

Date: 20-12-2021

EXPERIMENT NO: 05

AIM OF THE EXPERIMENT: Translate a nucleotide sequence and select the correct reading frame of the polypeptide from the output sequence.

THEORY:

Translation is the process of synthesizing amino acid sequence from the information present in the mRNA. The process is accomplished by ribosomes, with the help of tRNA molecules, in the cytosol.

The information present in the mRNA is a sequence of nucleotides, and 3 such nucleotides are read by the tRNA at a time called codon. Biologists have decoded this code and named it genetic code, and accordingly, today we know which codon specifies what amino acid. The genetic code is nearly universal and minor variations in codon usage, called codon Bias, are found in some specific organisms and specific organelles. We now have several genetic code dictionaries.

Bioinformatics tools for Translation:

Once the codons have been decoded, Bioinformatics has helped in translating mRNA or DNA sequences into amino acid sequence, using some

specific algorithms or softwares. However, there are two aspects to be looked into:

- (A) Codon bias: Since codon usage bias has been identified in certain organisms and organelles, we first need to know the source of the nucleotide, and select the genetic code to be used accordingly. Not all softwares have these in-built facilities for codon usage.
- (B) Selecting Open reading frame (ORF):

Since the sequence of nucleotides in the mRNA/DNA specifies the amino acid sequences, any deletion or insertion of nucleotides causes changes in the reading frame for the sequence, and as such the entire amino acid sequence is altered. There are three ORFs in any nucleotide sequence, named +3, +2, +1, -1, -2, and -3, each one of which provide different amino acid sequences.

#### MATERIALS:

- ① EMBOSS Transeq - It is a powerful and updated online software/tool maintained by the European Bioinformatics Institute. It allows usage of different genetic code dictionaries in one hand, and provides option for choosing ORFs.
- ② Computer with internet facility.
- ③ Notebook, pen, pencil, etc.

## PROCEDURE :

- ① Go to the EMBOS-Transseq homepage .  
(<https://www.ebi.ac.uk/Tools/em>)
- ② In search textbox paste a standard nucleotide sequence of coding for human mitochondria ribosome polypeptide .
- ③ Select frame and codon table .
- ④ Clicked the 'Submit' button .
- ⑤ Select various ORFs and translate multiple times .

## RESULTS :

Results were printed and attached.

