

## ABSTRACT

Healthcare-associated infections (HAIs) are infections that occur while receiving health care, developed in a hospital or other health care facility that first appear 48 hours or more after hospital admission, or within 30 days after having received health care. Previous research in Indonesia showed that HAIs occur in high numbers after surgical operations and with the use of invasive medical devices. HAIs can be caused by antibiotic-resistant pathogenic microorganisms, bacterial transmission from medical staff or the environment, or between patients. Recent genomic surveillance is often carried out to analyze the microbiome characteristics of the hospital environment using the Shotgun metagenomic DNA sequencing (SGS) technique. SGS is able to identify bacterial profiles, resistome populations, and characteristics of bacterial virulence factors.

This research aimed to determine the bacterial profile based on environmental isolates in the Pediatric Intensive Care Unit (PICU) of RSUP dr. Sardjito Yogyakarta using the Shotgun metagenomic DNA sequencing method. The specific objectives were to determine genomic surveillance based on taxonomy and the distribution of resistome and virulome genes in environmental isolates for infection control, and risk factors for Healthcare-Associated Infections (HAIs) in PICU patients associated with the presence of bacteria and the spread of resistome and virulome in the pediatric intensive care unit of Dr. Sardjito Yogyakarta within three months of observation. Odds Ratio and significance were assessed for various risk factors for the occurrence of HAIs in the pediatric intensive care unit of Dr. Sardjito General Hospital over a period of three months. The compliance percentage of hand hygiene is measured for the five moments of hand hygiene, and the results of the secondary data analysis are correlated with the genomic analysis of the presence of bacterial specimens in the PICU environment.

Data was collected from 81 patients and observations were made on healthcare workers in the pediatric intensive care unit. Data processing and analysis was performed to test hypotheses using chi-square tests and multiple logistic regression analysis. The research showed that a variety of bacteria, including bacteria from the "ESKAPE" group, are prevalent on the surfaces of medical equipment and in the PICU environment at RSUP dr. Sardjito Yogyakarta. Gender, length of hospital stay, and the use of medical devices such as urinary catheters, intubation, mechanical ventilation, nasogastric tubes, intravenous (IV) lines, and central venous catheters (CVC) are all risk factors for HAIs in PICU. The prescription of multiple types of antibiotics during treatment and antibiotic resistance (MDR and XDR) obtained from bacterial culture results also showed statistically significant associations with HAI occurrence. Additionally, medical procedures involving the use of IV lines and irrational antibiotic prescribing were found to be both confounders and risk factors for HAI.

**Keyword:** Healthcare-associated infections, ESKAPE pathogen, shotgun metagenomic DNA sequencing, environmental isolates, resistome.

## INTISARI

*Healthcare Associated Infections* (HAIs) yakni penyakit infeksi yang pertama muncul dalam waktu antara 48 jam dan empat hari setelah pasien masuk rumah sakit maupun di tempat pelayanan kesehatan lainnya, atau dalam waktu 30 hari setelah pasien keluar dari rumah sakit. Penelitian sebelumnya di Indonesia menunjukkan bahwa HAIs terjadi dalam jumlah yang tinggi setelah operasi bedah dan penggunaan alat medis invasif. HAIs dapat disebabkan oleh mikroorganisme patogen yang resisten terhadap antibiotik, penularan bakteri dari staf medis atau lingkungan, atau antara pasien. Pendekatan epidemiologi molekuler diperlukan untuk mempelajari kontribusi faktor risiko dan distribusi gen resistensi antibiotik pada bakteri MDR di lingkungan rumah sakit. Pemantauan genomik terkini sering dilakukan untuk menganalisis karakteristik mikrobioma di lingkungan rumah sakit menggunakan teknik Shotgun metagenomic DNA sequencing (SGS). SGS mampu mengidentifikasi profil bakteri, populasi resistome, dan karakteristik faktor virulensi bakteri.

Penelitian ini bertujuan untuk menentukan profil bakteri berdasarkan isolat lingkungan di Unit Perawatan Intensif Anak (PICU) RSUP dr. Sardjito Yogyakarta menggunakan metode Shotgun metagenomic DNA sequencing. Tujuan khususnya adalah untuk menentukan pemantauan genomik berdasarkan taksonomi dan distribusi gen resistome dan virulome pada isolat lingkungan untuk pengendalian infeksi, serta faktor risiko untuk HAIs pada pasien perawatan intensif anak yang terkait dengan keberadaan bakteri dan penyebaran resistome dan virulome di unit perawatan intensif anak RSUP dr. Sardjito Yogyakarta dalam tiga bulan pengamatan. Odds Ratio dan signifikansi dievaluasi untuk berbagai faktor risiko kejadian HAIs di unit perawatan intensif anak RSUP dr. Sardjito dalam periode tiga bulan. Persentase kepatuhan cuci tangan diukur untuk lima momen kebersihan tangan, dan hasil analisis data sekunder dikorelasikan dengan analisis genomik terkait keberadaan spesimen bakteri di lingkungan PICU.

Penelitian ini menunjukkan bahwa berbagai jenis bakteri, termasuk bakteri kelompok "ESKAPE", umum ditemukan di permukaan alat medis dan lingkungan PICU. Dari 81 pasien HAIs, jenis kelamin, lama rawat inap, dan penggunaan alat medis seperti kateter urin, intubasi, ventilasi mekanik, NGT, IV line, dan kateter vena sentral (CVC) merupakan faktor risiko untuk HAIs di PICU. Resep obat antibiotik yang menggunakan beberapa jenis antibiotik selama pengobatan dan resistensi antibiotik (MDR dan XDR) yang diperoleh dari hasil kultur bakteri juga menunjukkan hubungan yang signifikan secara statistik dengan kejadian HAI. Selain itu, prosedur medis yang melibatkan penggunaan jalur IV dan pemberian antibiotik secara tidak rasional juga ditemukan sebagai faktor risiko untuk HAI.

**Kata Kunci:** Healthcare-associated infections, Bakteri "ESKAPE", shotgun metagenomic DNA sequencing, environmental isolates, resistome.