Phylogenetic analysis of *Salmonella* serovars based on 16S rRNA gene sequences

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Abstrak

Kami telah menentukan sekuens gen 16S rRNA lengkap dari 15 Salmonella *spesies dengan metode* direct sequencing *gen produk amplifikasi PCR menggunakan primer universal. Persentase kemiripan antara urutan nukleotida di antara* Salmonella *spp sangat tinggi (97,4 % - 99,2%). Subsitusi basa terdapat sepanjang gen tersebut dengan dua hotspot, satu diantaranya adalah daerah variabel V6. Telah pula dideteksi daerah spesifik untuk* Salmonella *yang dapat dipergunakan untuk merancang pelacak gen yang spesifik spesies. Sisipan 9 bp dan delesi 5 bp ditemukan masing-masing pada* S. waycross, *dan* S. matopeni. *Hal ini sesuai dengan frekuensi mutasi yang tinggi di antara kuman salmonellae patogen. Serovar* Salmonella *tampaknya termasuk di dalam satu spesies yang dapat dibagi dalam 4 subcluster, hal mana tidak sesuai dengan skema klasifikasi Kauffman-White atau Le minor.* S. bovismorbificans *ternyata paling beragam di antara 15 serovar tersebut. Diharapkan analisis gen yang lengkap ini dapat meningkatkan pengetahuan mengenai hubungan filogenetik dan klasifikasi taksonomik dari serovar-serovar ini.*

Abstract

We determined the complete 16S rRNA gene sequences from 15 Salmonella *species through direct sequencing of PCR-amplified gene products using universal primers. Percentage similarity of sequences between* Salmonella *spp was very high (97.4 to 99.2%). Base subtitutions occurred throughout the gene with two apparent 'hotspots', one of which corresponded to the V6 variable region. We have also detected a* Salmonella*-specific region that can be used in the design of a species-specific gene found in* S. waycross *and* S. matopeni, *respectively, thus concurring with the known high mutational frequencies existing among pathogenic salmonellae. The* Salmonella *serovars appear to belong to a single species that can be divided into four subclusters which do not concur with the Kaufmann-White or Le Minor classification schemes.* S. bovismorbificans *was found to be most diverse among the 15 serovars studied. It is hoped that the complete sequence analysis of this gene will improve our understanding of phylogenetic relationships and taxonomic classification of these serovars.*

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