

## ■ РЕФЕРАТИ СТАТЕЙ, ОПУБЛІКОВАНИХ В «CYTOLOGY AND GENETICS», № 5, 2022 р.

### CPG METHYLATION OF THE PROXIMAL PROMOTER REGION REGULATES THE EXPRESSION OF NAC6D GENE IN RESPONSE TO HIGH TEMPERATURE IN WHEAT (*TRITICUM AESTIVUM*)

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*Methylation of DNA promoter sequences at the CpG islands has become a molecular tool for gene regulation. NAC6D gene is induced by different biotic and abiotic stimuli. The proximal promoter sequence of NAC6D was investigated for the impact of CpG methylation on its expression in response to high temperature in wheat. Gene expression was estimated by real time PCR and methylation of NAC6D promoter sequence was investigated by bisulfite sequencing. Results showed that NAC6D was highly induced by high temperature, whereas DNA methyltransferase 3 (Met3) was highly reduced by high temperature. Close investigation of NAC6D promoter methylation revealed that high temperature caused hypomethylation of the proximal promoter sequence. Twelve CpG sites showed low difference in methylation compared to the control (normal temperature, 25 °C), while 3 CpGs (-59, -169, -204) were extremely hypomethylated in response to high temperature compared to their methylation status under the normal condition. The induction of NAC6D was negatively correlated with Met3 suppression and methylation level at the CpG sites in the promoter region. Results prove that methylation greatly contribute to the regulation of NAC6D in response to high temperature. This will improve our current understanding of how plants respond to abiotic stresses at the molecular level and the integration of DNA methylation and epigenetics in the next generation plant breeding.*

**Key words:** NAC6D, promoter, methylation, CpG, Wheat, epigenetic, DNA methyltransferases, epialleles.

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### РЕГУЛЯЦІЯ ЕКСПРЕСІЇ ГЕНУ NAC6D У ПШЕНИЦІ (*TRITICUM AESTIVUM*) ШЛЯХОМ МЕТИЛЮВАННЯ СРГ ДІЛЯНКИ ПРОКСИМАЛЬНОГО ПРОМОТЕРА ЯК РЕАКЦІЯ НА ВИСОКІ ТЕМПЕРАТУРИ

Метилування промоторних послідовностей ДНК у СpG острівцях стало молекулярним інструментом генної регуляції. Ген NAC6D зазнає впливу різних біотичних та абіотичних факторів. Послідовність проксимального промотора NAC6D вивчали для встановлення впливу метилування СpG на його експресію як реакцію пшениці на високі температури. Експресію генів оцінювали за допомогою ПЛР у реальному часі, а метилування послідовності промотора NAC6D досліджували за використання бісульфітного секвенування. Результати продемонстрували, що за впливу високої температури відбувалась значна індукція NAC6D та суттєве зменшення ДНК-метилтрансферази 3 (Met3). Детальне вивчення метилування промотора NAC6D показало, що висока температура спричиняла гіпометилування послідовності проксимального промотора. Дванадцять ділянок СpG продемонстрували меншу різницю щодо метилування порівняно з контролем (нормальна температура, 25 °C), а 3 СpG (-59, -169, -204) були суттєво гіпометильованими у відповідь на високі температури порівняно з їхнім статусом метилування за нормальних умов. Індукція NAC6D мала негативну кореляцію з рівнем пригнічення та метилування Met3 в СpG острівцях у ділянці промотора. Результати доводять, що метилування здійснює значний вплив на регуляцію NAC6D у відповідь на високі температури. Ці дані поглиблюють наші поточні знання про те, як рослини реагують на абіотичні стреси на молекулярному рівні та на інтеграцію метилування ДНК і епігенетики у селекцію рослин наступного покоління.

