

Translation in Elizabethkingia anophelis R26

GRP#
25

Authors

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ABSTRACT

Elizabethkingia anophelis is a slightly yellow, non-motile, non-spore-forming, Gram negative rod. It was originally found in the gut of mosquitos, with the first outbreaks happening in Singapore and Central Africa. Following these cases E. anophelis been found to be resistant to most drugs. During our research we found twenty two genes that were responsible for translation. This is extremely relevant as Translation is the process in which cellular ribosomes create proteins.

INTRODUCTION

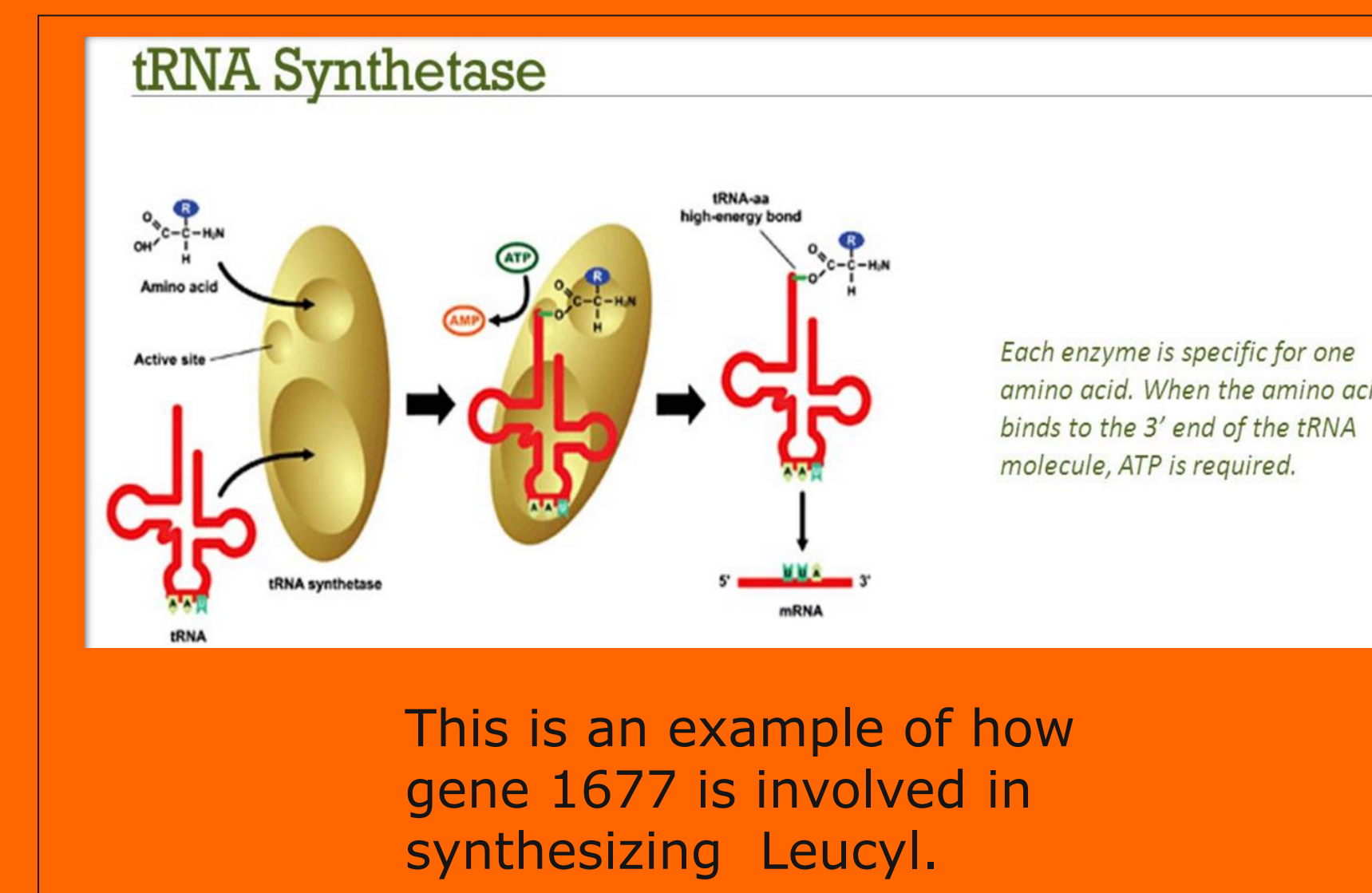
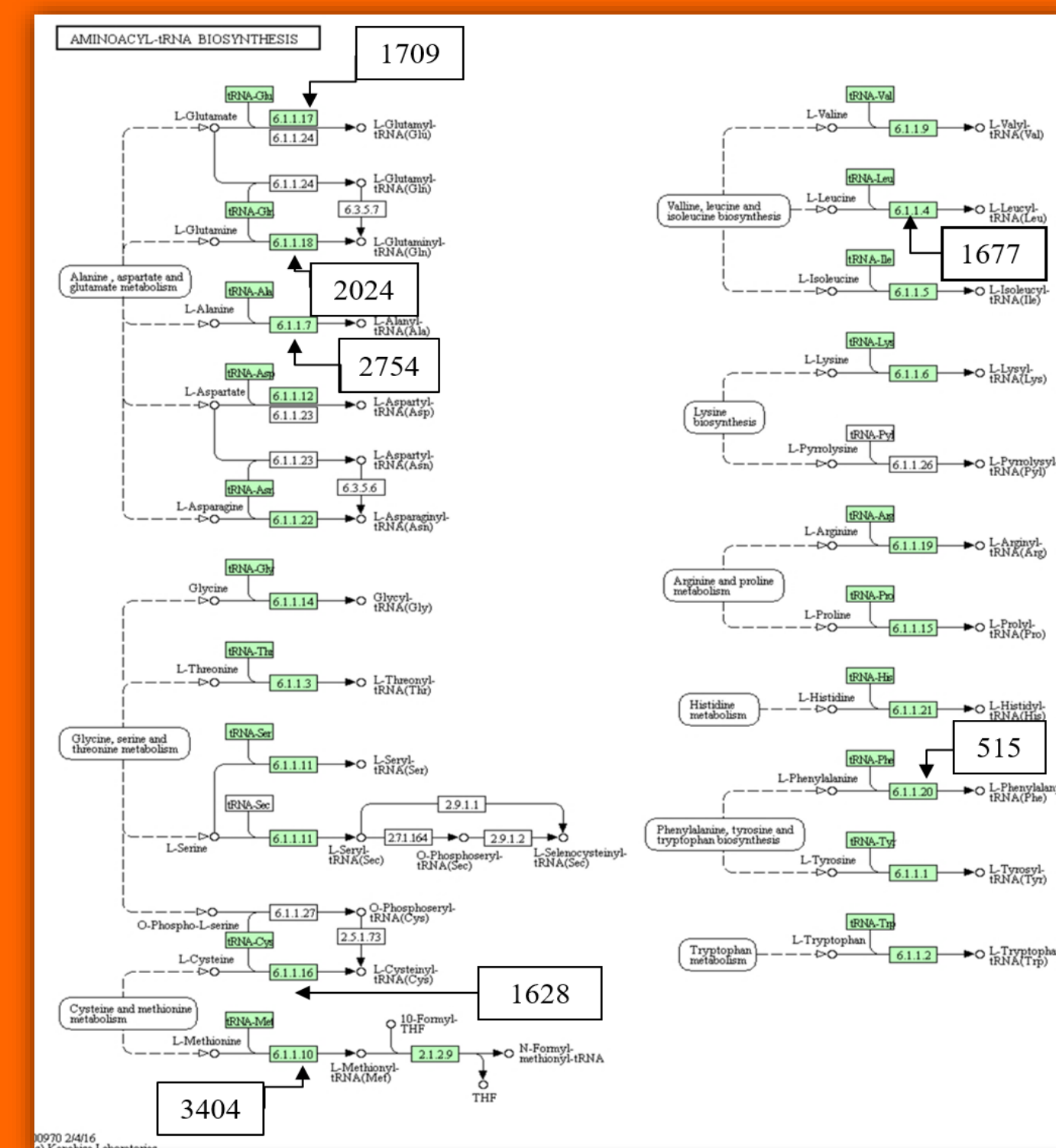
Elizabethkingia Anophelis R26 is a gram negative phylogenetic bacteria. People who contract this bacteria have died. We focused on the genes: 1677, 3404, 2754, 1628, 1709, 2024, and 515. These genes are all used to synthesize proteins. When introduced to the drugs Cephotoxin and Imipenem, these genes are not highly affected.

