

GENETIC VARIATION AND BIOINFORMATICS ANALYSIS OF THE TEF2 GENE OF *SORDARIA FIMICOLA*

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Abstract

The current study aimed to find out genetic variation and post-translational modifications of the eukaryotic translational elongation factor (eEF-1) due to environmental stress. Ribosomal translation factors are directly involved in protein translation and are greatly conserved but several studies have revealed that eEF1A is post-translationally modified. Six parental strains of *Sordaria fimicola* (S1, S2, S3, N5, N6, and N7) were subjected to amplify the TEF2 gene, and a comparison was made with reference species *Saccharomyces cerevisiae*. Different bioinformatics tools, i.e., Clustal W, PMes Server, PAIL and NetNES Servers, NetPhos 3.1, and Phyre2 were used for multiple sequence alignment, to identify methylation sites, acetylation sites on the protein, phosphorylation sites, and Protein 3D structure. The PTMs of *S. fimicola* strains were compared with PTMs of reference species. Out of the total, 329 nucleotides polymorphism was observed on five nucleotide positions. Altogether, a total of 13 sites (8Ser/4Thr/2Y) of phosphorylation modifications were observed in *S. cerevisiae* and *S. fimicola*. The polymorphism was observed at 23 sites in strains of SFS (S1, S2, and S3) while six polymorphic sites were present in NFS strains (NFS). The study reiterated that environmental stress causes genetic variation and ultimately leads to evolution.

Key words: Post-translational modification (PTM), Protein synthesis, *Sordaria fimicola*, Translation elongation factor, Eukaryotic elongation factor eEF1A.

Introduction

The eukaryotic translational elongation factor (eEF-1) complex plays both canonical and non-canonical functions in the cell. During the mechanism of protein synthesis, the protein complex subunits play a fundamental role, as it controls the delivery step of aa-tRNA during the elongation stage of translation. The role of eEF1A is attached with aminoacylated tRNAs and helps its transfer to the A-site of the translating 80S ribosome. Besides its well-established role in the elongation phase of translation, it also controls different cellular processes. The protein complex has two paralogs eEF1A and eEF1B, they are involved in aminoacyl-tRNAs delivery and catalyze them to the ribosomes A-site and act as guanine nucleotide exchange factor (GEF) respectively (Andersen *et al.*, 2003 & Khacho *et al.*, 2008).

eEF-1A is extensively post-translationally modified by lysyl acetylation, methylation (Cavallius *et al.*, 1993), ubiquitination, nitrosylation, glutathionylation, phosphorylation (Trauhj *et al.*, 2001), C-terminal methyl esterification (Zobel-Tropp *et al.*, 2000), and the attachment of ethanolamine phosphoglycerol (EPG) (Whiteheart *et al.*, 1989).

The functional and structural complexity of the proteome is enhanced greatly by spatial and temporal modifications termed as post-translational modifications, subjected to almost all the proteins after their translation. The role of PTMs in cellular processes can be understood by studying, analyzing, and predicting them *In Silico* by using different computational tools which are online available and are user-friendly webserver (Shi, 2019).

Furthermore, the 3D structure of the proteome can also help to predict the modified site of proteins. In the current study, we predict the most common PTMs as Phosphorylation, acetylation, glycosylation, and methylation by using different computational approaches.

Environmental extremes have a remarkable impact on the expression of genetic variation in individuals which leads toward evolution (Hoffman *et al.*, 1997). When there is a variation in physical conditions it affects reproductive growth, and when the perseverance of the conditions lead to long-lasting harm, these factors create environmental stress. Stress is an environmental factor that led to evolution and causes variation in living organisms (Parsons, 2005). Significant variation in morphological and physiological characteristics can be accomplished over inducing environmental stress (Weber, 1990 & Weber & Diggins, 1990). The research was undertaken to pursue the effect of stressful conditions on genetic variation and post-translational modifications in the translational elongation factor (eEF-1) complex in *Sordaria fimicola*.

For the present study, six parental strains of *S. fimicola* were used; the strains were earlier collected from Evolution Canyon (EC). Evolution canyon is considered as microclimate to study the relationship between climatic changes and genetic variation; the EC has two slopes; one is tropical, and the other is temperate. The south-facing slope (SFS) is dry, harsh, and has xeric conditions while the north-facing slope (NFS) is mesic, lush green, and moderate in terms of abiotic factors (Nevo, 1995). Strains S1, and S3, were collected from SFS, and N5, N6, and N7 were collected from NFS.

Methodology

Organism: Six various strains of *S. fimicola* (S1, S2, S3, N5, N6, and N7) were collected from molecular genetics and research laboratory, Department of Botany, University of Punjab, Lahore. The strains were earlier collected from Evolution Canyon (EC), Israel. EC has two opposite slopes one is a tropical Asian-African tropical south-facing slope (SFS) and the other is a temperate European north-facing slope (NFS).

