

**Identification of MDR (Multi-Drug Resistance) through the *Int1*  
(Integron Class 1) Gene in *Citrobacter freundii* in Chicken Eggs by using the  
PCR (Polymerase Chain Reaction) Method**

**Nindita Lestyana Putri**

**ABSTRACT**

Chicken eggs are a rich source of protein; therefore, eggs are easily contaminated by bacteria, especially bacteria from the Enterobacteriaceae family. *C. freundii* is a member of the Enterobacteriaceae family that can cause gastrointestinal infections in humans through the consumption of contaminated food. Besides being found on food, *C. freundii* is also often isolated from soil, water, feces, waste materials, and intestines. *C. freundii* plays an active role in carrying a resistance gene in the gastrointestinal tract of both humans and animals and can contaminate animal-based food products through feces. This study aimed to discover whether the MDR-coding gene, *Int1*, could be found in *C. freundii* isolates. The isolation and identification of *C. freundii* in this study used LB as the pre-enrichment medium, TTB as the enrichment medium, and the medium SSA as a selective medium, followed by Gram staining of colonies, biochemical tests (TSIA, Urea, SCA, SIM, MR-VP), carbohydrate fermentation tests (lactose, sucrose, glucose, mannitol, and maltose) and a validation test using the Vitek 2 machine. Tests for resistance to a number of antibiotics using the antibiotic disc diffusion method were conducted for streptomycin, gentamycin, chloramphenicol, erythromycin, tetracycline, oxytetracycline, doxycycline, amoxicillin, penicillin, oxacillin, cloxacillin, trimethoprim, and ciprofloxacin. The results study demonstrated that *C. freundii* was 100% resistant to erythromycin, amoxicillin, penicillin, oxacillin, and cloxacillin, and 33.3% resistant to ampicillin. The Polymerase Chain Reaction (PCR) analysis of *C. freundii* revealed DNA strand fragments at a fragment length of 346 bp. The PCR product sequencing analysis was conducted to see the homology of the DNA. The result of the homology was 91% by using the BLAST system.

