Transcript Factors Associated with Disease Resistance in Plants and Their Potential for Crop Improvement

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Abstract: **Transcription factors have a variety of functions that vary depending on the organism. In vertebrates, transcription factors, for example, are directly responsible for growth, with various classes of factors acting in different tissues. Transcription factors are especially important during embryonic development, so specific factors are required for pluripotent embryonic stem cell differentiation. Other factors' activity must also be maintained for stem cells to preserve their ability to transform into any cell type and self-renew. In this paper we are surveying Transcription Factors which protect plants against pathogens.**

Keywords – Transcription factor; disease resistance; abotic stress, pathogens

I. INTRODUCTION

Transcription factors are a form of protein that reads and interprets the genetic "blueprint" contained in DNA. They bind to DNA and aid in the start of a gene transcription increase or decrease programme. Plant disease resistance works in two ways to protect plants from pathogens: pre-formed structures and chemicals, and immune system responses triggered by infection**.** [wiki].
Transcription factors (TFs) are key regulators of gene expression, modulating key aspects of plant function such as responses to environmental factors and hormones, as well as cell differentiation and organ development [Elamin et.al].Transcription factors may either activate or repress a gene's transcription, which is a key factor in determining whether a gene functions at any given time[cooper et.al].

Phytopathogenic microorganisms have a direct impact on crop plant survival and productivity. Transcription factors (TFs) play a key role in the body's response to biotic stresses like insect attack and pathogen infection. Many TF families have previously been identified as differentially expressed in plants in response to bacterial, fungal, and viral infection in the face of such adversity. Recent advances in understanding the structure, function, signal regulation, and interaction of transcription factors with other proteins in response to pathogens are highlighted in this study. Because of their abundance, we concentrate on three transcription factor families: ERF, bZIP, and WRKY[Feng et.al].

II. TRANSCRIPT FACTORS ASSOCIATED WITH DISEASE RESISTANCE

AP2/ERF: Because of their ability to react to multiple stimuli and control various stresses, AP2/ERFs may form a more complex stress response network. Abiotic stresses cause AP2/ERFs to react in different ways: some are induced quickly and constantly, while others are controlled by prolonged stress, implying that they may have reciprocal influence on each other's work [Xieet.al].

The basic leucine zipper (bZIP) gene family is one of the most important transcription factor families in plants, with members involved in a variety of biological processes including light signalling, seed maturation, flower growth, and abiotic and biotic stress responses[wang et.al. The Arabidopsis genome sequence includes 75 different members of the bZIP family, with around 50 of them being new to science. The AtbZIP family can be divided into ten classes using common domains. We address the interacting proteins and study the
available data on bZIP functions in the sense of subgroup membership. This is needed for a complete functional characterization of bZIP transcription
factors in plants, as well as the identification of functional redundancies among AtbZip transcription factors [Jacoby et.al]

TF	Resistance Against	REFERENCE
AP2/ERF	Disease Resistance	[7,11]
BZIP	Disease Resistance	[7,11,14]
WRKY	Disease Resistance	[5,7,11,16]
NAC	Disease Resistance	[6,7,11,17]
BHLP	Disease Resistance	[6,7,11]
MYB	Disease Resistance	[6,7,11]
Tri-Helix	Disease Resistance	[7,11]
TGA	Disease Resistance	[7,8,11]
RAV	Disease Resistance	[7,9,11]
EMT	Disease Resistance	[7,10,11]

Table 1: Transcript Factors associated with disease resistance.

One of the largest families of transcriptional regulators found exclusively in plants is the WRKY transcription factors. They play a variety of roles in plant disease resistance, abiotic stress responses, nutrient deficiency,

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senescence, seed and trichome growth, embryogenesis, and other hormone-controlled developmental and hormonal processes. In different homo- and heterodimer combinations, WRKYs may serve as transcriptional activators or repressors[Bhakshi et.al].

NAC transcription factors (NAM, ATAF1,2, and CUC2) are one of the largest transcription factor families found in plants, and they play a role in a variety of developmental and signalling processes. The basic genomic, biochemical, and evolutionary specifics of NAC TFs have not been identified, despite the availability of detailed genomic information from a variety of plant species. NAC TFs also encode many novel chimeric proteins and control a complex interactome network, according to the findings. Several NAC proteins were discovered to encode other functional signature motifs in addition to the NAC domain[Mohantha et.al] .

III. IDENTIFICATION OF TRANSCRIPTION FACTOR CONTEXTS IN LITERATURE USING MACHINE LEARNING APPROACHES

Various machine learning techniques are used for identification of Transcription factors [Yang et.al] In the literature, a text-classification system is designed to automatically recognise contexts relevant to transcription factors. A learning model is built around a collection of biological features (such as protein and gene names, interaction words, and other biological terms) that are thought to be important to the task. To engineer such features, we used context information from established biological resources (MeSH and GO). Training datasets that are both weak and noisy have been established. Three machine-learning methods, as well as a vote-based merging of individual approaches and/or separate training datasets, are examined. The system produced highly promising results, with a 90% accuracy rate.

At the genome-scale, this workflow [Yayego et.al] included numerical prediction, knowledge-based classification, and experimental validation of candidate TFs .TFpredict is a machine learning algorithm that predicts whether a protein is a TF based on sequence homology.

DeepTFactor is a deep learning-based platform that uses protein sequences as inputs to predict transcription factors. DeepTFactor's reasoning mechanism was deciphered, indicating that DeepTFactor studied DNA-binding domains of TFs inherently. DeepTFactor predicted 332 TFs in E. coli K-12 MG1655, three of which were experimentally validated using ChIP-exo experiments to classify genome-wide binding sites.

Liu et.al addressed by combining the Cox PH model with the random forest algorithm, a groundbreaking process for selecting transcription factor variables and evaluating prognostic prediction power was developed. They chose the top five transcription factors and used Cox PH regression to build a prediction model.Validatedpredictive model using Kaplan-Meier analysis on four separate publicly accessible datasets (GSE39582, GSE17536,

GSE37892, and GSE17537) from the GEO database, which included 925 colon cancer patients.

XGBoost was applied to build a classifier that predict TFs that prefer methylated DNA[Meng et.al]

Using machine learning algorithms, researchers [Rostam et.al] developed a simple and fast imaging-based method for identifying different macrophage functional phenotypes based on cell size and morphology. Fluorescent microscopy was used to examine the morphology of various cell types, which were stained with DAPI and phalloidin for nucleus and actin distribution, respectively. We were able to effectively classify M1 and M2 phenotypes by analysing their morphology alone, and we were able to differentiate them from naive macrophages and monocytes with an average accuracy of 90%.

IV . CONCLUSION

This paper summarizes the transcript factors associated against pathogens and machine learning algorithms used in identification of transcript factors.

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