DNA extraction: Total genomic DNA extraction was performed by taking perithecia of *Sordaria fimicola*, which were already cultured on potato dextrose agar (PDA) media by following the protocol described by Pietro *et al.*, 1995. The quality and quantity of DNA were examined by running the 1% agarose gel electrophoresis and spectrophotometrically for different DNA samples. The gel was visualized under UV light of Gel documentation system (Syngene Germany). The DNA was stored at -20 until further use.

Primer design and PCR amplification: To amplify *tef2* gene primers were designed manually and by using primer 3 plus software available at <https://primer3plus.com>. Primers were used to amplify the candidate gene; of Boiron, Germany has given in (Table 1).

Touch down PCR conditions was used for the amplification purpose, a total volume of 20 µl was prepared by adding 10 µl master mix, 2.5 µl of gDNA, 1 µl of forward primer and 1 µl of reverse primer, and 5.5 µl of dd H₂O. The PCR amplicons were separated on 1% agarose gel stained with ethidium bromide (BIORAD) along with 1kb DNA ladder (Invitrogen) and visualized under ultraviolet rays in the Gel Doc system. The amplicons were sent to Macrogen Korea for sequencing. Nucleotides sequences were aligned by using Clustal Omega O software of the *tef-2* gene of *S. cerevisiae* (Accession number FR774388) and of *S. fimicola*.

Prediction of PTMS: Various computational tools to predict PTMs of TEF2 gene were used like YinOYang 1.2 (www.cbs.dtu.dk/services/YinOYang/) for glycosylation, Netphos 3.1 (www.cbs.dtu.dk/services/NetPhos/) for phosphorylation, PAIL (bdmpail.biocuckoo.org/) for acetylation and ModPred (montana.informatics.indiana.edu/ModPred/faq.html) for methylation on different amino acid residues.

Prediction of protein 3D structure: Phyre2 (Protein Homology/analogy Recognition Engine V 2.0)

bioinformatics tool available at <http://www.sbg.bio.ic.ac.uk/~phyre2> was used to predict 3D structures and functions of elongation factor complex protein. PyMol molecular system and BioLip were used to visualize structures of protein and to predict ligand-protein interaction.

Results

Single nucleotide polymorphism (SNP) analysis: The sequences of all six strains of *S. fimicola* (S1, S2, S3, N5, N6, and N7) were aligned along with reference species *S. cerevisiae* with the online available tool Clustal Omega 3 to observe polymorphism among various strains of *S. fimicola*. The polymorphism was observed at 23 sites in *S. fimicola* strains, out of which 17 sites were observed in SFS strains (S1, S2, and S3) while six polymorphic sites were present in NFS strains (N5, N6, and N7) the results have been shown in (Figs. 1 & 2).

Prediction of phosphorylation: Protein phosphorylation majorly occurs on serine (S), threonine (T), and tyrosine (Y). For the elongation factor 1 protein of *S. cerevisiae*, phosphorylation was predicted at 13 serine (S), 16 threonines (T), and 3 tyrosine (Y) residues at various positions in the amino acid sequence. Phosphorylation was predicted at 13 serine (S), 17 threonines (T), and 3 tyrosine (Y) residues of S1, S2, and S3 strains. Phosphorylation for N5, N6, and N7 strains was observed at 14 serine (S), 15 threonines (T), and 3 tyrosine (Y) residues. Results have been shown in (Table 2).

Prediction of O-glycosylation: YinOYang 1.2 server results have shown in Table 3 and Graphical representation (Fig. 3) indicates that in *S. cerevisiae* O-glycosylation for elongation factor 1 protein was predicted at 3 serine (S), 5 threonines (T). O-glycosylation was predicted at 3 serine (S) and 8threonine (T) residues at the sequence of amino acids in S1, S2, and S3 strains. While 3 serine (S) and 5 threonine (T) residues were observed for O-glycosylation in N5, N6, and N7 strains.

Table 1. Primers sequences used to amplify *tef2* gene.

Sr. No.	Name	Sequence (°)	Expected product length (bp)	Tm
1.	TEFF1	ATGGGTAAAGAGAAGTCTCA	421	52
2.	TEFR1	CATTGACGGAGTCCATCT		53
3.	TEFF2	TGGGACGAATCCATTCCA	420	52
4.	TEFR2	CACCTGGAACACCTTGTTCC		58
5.	TEFF3	GTTCCAGGTGACAACGTTGG	460	58
6.	TEFR3	TTTGAGCAGCCTTGTAACC		56

Table2. Phosphorylation prediction on serine, threonine and tyrosine residues in *S. fimicola* and *S. cerevisiae*.

