



Research Paper

**PHYLOGENETIC TREE CONSTRUCTION OF BIOSURFACTANT
PRODUCING ORGANISMS**

Yusuf Talib¹, Amena Farooqui¹, Mehvish Fatema¹ and Wajed Khan²

¹ Department of Biotechnology,
Dr.Rafiq Zakaria Campus,
Maulana Azad College, Aurangabad.

²Department of Microbiology,
Dr.Rafiq Zakaria Center for Higher Learning and Advacned Research,
Dr. Rafiq Zakaria Campus, Aurangabad
India.

Abstract

Phylogenetic Tree is the graphical represent which display the relation between organisms, species or genomic sequence, Phylogenetic is the study of the evolutionary history of living organism using tree like diagrams to represent pedigrees of these organisms. Phylogenetic treats a species as a group of lineage- connected individuals over time taxonomy, the classification of organism according to similarity has been richly informed by Phylogenetic but remains methodologically and logically distinct. Phylogenetic also helps user to extract the relationship between species or organism in pictorial form which useful to easily understand Phylogenetic is known as Phylogenetic Tree Analysis. For tree construction we selected Biosurfactant as a genetic marker for selection of organisms (Dietzia spc was selected for study), on the base of E-Value we proceeded to sort out the organisms which will help to plot the evolutionary tree with the help of Bioinformatics applications.

Key words: *Biosurfactant, Evolution, Programmes for Phylogenetic Tree Construction.*

INTRODUCTION

Biosurfactant

Several prokaryotes and eukaryotes produce surface-active molecules, which are generically known as biosurfactants. These molecules present two distinct moieties: a hydrophilic and a hydrophobic one, and it is this combination that allows the microorganism to interact with hydrophobic substrates or surfaces. Biosurfactant reduce the interfacial tension and/or produce stable emulsions with insoluble compounds like hydrocarbon(1).

Phylogenetic inference is the process of developing hypothesis about the evolutionary relatedness of organisms based on their observable characteristics. Traditionally phylogenetics analyses have been based on the gross anatomy of species(2).when linaneaus developed the system of classification into kingdom, phyla

genera, and species, the early biologists sorted living things into a symbolic tree of life. this tree based representation of the relationships among species is a phylogenetic tree.

Evolutionary distance between pairs of sequence, relative to other sequences in an input data set, is one way to assign branch length(3). While a phylogeny of species generally has as root, assuming that all species have a specific common ancestor, a phylogenetic tree derived from sequence data may be rooted or unrooted.

MATERIALS AND METHODS

Programs

Various programs are available for Phylogenetic tree analysis, for generating a tree we need to first align the sequences (figure1) For alignment BLAST method has been utilized to get the most closely related sequences on the basis of E-value, which has been extracted from NCBI Database, after getting the similarity sequences we had proceed for construction of Phylogenetic Tree which is performed by using CLUSTALX2 application (figure 2) which is windows based programme for offline alignment, takes input in fasta file format and provides the output in .dnd, .aln,.phy form, these output is further used as a input in PHYLIP program.

[illegible]

Figure 1

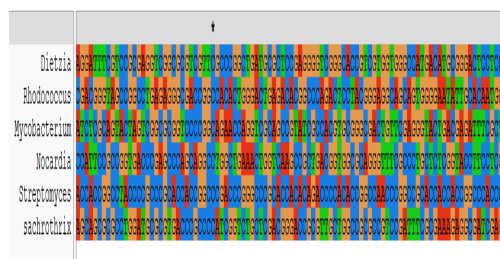


Figure 2

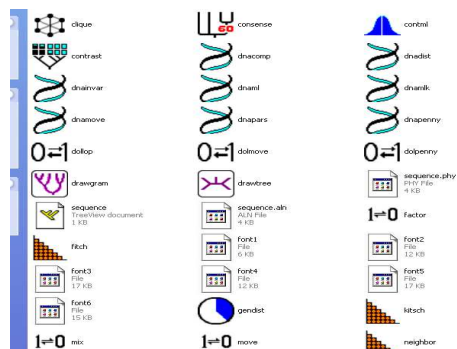


Figure 3

```
drawgram.exe: can't find input tree file "intree"
Please enter a new file name: sequence.dnd
DRAWGRAM from PHYLIP version 3.68
Reading tree ...
Tree has been read.
Loading the font ...
drawgram.exe: can't find font file "fontfile"
Please enter a new file name: font3
Font loaded.

Rooted tree plotting program version 3.68
Here are the settings:
B Screen type (IBM PC, ANSI): IBM PC
P Final plotting device: Postscript printer
P Previewing device: PS Windows display
H Tree groups: Horizontally
S Tree style: Phenogram
B Use branch lengths: Yes
L Angle of labels: 90.0
D Scale of branch length: Automatically rescaled
D Depth/Breadth of tree: 0.53
I Stem-length/ree-depth: 0.95
C Character ht /tip space: 0.3333
A Ancestral nodes: Weighted
F Font: Times-Roman
H Horizontal margins: 1.65 cm
M Vertical margins: 2.16 cm
E Pages per tree: one page per tree

Y to accept these or type the letter for one to change
Y
Preview window displayed... press "Change" button to return to menu.
Done.
Press enter to quit.
```

Figure 4

Phylogenetic tree construction

After getting output from clustalx in .dnd file, .aln file, we provided the sequence as input to the PHYLIP program (figure 3) which construct the tree using UPGMA and NJ method, which provides the information of root and branches attached with the help of genetic marker. PHYLIP has two different programs which helps to make rooted and unrooted tree here we selected only rooted tree by using drawgram program (figure 5).

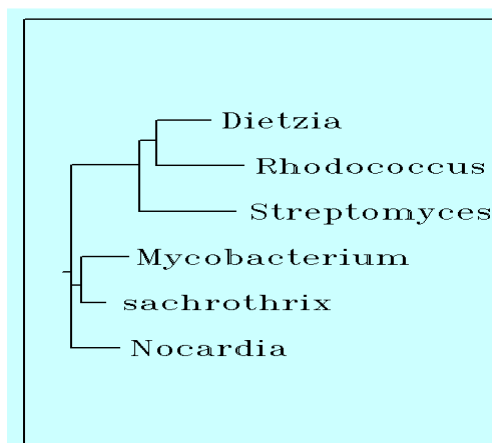


Figure 5

RESULTS

For construction purpose we have selected the Biosurfactant producing organism *Dietzia* spc, with the help of sequence similarity using E-Value we had selected 5 different sequences obtained from different spc, like *Nocardia*, *Sachrothrix*, *Mycobacterium*, *Streptomyces* and *Rhodococcus*, on that sequence similarity they do also have the ability for Biosurfactant production, further there sequence has been downloaded from the public databank and again realigned for tree generation purpose that alignment will give a score which help them to stand on the Phylogenetic tree, those extracted file has been submitted to clustalX for Aligned and then for PHYLIP to draw the tree and provide the internal and external nodes.

Which shows the 3 different groups has been plotted 1st is of *Nocardia* spc, 2nd is of *mycobacterium* and *sachrothrix* species and last group which shows the degree of similarity consists of our query sequence *Dietzia*, *Rhodococcus*, *Streptomyces*. These three are diversified by the evolution time factor.

DISCUSSION

Phylogenetic tree construction is one of the main stream to have the knowledge of evolutionary relationship between different organism. Phylogenetic tree can be constructed in rooted form.

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