MATERIALS AND METHODS

We started by navigating to the Patric Database. Next, we clicked on the Pathways tab and clicked on translation. Clicked on Aminoacyl tRNA biosynthesis. Clicked on the Gene 6.1.1.4. Click on the ID under the Patric ID tab. Click on the view NT sequence link and copy the NT sequence into the clipboard. Navigated to the Blast site from D2L. Paste the NT sequence into the FASTA format box, and click search. Find and copy the Rast number for the gene, which was 1677. Go to the Rast Database on the Online Genomic Database tab. Go to Elizabethkingia Anophelis R26 and click View Details. Click on Browse Annotated Genome in SEED Viewer. Click on the highlighted "here". Paste the Rast ID in the Feature ID search bar. Click on the Feature ID of the gene that appears. Screenshot the visual region information for the gene in Elizabethkingia Anopheles R26. Repeat the same steps for genes 6.1.1.16, 6.1.1.17, 6.1.1.18, and 6.1.1.20. We then went to the excel spreadsheet of RNA sequence data fold changes in D2L and found the Rast numbers in the spreadsheet to see whether our genes were transcribed in the control group, a group where Cefotax was introduced, and a group where Imipenem was introduced.

RESULTS

In our study, we went to different online databases to find our genes. The genes that we found were a part of pathway named aminoacyl-tRNA biosynthesis. This particular pathway is involved with translation, and in this pathway we found a total of 22 genes that were involved with translation. These genes are shown in figure 1. We also found that our genes code for enzymes that charge the tRNA with an amino acid for translation. Our genes are responsible for the synthesis of Leucyl, Alanyl, Methionyl, Cysteinyl, Glutamyl, Glutaminyl, and Phenylalanyl.



This is an example of how gene 1677 is involved in synthesizing Leucyl.

Fig. 1: All numbers in boxes are genes

After we acquired the DNA sequences for these genes we looked to see if they were transcribed, and how the number of transcriptions changed from exposure to the drugs Cefotax and Imipenem.

A change of +50% or -50% is significant.

Genes	Groups	Control	Cefotax	Imipenem
1677		124	170	134
2754		1841	2458	1498
3404		3	4	5
1628		83	42	124
1709		383	352	354
2024		18	19	18
515		8	5	13

DISCUSSION

The purpose of the research was to determine whether or not the genes related to translation were "turned on" or expressed in the Elizabethkingia anophelis R26 virus. Through our research and using databases Rast Patric and BLAST we were able to determine that the genes that we had chosen were in fact expressed in Elizabethkingia anophelis R26. In order to be able to determine whether or not all of the genes are related to translation in Elizabethkingia anophelis 26, we would need to look at the other 14 out of 22 genes that were shown in the Patric database to be used in the process of translation.

REFERENCES

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