

ABSTRACT

Post translational modifications (PTMs) take place naturally at different amino acid residues of protein to modify its functions. The aim of present study was to explore genetic diversity among different strains of *Sordaria fimicola*. Nucleotide sequences of *clr-1* and *clr-2* genes and their subsequent protein sequences were compared with nucleotide and protein sequences of reference organism (*Neurospora crassa*) to find out variations. Nucleotide variations were found at 15 different positions for *clr-1* gene and 9 for *clr-2* gene among SFS and NFS strains of *S. fimicola*, while 9 variations were found in the protein sequence of *clr-1* and 7 in the *clr-2* protein. Genetic variations in the nucleotide sequence also affect subsequent protein sequences therefore PTMs of *clr-1* and *clr-2* proteins in *S. fimicola* strains and *N. crassa* were analyzed using different bioinformatics tools. Similar glycosylation sites (408T, 414S, 705S, 1023T) and methylation sites (R431) were observed in the protein sequences of *clr-1* and *clr-2*. Variations were found in *clr-1* protein at phosphorylation sites (76S, 245S, 373Y, 571T, 576S, 792S) and nuclear export signals (19L) while *clr-2* revealed phosphorylation at 226S, 407S, 706S, 1025S residue and peptide cleavage at peptide number 406. These results suggest that stressful environmental conditions induce **genetic variations in the nucleotides which subsequently affect the multi-functionality of proteins.**