IDENTIFICATION AND ANTIMICROBIAL SUSCEPTIBILITY OF *ENTEROBACTERIACEAE* BACTERIA ISOLATED FROM FECES OF BIRDS OF PARADISE (PARADISAEIDAE)

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Bogor, July 2025

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ABSTRAK

RANGGA ATHAYA DEFAN. Identifikasi dan Sensitivitas Antimikroba Bakteri *Enterobacteriaceae* yang Diisolasi dari Feses Burung Cendrawasih (Paradisaeidae). Dibimbing oleh DORDIA ANINDITA ROTINSULU dan ARIEF BOEDIONO.

Burung cendrawasih (Paradisaeidae) adalah keluarga burung yang berasal dari Papua dan wilayah sekitarnya, yang saat ini terancam oleh hilangnya habitat dan perdagangan satwa liar ilegal. Upaya konservasi telah menyebabkan penempatan mereka di fasilitas eksitu, sehingga menjaga kesehatan mereka menjadi prioritas. Namun, pengobatan infeksi bakteri pada burung-burung ini semakin menantang akibat meningkatnya resistensi antimikroba (AMR) secara global. Studi ini bertujuan mengidentifikasi bakteri *Enterobacteriaceae* yang diisolasi dari feses burung cendrawasih dalam penangkaran dan menguji kepekaannya terhadap antimikroba. Sampel feses dari sepuluh individu yang berasal dari lima spesies dikultur pada media selektif. Sebanyak 24 isolat Gram-negatif diidentifikasi melalui uji biokimia. Genus paling umum adalah *Citrobacter* (50%), diikuti oleh *Enterobacter* (20,83%), *Klebsiella* (12,5%), *Salmonella* (4,17%), *Proteus* (4,17%), *Escherichia* (4,17%), dan *Pantoea* (4,17%). Pengujian kepekaan antimikroba menggunakan metode difusi cakram Kirby-Bauer dilakukan terhadap doksisiklin, ampisilin, gentamisin, siprofloksasin, kloramfenikol, dan trimetoprim-sulfametoksazol. Ditemukan resistensi tinggi terhadap doksisiklin (66,6%). diikuti oleh ampisilin (12,5%) dan kloramfenikol (4,17%). Kepekaan intermediat ditemukan terhadap ampisilin (16,67%), siprofloksasin (8,33%), dan gentamisin (4,17%). Semua isolat (100%) menunjukkan kepekaan terhadap trimetoprim-sulfametoksazol. Tidak terdapat isolate yang *multidrug-resistant*. Hasil ini menyoroti pentingnya pemantauan rutin dan penggunaan antibiotik yang bijaksana dalam program konservasi eksitu.

Kata kunci: Cendrawasih, *Enterobacteriaceae*, konservasi eksitu, resistansi antimikrobial

ABSTRACT

RANGGA ATHAYA DEFAN. Identification and Antimicrobial Susceptibility of *Enterobacteriaceae* Bacteria Isolated from Feces of Birds-of-Paradise (Paradisaeidae). Supervised by DORDIA ANINDITA ROTINSULU and ARIEF BOEDIONO.

Birds-of-paradise (Paradisaeidae) are a family of bird native to New Guinea and surrounding regions, currently threatened by habitat loss and illegal wildlife trade. Conservation efforts have led to their placement in ex-situ facilities, where maintaining their health is a priority. However, the treatment of bacterial infections in these birds poses increasing challenges due to the global rise in antimicrobial resistance. This study aimed to identify *Enterobacteriaceae* bacteria isolated from the feces of captive birds-of-paradise and assess their antimicrobial susceptibility. Fecal samples from ten individuals across five species were cultured on selective media. A total of 24 Gram-negative isolates were identified through biochemical testing. The most prevalent genus was *Citrobacter* (50%), followed by *Enterobacter* (20.83%), *Klebsiella* (12.5%), *Salmonella* (4.17%), *Proteus* (4.17%), *Escherichia* (4.17%), and *Pantoea* (4.17%). Antimicrobial susceptibility testing using the Kirby-Bauer disc diffusion method was conducted against doxycycline, ampicillin, gentamicin, ciprofloxacine, chloramphenicol, and trimethoprim-sulfamethoxazole. High resistance to doxycycline (66.6%) was observed. Followed by ampicillin (12.5%) and chloramphenicol (4.17%). Intermediate susceptibility was observed to ampicillin (16.67%), ciprofloxacine (8.33%), and gentamicin (4.17%). All isolates (100%) showed susceptibility to trimethoprim-sulfamethoxazole. None of the isolates were multidrug-resistant. These results highlight the importance of routine monitoring and prudent antibiotic use in ex-situ conservation programs.

