Annotation of the *Propionibacterium acnes 266* Genome on Locus Tags PAZ_c00130 and PAZ_c00160.

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Abstract

Two genes from the microorganism *Propionibacterium acnes* 266 (PAZ_c00130 and PAZ_c00160) were annotated using the collaborative genome annotation website GENI-ACT. The Genbank proposed gene product name for each gene was assessed in terms of the general genomic information, amino acid sequence-based similarity data, and cellular localization data. The Genbank proposed gene product name did not differ significantly from the proposed gene annotation for either of the two genes and as such, the genes appear to be correctly annotated.

Introduction

Propionibacterium acnes is an aerotolerant anaerobic, slow growing, gram positive bacterium (Wikipedia, 2017). Strains of *P. acnes* are found among the diverse community of bacteria in the adult human skin where they live off fatty acids secreted by sebaceous glands (Kasimatis et al., 2013 and Wikipedia, 2017).

P. acnes can cause or contribute to skin disorders that result in acne if over abundant. Historically, *P. acnes* has been connected to development of acne vulgaris which is a skin disease affecting more than 80% of adolescents in the U.S.(Kasimatis et al., 2013). The antibiotics commonly used to treat acnes vulgaris are erythromycin, clindamycin, doxycycline and minocycline. *P. acnes* glows orange in black light and is killed when exposed to ultraviolet light and light near the ultraviolet range. Therefore, P. acnes infections can be treated with phototherapy (Wikipedia, 2017).

According to Kasimatis et al. (2013), skin health may depend on the different *P* acnes strains as some are beneficial and others are pathogenic. Therefore, it is important to understand the genetic differences between various strains of *P* acnes to contribute to human skin health.

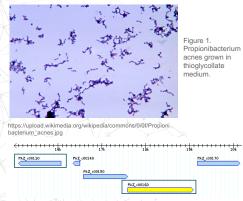


Figure 2. The locus tags and relative position of the genes under investigation in this research

Methods

Modules of the GENI-ACT (http://www.geni-act.org/) were used to complete *Propionibacterium acres* 266 genome annotation . The modules are described below:

Modules	Activities	Questions Investigated
Module 1- Basic Information Module	DNA Coordinates and Sequence, Protein Sequence	What is the sequence of my gene and protein? Where is it located in the genome?
Module 2- Sequence-Based Similarity Data	Blast, CDD, T-Coffee, WebLogo	Is my sequence similar to other sequences in Genbank?
Module 3- Cellular Localization Data	Gram Stain, TMHMM, SignalP, PSORT, Phobius	Is my protein in the cytoplasm, secreted or embedded in the membrane?

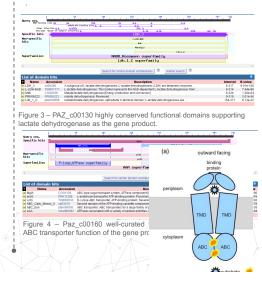
Results

PAZ_c00130:

The initial proposed product of this gene by GENI-ACT was an L-lactate dehydrogenase. This gene product proposal was supported by the top BLAST hits for the amino acid sequence, the presence of well-curated protein functional domains within the amino acid sequence, and the cellular location of the amino acid sequence. As such, the proposed annotation is an L-lactate dehydrogenase.

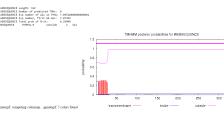
PAZ_c00160:

The initial proposed product of this gene by GENI-ACT was a ribose ABC transporter. This gene product proposal was supported by the top BLAST hits for the amino acid sequence, the presence of well-curated functional domains within the amino acid sequence, and the cellular location of the amino acid sequence. As such, the proposed annotation is a ribose ABC transporter.



Cellular localization of PAZ_c00130:

According to Garvie (1980), lactate dehydrogenases are cytoplasmic enzymes. Therefore, the gene product for PAZ_c00130 should be located in the cytoplasm. The TMHMM software supported intracellular localization as it predicted no transmembrane helixes. SignalP further supported this assessment as it predicted no signal peptide. The final prediction of PSORT-B was Cytoplasmic with a score of 9.97. Oddly enough, Phobius predicted the gene product to be non-cytoplasmic. All results considered, the gene product of PAZ_c00130 is very likely located in the cytoplasm.



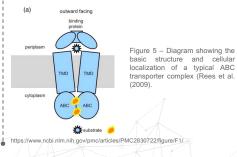
glot in postscript, script for making the plot in graphot, data for plot

Figure 4 – PAZ_c00130 TMHMM results displaying 0 transmembrane helixes.

Cellular localization of PAZ_c00160:

TMHMM showed no transmembrane helixes suggesting that the gene product does not reside in the cytoplasmic membrane of the cell. SignalP predicted no signal peptide suggesting that the gene product is not located outside the cell. PSORT-B gave a final prediction of cytoplasmic membrane location with a high score of 9.99. Finally, Phobius predicted the protein to reside outside the cell. Given the mixed results, it is too difficult to draw a conclusion for the location of this protein.

ABC transporters tend to consist of four domains with two in the membrane and two in the cytoplasm (Rees et al. 2009). Therefore, it is possible for the protein of PAZ_c00160 to reside either in the cytoplasmic membrane or the cytoplasm.



Conclusion

The GENI-ACT proposed gene product did not differ significantly from the proposed gene annotation for both of the genes and as such, the genes appear to be correctly annotated by the computer database.

Gene Locus	Geni – Act Gene Products	Proposed Annotation
Paz_c00130	L-lactate dehydrogenase	L-lactate dehydrogenase
Paz_c00160	Ribose ABC transporter	Ribose ABC transporter

References

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