



Editorial Note on Antisense Transcripts of *MIR398* Genes Suppress *MicroR398* processing and Attenuate Plants

Glory Thomas

Department of Biotechnology, North-Western University, USA

*Corresponding Author's E-mail: agriscience.7@gmail.com

EDITORIAL

MiRNAs (microRNAs) are small RNAs that repress the expression of their target genes at post-transcriptional levels¹. In plants, appropriate miRNA accumulation depends on the activity of the nuclear proteins HYPONASTIC LEAVES1 (HYL1), DICER-LIKE1 (DCL1), SERRATE (SE), and AGONAUTE1 (AGO1). These proteins are thought to function together to catalyze the processing of Pri-miRNAs and pre-miRNAs. In the study reported here, We Endeavored to know the molecular relationship between MIRNA genes and their cis-NATs in miRNA processing and gene regulation in response to heat. Functional analysis indicated that the processing of pri-miR398b/c is suppressed by their cis-NATs. This finding provides insight into the function of cis-NATs in miRNA-guided gene silencing and will thus facilitate the genetic manipulation of organic phenomenon for Thermotolerance in eukaryotes.

Nearly all nonlethal mutants of DCL1, HYL1, and SE display multiple morphological, physiological, and biochemical aberrations⁸. Theoretically, the pleiotropic effects of DCL1, HYL1, and SE mutations are due to the reduced accumulation of miRNAs and increased expression of miRNA-directed targets. Because miRNAs can silence their target genes¹⁰, MIRNA genes and artificial miRNAs are broadly used for identification of gene function in plants and for genetic manipulation of agricultural traits for top yield and quality. For unknown reasons, however, these MIRNA genes frequently don't add many plants. The pandemic

has featured imbalances in our social orders, supply chains and markets. A few nations and organizations have been more earnestly hit by the pandemic. Also, changes to review approaches can make it significantly harder for organizations in lower pay nations.

Natural antisense transcripts (NATs), a category of RNAs containing sequences complementary to sense mRNAs, comprise a group of prominent and sophisticated regulatory RNAs. Recent genomic studies using computational prediction methods and experimental identification approaches have revealed an outsized number of NATs. NATs are often divided into cis-NATs, which are transcribed from opposing DNA strands at an equivalent genomic locus, and trans-NATs, which are transcribed from separate genomic loci. Cis-NATs successively are often categorized into three types: convergent (3'-end overlap), divergent (5'-end overlap), and enclosed (one transcript encompassing the other). Studies have revealed that cis-NATs can participate during a broad range of regulatory events. Evidence has been uncovered for the involvement of cis-NATs in translation initiation mRNA stability transcription termination alternative splicing RNA editing DNA methylation histone methylation small interfering RNA (siRNA)-induced gene silencing and translational enhancement have shown that antisense transcription is related to miRNA-targeted mRNAs in Arabidopsis. Albeit several cis-NATs are known to require part in gene regulatory events, the role of the many cis-NATs is unclear.