**Ключові слова:** NAC6D, промотор, метилування, СpG, пшениця, епігенетичний, метилтрансферази ДНК, епіалелі.

#### REFERENCES

- Akimoto K, Katakami H, Kim H et al. (2007) Epigenetic inheritance in rice plants *Ann Bot* 100(2):205–217. doi: 10.1093/aob/mcm110  
Alotaibi S, El-Shehawi AM, Elseehy MM. (2020). Heat

- shock proteins expression is regulated by promoter CpG methylation/demethylation under heat stress in wheat varieties Pakistan J Biol Sci 23(10):1310–1320. doi: 10.3923/pjbs.2020.1310.1320
- Becker C, Weigel D. (2012) Epigenetic variation: origin and transgenerational inheritance Cur Opin Plant Biol 15(5):562–567. doi: 10.1016/j.pbi.2012.08.004.
- Berdasco M, Alcázar R, Garcíá-Ortiz MV et al. (2008) Promoter of DNA Hypermethylation and Gene Repression in Undifferentiated Arabidopsis Cells PLoS ONE 3(10):e3306. doi: 10.1371/journal.pone.0003306
- Bird A. (2002) DNA methylation patterns and epigenetic memory Genes Develop 16(1):6–21. doi: 10.1101/gad.947102
- Bräutigam K, Vining KJ, Lafon-Placette C et al. (2013) Epigenetic regulation of adaptive responses of forest tree species to the environment Ecol Evol 3(2):399–415. doi: 10.1002/ece3.461
- Bucherna N, Szabo E, Heszky LS et al. (2001) DNA methylation and gene expression differences during alternative *in vitro* morphogenic processes in eggplant (*Solanum melongena* L.) *In vitro* Cellular and Developmental Biology-Plant 37:672–677. <https://doi.org/10.1007/s11627-001-0117-8>
- Carr IM, Valleley EMA, Cordery SF et al. (2007) Sequence analysis and editing for bisulphite genomic sequencing projects Nucl Acids Res 35(10):e79. doi: 10.1093/nar/gkm330
- Chan SW, Henderson IR, Jacobsen SE. (2005) Gardening the genome: DNA methylation in Arabidopsis thaliana Nat Rev Genet 6(5):351–360. doi: 10.1038/nrg1601
- Colaneri AC, Jones AM. (2013) Genome-wide quantitative identification of DNA differentially methylated sites in Arabidopsis seedlings growing at different water potential PLoS One 8(4):e59878. doi: 10.1371/journal.pone.0059878
- Conrath U. (2011) Molecular aspects of defence priming Trends in Plant Sci 16(10):524–531. doi: 10.1016/j.tplants.2011.06.004
- Dai Y, Nil Z, Dai J et al. (2005) Isolation and expression analysis of genes encoding DNA methyltransferase in wheat (*Triticum aestivum* L.) Biochim Bioph Acta 1729(2):118–125. doi: 10.1016/j.bbaexp.2005.04.001
- Demeulemeester M, Van Stallen N, De Proft M. (1999) Degree of DNA methylation in chicory (*Cichorium intybus* L.): influence of plant age and vernalization Plant Sci 142(1):101–108
- Deng S, Dai H, Arenas C et al. (2014) Transcriptional Silencing of Arabidopsis Endogenes by Single-Stranded RNAs Targeting the Promoter Region Plant Cell Physiol 55(4):823–833. doi: 10.1093/pcp/pcu025
- El-Shehawi A. (2020). Heat Shock Proteins Expression Is Regulated by Promoter CpG Methylation/demethylation under Heat Stress in Wheat Varieties. Pakistan J Biol Sci PJBS 23(10):1310–1320
- El-Shehawi AM, Fahmi AI, Elseehy MM, Nagaty HA. (2013). Enhancement of nutritional quality of wheat (*Triticum aestivum*) by metabolic engineering of isoflavone pathway Amer J Biochem Biotechnol 9(4): 404–414
- Elseehy MM. (2020). Differential transgeneration methylation of exogenous promoters in T1 transgenic wheat (*Triticum aestivum*) Cytol Genet 54(5):493–504
- Elseehy, M. M., & El-Shehawi, A. M. (2018). Expression Profile of Wheat DNA Methyltransferases Genes in Egyptian Wheat (*Triticum Aestivum*) Varieties Under PEG Induced Dehydration. Alexandria Science Exchange Journal, 39(OCTOBER-DECEMBER), 695-701.
- Elseehy MM, El-Shehawi AM. (2020). Methylation of exogenous promoters regulates soybean isoflavone synthase (GmIFS) transgene in T0 transgenic wheat (*Triticum aestivum*). Cytol Genet 54(3):12. <https://doi.org/10.3103/S0095452720030032>
- Fedoroff NV. (2012) Presidential address. Transposable elements, epigenetics, and genome evolution. Science. 338(6108):758–67. doi: 10.1126/science.338.6108.758.
- Guérin C, Roche J, Allard V et al. (2019) Genome-wide analysis, expansion and expression of the NAC family under drought and heat stresses in bread wheat (*T. aestivum* L.) PLoS One 14(3):e0213390. doi: 10.1371/journal.pone.0213390
- Guo W, Zhang J, Zhang N et al. (2015) The wheat NAC transcription factor tanac21 is regulated at the transcriptional and post-translational levels and promotes heat stress tolerance in transgenic Arabidopsis PLoS ONE 10(8):e0135667. doi:10.1371/journal.pone.0135667
- Han S, Wagner D. (2014) Role of chromatin in water stress responses in plants J Exp Bot 65(10):2785–2799. doi: 10.1093/jxb/ert403
- Hauben M, Haesendonckx B, Standaert E et al (2009) Energy use efficiency is characterized by an epigenetic component that can be directed through artificial selection to increase yield Proc Natl Acad Sci USA 106(47):20109–20114. doi: 10.1073/pnas.0908755106
- Heilersig BHJB, Loonen AEHM, Janssen EM et al. (2006) Efficiency of transcriptional gene silencing of GBSSI in potato depends on the promoter region that is used in an inverted repeat Mol Gen Genom 275(5):437–449. doi: 10.1007/s00438-006-0101-4
- Ikeuchi M, Iwase A, Sugimoto K. (2015) Control of plant cell differentiation by histone modification and DNA methylation Curr Opin Plant Biol 28:60–67. doi: 10.1016/j.pbi.2015.09.004

