Annotation of Five Genes in the DNA Mismatch Repair Pathway of *Kytococcus Sedentarius*

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Abstract

Background information: Kytococcus sedentarius is an opportunistic pathogen that can survive under certain environmental conditions. Understanding the genetics of this organism and its biologic pathways can lead to additional treatment in addition to possible uses of the protein products.

Methods: This study used the IMG-AC website to record data in a digital notebook. The gene details page was accessed for basic information on each gene. Databases such as BLAST, CDD, TIGRFAM, PDB, PSORT-B, MetaCyc, and Prosite were used to generate data as used in the analysis.

Results

5. PDB crystal structures of (A) helicase, (B) ligase, (C) polymerase subunit, and (D) single stranded DNA leading protein.

6. A TIGRFAM to protein product. Five of the genes were involved in the DNA mismatch repair pathway of *K. sedentarius*.

Conclusions

This study confirmed the proposed annotations of the genes involved in the DNA mismatch repair pathway of *K. sedentarius*. Searches with BLAST found the same amino acid sequences present in other organisms indicating a high amount of conservation. A high amount of sequence conservation was also seen in the Web-logos.

Literature Cited


