STUDI POLIFASIK *Salmonella* spp. PENYEBAB DEMAM ENTERIK DI YOGYAKARTA

INTISARI

Menurut WHO, demam enterik menjadi salah satu penyakit endemik di Indonesia dengan prevalensi sebesar 358–800 per 100.000 kasus dan persentase kematian sebesar 1–5%. Selain jumlah kasus yang tinggi, hasil dari uji untuk deteksi demam enterik masih memiliki kekurangan, salah satunya hasil positif palsu. Oleh karena itu, dibutuhkan kajian diversitas yang bersifat diskriminatif terhadap anggota *Salmonella* spp. dengan pendekatan sistematik polifasik. Penelitian ini dilakukan dengan tujuan menganalisa diversitas strain anggota *Salmonella* spp. yang berasal dari kota Yogyakarta berdasarkan pendekatan polifasik, dengan menganalisa karakteristik uji biokimia dan serologi, profil protein, gen *16S rRNA*, dan uji sensitivitas terhadap antibiotik. Sebanyak 18 sampel *Salmonella* spp. yang dikoleksi dari RSUP Sardjito, RS Akademik UGM, dan Balai Laboratorium Kesehatan dan Kalibrasi Yogyakarta. Untuk identifikasi *Salmonella* spp., pewarnaan Gram, uji biokmia, dan uji sensitivitas terhadap 18 jenis antibiotik digunakan metode uji dengan Vitek-2 dan uji similaritas menggunakan aplikasi MVSP. Uji profil protein dilakukan dengan metode SDS-PAGE dan dianalisis dengan perhitungan berat molekul berdasarkan Retention factor (Rf) dan persamaan linier (Y = a + bX). Analisis gen *16S rRNA* dilakukan dengan metode ekstraksi DNA, amplifikasi gen *16S rRNA*, elektroforesis, dan sekuensing DNA yang kemudian dianalisis menggunakan perangkat lunak MEGA. Hasil identifikasi yang diperoleh dari penelitian ini yakni terdeteksi *Salmonella* spp., *Salmonella typhi*, *Salmonella paratyphi* A, *Salmonella paratyphi* B. Dari uji aktivitas biokimia memberikan hasil bahwa semua isolat menunjukkan adanya aktivitas fermentasi D-Glukosa, D-Maltosa, D-Manitol, D-Manosa, D-Trehalosa, dan kumarat. Dari hasil uji biokimia, uji serologi, dan uji morfologi didapatkan similaritas tertinggi pada A11 dan A14 (100%). Pada uji sensitivitas antibiotik, *Salmonella* spp. memiliki sensitivitas tertinggi terhadap tigesiklin, sedangkan resistensi tertinggi terhadap sefazolin, amikasin, dan gentamisin. Hasil yang didapatkan dari analisis profil protein yakni A6 dan A7 mirip (similaritas 89%). Pada uji karakteristik dengan gen *16S rRNA* didapatkan hasil berupa kekerabatan yang dekat antara C2-A17, A7-A2, A9-A3, C1-A4, A6-A14. Kesimpulan dari penelitian ini yakni; berdasar uji biokimia, semua sampel masih dalam satu spesies, tidak ada karakter yang berbeda berdasarkan urutan gen *16S rRNA*, dan semua sampel sensitif terhadap tigesiklin dan resisten terhadao sefazolin, amikasin, dan gentamisin.

Kata kunci: Demam enterik; tifoid; *Salmonella*; Polifasik; molekuler

POLYPHASIC STUDY OF *Salmonella* spp. CAUSES OF ENTERIC FEVER IN YOGYAKARTA

ABSTRACT

According to WHO, enteric fever is an endemic disease in Indonesia with a prevalence of 358–800 per 100,000 cases and a mortality rate of 1–5%. Apart from the high number of cases, the results of tests for detecting enteric fever still have drawbacks, one of which is false positive results. Therefore, discriminative diversity studies are necessary among *Salmonella* spp. with a polyphasic systematic approach. This research aims to analyze the diversity of strains of members of *Salmonella* spp. collected from the city of Yogyakarta based on a polyphasic approach, precisely by analyzing the characteristics of biochemical and serology tests, protein profiles, the *16S rRNA* gene, and antibiotic sensitivity tests. A total of 18 samples of *Salmonella* spp. were collected from Sardjito Hospital, UGM Academic Hospital, and Yogyakarta Health and Calibration Laboratory Center. Vitek-2 was used to identify *Salmonella* spp., Gram staining, biochemical testing, and sensitivity testing to 20 types of antibiotics, and the similarity test was done using the MVSP software. The protein profile test was conducted using the SDS-PAGE method and analyzed by calculating the molecular weight based on the Retention factor (Rf) and linear equation (Y = a + bX). Analysis of the *16S rRNA* gene was conducted using DNA extraction, *16S rRNA* gene amplification, electrophoresis, and DNA sequencing method which was then analyzed using MEGA software. The identification results obtained from this research were detected *Salmonella* spp., *Salmonella* typhi, *Salmonella* paratyphi A, *Salmonella* paratyphi B. The biochemical activity test showed the result that all samples showed glucose fermentation of D-Glucose, D-Maltose, D- Mannitol, D-Mannose, D-Trehalose, and coumarate. From the results of biochemical tests, serological tests, and morphological tests, the highest similarity was obtained between strains A11 and A14 (100% similarity). In antibiotic sensitivity test, *Salmonella*spp. has the highest sensitivity to tigecycline, while the highest resistance is to cefazolin, amikacin, and gentamicin. The results obtained from protein profile analysis were that A6 and A7 were similar (89% similarity). In the characteristic test with the *16S rRNA* gene, results were obtained in the form of close relatives between C2-A17, A7-A2, A9-A3, C1-A4, and A6-A14. The conclusions from this research are; based on biochemical tests, all samples were still in the same species, there were no different characters based on the *16S rRNA* gene sequence, and all samples were sensitive to tigecycline and resistant to cefazolin, amikacin, and gentamicin.

Keywords: enteric fever; typhoid; *Salmonella*; polyphasic; molecular