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The Transcriptome of Carnation (Dianthus Caryophyllus) of Elicited Cells with Fusarium Oxysporum f.sp. Dianthi

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Abstract : Carnation (Dianthus caryophyllus) is one of the most important products of exportation in the floriculture industry worldwide. Fusariosis is the disease that causes the highest losses on farms, in particular the one produced by Fusarium oxysporum f.sp. dianthi, called vascular wilt. Gene identification and metabolic routes of the genes that participate in the building of the plant response to Fusarium are some of the current targets in the carnation breeding industry. The techniques for the identifying of resistant genes in the plants, is the analysis of the transcriptome obtained during the host-pathogen interaction. In this work, we report the cell transcriptome of different varieties of carnation that present differential response from Fusarium oxysporum f.sp. dianthi attack. The cells of the different hybrids produced in the outbreeding program were cultured in vitro and elicited with the parasite in a dual culture. The isolation and purification of mRNA was achieved by using affinity chromatography Oligo dT columns and the transcriptomes were obtained by using Illumina NGS techniques. A total of 85,669 unigenes were detected in all the transcriptomes analyzed and 31,000 annotations were found in databases, which correspond to 36.2%. The library construction of genic expression techniques used, allowed to recognize the variation in the expression of genes such as Germin-like protein, Glycosyl hydrolase family and Cinnamate 4-hydroxylase. These have been reported in this study for the first time as part of the response mechanism to the presence of Fusarium oxysporum.

Keywords : Carnation, Fusarium, vascular wilt, transcriptome
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