Organism	Serine	Threonine	Tyrosine	Kinases
<i>S. cerevisiae</i>	6, 18, 21, 53, 107, 157, 192, 273, 289, 314, 356, 381, 438	22, 72, 82, 88, 106, 142, 172, 240, 267, 277, 284, 285, 341, 430, 442, 449	56, 85, 252	PKC, PKG, unsp, PKA, p38MAPK, cdk5, CKII, INSR, cdc2, DNAPK, PKB
Total	13	16	03	11
SFS strains of <i>S. fimicola</i>	6, 18, 21, 53, 107, 157, 192, 237, 289, 314, 356, 381, 394	22, 72, 82, 88, 106, 142, 172, 240, 267, 277, 284, 285, 341, 363, 430, 442, 449	56, 85, 252	PKC, PKG, unsp, PKA, p38MAPK, cdk5, CKII, INSR, cdc2, DNAPK, PKB
Total	13	17	03	11
NFS strains of <i>S. fimicola</i>	6, 18, 21, 53, 107, 157, 192, 225, 237, 289, 314, 356, 381, 438	22, 72, 82, 88, 106, 142, 240, 267, 277, 284, 285, 341, 430, 442, 449	56, 85, 252	PKC, PKG, unsp, PKA, p38MAPK, cdk5, CKII, INSR, cdc2, DNAPK, PKB
Total	14	15	03	11

Highlighted areas show polymorphisms on that site; Red highlighted areas show polymorphisms on that site while yellow highlighted areas show conserved sites

S3	AACATGATTACTGGTACTTCTCAAGCTGACTGTGCTATCTTGATTATTGCAAGGTGGTGTC	360
S1	AACATGATTACTGGTACTTCTCAAGCTGACTGTGCTATCTTGATTATTGCAAGGTGGTGTC	360
S2	AACATGATTACTGGTACTTCTCAAGCTGACTGTGCTATCTTGATTATTGCAAGGTGGTGTC	360
Ref.	AACATGATTACTGGTACTTCTCAAGCTGACTGTGCTATCTTGATTATTGCTGGTGGTGTC	360
N6	ATCATGATTACTGGTACTTCTCAAGCTGACTGTGCTATCTTGATTATTGCTGGTGGTGTC	360
N5	ATCATGATTACTGGTACTTCTCAAGCTGACTGTGCTATCTTGATTATTGCTGGTGGTGTC	360
N7	ATCATGATTACTGGTACTTCTCAAGCTGACTGTGCTATCTTGATTATTGCTGGTGGTGTC	360

S3	GGTGAATTCGAGCCGGTATCTCTAAGGATGGTCAAACCAGAGAACACCTTTGTTGGCT	420
S1	GGTGAATTCGAGCCGGTATCTCTAAGGATGGTCAAACCAGAGAACACCTTTGTTGGCT	420
S2	GGTGAATTCGAGCCGGTATCTCTAAGGATGGTCAAACCAGAGAACACCTTTGTTGGCT	420
Ref.	GGTGAATTCGAGCCGGTATCTCTAAGGATGGTCAAACCAGAGAACACCTTTGTTGGCT	420
N6	GGTGAATTCGAGCCGGTATCTCTAAGGATGGTCAAACCAGAGAACACGCTTTGTTGGCT	420
N5	GGTGAATTCGAGCCGGTATCTCTAAGGATGGTCAAACCAGAGAACACGCTTTGTTGGCT	420
N7	GGTGAATTCGAGCCGGTATCTCTAAGGATGGTCAAACCAGAGAACACGCTTTGTTGGCT	420

S3	TTCACCTTGGGTGTTAGACAATTGATTGTTGCTGTCAACAAGATGGACTCCGTCAAATGG	480
S1	TTCACCTTGGGTGTTAGACAATTGATTGTTGCTGTCAACAAGATGGACTCCGTCAAATGG	480
S2	TTCACCTTGGGTGTTAGACAATTGATTGTTGCTGTCAACAAGATGGACTCCGTCAAATGG	480
Ref.	TTCACCTTGGGTGTTAGACAATTGATTGTTGCTGTCAACAAGATGGACTCCGTCAAATGG	480
N6	TTCACCTTGGGTGTTAGACAATTGATTGTTGCTGTCAACAAGATGGACTCCGTCAAATGG	480
N5	TTCACCTTGGGTGTTAGACAATTGATTGTTGCTGTCAACAAGATGGACTCCGTCAAATGG	480
N7	TTCACCTTGGGTGTTAGACAATTGATTGTTGCTGTCAACAAGATGGACTCCGTCAAATGG	480

S3	GAAGCTACCTCCAACGCTCCATGGTACAAGCGTTGGGAAAAGGAAACCAAGGCCGGTGTC	660
S1	GAAGCTACCTCCAACGCTCCATGGTACAAGCGTTGGGAAAAGGAAACCAAGGCCGGTGTC	660
S2	GAAGCTACCTCCAACGCTCCATGGTACAAGCGTTGGGAAAAGGAAACCAAGGCCGGTGTC	660
Ref.	GAAGCTACCTCCAACGCTCCATGGTACAAGCGTTGGGAAAAGGAAACCAAGGCCGGTGTC	660
N6	GAAGCTACCTCCAACGCTCCATGGTACAAGCGTTGGGAAAAGGAAACCAAGGCCGGTGTC	660
N5	GAAGCTACCTCCAACGCTCCATGGTACAAGCGTTGGGAAAAGGAAACCAAGGCCGGTGTC	660
N7	GAAGCTACCTCCAACGCTCCATGGTACAAGCGTTGGGAAAAGGAAACCAAGGCCGGTGTC	660

