

## Abstract

*Xenorhabdus* is a bacteria genus of the family Enterobacteriaceae. Bacteria of this genus form a mutualistic relationship with *Steinernema* entomopathogenic nematodes. More so, their antimicrobial production serves as a potential source of novel antibiotics in the wake of growing antimicrobial resistance. This study aimed to establish the phylogenetic relationship of three *Xenorhabdus* isolates to the 24 described species of the genus based on the 16s rRNA gene. Secondly, it aimed to determine the antibiotic activity of the three *Xenorhabdus* isolates from Kenya. Six 16s rRNA sequences were isolated in this study while 184 sequences were obtained from public databases compiling a data-set of 190 sequences. Phylogenetic reconstruction was done using maximum likelihood method with a bootstrap test of phylogeny of 500 replicates. The phylogenetic reconstruction identified the isolates as *Xenorhabdus griffinae* L67, *Xenorhabdus griffinae* XN45 and a novel *Xenorhabdus* species. This is the first record of *Xenorhabdus griffinae* in Kenya. The antibiotic activities of the isolates were assessed by analysis of the inhibitory effect of the whole broth extracts, organic fractions and aqueous fractions. *Xenorhabdus griffinae* L67, *Xenorhabdus griffinae* XN45 and *Xenorhabdus* sp. P48 produced antibiotics effective against gram-positive bacteria. *Xenorhabdus griffinae* L67 produced water-soluble antibiotics active against gram-positive bacteria. *Xenorhabdus griffinae* XN45 produced antibiotics that readily dissolved in dimethyl sulfoxide. These were inhibitory to Methicillin resistant *Staphylococcus aureus*. The organic solvent fraction of *Xenorhabdus griffinae* L67 had a peak uv absorption at 218nm. This indicated the presence of peptide antimicrobials from *Xenorhabdus griffinae* that were active against Methicillin resistant *Staphylococcus aureus*.