The relatively higher MBC/MIC ratios for MRSA, E. coli, and C. albicans imply that higher dosages or combination treatments may be necessary for these pathogens.The cytoplasm exhibits a consistent electron density, indicating that there is no leakage or disruption of intracellular contents.Although C. albicans showed inhibition at a lower concentration, the bacteriostatic nature of the extract (MBC/MIC ratio of 8) suggests it may need to be supplemented with other antifungal agents for complete eradication, especially in immunocompromised patients where fungal infections can be more severe.The MIC and MBC results for MP fruit extract underline its significant antimicrobial potential, particularly as a bactericidal agent against MDR bacterial strains such as Enterococcus faecalis and Salmonella typhi.The study of the antibiofilm activity of Murraya paniculata fruit extract against several pathogenic organisms, including MDR bacteria and Candida albicans, demonstrates its potential to inhibit biofilm formation.Future research should focus on isolating specific bioactive compounds, determining optimal dosing, and exploring synergistic effects with other antimicrobial agents to enhance its efficacy against resistant pathogens.While it also shows efficacy against MRSA, E. coli, and Candida albicans, these organisms require higher concentrations for bactericidal or fungicidal activity, suggesting moderate resistance.The ultrastructural analysis and antibiofilm activity results of MP fruit extract provide insights into its mechanism of action against Staphylococcus aureus and other pathogenic organisms.This weakening may make the cells more susceptible to osmotic stress and environmental factors, suggesting a possible mechanism by which the extract compromises the bacteria's defenses.These findings support further exploration of MP fruit extract as a natural antimicrobial, with potential applications in bacterial and fungal infections.The spherical, cocci-shaped cells are densely packed with .intact cell walls, indicative of a healthy bacterial structure