S3	GCTGGTGTTACCACTGAAGTCAAGTCCGTTGAAATGCATCACGAACAATTGGAACAAGGT	900
S1	GCTGGTGTTACCACTGAAGTCAAGTCCGTTGAAATGCATCACGAACAATTGGAACAAGGT	900
S2	GCTGGTGTTACCACTGAAGTCAAGTCCGTTGAAATGCATCACGAACAATTGGAACAAGGT	900
Ref.	GCTGGTGTTACCACTGAAGTCAAGTCCGTTGAAATGCATCACGAACAATTGGAACAAGGT	900
N6	GCTGGTGTTACCACTGAAGTCAAGTCCGTTGAAATGCATCACGAACAATTGGAACAAGGT	900
N5	GCTGGTGTTACCACTGAAGTCAAGTCCGTTGAAATGCATCACGAACAATTGGAACAAGGT	900
N7	GCTGGTGTTACCACTGAAGTCAAGTCCGTTGAAATGCATCACGAACAATTGGAACAAGGT	900

S3	ACCGTCATTGTTTTGAACCATCCAGGTCAAATCTGCTGGTTACTCTCCAGTTTTGGAT	1080
S1	ACCGTCATTGTTTTGAACCATCCAGGTCAAATCTGCTGGTTACTCTCCAGTTTTGGAT	1080
S2	ACCGTCATTGTTTTGAACCATCCAGGTCAAATCTGCTGGTTACTCTCCAGTTTTGGAT	1080
Ref.	ACCGTCATTGTTTTGAACCATCCAGGTCAAATCTGCTGGTTACTCTCCAGTTTTGGAT	1080
N6	ACCGTCATTGTTTTGAACCATCCAGGTCAAATCTCTGCTGGTTACTCTCCAGTTTTGGAT	1080
N5	ACCGTCATTGTTTTGAACCATCCAGGTCAAATCTCTGCTGGTTACTCTCCAGTTTTGGAT	1080
N7	ACCGTCATTGTTTTGAACCATCCAGGTCAAATCTCTGCTGGTTACTCTCCAGTTTTGGAT	1080

S3	TGTCACACTGCTCACATTGCTTGTAGATTCGACGAATTGTTGGAAAAGAACGACAGAAGA	1140
S1	TGTCACACTGCTCACATTGCTTGTAGATTCGACGAATTGTTGGAAAAGAACGACAGAAGA	1140
S2	TGTCACACTGCTCACATTGCTTGTAGATTCGACGAATTGTTGGAAAAGAACGACAGAAGA	1140
Ref.	TGTCACACTGCTCACATTGCTTGTAGATTCGACGAATTGTTGGAAAAGAACGACAGAAGA	1140
N6	TGTCACACTGCTCACATTGCTTGTAGATTCGACGAATTGTTGGAAAAGAACGACAGAAGA	1140
N5	TGTCACACTGCTCACATTGCTTGTAGATTCGACGAATTGTTGGAAAAGAACGACAGAAGA	1140
N7	TGTCACACTGCTCACATTGCTTGTAGATTCGACGAATTGTTGGAAAAGAACGACAGAAGA	1140

S3	TCTGGTAAGAAGTTGGAAGACCATCCAAAGTTCTTGAAGTCCGGTGACGCTGCTTTGGTC	1200
S1	TCTGGTAAGAAGTTGGAAGACCATCCAAAGTTCTTGAAGTCCGGTGACGCTGCTTTGGTC	1200
S2	TCTGGTAAGAAGTTGGAAGACCATCCAAAGTTCTTGAAGTCCGGTGACGCTGCTTTGGTC	1200
Ref.	TCTGGTAAGAAGTTGGAAGACCATCCAAAGTTCTTGAAGTCCGGTGACGCTGCTTTGGTC	1200
N6	TCTGGTAAGAAGTTGGAAGACCATCCAAAGTTCTTGAAGTCCGGTGACGCTGCTTTGGTC	1200
N5	TCTGGTAAGAAGTTGGAAGACCATCCAAAGTTCTTGAAGTCCGGTGACGCTGCTTTGGTC	1200
N7	TCTGGTAAGAAGTTGGAAGACCATCCAAAGTTCTTGAAGTCCGGTGACGCTGCTTTGGTC	1200

Fig. 1. Pairwise alignment of nucleotide sequence of Tef2 gene in *S. fimicola* and *S. cerevisiae* red lines indicates the Single nucleotide polymorphisms (SNPs).

