METHYLATION OF EXOGENOUS PROMOTERS REGULATES SOYBEAN ISOFLAVONE SYNTHASE (GMIFS) TRANSGENE IN T0 TRANSGENIC WHEAT (*TRITICUM AESTIVUM*)

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DNA methylation is one epigenetic strategy for gene regulation in living organisms. In this study, the expression of soybean isoflavone synthase (GmIFS) transgene in T0 transgenic wheat plants was investigated at the RNA and the final product genestin level. T0 plants showed variations in the GmIFS expression. Methylation status of the exogenous promoters (35S or Oleocin (OL)) proximal sequence was investigated in T0 plants using bisulphite sequencing to disclose their methylation in parallel with the GmIFS level of expression. Results concluded that the high GmIFS expressers of T0 plants exhibited high methylation of exogenous promoter proximal sequences as well as low expression of DNA methyltransferases (Mets). Variation in GmIFS was associated with the level of methylation in the 35S or OL promoters. High expression of GmIFS was negatively correlated with methylation level of 35S and OL promoter proximal regions. In 35S promoter, methylation level of the CpG sites −56 and −88 is strongly linked to GmIFS expression and is involved in the regulation of GmIFS gene. In OL promoter, the CpG site could be involved in the regulation of the GmIFS. Wheat Met3 expression varied among T0 transgenic plants. Its expression profile could explain the regulation of GmIFS transgene by methylation.

Key words: Transgenic, Wheat, Epigenetic, Methylation, Promoter, DNA methyltransferase.

МЕТИЛЮВАННЯ ЕКЗОГЕННИХ ПРОМОТЕРІВ РЕГУЛЮЄ ТРАНСГЕН СИНТАЗИ ІЗОФЛАВОНУ СОЇ (GMIFS) У ТРАНСГЕННІЙ ПШЕНИЦІ T0 (*TRITICUM AESTIVUM*)

Метилювання ДНК – це одна з епігенетичних стратегій регуляції генів у живих організмах. У цьому дослідженні було проведено вивчення експресії трансгену синтази ізофлавону сої (GmIFS) у T0 рослинах трансгенної пшениці на рівні РНК та рівні геністину у кінцевому продукті. T0 рослини продемонстрували відмінності експресії GmIFS. Статус метилювання проксимальних послідовностей екзогенних промотерів (35S або олеозин (OL)) у T0 рослинах досліджували за використання бісульфітного секвенування з метою виявлення їхнього метилювання одночасно з рівнем експресії GmIFS. Результати продемонстрували, що значні експресори GmIFS T0 рослин мали високий рівень метилювання проксимальних послідовностей екзогенного промотера, а також низький рівень експресії метилтрансфераз ДНК (Mets). Відмінності в GmIFS були пов'язані з рівнем метилювання в промотерах 35S або OL. Високий рівень експресії GmIFS мав негативну кореляцію з рівнем метилювання проксимальних ділянок промотера 35S і OL. У промотері 35S рівень метилювання сайтів CpG −56 і −88 суттєво пов'язаний з експресією GmIFS і залучений до регуляції гену GmIFS. У промотері OL сайт CpG може бути залучений до регуляції GmIFS. Експресія Met3 пшениці була різною для різних T0 трансгенних рослин. Можливо, профіль її експресії пояснює регуляцію трансгену GmIFS шляхом метилювання.

Ключові слова: трансгенний, пшениця, епігенетичний, метилювання, промотер, метилтрансфераза ДНК.

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