Annotation of the Kytococcus sedentarius Genome from DNA Coordinates 364717 to 370640

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Abstract

Annotations are part of genome data that can be done by computational means before a genome sequence is deposited in Genbank (Koonin et al., 2003). The leading website, GEN-ACT (www.geni-act.org) is an annotation collaboration tool that provides a set of tools to genomics bioinformaticians and project designing reusables to facilitate genomics research was used to annotate 5 consecutive genes of Kytococcus sedentarius (Ksed_03790-Ksed_03830). The methods and data flow were evaluated and each gene was assessed. Following steps were taken. The assessment of amino acid sequence similarly to be done by looking the redundancy in the genetic code, the structure-based evidence from the amino acid sequence to find similarity in the structures of fundamental domains, the cellular localization data to determine where in the cell the protein is encoded, the potential alternative open reading frames, and the possibility of horizontal gene transfer. The data obtained manually matched the computor's data for the corresponding gene product names.

Introduction

Kytococcus sedentarius is the only bacterium known to use that produces the antibiotic chitinase Aand B which is used as a T(2) (Tissel localization) for increased milk production efficiency in dairy cows. (Whitman et al., 2012). But Kytococcus is an opportunistic pathogen. It has been isolated from varying environments, including human skin, groundwater, and even airline cabins. Kytococcus sedentarius can cause dermatological infections like pilomatrixylosis (not in India). It is a Gram-positive organism that grows as a spherical spore in all tissues which can be arranged in cubical packets. It is non-encapsulated and does not form endospores. It is strictly aerobic and chemolithoautotrophic. requires methylene and other amino acids for growth, and grows well in N-acetylaspartylglycine (NAG) concentrations at 80°C and 35°C.

Methods and Materials

Modules of the GEN-ACT (http://www.geni-act.org) were used to complete Kytococcus sedentarius genome annotations as described below.

Results

Kytococcus sedentarius 03790:
The top BLASTN hits were Enterobacter Coli O157 and Serpinius profundius and the COG Names were Maltose binding periplasmic protein MalE [Carbohydrate transport and metabolism] and PmD [Pentapeptide/putrescine-binding periplasmic protein (membrane transport and metabolism)]. The only gene name found was Maltose transport system permease component. Ksed_03790 was annotated as a maltose-binding ATPase periplasmic protein. According to the phylogenetic tree, it seems as though Kytococcus sedentarius has evolved independently from other bacteria. Thus, this bacterium is an extremely good model for study. There is no similar sequence in other databases.

Kytococcus sedentarius 03800:
Genbank-proposed gene product name is Periplasmic membrane protein. Top BLAST hits suggest ABC type sugar transporters. Top COG hits are sugar transporters. These components confirm that protein produced is a sugar transporter.

Figure 5 - Ksed_03790: The SignalP graph results show that the cleavage site is between pos 28 and 29.

Figure 6 - Ksed_03800: The phylogenetic tree shows Kytococcus sedentarius is closely related to some organisms such as Ochrobactrum pelagiosolvens and Serpinius profundus. and they may be a closer spore from similar pathways.

Figure 7 - Data from Phobius prediction graph indicates that there is an extremely low probability of appearing in the non-photosynthetic region and a high probability of appearing in the photosynthetic region.

Kytococcus sedentarius 03810:
Top BLAST hits Maltose transport system permease protein MalE. COG hits include: ABC-type maltose transporter (Carbohydrate transport and metabolism). The top BLAST hits suggest ABC type sugar transporters. Top COG hits are sugar transporters. These components confirm that protein produced is a sugar transporter.

Figure 8 - Eight transmembrane helices in Ksed_03810.

Kytococcus sedentarius 03820:
Top BLAST hit is MalE maltose transport system permease protein MalE. The protein is a maltose binding ATPase periplasmic protein. Ksed_03820 was annotated as a maltose-binding ATPase periplasmic protein. Ksed_03820 was also annotated as a lipoprotein.

Kytococcus sedentarius 03830:
Top BLAST hit is MalE maltose transport system permease protein MalE. The protein is a maltose-binding ATPase periplasmic protein. Ksed_03830 was also annotated as a lipoprotein.

Conclusion

The GEN-ACT proposed gene product did not differ significantly from the proposed gene annotation for each of the genes in the group; therefore, the genes appear to be correctly annotated by the computer database.

References


Kytococcus sedentarius, the organism associated with pitted keratolysis, produces keratin-degrading enzymes. Longhaye et al. (2002)

GEN-ACT Guiding Education through Novel Investigation, Developing Next-generation Academic Scientists (http://www.geni-act.org)

Genome annotation: data flow and performance, 5.1.1 Sequence strategies

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