureus* isolates. The results of the antibiotic sensitivity tests are summarized in Table 2.

Hososaka et al., (2007) reported that from 480 *S. aureus* strains, 6 were MRSA but oxacillin-sensible (OS-MRSA). Our results show that the carriage of MRSA exists among healthy children. Therefore continuing surveillance is needed to more accurately assess the prevalence, epidemiology of community-acquired infection and to develop strategies that will improve therapy and control the spread.