S1	MGKEKSHINLVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVL	60
S2	MGKEKSHINLVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVL	60
S3	MGKEKSHINLVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVL	60
Ref.	MGKEKSHINLVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVL	60
N7	MGKEKSHINLVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVL	60
N5	MGKEKSHINLVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVL	60
N6	MGKEKSHINLVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVL	60

S1	DKLKAERERGITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGV	120
S2	DKLKAERERGITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGV	120
S3	DKLKAERERGITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGV	120
Ref.	DKLKAERERGITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGV	120
N7	DKLKAERERGITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGV	120
N5	DKLKAERERGITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGV	120
N6	DKLKAERERGITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGV	120

S1	GEFVAGISKDGGQTREHALLAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETSNIKKVG	180
S2	GEFVAGISKDGGQTREHALLAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETSNIKKVG	180
S3	GEFVAGISKDGGQTREHALLAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETSNIKKVG	180
Ref.	GEFVAGISKDGGQTREHALLAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETSNIKKVG	180
N7	GEFVAGISKDGGQTREHALLAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETSNIKKVG	180
N5	GEFVAGISKDGGQTREHALLAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETSNIKKVG	180
N6	GEFVAGISKDGGQTREHALLAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETSNIKKVG	180

S1	YNPKTVPFVPISGWNGDNMIEATSNAPWYKRWKETKAGVVKGKTLLEAIDAIEQPSRPT	240
S2	YNPKTVPFVPISGWNGDNMIEATSNAPWYKRWKETKAGVVKGKTLLEAIDAIEQPSRPT	240
S3	YNPKTVPFVPISGWNGDNMIEATSNAPWYKRWKETKAGVVKGKTLLEAIDAIEQPSRPT	240
Ref.	YNPKTVPFVPISGWNGDNMIEATSNAPWYKRWKETKAGVVKGKTLLEAIDAIEQPSRPT	240
N7	YNPKTVPFVPISGWNGDNMIEATSNAPWYKRWKETKAGVVKGKTLLEAIDAIEQPSRPT	240
N5	YNPKTVPFVPISGWNGDNMIEATSNAPWYKRWKETKAGVVKGKTLLEAIDAIEQPSRPT	240
N6	YNPKTVPFVPISGWNGDNMIEATSNAPWYKRWKETKAGVVKGKTLLEAIDAIEQPSRPT	240

S1	DKPLRLPLQDVYKIGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVKSVMHHEQLEQG	300
S2	DKPLRLPLQDVYKIGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVKSVMHHEQLEQG	300
S3	DKPLRLPLQDVYKIGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVKSVMHHEQLEQG	300
Ref.	DKPLRLPLQDVYKIGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVKSVMHHEQLEQG	300
N7	DKPLRLPLQDVYKIGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVKSVMHHEQLEQG	300
N5	DKPLRLPLQDVYKIGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVKSVMHHEQLEQG	300
N6	DKPLRLPLQDVYKIGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVKSVMHHEQLEQG	300

S1	VPGDNVGFNVKNVSVKEIRRGVCGDAKNDPPKGCASFNATVIVLNHPGQISAGYSPVLD	360
S2	VPGDNVGFNVKNVSVKEIRRGVCGDAKNDPPKGCASFNATVIVLNHPGQISAGYSPVLD	360
S3	VPGDNVGFNVKNVSVKEIRRGVCGDAKNDPPKGCASFNATVIVLNHPGQISAGYSPVLD	360
Ref.	VPGDNVGFNVKNVSVKEIRRGVCGDAKNDPPKGCASFNATVIVLNHPGQISAGYSPVLD	360
N7	VPGDNVGFNVKNVSVKEIRRGVCGDAKNDPPKGCASFNATVIVLNHPGQISAGYSPVLD	360
N5	VPGDNVGFNVKNVSVKEIRRGVCGDAKNDPPKGCASFNATVIVLNHPGQISAGYSPVLD	360
N6	VPGDNVGFNVKNVSVKEIRRGVCGDAKNDPPKGCASFNATVIVLNHPGQISAGYSPVLD	360

S1	CHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAALVKFVPSKPMCVEAFSEYPPLG	420
S2	CHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAALVKFVPSKPMCVEAFSEYPPLG	420
S3	CHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAALVKFVPSKPMCVEAFSEYPPLG	420
Ref.	CHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAALVKFVPSKPMCVEAFSEYPPLG	420
N7	CHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAALVKFVPSKPMCVEAFSEYPPLG	420
N5	CHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAALVKFVPSKPMCVEAFSEYPPLG	420
N6	CHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAALVKFVPSKPMCVEAFSEYPPLG	420

S1	RFAVRDMRQTVAVGVKSVDKTEKAAKVTCAAQKAAKK*	458
S2	RFAVRDMRQTVAVGVKSVDKTEKAAKVTCAAQKAAKK*	458
S3	RFAVRDMRQTVAVGVKSVDKTEKAAKVTCAAQKAAKK*	458
Ref.	RFAVRDMRQTVAVGVKSVDKTEKAAKVTCAAQKAAKK-	458
N7	RFAVRDMRQTVAVGVKSVDKTEKAAKVTCAAQKAAKK*	458
N5	RFAVRDMRQTVAVGVKSVDKTEKAAKVTCAAQKAAKK*	458
N6	RFAVRDMRQTVAVGVKSVDKTEKAAKVTCAAQKAAKK*	458

Fig. 2. Pairwise alignment of the amino acid sequence of EF1 protein in six strains of *S. fimicola* and *S. cerevisiae*. Alphabets in red representing the PTMs sites on Ser/Thr/Y and Lysine residue for potential acetylation, glycosylation and phosphorylation. Alphabets in Grey representing polymorphic sites.

