DO NOT CONSIDER FOR TALK

2025 SEA Symposium Abstract

University of Lagos

Lagos

Corresponding Faculty Member: Imade Nsa (insa@unilag.edu.ng)

Genome insights into Mugiwara and Ceiling fan

Ifunanya O Okoli, Opeoluwa S Aworetan, Adeyanju E Tomi, Fuad Jebe-Abdulli, Modesola Onikoro, Oluwafoyinsolami Adisa, Gloria A Omogwigho, Oluwatunkunmi Okupa, Fuhad T Lawal, Grace Immanuel, Evans Oleka, Chibueze Uchegbu, Emmanuel Ajayi, Opeoluwa Aworetan, Tomiwa Adeyanju, Faith Onyekachi, Ezichukwu E Ejiofor, Hauwa Kamselem, Shina O Abidoye, Imade Y Nsa, Matthew O Ilori

Mugiwara and CeilingFan are both Siphoviridae phages belonging to Cluster BE, Subcluster BE2, with genomes of 132,946 bp (CeilingFan) and 133,330 bp (Mugiwara). Annotation tools used were DNA Master, NCBI BLAST, Phamerator, Starterator, GeneMark, Glimmer, and HHPred. DNAMaster called 248 ORFs, 45 RNAs for CeilingFan, and 250 ORFs, 43 RNAs for Mugiwara (Phamerator: 261 ORFs for CeilingFan, 255 for Mugiwara). Gene function was predicted using Phamerator, HHPred, and BLAST.
CeilingFan ORFs include 73.09% forward and 26.9% reverse genes, with no orphams. ATG (70.9%), GTG (14.5%), and TTG (9.6%) are the most common start codons. Its longest gene (6,300 bp) encodes the Tape Measure protein, while the shortest (105 bp) is a hypothetical protein. Three genes were manually added: genes 188 and 190 (tRNAs) and gene 189 (a hypothetical protein). Mugiwara has 72.8% forward and 27.2% reverse genes, with seven orphams. Its most frequent start codons are ATG (80.8%), GTG (12.4%), and TTG (8.8%). The longest gene (6,288 bp) encodes the Tape Measure protein, while the shortest (99 bp) encodes hypothetical proteins. CeilingFan has 63 ORFs and Mugiwara 42 ORFs with shared functions, including the major tail protein, portal protein, and DNA primase.
Synteny between CeilingFan and Mugiwara is evident from 191 shared phams and 75.96% similarity in G+C content, highlighting conserved genes essential for bacterial infection. These include hypothetical proteins, enzyme-coding genes like transglycosylases, and structural proteins such as Tail Assembly Chaperone. Both resemble lytic phages Spilled and Quaran19 (GCS: 86.5% and 86.4%) and LukeCage and Bordeaux (GCS: 76.8% and 76.4%), confirming their classification within Subcluster BE2. Synteny extends across subcluster members, though some variations exist due to orphams (Phage Spilled), gene position shifts, or unique genes, reflecting evolutionary adaptations.