**Regulation of *asl-1* transcription factor in *Neurospora crassa***

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**Abstract**

Transcription factors (TFs) binds to the upstream regulatory elements of genes in the promoter and enhancer regions of DNA and regulate transcription. The Activating-transcription factor (ATF) belongs to the basic leucine zipper (bZIP) family. The bZIP family of transcriptional regulators contains a basic region that mediates nuclear localization and DNA binding and a leucine zipper that forms homodimer or heterodimers with other bZIP-type TFs. *Atf-1* gene encodes an ATF/CREB family transcriptional factor**.** Atf1 was first described in *Schizosaccharomyces pombe.* The functional domain of ATF1 possess discrete sequence motifs namely OSA, HRA, HRR and bZIP. Osmotic Stress Activation (OSA) helps in mitigating osmotic stress. HRA helps in activating recombination while HRR repress recombination. Although ATF2 of human maintains cellular homeostasis and pathological processes, altered expression of ATF2 leads to the occurrence of various disorders. bZIP TF Sko1 or ATF/CREB is one of the common targets found in yeast as well as mammals against antifungal drug. The Sko1 homolog of *N.crassa,* ASL-1 (NCU01345), is an essential gene, required for ascospore viability. Studies conducted on the *Atf1* orthologs in other fungal taxa including *N. crassa*, *Aspergillus nidulans*, *Aspergillus fumigatus* and *Fusarium graminearum* has unravelled the versatile role of Atf1ranging from vegetative growth and development, coordination of stress response and secondary metabolism to virulence in pathogenic fungi. Studies have reported that Atf1 orthologs orchestrate environmental stress response of fungi. **Our primary focus is to understand the mechanisms of transcriptional regulation of *asl-1* in *N. crassa.***

**Keywords: *asl-1*, Transcription factor, *N.crassa,* stress adaptation.**