INTISARI

Analisis Molekuler dan Imunologis Sistem Pertahanan *Streptococcus* spp. yang Diisolasi dari Pernapasan Anjing dan Kucing di Semarang dan Daerah Istimewa Yogyakarta

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Streptococcus merupakan bakteri penyebab infeksi saluran pernapasan pada anjing dan kucing serta berpotensi zoonosis. *Streptococcus canis* adalah spesies yang paling sering diisolasi dan memiliki faktor virulensi yang berperan dalam patogenesitas serta penghindaran fagositosis oleh makrofag. Kajian tentang infeksi *Streptococcus* pada hewan kesayangan masih terbatas. Penelitian ini bertujuan mengisolasi dan mengidentifikasi *Streptococcus* spp. dari sampel klinis anjing dan kucing, mendeteksi gen virulensi terkait antifagositosis, serta mengevaluasi interaksi bakteri dengan makrofag secara *in vitro*. Sebanyak 55 sampel swab nasal dan/atau orofaring dikoleksi dari anjing (n = 3) dan kucing (n = 52) bergejala pernapasan di Semarang dan Daerah Istimewa Yogyakarta. Isolasi bakteri dilakukan dengan inokulasi pada plat agar darah (PAD), pewarnaan Gram, dan uji katalase. Identifikasi molekuler dilakukan dengan *polymerase chain reaction* (PCR) menggunakan primer 16S rRNA *Streptococcus* spp., gen spesies spesifik, dan gen pengkode *M- like* protein (SCM). Aktivitas fagositosis diuji secara *in vitro* menggunakan sel makrofag RAW 264 dengan penghitungan indeks fagositosis dan diolah secara statistik dengan T-test. Hasil penelitian menunjukkan 32 isolat terkonfirmasi *Streptococcus* spp. berdasarkan isolasi fenotipik dan deteksi gen 16S rRNA. *Streptococcus canis* sebagai spesies dominan sebanyak 25 isolat (25/32, 78,13%), sementara spesies *S. dysgalactiae* dan *S. equi* subsp. *zooepidemicus* tidak terdeteksi pada sampel yang diuji. Gen *scm* terdeteksi pada 32% (8/25) isolat *S. canis*. Isolat yang membawa gen *scm* menunjukkan indeks fagositosis yang lebih rendah (3,64 ± 0,93) dibandingkan isolat tanpa gen *scm* (5,88 ± 1,19). Hal ini berkaitan dengan peran protein M dalam menghambat proses opsonisasi. Berdasar analisis statistik menunjukkan adanya perbedaan yang signifikan antara kelompok isolat membawa gen *scm* dengan kelompok isolat tanpa gen *scm* ($p < 0,05$). Hasil ini menunjukkan bahwa *Streptococcus* spp. khususnya *S. canis* berperan penting pada kasus infeksi pernapasan anjing dan kucing. Keberadaan gen *scm* pada *S. canis* berkontribusi secara signifikan terhadap kemampuan bakteri menghindari eliminasi oleh sel makrofag.

Kata Kunci: *Streptococcus* spp., Faktor Virulensi, Makrofag, Infeksi Pernapasan, Hewan Kesayangan

ABSTRACT

Molecular and Immunological Analysis of the Defense System of *Streptococcu*s spp. Isolated from the Respiratory Tracts of Dogs and Cats in Semarang and the Special Region of Yogyakarta

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Streptococcus spp. are bacterial pathogens associated with respiratory tract infections in dogs and cats and have zoonotic potential. *Streptococcus canis* is the most frequently isolated species and possesses virulence factors that contribute to pathogenicity and evasion of macrophage-mediated phagocytosis. Studies on Streptococcus infections in companion animals remain limited. This study aimed to isolate and identify *Streptococcus* spp. from clinical samples of dogs and cats, detect virulence genes associated with anti-phagocytic mechanisms, and evaluate bacterial–macrophage interactions in vitro. A total of 55 nasal and/or oropharyngeal swab samples were collected from dogs (n = 3) and cats (n = 52) showing respiratory clinical signs in Semarang and the Special Region of Yogyakarta, Indonesia. Bacterial isolation was performed using blood agar plates, followed by Gram staining and catalase testing. Molecular identification was conducted by polymerase chain reaction (PCR) using *Streptococcus* spp. 16S rRNA primers, species-specific gene primers, and primers for the M-like protein–encoding gene (SCM). Phagocytic activity was assessed in vitro using RAW 264 macrophage cells by calculating the phagocytic index, and statistical analysis was performed using a t-test. The results showed that 32 isolates were confirmed as *Streptococcus* spp. based on phenotypic characterization and 16S rRNA gene detection. *Streptococcus canis* was identified as the dominant species, accounting for 25 isolates (25/32, 78,1%), while *S. dysgalactiae* and *S. equi* subsp. *zooepidemicus* were not detected in the tested samples. The *scm* gene was detected in 32% (8/25) of *S. canis* isolates. Isolates carrying the *scm* gene exhibited a lower phagocytic index (3,64 ± 0,93) compared to isolates lacking the gene (5,88 ± 1,19), which is associated with the role of M protein in inhibiting opsonization. Isolates harboring the *scm* gene exhibited significantly lower phagocytic indices compared to isolates lacking the gene. Statistical analysis revealed a significant difference between the two groups ($p < 0.05$). These findings indicate that *Streptococcus* spp., particularly *S. canis*, play an important role in respiratory infections in dogs and cats. The presence of the *scm* gene in *S. canis* significantly contributes to the bacterium's ability to evade elimination by macrophages.

Keywords: *Streptococcus* spp., Virulence Factors, Macrophage, Respiratory Infection, Companion Animal