

# Chaetocin Affect Photosynthesis of *Nicotiana tabacum* under Abiotic Stress

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## ABSTRACT

Epigenetic regulation of gene expression plays an important role in plant growth, development, and response to abiotic stresses. Due to increasing pollution and global warming, the environmental condition is getting worse for living organisms and plants. The growth and productivity of crop plants worldwide are severely affected by abiotic stress conditions. In present study, we have studied the effect of histone methyltransferase inhibitor chaetocin in tobacco plant under different abiotic stresses like drought, cold, and salinity. In our present study, we have found that photosynthesis is lowered in control plants by chaetocin under abiotic stresses in the presence of chaetocin. Our study will help understand the epigenetic regulation of photosynthesis and identify stress-responsive genes to understand the mechanism that reduces crop yield.

**Keywords:** Abiotic stress, Chaetocin, Histone methyltransferase.

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## INTRODUCTION

**S**tress in plants refers to any external condition that is not ideal for its growth. Due to sessile nature, plants have to deal with these external environmental conditions that are changing continuously. Stress in plants can lead to a reduction in their growth, damage them or result in death. These stress conditions pose a severe threat for agriculture crops as the crop yield decreases significantly (Wang *et al.*, 2003; Wania *et al.*, 2016). Abiotic stress consists of different environmental conditions like high temperature, cold, light, salinity, deficit or excessive water, radiation, etc. Due to increasing pollution and global warming, the environmental condition is getting worse for living organisms and plants. Growth and productivity of crop plants worldwide are severely affected by abiotic stress conditions. Plants response to abiotic stress is a complex process (Skurycz *et al.*, 2010; Cramer *et al.*, 2010), resulting in temporary or permanent changes in plant physiology. Abiotic stress response in plants is interconnected and occurs in expression changes in number of genes. Our present study uses histone modification inhibitors to study plant physiology concerning gas exchange parameters i.e. photosynthesis, transpiration, and water use efficiency.

Epigenetic regulation of gene expression consists of DNA methylation and post-translational histone modifications. Histone modifications consist of acetylation, methylation, ubiquitylation, sumoylation of lysine and arginine residues (Strahl and Allis, 2000). In this study, we focused on histone methylation which was discovered in 1960 at the  $\alpha$ -amino group of lysine residue in histone protein (Allfrey and Mirsky, 1964; Murray, 1964). Histone methylation on lysine residue can be mono-, di-, tri-methylated, whereas methylation on arginine residue can be mono-, di-methylation symmetrical or dimethylation asymmetrical (Greer and Shi, 2012). Histone methylation on lysine is tightly regulated by methyltransferases (KMTs) and demethylases (KDMs). First histone KMT (KMT1A) was discovered in the year 2000 by Thomas Jenuwein and coworkers (Rea *et al.*, 2000). KMTs contain an enzymatic SET domain made up of 130 amino acids and are the largest among

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the two KMTs family (Dillon *et al.*, 2006). The KMTs does not contain SET domain (v. 3.2.1). Both the KMTs class of enzymes uses S-adenosyl methionine as the methyl group donor (Dillon *et al.*, 2006). KMTs are specific in lysine methylation.

On the other hand the first histone demethylase KDM1A was discovered by Yang Shi and David Allis (2003) and contain Flavin adenine dinucleotide dependent amine oxidase domain for demethylase activity. Other classes of demethylases were also observed like Jumonji C (Jumonji C) and JmjN domain (Shi and Allis, 2006).

Chaetocin is a fungal metabolite from *Chaetomium* with antimicrobial and cytostatic activity. It is a molecular dimer of two five-membered rings. It is a competitive inhibitor of S-adenosyl methionine, an inhibitor for lysine-specific methyltransferase. It is a compound useful in epigenetic gene regulation (Rea *et al.*, 2006). Chaetocin is specific for S-adenosyl methionine histone H3 at lysine 9 and is best suited for studying mediated gene silencing (Greiner *et al.*, 2006). In our study we have used Chaetocin to study the effect of histone methylation on the physiology of plants under abiotic stresses. This study will help understand the mechanism that reduces crop yield and about how epigenetic regulation of gene expression affects plant physiology and their response in abiotic stress.