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Whole genome sequence and comparative genomics analysis of multidrug-resistant *Staphylococcus xylosus* NM36 isolated from a cow with mastitis in Basrah city

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Abstract

Background *Staphylococcus xylosus* is a coagulase-negative, gram-positive coccus that is found in the environment and as a commensal organism on the skin and mucosal surfaces of animals. Despite the fact that *S. xylosus* is considered a nonpathogenic bacterium, several studies have linked *S. xylosus* to opportunistic infections in both animals and humans. During an investigation of mastitis-causing agents in the governorate of Basrah, Iraq, we identified an antibiotic-resistant strain of *S. xylosus* NM36 from a milk sample from a cow with chronic mastitis. In addition to robust biofilm formation, multiple antibiotic resistance phenotypes were found. To further understand the genetic background for these phenotypes, the full genome of *S. xylosus* NM36 was analyzed.

Results The genome consisted of a single circular 2,668,086 base pairs chromosome containing 32.8% G + C. There were 2454 protein-coding sequences, 4 ribosomal RNA (rRNA) genes, and 50 transfer RNA (tRNA) genes in the genome. In addition, genetic variation was studied by searching sequence data against a representative reference genome. Consequently, single-nucleotide polymorphism analysis was conducted and showed that there were 46,610 single-nucleotide polymorphisms (SNPs), 523 insertions, and 551 deletions. In order to overcome antibiotics, *S. xylosus* NM36 had been armed with several antibiotic resistance genes from several groups and families. The genome annotation service in PathoSystems Resource Integration Center (PATRIC) and Rapid Annotation using Subsystem Technology (RAST) annotation servers showed that there are multiple antimicrobial resistance elements, including antibiotic inactivation enzymes (BlaZ family, FosB), antibiotic resistance gene clusters (TcaB, TcaB2, TcaR), proteins involved in methicillin resistance (LytH, FmtA, FemC, HmrB, HmrA), TetR family transcriptional regulators, and efflux pumps conferring antibiotic resistance (NorA). In addition, we investigated and categorized the biofilm and quorum-sensing elements of the NM36 strain and found that it has multiple subsets of biofilm regulators, confirming its pathogenic nature.

Conclusions These findings necessitate a reevaluation of microbial and clinical interventions when dealing with coagulase-negative staphylococci, particularly in the context of studies pertaining to public health. This is the first time, to our knowledge, that the entire genome of *S. xylosus* has been sequenced in Iraq.

Keywords *Staphylococcus xylosus*, Whole genome sequencing, Mastitis, Biofilm, Antibiotic resistance

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