

EFFECTS OF DNA METHYLATION ON THE DEVELOPMENT OF SOYBEAN SEEDLINGS (GLYCINE MAX L. MERR.)

III Simpósio Internacional de Atualização em Genética e Melhoramento de Plantas, 0^a edição, de 24/05/2021 a 26/05/2021
ISBN dos Anais: 000

COELHO; Fernanda Silva¹, SANGI; Sara², MORAES; Juliana³, BALLESTEROS; Helkin Giovanni Forero⁴,
HEMERLY; Adriana⁵, GRATIVOL; Clícia⁶

RESUMO

DNA methylation is an important epigenetic mechanism that regulates several plant development processes. Some studies have shown that DNA methylation plays a central role in genome organization, imprinting, transposon silencing, and regulation of gene expression. Despite previous studies related to the methylation profile in soybean, there are no studies on the effect of this epigenetic mechanism on the development of soybean seedlings. Thus, this work aimed to evaluate the effect of DNA methylation on the development of soybean seedlings treated with methylation inhibitors. Soybean seedlings were grown for 7 days in tubes with MS $\frac{1}{2}$ force medium containing the methylation 5-azacytidine inhibitor (100 μ M) arranged in DIC in the BOD. Phenotypic and biochemical analyses of the shoot and the root were performed. We also analyze the root structure and measure the chlorophyll concentration in the leaves. The treatment with methylation inhibitor caused length reductions in the length of the shoot and roots, also in fresh mass, and in dry mass only in the roots. However, there was no difference between the dry mass of the shoot between the control and the treated. Surprisingly, the shoots and roots treated with inhibitor have higher biomass compared to control seedlings. Seedling leaves treated with inhibitor have a reduction in the content of chlorophyll *a*, *b*, and carotenoids, which suggests a reduction in photosynthetic efficiency. There is a higher concentration of proteins and triglycerides in the aerial part and root of the tract than in the control. The analysis of the root meristem showed variation in the size of the nuclei in the columella region and the cap region of the treated seedling concerning the control. The data obtained so far, suggest that DNA methylation plays an important role in the regulation of cell division, which influences the correct development of soybean.

PALAVRAS-CHAVE: epigenetic marks, soybean root, cell division

¹ Universidade Estadual do Norte Fluminense Darcy Ribeiro, fernandacoelho.cederj@gmail.com

² Universidade Estadual do Norte Fluminense Darcy Ribeiro, sarasm.sangi@gmail.com

³ Universidade Estadual do Norte Fluminense Darcy Ribeiro, julianalopesmoraes16.6@gmail.com

⁴ Universidade Federal do Rio de Janeiro, helfos85@gmail.com

⁵ Universidade Federal do Rio de Janeiro, hemerly.adriana@gmail.com

⁶ Universidade Estadual do Norte Fluminense Darcy Ribeiro, cgrativol@uenf.br