



Epigenetic modifications are required for herbicide detoxification in Arabidopsis thaliana

Catarine Markus¹, Viviane Rostirola Elsner², Giliardi Dalazen³, Alexandre Pisoni⁴, Ales Pecinka⁵, Aldo Merotto Junior⁶

Federal University of Rio Grande do Sul, Porto Alegre, RS, Brazil¹, Centro Universitário Metodista, Porto Alegre, RS, Brazil², Federal University of Rio Grande do Sul, Porto Alegre, RS, Brazil³, Federal University of Rio Grande do Sul, Porto Alegre, RS, Brazil⁴, Max Planck Institute for Breeding Research, Cologne, NRW, Germany⁵, Federal University of Rio Grande do Sul, Porto Alegre, RS, Brazil⁶

Epigenetic regulation includes DNA methylation and histone modifications, which are important for plant development and stress mitigation. Currently this mechanism is hypothesized to be involved with herbicide resistance. The aim of this study is to evaluate whether herbicides can cause epigenetic changes that may be important for evolution of herbicide resistance. Two specific experiments for epigenetics analysis were carried out using Arabidopsis thaliana. The herbicides used were imazethapyr, glyphosate and 2,4-D at sublethal doses of 11, 72 and 81 g ha⁻¹, respectively. The first experiment was performed with *A. thaliana* L5 and heat stress was used as positive control. The second experiment was performed with 15 different mutants associated with specific pathways of epigenetic modifications and the wild type Col-0 (WT). The mutant that presented biggest change in herbicide susceptibility compared to WT was used for RNA-seq analysis, performed 48 hours after herbicide application. Herbicide treatments led to global modifications of DNA methylation, lower than heat stress. Some mutants affected in DNA and specific histone methylation modifications presented changing in herbicide susceptibility. The ros1 mutant showed 20-30% (P <0.01) increase in susceptibility to imazethapyr compared to WT. ROS1 (REPRESSOR OF SILENCING 1) is a 5methylcytosine glycosylases that is a repressor of transcriptional gene silencing. Thus, in ros1 genes that are important for herbicide detoxification may be not expressed, increasing the herbicide susceptibility. In fact, the analysis of RNA-seq showed 66 genes high expressed in WT and low expressed in ros1. Some of these genes are putative involved with herbicide detoxification. The results indicate that the evaluated herbicides can change specific epigenetics pathways. This is promising to understanding the evolution of herbicide resistance as well as the regulation of current processes of resistance still not completely understood.

Palavras-chave: Epigenetics, DNA methylation, herbicide susceptibility, imazethapyr