Karakteristik dan hubungan resistom dan tingkat kekebalan gentamisin, klindamisin dan minosiklin pada isolat klinis staphylococcus aureus kebal metisilin = The gentamicin, clindamycin and minocycline resistome and minimum inhibitory concentration characteristics and relations in clinical methicillin-resistant staphylococcus aureus.

Irandi Putra Pratomo, author

Abstrak

Latar belakang: Antibiotik gentamisin (GEN), klindamisin (CLI) dan minosiklin (MIN) digunakan dalam penanganan infeksi Staphylococcus aureus kebal metisilin (methicillin-resistant Staphylococcus aureus, MRSA). Teknologi next-generation sequencing (NGS) merupakan metode mutakhir yang digunakan untuk pemetaan pola kekebalan kuman untuk pengendalian infeksi di suatu fasilitas pelayanan kesehatan. Penelitian ini bertujuan untuk mengetahui profil genom isolat MRSA klinis melalui pemeriksaan NGS.
Metode: Proses sequencing DNA menggunakan Illumina® MiSeq dilakukan pada 92 isolat MRSA klinis yang diperoleh dari pasien yang dirawat di Hiroshima University Hospital, Hiroshima, Jepang sehingga didapatkan masing-masing susunan genom de novo. Susunan genom de novo tersebut kemudian dianalisis in silico menggunakan ResFinder sehingga didapatkan profil genom kekebalan antibiotik kuman. Data ini kemudian dianalisis bersama data fenotip kadar hambat minimum (KHM) GEN, CLI, dan MIN.
Hasil: Penelitian ini menunjukkan MRSA aac(6')aph(2")+,spc+, ermA+,tetM+ merupakan isolat terbanyak (42/92) dan memiliki KHM GEN >16 mg/L (40/42), CLI >4 mg/L (26/42) dan MIN >8 mg/L MIN (30/42). Deteksi gen aac(6')aph(2") berhubungan dengan KHM GEN (p<0,001), deteksi gen ermA berhubungan dengan KHM CLI (p<0,001) dan deteksi gen tetM berhubungan dengan KHM MIN (p<0,001). Deteksi bersamaan aac(6')aph(2")-spc-ermA-tetM berkorelasi dengan KHM GEN (c= 0,398, p <0,001), CLI (c= 0,448, p <0,001) dan MIN (c= 0,515, p <0,001).
Kesimpulan: Penelitian ini menunjukkan korelasi fenotip KHM dan genotip kekebalan antibiotik GEN, CLI dan MIN pada MRSA. Teknologi NGS berpotensi sebagai uji cepat deteksi kekebalan antibiotik pada kasus infeksi MRSA yang merupakan bagian dari upaya pengendalian infeksi.
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Background: Gentamicin (GEN), clindamycin (CLI) and minocycline (MIN) are amongst the widely used antibiotic treatments in methicillin-resistant Staphylococcus aureus (MRSA) infection. The emerging next-generation sequencing (NGS) technology provides antibiotic resistance pattern mapping to be inferred as a consideration in healthcare infection control policy. The subjective of this study is to reveal genomic resistome using NGS and to correlate the resistome with the phenotype of antibiotic resistance represented as minimum inhibitory concentration (MIC) between clinically isolated MRSA specimens.
Methods: Illumina® MiSeq was used to sequence and to de novo assembly the genomic DNA of 92 MRSA specimens obtained from the patients treated in Hiroshima University Hospital, Hiroshima, Japan. Resistome was determined by feeding the de novo genome assembly to ResFinder annotation tool prior to correlation analysis with MIC data. These procedures were performed during GEN, CLI and MIN susceptibility observation.
Results: The aac(6')aph(2")+,spc+, ermA+,tetM+ MRSA strains were revealed to be predominant (42/92) of

which were possessing GEN MIC >16 mg/L (40/42), CLI MIC >4 mg/L (26/42) and MIN MIC >8 mg/L MIN (30/42). This study also revealed the correlation of aac(6')aph(2'') and GEN MIC ($p<0.001$), ermA and CLI MIC ($p<0.001$), and tetM and MIN MIC ($p<0.001$). Simultaneous detection of aac(6')aph(2'')-spc-ermA-tetM was correlated with GEN MIC ($c= 0.398$, $p <0.001$), CLI MIC ($c=0.448$, $p <0.001$), and MIN MIC ($c= 0.515$, $p <0.001$).

Conclusions: This study showed correlation between the MIC and resistome of GEN, CLI and MIN in MRSA. The emerging NGS technology provides promising method in rapid detection of antibiotic resistance in MRSA thus feasible for infection control near in the future.