Table 3. Prediction of O-glycosylation, Acetylation and Methylation in various strains of *S. fimicola* and *S. cerevisiae*.

Organisms	O-glycosylation	Acetylation	Methylation
	Residues Serine (S) and Threonine (T)	Residue Lysine (K)	Residue Arginine (R)
<i>S. cerevisiae</i>	107S, 185T, 204T, 237S, 284T, 285T, 352S, 449T	23, 39, 54, 58, 180, 225, 227, 245, 319, 387, 396, 404, 409, 440, 444, 447, 450, 453, 457, 460, 461	7, 11, 18
Total	8	21	3
SFS	107S, 185T, 204S, 216T, 237S, 284T, 285T, 352T, 449T	4, 6, 21, 37, 52, 56, 178, 223, 225, 243, 317, 385, 394, 402, 407, 448, 451, 455, 458, 459	2, 4, 7
Total	9	20	3
NFS	107S, 185T, 204T, 237S, 284T, 285T, 352S, 449T	4, 6, 21, 37, 52, 56, 178, 223, 225, 243, 317, 384, 385, 394, 402, 407, 438, 442, 445, 448, 451, 455, 458, 459	2, 4, 7
Total	8	23	3

Highlighted areas show polymorphisms on that site; Red highlighted areas show polymorphisms on that site while yellow highlighted areas show conserved sites

Prediction of methylation: Methylation at three arginine residues (R7, R11, and R18) was predicted in *S. cerevisiae* reference species. While (R2, R4, and R7) positions were investigated for methylation in all six strains of *S. fimicola*. R7 site seems to be a conserved site in all strains of *S. fimicola* and reference organisms.

Prediction of acetylation: (PAIL) server results have shown in (Table 3), acetylation at lysine (K) residue was investigated at 21 positions in *S. cerevisiae*. In the S1, S2, and S3 strains of *S. fimicola*, acetylation was found at 20 lysine residues and 24 sites were observed in the N5, N6, and N7 strains (Table 2). Only 225 lysines (k) position was found to be conserved in *S. cerevisiae* and *S. fimicola*.

Prediction of 3D protein structure: Phyre2 (Protein Homology/analogy Recognition Engine V 2.0) online server tool available at <http://www.sbg.bio.ic.ac.uk/~phyre2> was used to visualize the 3D structure of elongation factor alpha 1 protein of S1 strain, N7 strains, and reference strain of *S. cerevisiae*. Graphical dissimilarities in the orientation of alpha and beta-helix were found in all the experimental strains due to the occurrence of variation in amino acid sequences (Fig. 4). The motifs shown in the helical form are α -helix, motifs in arrow form are β -sheets and it also shows the loop regions for the attachment of ligand.

Discussion

According to different studies effect of environmental stress can be positively associated with genetic variation in individuals (Parsons, 2005). In the present study genetic variation was observed in SFS strains that encounter environmental stress as compared to NFS strains. The six strains of *S. fimicola* S1, S2, S3, N5, N6, and N7 were used to amplify the *tef-2* gene to investigate natural polymorphisms. Point mutations at four positions (112, 454, 674, and 1293) were found between *S. fimicola* sequences (FR774388) and the reference species.

Natural polymorphisms were at nineteen other positions. The 28C, 211T, 324T, 371T, 671G, 867G, 922G, 1048A, 1088G, 1172G, and 1322T variants were observed only in SFS strains while variations at position the 302T variant were present only in N5 strain and 643C in N6, 510G in N7 while 780C only in S2 strains. A total of 23 point mutations were observed in the exonic region of the *tef-2* gene in which SFS strains showed more polymorphic

sites these results are in accordance with Arif *et al.*, (2017) who studied single nucleotide polymorphism in frequency clock and Mating Type a-1 proteins encoding genes and results showed that more genetic variation was observed in SFS strains than NFS strains. Similar findings were also reported by Hosid *et al.*, (2008), which revealed that there is a relationship between genetic variation and environmental stress in the soil fungus *Emericella nidulans*. Environmental stresses contribute to genetic variation and change the gene frequencies, and ultimately lead towards evolution (Hoffman & Parsons, 1991).

It is reported that translation elongation factors are extremely conserved among various species and in addition to protein synthesis they might play a crucial role in other biological processes (Dever *et al.*, 2018). EF-2 catalyzes the translocation of peptidyl-tRNA on the ribosome (Riis *et al.*, 1990). Chen *et al.*, (2019) worked on characterization and expression of translation elongation factor 2 from *Dermatophagoides farina*.

