

**COMBINING GENE AND GENOME MUTATIONS IN MAIZE
BREEDING FOR GRAIN PROTEIN CONTENT AND QUALITY**

**Andrei PALII¹, Grigorii BATIRU¹, Galina COMAROVA¹, Alexandr ROTARI²,
Dumitru COJOCARI¹**

¹State Agrarian University of Moldova;

²Institute of Crop Sciences "Porumbeni", Pascani, Republic of Moldova

Maize is an important source of vegetable protein, but compared to other cereals, it contains a relatively small amount of protein in grains (about 10%). At the same time, the biological value is low due to the limitation of essential amino acids, lysine and tryptophan. By various methods of amelioration (selection, polyploidy, mutagenesis, wide hybridization), the protein level can be increased considerably and the biological value can be elevated by using spontaneous mutations such as *opaque-2* (*O2*) gene that increase lysine content in protein. In our research we study the possibility of combining genome-wide (polyploidy) and gene (gene *O2*) mutations in order to increase the quantity and quality of grain protein. This paper presents the results of the evaluation of protein and lysine content in diploid and tetraploid maize with the *o2* gene in the year of vegetation 2017. As research material we used diploid and tetraploid forms with *opaque-2* gene belonging to two hybrids homologated in Moldova Chişiniovschi 307 PL and Chisiniovschi 401 L. The tetraploid forms were obtained by colchicization at the Department of Plant Biology of the State Agrarian University of Moldova during 2010-2011 and are maintained in populations. The weather conditions during the growing season were within the normal range for corn growing. Biochemical analyzes of diploid and tetraploid *o2* grains were performed by infrared spectroscopy on the IR 4500 (US) and also using classic methods. These analyzes were performed in the Biochemistry Laboratory of the Institute of Crop Production "Porumbeni" under the direction of Dr. E. Rotari. Growth of tetraploid plants was slower and habitus at flowering was shorter than diploid forms. The tetraploid ears were shorter, filling - lower, and larger grains. All of these features are specific for tetraploids, are largely genotype dependent and should be considered in biochemical analyzes. Since grain filling is lower and the grains are larger, the protein content is also higher. To minimize this, during the flowering period, tetraploid plants were pollinated abundantly several times until the stigmas were dried. Generally, the higher the degree of heterozygosity of the tetraploid genotype, the more ears are filled. For biochemical analyzes, samples were prepared only from well-filled ear. As expected, the protein content in the tetraploid grains at all genotypes was on average one percent absolute value higher than in diploid grains, but varied widely among the populations, which denotes genotypic specificity in determining this index. The level of lysine in the dry matter was about fifty percent relative value higher, but related to protein content, did not differ essentially compared to diploids. The obtained results demonstrate the possibility of increasing protein content and its quality by polyploidy in maize genotypes with the *o2* gene.