- Jones L, Ratcliff F, Baulcombe DC. (2001) RNA-directed transcriptional gene silencing in plants can be inherited independently of the RNA trigger and requires Met1 for maintenance *Curr Biol* 11(10):747–757. doi: 10.1016/s0960-9822(01)00226-3
- Kathiria P, Sidler C, Golubov A et al. (2010) Tobacco mosaic virus infection results in an increase in recombination frequency and resistance to viral, bacterial, and fungal pathogens in the progeny of infected tobacco plants *Plant Physiol* 153(4):1859–1870. doi: 10.1104/pp.110.157263
- Law JA, Jacobsen SE. (2010) Establishing, maintaining and modifying DNA methylation patterns in plants and animals *Nat Rev Genet* 11(3):204–220. doi: 10.1038/nrg2719
- Li Y, Tollefsbol TO. (2011) DNA methylation detection: Bisulfite genomic sequencing analysis *Methods Mol Biol* 791:11–21. doi: 10.1007/978-1-61779-316-5\_2
- Lira-Medeiros CF, Parisod C, Fernandes RA et al. (2010) Epigenetic variation in mangrove plants occurring in contrasting natural environment *PLoS One* 5(4):e10326. doi: 10.1371/journal.pone.0010326
- Livak KJ, Schmittgen TD. (2001) Analysis of relative gene expression data using real-time quantitative PCR and the 2<sup>-</sup>(-Delta Delta C(T)) *Meth Meth*. 25(4):402–408. doi: 10.1006/meth.2001.1262
- Lopez CMR, Wilkinson MJ. (2015) Epi-fingerprinting and epi-interventions for improved crop production and food quality. *Front. Plant Sci.* 6:397. doi: 10.3389/fpls.2015.00397
- Lu M, Sun QP, Zhang DF et al. (2015) Identification of 7 stress-related NAC transcription factor members in maize (*Zea mays* L.) and characterization of the expression pattern of these genes *Biochem Biophys Res Commun* 462(2):144–1450. doi: 10.1016/j.bbrc.2015.04.113
- Matzke MA, Primig M, Trnovsky J et al. (1989) Reversible methylation and inactivation of marker genes in sequentially transformed tobacco plants *EMBO J* 8(3):643–649. PMID: 16453872
- Moyano E, Martínez-Rivas FJ, Blanco-Portales R et al. (2018) Genome-wide analysis of the NAC transcription factor family and their expression during the development and ripening of the *Fragaria × ananassa* fruits *PLoS One* 13(5):e0196953. doi: 10.1371/journal.pone.0196953
- Nakashima K, Takasaki H, Mizoi J et al. (2012) NAC transcription factors in plant abiotic stress responses *Biochim Biophys Acta* 1819(2):97–103. doi: 10.1016/j.bbagr.2011.10.005
- Nuruzzaman M, Manimekalai R, Sharoni AM et al. (2010) Genome-wide analysis of NAC transcription factor family in rice *Gene* 465(1–2):30–44. doi: 10.1016/j.gene.2010.06.008
- Pinheiro GL, Marques CS, Costa MDBL et al. (2009) Complete inventory of soybean NAC transcription factors: Sequence conservation and expression analysis uncover their distinct roles in stress response *Gene*. 444(1–2):10–23. doi: 10.1016/j.gene.2009.05.012
- Qin D, Wu H, Peng H et al. (2008) Heat stress-responsive transcriptome analysis in heat susceptible and tolerant wheat (*Triticum aestivum* L.) by using Wheat Genome Array *BMC Genomics* 9:432. doi: 10.1186/1471-2164-9-432