The structure and dynamics of proteome altered due to post-translational modifications which occur in almost every kind of protein after its synthesis. Various types of PTMs such as acetylation, phosphorylation, glycosylation, or methylation can be studied by using different computational tools.

Phosphorylation is the ubiquitous kind as it was reported that 30% of the total protein undergo the process of phosphorylation at least at one position. Protein kinases are the enzymes involved in the process of phosphorylation while protein phosphatases remove the chemical group as it is a kind of reversible PTM (Pinna, 1996 & Cohen, 2002). The present study reported a total of 32 phosphorylation sites of TEF2 protein in *S. cerevisiae* which included 13 Serine residues, 16 Threonine residues and 3 Tyrosine residues. In south-facing strains (S1, S2, S3), 13 Serine residues, 17 Threonine residues, and 3 Tyrosine residues were predicted as phosphorylation sites and variation occurred at 394S, 142T, 363T residues which were not found in reference organism but present in SFS strains (Table 2). In North-facing strains (N5, N6, N7), 14 Serine residues, 15 Threonine residues, and 3 Tyrosine residues were investigated as phosphorylation sites and variation occurred at 225S residue which was present in NFS strains but not found in reference organism (Table 1). Chen *et al.*, (2019) reported 31 phosphorylation sites of TEF2 in *Dermatophagoides farina* which included 17 Serine residues 8 Threonine residues and 6 Tyrosine residues.

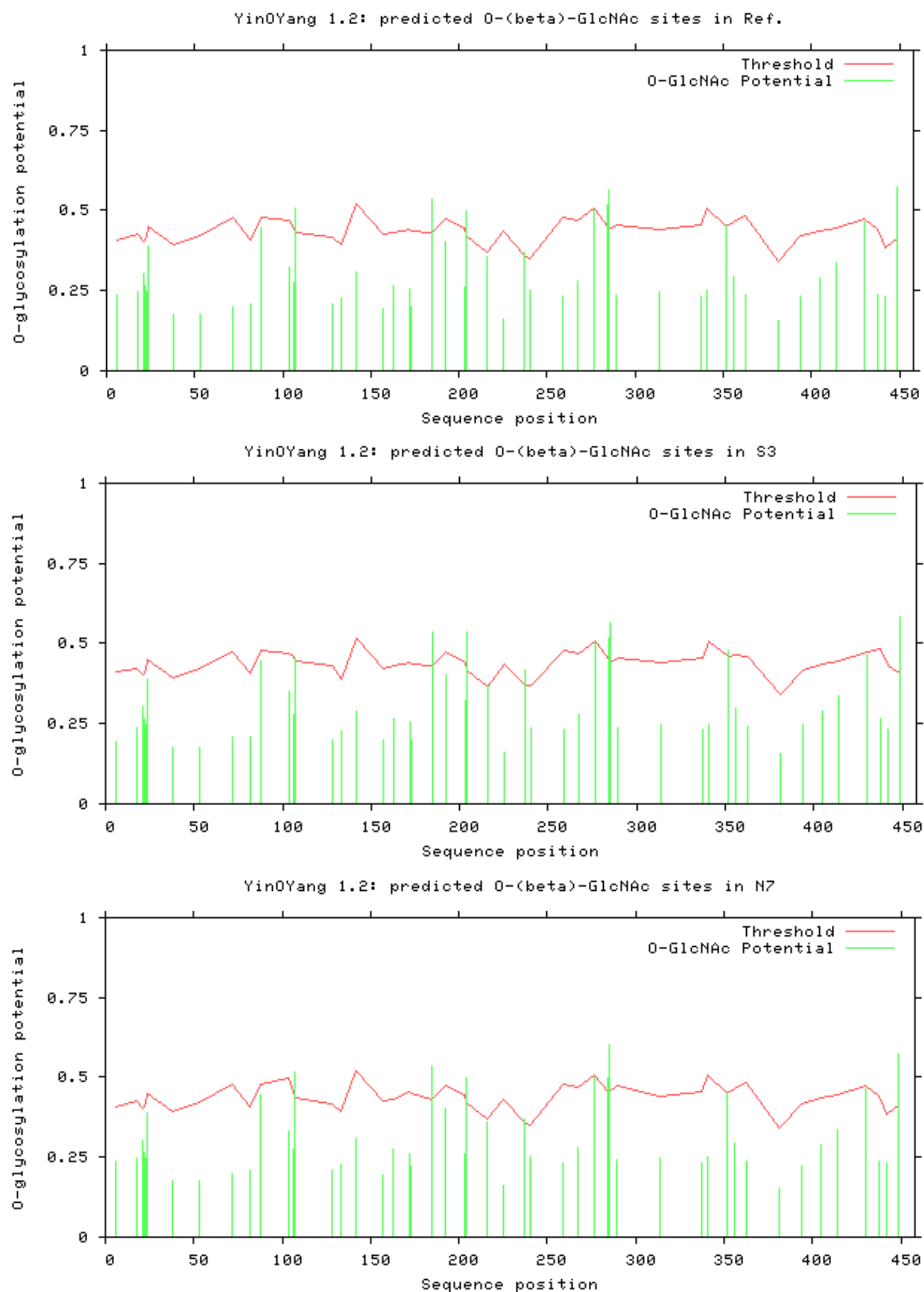


Fig. 3. Graphical representation of Prediction of Potential Glycosylation and YinOYang sites in *S. cerevisiae* (A), SFS strains (B) and NFS strains (C) of *S. fimicola* at 0.5 thresholds.

