

Using the Annotation of the *K. sedentarius* Genome to enhance STEM Experiences

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Abstract

A group of consecutive 7 genes from the microorganism *Kytococcus sedentarius* (Ksed_04170 – Ksed_04230) were annotated using the collaborative genome annotation website GENI-ACT. The Genbank proposed gene productname for each gene was assessed in terms of the general genomic information, amino acid sequence-based similarity data, structure-based evidence from the amino acid sequence, cellular localization data, potential alternative open reading frames, enzymatic function, presence or absence of gene duplication and degradation, the possibility of horizontal gene transfer, and the production of an RNA product. The Genbank proposed gene product name did not differ significantly from the proposed gene annotation for each of the genes in the group and as such, the genes appear to be correctly annotated by in the r database.

Introduction

After school activities are meant to relieve stress from the average school day and encourage students to participate in extracurricular activities that differentiate from what they do in the classroom. Also some extracurricular activities are meant to influence students to take interest in different things that could possibly affect their future in and out of school. This statement is supported through my very own experience. Earlier this school year I joined an after school club known as BAASE. BAASE is a new afterschool club; BAASE stands for Biology And Afterschool Science Explorations.

Throughout the school year we have been researching genomics and it has had a great effect on our group after school. In the beginning of the school year, when we started, a lot of us weren't sure what we wanted to do or didn't think about what we wanted to do. However, then we began working and working towards our research after school and learning more everyday about genomics. This research began to influence the way that we thought about our future and what we want to do as a career when we become adults.

Kytococcus sedentarius, a gram positive bacterium and a chemoheterotroph was used as an organism of interest for this project. This bacterium was selected because it has yet to have been thoroughly studied utilizing bioinformatics (Sims et al., 2009).

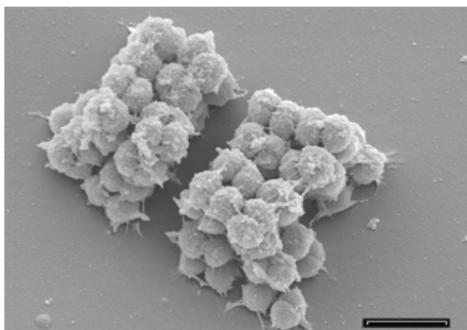


Photo credit: Dr. Manfred Rohde at Helmholtz Centre for Infection Research, Braunschweig, Scale = 2 µm.

