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Single nucleotide polymorphism in the genome of *Salmonella Enteritidis* and implications for controlling an important foodborne pathogen

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Genetic variation among microbes remains the basis for developing tools for pathogen identification and characterization and the advent of whole genome sequencing has now provided an opportunity to generate unambiguous laboratory results that could be used to effectively manage and control an important foodborne pathogen such as *Salmonella enterica* serovar Enteritidis (SE). The observed clonality of SE organisms has been interpreted, with some justification, as a demonstration of limited genetic variation. Consequently, conventional subtyping tools have been shown to be poorly discriminatory for assessing the relatedness or otherwise, among isolates and has hindered an objective assessment of the food source of infection outbreaks in humans. Single nucleotide polymorphism (SNP) is one of the most important types of genetic variation observed in the genome of SE. We have analyzed a total of 146 genomes of SE including all published sequences (n=128) and unpublished but finished genomes (n=18) and found a total of 7,648 SNPs. A significant proportion (21%) was present in intergenic locations while a majority (79%) occurred among a diverse collection of coding sequences. Despite the spread of the SNPs across the entire SE genome, the occurrence of different SNPs in a non-random manner, i.e., linkage disequilibrium provides the opportunity to characterize isolates, cluster related isolates and determine genetic distances among different isolates. SNP variation in the SE genome has been exploited to develop a new, robust, cost-effective, sensitive and specific subtyping tool for SE using a real time-polymerase chain reaction (SE-SNP-PCR) that measures fluorescence based on the presence of one SNP allele or the other at each of 60 loci distributed across the genome. It was identified a total of 16 circulating SE clades in Canada. The new test reliably demonstrated relatedness between human isolates, food and animal isolates in a distinct geographical region in Canada, and should be useful to comprehensively describe genetic distances between isolates and to develop an evolutionary map of SE.

Biography

Dele Ogunremi is a research scientist at the Canadian Food Inspection Agency, Ottawa Laboratory Fallow field, and is a trained veterinarian with doctoral and postdoctoral training in Molecular Biology and Immunology. He graduated with DVM (1984) and MVSc (1986) from the University of Ibadan, Nigeria and PhD from the University of Saskatchewan, Canada (1993), where he also completed a postdoctoral training (1996). His research interests include the application of genomics sequencing technology to detect, identify and characterize foodborne microbial pathogens. He has generated, assembled and characterize Salmonella and Listeria genomes. Recently he completed the development of genomics based single nucleotide polymorphism genotyping test for Salmonella Enteritidis. He has played a lead role in the establishment of the Pulse Field Gel Electrophoresis at the Canadian Food Inspection Agency. His research work has been protected by patents granted in Canada, United States and New Zealand.

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