IDENTIFICATION OF SOME MOLECULAR MARKERS ASSOCIATED WITH RESISTANCE OF SOME OILSEED RAPE CULTIVARS (*BRASSICA NAPUS* L.) AT THE PATHOGEN *VERTICILLIUM LONGISPORUM*

Mădălina - Cristina BURLACU (ARSENE)[1], Dănuţ-Petru SIMIONIUC[1], Florin Daniel LIPŞA[1], Eduard LĂZĂRESCU[1]

e-mail: burlacucmadalina@yahoo.com

Abstract

Oilseed rape (*Brassica napus* L) is a relative young species which appeared a few hundred years ago through a spontaneous interspecific hybridization between cabbage (*Brassica oleracea* L.) and turnip rape (*Brassica rapa* L.) (Rygulla et.al., 2007). Among the main diseases that can affect the oilseed rape culture we can find also verticillium wilt caused by the pathogen *Verticillium longisporum.* The mycelium is colonizing the vascular system of the plant and cause his obstruction, so due to the water stress the plant can die. Because, until now there are no available approved chemicals to prevent this disease, the phytosanitary control of this disease can be realized by cultivating some resistant varieties. The aim of this study was utilization of the SSR markers to identify some resistance sources of oilseed rape to *Verticillium longisporum* pathogen attack. For this purpose we used a number of 130 oilseed rape cultivars which were artificially infected with the pathogen *V. longisporum*. For the molecular studies, we used 51 SSR markers which amplified a number of 139 specific fragments. Correlating the molecular data obtained after the SSR analysis and the phenotypic data obtained after the artificial infection, we identified 18 SSR markers associated with resistance to *V. longisporum.* This results are very important for the next studies regarding the breeding of oilseed rape, for the identification of the resistance genes to *V. longisporum*.

Key words: molecular markers, association, rezistance