Methods and Materials

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

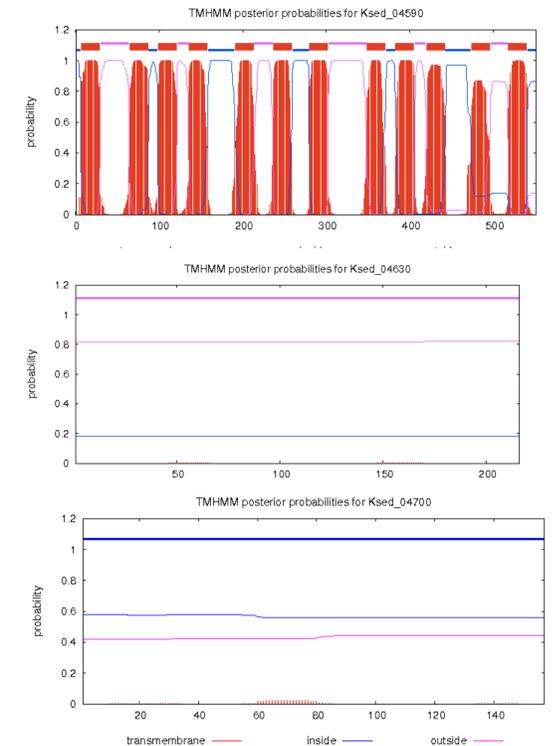
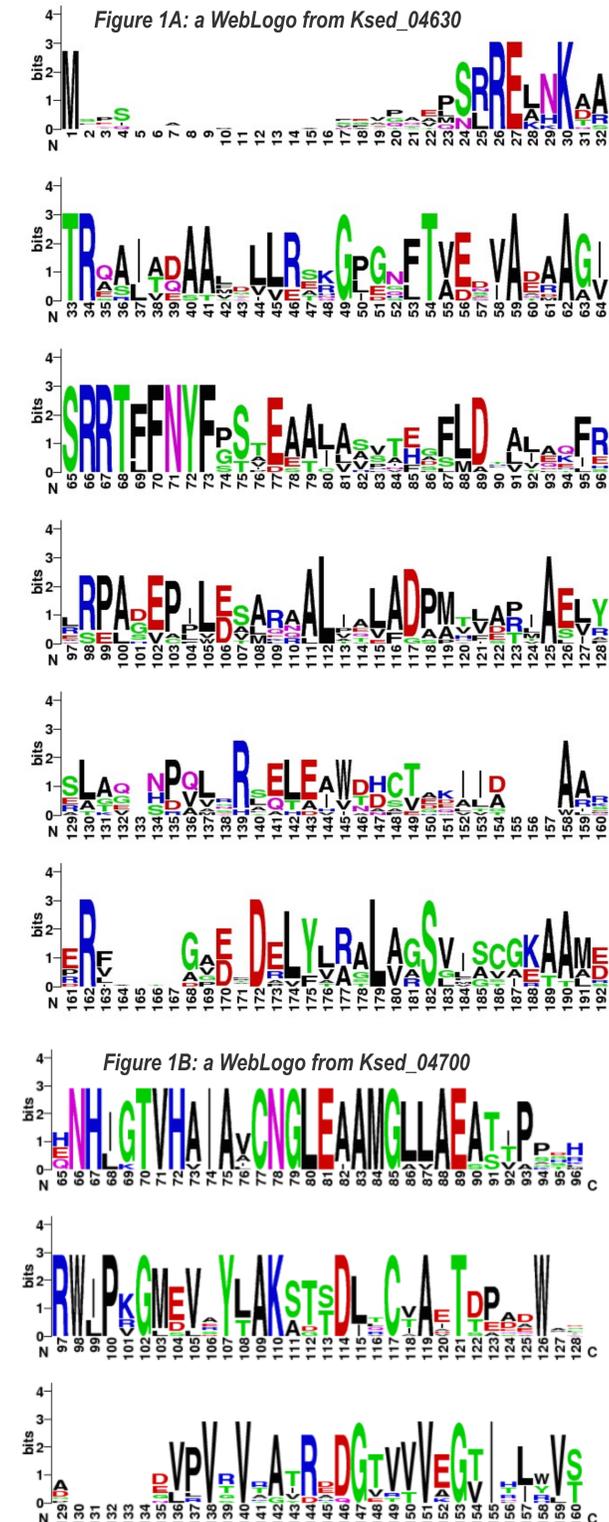
Modules	Activities	Questions Investigated
Module 1- Basic Information Module	DNA Coordinates and Sequence, Protein Sequence	What is the sequence of my gene and protein? Where is it located in the genome?
Module 2- Sequence-Based Similarity Data	Blast, CDD, T-Coffee, WebLogo	Is my sequence similar to 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?
Module 4- Alternative Open Reading Frame	IMG Sequence Viewer For Alternate ORF Search	Has the amino acid sequence of my protein been called correctly by the computer?
Module 5- Structure-Based Evidence	TIGRFam, Pfam, PDB	Are there functional domains in my protein?
Module 6- Enzymatic Function	KEGG, MetaCyc, E.C. Number,	In what process does my protein take part?
Module 7- Gene Duplication/ Gene Degradation	Paralog, Pseudogene	Are there other forms of my gene in the bacterium? Is my gene functional?
Module 8- Evidence for Horizontal Gene Transfer	Phylogenetic Tree,	Has my gene co-evolved with other genes in the genome?
Module 9- RNA	RFAM	Does my gene encode a functional RNA?

Results

Throughout the project presented to us by The University of Buffalo (UB) my group would be varied in our motivation to complete the project. But within our procrastination was an underlying urge to learn more. One reason we fell a little bit behind is because we would ask so many off-shoot questions and get sidetracked on the science of the cells of *Kytococcus sedentarius*. We wanted to know everything we could about trans-membranous proteins and about the genome of *Kytococcus sedentarius*. This project has further pushed 2 out of our 3 members to pursue careers in the STEM field. Tyler Allen wants to pursue engineering while Chris Lozada wants to be a physician. Our 3rd member Zac VanKoevering has used this experiment to realize that he does not want a career in the STEM field but that he enjoys STEM topics as something that he's interested in pursuing later on in life. Without after-school STEM activities, these realizations may never have happened.

Furthermore, the project presented to us by UB has made me personally more intrigued to learn about gene mapping and the careers that follow it. As we have gone through the charting of our individual gene strands we have realized the unique complexities of DNA and how far they go into determining an organism's life. DNA is the future. Gene mapping to find flaws or things that are undesirable is how we push into the history books. The after school STEM activities reinforcing us to follow that path are sending us into the future. While English and history classes are essential, if we as a race want to thrive and to defy our known boundaries then STEM activities and classes must be pursued. This is how we leave our mark on the world.

During the project, two activities piqued the group's interest. WebLogo and Transmembrane topology graphing were of interest.



Conclusion

By having after-school STEM activities available to students, it increases awareness for the types of jobs that are out there involving STEM. Also, science programs in high schools can be slow and drawn-out because of the variety in the learning speed of students. The setting of the classroom requires the instructor to go at one pace for everyone, but in after-school activities instructors can better individualize how instruction is happening. Within my group, 2 of us were 3 modules ahead of the rest of the group, but in the end we all learned what was necessary. This way of instruction gives more flexibility to how someone is educated. I personally feel as if I have learned more from after-school STEM activities than I have in a classroom setting for the same area.

References

Sims et al. (2009). Complete genome sequence of *Kytococcus sedentarius* type strain (541T). *Standards in Genomic Sciences*, 12 - 20.

Acknowledgments

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