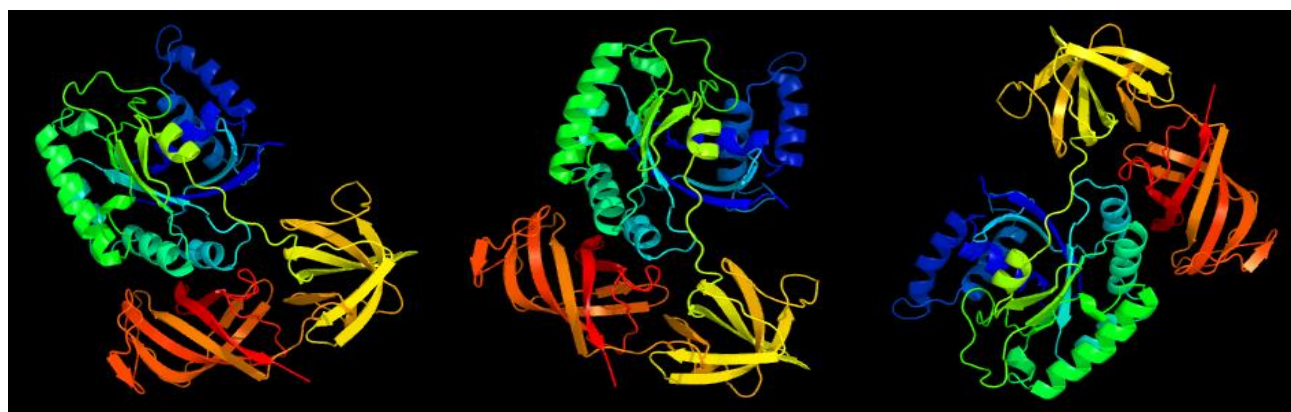


Fig. 4. 3D structure of translation elongation factor alpha 1 protein in *S. cerevisiae* (Left), SFS (Center) and NFS (Right) of *S. fimicola*. Image coloured by rainbow N → C terminus. *S. cerevisiae* = Model dimensions (Å): X: 77.549 Y: 51.010 Z: 69.994 SFS= Model dimensions (Å): X: 77.549 Y: 51.010 Z: 69.994 NFS= Model dimensions (Å): X: 78.134 Y: 51.010 Z: 69.994.

Present work investigated O-glycosylation at Serine and Threonine residues in tef2 protein of *S. fimicola*. Eight *O*-glycosylated sites were predicted in *S. cerevisiae* as well as in NFS strains while nine *O*-glycosylated sites were investigated in SFS strains. Six *O*-glycosylated sites (107S, 185T, 237S, 284T, 285T, 449T) were found to be conserved among reference organisms, SFS strains, and NFS strains. Gonzalez *et al.*, (2012) studied *O*-glycosylation in secretory proteins of eight fungal genomes. Bukhari *et al.*, (2020) also reported glycosylation sites in *S. fimicola* by using YinOYang 1.2 server.

Lysine acetylation is a ubiquitous kind of PTMs of proteins and is known to play a key role in broad-spectrum cellular functions (Kim *et al.*, 2006 & Zhao *et al.*, 2010). In the TEF2 protein of *S. cerevisiae*, acetylation was predicted at 21 Lysine residues. In SFS strains, Lysine acetylation was predicted at 20 sites, and in NFS strains, Lysine acetylation ion was predicted at 24 sites. Single acetylation site (225K) was found to be conserved in the organism, SFS strains, and NFS strains.

In *S. cerevisiae*, there are 166 methyltransferases found when methyltransferase genes are searched in the *S. cerevisiae* genome database (White, 2019). A great number of the identified methyltransferases in the yeast *S. cerevisiae* modify ribosomal components, indicating that methylation of translational components is significant for cellular functions (Clarke, 2013). The current study reported that Arginine methylation at 3 sites of *S. cerevisiae*, SFS, and NFS strains in TEF2 protein. Single methylation site 7R was found to be conserved between *S. cerevisiae*, SFS strains, and NFS strains.

Conclusion

The present work was performed to detect polymorphism and post-translational modifications by using different computational techniques in the TEF2 gene in *S. fimicola*. Significant differences in the gene sequences and their reflections upon post-translational modifications of proteins were observed. So, it is found that genetic variation may occur under stressful environmental conditions in nucleotide sequence of tef 2 genes. This is shown by the presence of some different and some conserved PTM sites for translation elongation factor alpha 1 in each strain of *S. fimicola*.

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