

Genotyping of salmonella spp. on the basis of CRISPR (clustered regularly interspaced short palindromic repeats)

ABSTRACT

Aims: The CRISPR locus in Salmonella genome is comprised of three main components which are the (CRISPR-associated) cas genes, an AT-rich leader sequence and the CRISPR array. The length of CRISPR array is determined by the number of spacers within it and varies not only among different organisms but also varies among the bacterial serotypes and strains. This present study aimed at determining if the CRISPR array in Salmonella spp. could be applied to establish a correlation between serogroup type and the fingerprint generated by CRISPR typing.

Methodology and results: A total of 30 Salmonella samples were obtained from the Veterinary Diagnostic Laboratory, Kota Kinabalu, Sabah. Salmonella serogroup was determined using the slide agglutination test. Four different serogroups were identified which were serogroup B, C, D, and E. Deoxyribonucleic acid (DNA) was extracted and polymerase chain reaction (PCR) was performed using primers which were designed to amplify the CRISPR array in Salmonella genome. Our results indicate that there is a positive correlation between serogroup results obtained using slide agglutination test and the profile generated by CRISPR typing.

Conclusion, significance and impact of study: CRISPR typing has the potential to be applied for the genotyping of Salmonella bacteria.