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MOLECULAR AND GENETIC ASPECTS OF THE RESISTANCE OF LEGUMINOUS PLANTS TO BIOTIC STRESS FACTORS

Biotic stresses are a serious threat to global food security. The origin of new pathogens/insect races due to climatic and/or genetic factors is a major challenge for plant breeders in breeding biotic stress resistant crops. Molecular genetics approaches like mutation, marker assisted selection (MAS), genomics, recombinant DNA technology, targeted induced local lesions in genome (TILLING), and virus induced gene silencing (VIGS) were adapted by breeders to develop effective resistance in crop plants in a shorter time. Significant progress can already be seen in the development of genomic resources for model species of Medicago, Lotus, major legumes (soybean, common bean, peanut), and minor legume crops (cowpea, chickpea, pigeon pea). The objectives of this research were to evaluate soybean and chickpea mutant lines, obtained by gamma-irradiation at the Institute of Genetics, Plant Physiology and Protection, through simple sequence repeat (SSR) molecular-genetic and immunological analysis. SSR analysis has been provided with the use of 22 SSR primers. Development of dendrograms based on the immunological and molecular genetics analyses of each particular line and determination of genetic features of studied genotypes have been done. The production indices of mutants were assessed in vivo. The gene effects involved in controlling soybean genotypes interactions with fungal/bacterial pathogens, and polymorphism of SSR markers for soybean and chickpea have been established. A high degree of similarity has been found for soybean, chickpea plant response to Fusarium oxysporum Schlecht. emnd Snyd., and SSR markers polymorphism from different linkage groups, which indicates a polygenic control of the reaction and the opportunity to use molecular markers to identify resistant genotypes. SSR molecular markers which show high polymorphism of soybean and chickpea genotypes have been identified. The results show a future perspective for utilization of SSR analysis in the national soybean and chickpea breeding programme.

Country or International Organization

Republic of Moldova

Primary author: Prof. CORETCHI, Liuba (National Centre of Public Health, Academy of Sciencis of Moldova)

Co-authors: Mr CLICIUC, Dinu (Institute of Genetics, Plant Physiology and Protection); Dr BONDARENCO, Ecaterina (Institute of Genetics, Physiology and Plant protection)

Presenter: Prof. CORETCHI, Liuba (National Centre of Public Health, Academy of Sciencis of Moldova)

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