# Karakterisasi Genomik, Faktor Virulensi, Gen Resistensi Antibiotik, dan Lokus Kapsul Polisakarida Streptococcus pneumoniae Serotipe 3 = Genomic characterization, virulence factor, antibiotic resistance gene, and capsule polysaccharide locus of serotype 3 Streptococcus pneumoniae isolates

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Abstrak

Streptococcus pneumoniae serotipe 3 masih menjadi penyebab utama morbiditas dan mortalitas pada pasien yang terinfeksi pneumokokus. Penelitian ini bertujuan untuk menganalisis karakteristik genom, faktor virulensi, gen resistensi antibiotik, dan lokus kapsul polisakarida (cps) dari 19 isolat tersimpan S. pneumoniae serotipe 3 pada kelompok usia anak-anak dan dewasa dari berbagai wilayah di Indonesia. Karakterisasi genomik dilakukan dengan teknik whole-genome sequencing menggunakan platform Illumina, kemudian dilanjutkan dengan analisis bioinformatika menggunakan pipeline ASA3P, PathogenWatch, ABRIcate, dan GeneViewer. Pada penelitian ini ditemukan galur ST451-GPSC234 (n=5), ST180-GPSC12 (n=4), ST458-GPSC51 (n=2), ST3805-GPSC12 (n=2), ST4909-GPSC363 (n=2), ST700-GPSC10 (n=1), ST5292-GPSC309 (n=1), ST505-GPSC 12 (n=1), dan ST4233 (n=1). Selain itu, ditemukan isolat resisten terhadap tetracycline (42%) yang dibawa oleh gen determinan tetM4, tetM8, tetM12, dan tet32; chloramphenicol (10%) yang dibawa oleh gen catPC194; dan co-trimoxazole (5%) yang dibawa oleh gen folA dan folP. Penelitian menemukan galur ST700-GPSC10 tidak memiliki gen cpsA, cpsB, cpsC, cpsD, dan tnp pada lokus cps serta tidak memiliki gen penanda faktor modulasi imun meliputi gen cps4A, cps4B, cps4C, cps4D, igA dan zmpC. Penelitian ini menunjukkan isolat S. pneumoniae serotipe 3 memiliki keragaman genetik tinggi dengan karakteristik genom unik yang dapat berkontribusi terhadap patogenesis serotipe 3.

......Streptococcus pneumoniae serotype 3 remains a major cause of morbidity and mortality in pneumococcal infected patients. This study aimed to analyse genomic profiles, virulence factors, antibiotic resistance, and capsular polysaccharide (cps) loci of 19 archived isolates of S. pneumoniae serotype 3 in children and adult groups from various regions in Indonesia. Genomic characterization was performed by whole-genome sequencing technique using Illumina platform, followed by bioinformatics analysis using ASA3P, PathogenWatch, ABRIcate, and GeneViewer pipelines. This study found ST451-GPSC234 (n=5), ST180-GPSC12 (n=4), ST458-GPSC51 (n=2), ST3805-GPSC12 (n=2), ST4909-GPSC363 (n=2), ST700-GPSC10 (n=1), ST5292-GPSC309 (n=1), ST505-GPSC 12 (n=1), dan ST4233 (n=1). The isolates were found to be resistant to tetracycline (42%) carried by tetM4, tetM8, tetM12, and tet32 genes; chloramphenicol (10%) carried by catPC194 gene; and co-trimoxazole (5%) carried by folA and folP genes. This finding revealed that ST 700-GPSC 10 lacks of cpsA, cpsB, cpsC, cpsD, and tnp genes in cps locus and devoid immune modulation factor genes including cps4A, cps4B, cps4C, cps4D, igA, and zmpC. This study suggest that S. pneumoniae serotype 3 isolates have high genetic diversity with unique genomic characteristics that may contribute to pathogenesis of serotype 3