Genomic Insights into the Resistome and Virulence of *Nocardia pneumoniae* from a Post-operative Ocular Infection

Veena Radhakrishnan[a], Lalitha Prajna[b], Bharanidharan Devarajan[c], Jeyaraman Jeyakanthan[a*]

[a]Structural Biology and Bio-Computing Lab, Department of Bioinformatics, Science Block, Alagappa University, Karaikudi, 630 004, Tamil Nadu, India

[b]Department of Ocular Microbiology, Aravind Eye Care System, No.1 Anna Nagar, Madurai, 625020, Tamil Nadu, India

[c]Department of Microbiology, Aravind Medical Research Foundation, No.1 Anna Nagar, Madurai, 625020, Tamil Nadu, India

* Corresponding author.

E-mail address: jjbioinformatics@gmail.com (J. Jeyakanthan).

Abstract

Nocardia pneumoniae is an emerging opportunistic pathogen in postoperative ocular infections; however, the genomic determinants of its virulence and antibiotic tolerance remain under-characterized. In this study,we performed whole-genome sequencing and comparative genomic analysis of *Nocardia pneumoniae* strain JJAEH01, isolated from a post-operative ocular infection. The assembled genome spans approximately ~7.53 Mb with a GC content of 68.15%, and demonstrated >99% sequence similarity to reference N. pneumoniae genomes based on FastANI analysis, confirming its taxonomic identity. Pan-genome comparative analysis using Panaroo revealed multiple virulence-associated systems, including Type VII secretion components espG1 and eccB1, toxin-antitoxin modules vapB and vapC,siderophore-mediated iron acquisition systems irtA/irtB and yfiY with additional oxidative-stress gene regulators, all supporting roles in intra-host survival and immune evasion. Resistome profiling identified glycopeptide-associated vanY/vanW homologs, rifamycin-associated genes rox and rpoC, and stress-response pathways iniA/iniC, together with an expanded repertoire of multidrug efflux pumps, suggesting intrinsic tolerance to several antibiotic classes and the capacity to withstand mercury and other heavy metal stressors. The integrated antimicrobial resistance and virulence architecture of strain JJAEH01 underscores the pathogenic versatility and adaptive potential of *N. pneumoniae* in

clinical settings and highlights the value of whole-genome sequencing to support early diagnosis, refine antimicrobial decision-making, and ultimately improve clinical outcomes in postoperative ocular infections.

Keywords: *Nocardia pneumoniae*, whole-genome sequencing, antimicrobial resistance, virulence, postoperative ocular infection, rifamycin resistance.