- Saidi MN, Mergby D, Brini F. (2017) Identification and expression analysis of the NAC transcription factor family in durum wheat (*Triticum turgidum* L. ssp. durum) *Plant Physiol Bioche* 112:117–128. doi: 10.1016/j.plaphy.2016.12.028
- Saze H, Tsugane K, Kanno T et al. (2012) DNA methylation in plants: relationship to small RNAs and histone modifications, and functions in transposon inactivation *Plant and Cell Physiol* 53(5):766–784. doi: 10.1093/pcp/pcs008
- Song Q, Zhang T, Stelly DM et al. (2017) Epigenomic and functional analyses reveal roles of epialleles in the loss of photoperiod sensitivity during domestication of allotetraploid cottons *Genome Biol* 18(1):99. doi: 10.1186/s13059-017-1229-8
- Suzuki MM, Bird A. (2008) DNA methylation and landscapes: provocative insights from epigenomics *Nat Rev Genet* 9(6):465–476. doi: 10.1038/nrg2341
- Takatsuka H, Umeda M. (2015) Epigenetic Control of Cell Division and Cell Differentiation in the Root Apex *Front Plant Sci* 6:1178. doi: 10.3389/fpls.2015.01178
- Takuno S, Gaut BS. (2012) Body-methylated genes in *Arabidopsis thaliana* are functionally important and evolve slowly *Mol Biol Evol* 29(1):219–227. doi: 10.1093/molbev/msr188
- Tolley BJ, Woodfield H, Wanchana S. (2012) Light-regulated and cell-specific methylation of the maize PEP promoter *J Experim Bot* 63(3):1381–1390. doi: 10.1093/jxb/err367
- Tricker PJ, Lopez CM, Gibbings G et al. (2013) Transgenerational, dynamic methylation of stomata genes in response to low relative humidity *International J Mol Sci* 14(4):6674–6689. doi: 10.3390/ijms14046674
- Uauy C, Distelfeld A, Fahima T et al. (2006) NAC Gene Regulating Senescence Improves Grain Protein, Zinc and Iron Content in Wheat *Sci* 314(5803):1298–1301. doi: 10.1126/science.1133649
- Wang WS, Pan YJ, Zhao XQ et al. (2011) Drought-induced site-specific DNA methylation and its association with drought tolerance in rice (*Oryza sativa* L.) *J Experim Bot* 62(6):1951–1960. doi: 10.1093/jxb/erq391
- Wei X, Song X, Wei L et al. (2017) An epiallele of rice

- AK1 affects photosynthetic capacity J Integr Plant Biol 59(3):158–163. doi: 10.1111/jipb.12518
- Yaish MW. (2017) Epigenetic modifications associated with abiotic and biotic stresses in plants: an implication for understanding plant evolution Front Plant Sci 8:1983. doi: 10.3389/fpls.2017.01983
- Yaish MW, Al-Lawati A, Al-Harrasi I et al. (2018) Genome-wide DNA methylation analysis in response to salinity in the model plant caliph medic (*Medicago truncatula*) BMC Genomics 19(1):78. doi: 10.1186/s12864-018-4484-5
- Yong-Villalobos L, González-Morales SI, Wrobel K et al. (2015) Methylome analysis reveals an important role for epigenetic changes in the regulation of the Arabidopsis response to phosphate starvation Proc Natl Acad Sci 112(52):E7293–302. doi: 10.1073/pnas.1522301112
- Zilberman D. (2017) An evolutionary case for functional gene body methylation in plants and animals Genome Biol 18(1):87. doi: 10.1186/s13059-017-1230-2

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