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DEVELOPMENT OF EMS MUTAGENIZED SOYBEAN POPULATION FOR IDENTIFICATION OF *Phakopsora pachyrhizi* SUSCEPTIBILITY GENES / Desenvolvimento de uma população mutagenizada de soja para identificar genes que conferem suscetibilidade à *Phakopsora pachyrhizi*. V.M. STOCK¹; G. MARIN-RAMIREZ¹; T.C. BROMMONSCHENKEL¹; S.H. BROMMONSCHENKEL¹. ¹Dept. Of Plant Pathology, Federal University of Viçosa, Viçosa, Brasil. E-mail: shbromo@ufv.br

The susceptibility of plants to microbial pathogens involves molecular interactions between microbial effectors and host targets. The objective of this study was to create a large mutagenized soybean population to screen for *P. pachyrhizi* susceptibility genes. We treated 30,000 soybean seeds from cultivar TMG 4182 with different EMS dosages (0,2 to 1,0%). Germinated seeds (M1 seeds) were planted in the field and the plants were individually harvested, making up one population with 4000 M2 plants. Twenty-two seeds from each M2 mutant line are being screened with *P. pachyrhizi* PPUFV02 isolate. In a preliminary study, we have screened progenies from 358 mutant lines. The progenies of 154 lines showed phenotypic variations, such as plant growth (dwarfism), color (albinism, chlorosis), leaf morphological changes/lethal mutations, with segregation indicative of recessive inheritance. Plants from one M2 line did not display visible disease symptoms and reddish brown (RB) lesions were observed in plants from nine M2 lines. These selected plants will be further tested for disease resistance. These preliminary results indicates that this population is an important genetic resource to identify and clone soybean genetic determinants that encode proteins target by *P.pachyrhizi* effectors.

Key words: *Glycine max*; Asian soybean rust, susceptibility genes