Keywords: Antimicrobial resistance, birds-of-paradise, *Enterobacteriaceae*, ex-situ conservation

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as one of the requirements to obtain the Bachelor's degree
in
School of Veterinary Medicine and Biomedical Sciences

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PREFACE

Praise and gratitude the writer extends to Allah subhanahu wa ta'ala for His blessings, through which this scientific work has been completed. This research was carried out from September 2024 to February 2025 under the title "Identification and Characterization of *Enterobacteriaceae* Bacteria Isolated from Feces of birds-of-paradise (Paradisaeidae)."

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The author is aware that there are shortcomings in the writing of this scientific work, both in terms of the writing and the data presented. Therefore, the author welcomes constructive criticism and suggestions for future improvement. Hopefully, this scientific work will be beneficial to those who need it and will contribute to the advancement of science.

Bogor, July 2025

Rangga Athaya Defan

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

1 INTRODUCTION

1.1 Background

Birds-of-Paradise are birds that belong to the Paradisaeidae family. They can be found all over the island of New Guinea and its surrounding islands, which includes the Misool Island, the Japen Island, the Aru Island, and the Sarawati Island. Additionally, two birds-of-paradise species have also been reported as the native species of the Moluccas Islands and north-eastern Australia (Heads 2008). According to Helm-Bychowski and Cracraft (1993), about 90 Phylogenetic species are scattered across the island of New Guinea and its surroundings. birds-of-paradise are known for their display of beautiful feathers and mating dances to attract females (Frith and Beehler 1998). Because of their beautiful feathers, birds-of-paradise tend to be a target for poachers.

Jagat Satwa Nusantara (JSN) is a zoological park organized into three key sections, each showcasing a major animal group: “Dunia Air Tawar”, which showcases freshwater aquatic faunas, “Museum Komodo”, which showcases herpetofaunas, and “Taman Burung”, which showcases avian faunas (Avifauna). Jagat Satwa Nusantara operates as an ex-situ conservation site for many animals around the world, especially endemic animals to Indonesia. As an ex-situ conservation site, JSN preserves species outside their natural habitat. Ex-situ conservations provide shelter and rehabilitation for animals, before eventually reintroducing them back into the wild if possible. Ex-situ conservation sites also complement In-situ conservation sites by initiating breeding programs for endangered animals to increase their population (Mahanayak 2024).

Bacteria are microscopic organisms that are present in almost every living and non-living thing. They play a major role in our everyday life, whether it is beneficial or harmful (Baron 1996). Although only a small fraction of bacteria in the world are pathogenic, bacterial infections are caused by pathogenic bacteria that could affect animals or humans and become a major reason of certain illnesses or even death (Doron and Gorbach 2008). Naturally, a healthy animal’s intestine contains a wide range of intestinal microbe, that lives in symbiosis with its host. Gut microbiomes help the body regulate physiological functions, such as digestion and absorption of food, immune functions, and metabolization of food (Jandhyala *et al*. 2015). Naturally occurring microflora in an animal or human’s intestine are some species from the *Enterobacteriaceae* family. This diverse range of microflora could raise another problem within the community, which is antimicrobial resistance. Bacteria are capable of transferring their resistance gene. through several methods, such as conjugation and natural transformation (Jandhyala *et al*. 2015; Krisnawati *et al*. 2023). The constant mutation of genes, becoming more resistant to antimicrobials, has been a global concern for a while (Prestinaci *et al*. 2015). The natural environment and its inhabitants have the potential to previously unknown antimicrobial resistance genes of bacterial pathogens. This concern suggests a potential role of wildlife, such as the birds-of-paradise to be a potential carrier of an unknown antimicrobial resistance gene (Martínez 2008)

1.2 Problem Statement

The health of Birds-of-Paradise in ex-situ conservation is very important, as they are a protected animals under government regulations. However, current research on the bacteria in their digestive system is still limited. This knowledge gap poses significant challenges for veterinarians in ex-situ conservation to maintain the health of these birds, as understanding bacteria and their potential impacts is critical for bacterial disease prevention and treatment. There is also an urgent need to study the antimicrobial resistance of isolated bacteria to ensure appropriate antimicrobial treatment that can be applied if birds become ill. Without this understanding, there is a risk of ineffective treatment and the risk of accelerating the development of antimicrobial-resistant bacterial strains, which would limit the resources available to protect this rare species. This study aims to address this gap by investigating bacterial identification and resistance profiles, supporting more informed veterinary care for captive birds of paradise.

1.3 Objective

This research aims to identify *Enterobacteriaceae* bacteria from fecal samples of birds-of-paradise. The study also includes antimicrobial resistance testing to determine the sensitivity of these bacteria to various antimicrobials. The findings could help veterinarians choose appropriate antimicrobial treatments for captive birds-of-paradise and potentially prevent the development of antimicrobial-resistant bacterial strains.

1.4 Benefits

The results of this research are to provide information about *Enterobacteriaceae* bacteria isolated from feces of birds-of-paradise and their antimicrobial susceptibility. The data obtained from bacterial identification and antimicrobial resistance testing is useful for veterinarians in planning effective treatment for captive birds-of-paradise in implementing preventive measures towards antimicrobial resistance.