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BOOK OF ABSTRACTS

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Content

RESULTS:

The results have shown that treated wheat and barley varieties had different reactions to applied doses of gamma irradiation. Germination of both wheat varieties was very good at all applied doses (over 90%), and there was no significant difference in the germination rate among doses or varieties. However, barley seeds were more susceptible to gamma irradiation, where doses of 300, 450 and 600 Gy reduced germination rate for 14.2, 33.2 and 42.1%, respectively. The seedlings' growth was more affected by irradiation treatment then germination process in both wheat and barley varieties. The dose of 300 Gy was lethal for Rudnik and NS-40S, while Simonida expressed higher tolerance regarding this dose. Accordingly, the dose of 210 Gywas identified as GR50 for varieties Rudnik and NS-40S, while 310 Gy was determined for Simonida. These doses were used for the treatment of 2000 seeds of each variety and mutation populations were produced. Further, mutation populations of these cereal crops will be used in a breeding programs for creating the varieties with increase resilience to climate change.

CONCLUSIONS:

Gamma irradiation had negative effect on seed germination and growth in wheat and barley varieties, but the varieties had different reactions to applied doses. The GR50 values were identified for each variety and used for production of mutation populations. The obtained populations will be used in wheat and barley breeding programs for improved tolerance to climate change.

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T4-P-16 Molecular diversity of autumn garlic genotypes using SSR markers

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KEYWORDS: classification; germplasm collection; microsatellites

INTRODUCTION:

Garlic (*Allium sativum L.*) is one of the most important *Allium* species in terms of worldwide production and various usages in human nutrition, medicine, pharmacy and cosmetics. Basic method of garlic propagation is vegetative and creation of new varieties is mainly achieved by clonal selection. The characterization and preservation of samples in germplasm collections is of crucial importance in plant breeding, as well as availability of information about number and characteristics of samples in gene banks. Since pheotypic traits can vary significantly under the influence of environmental factors the characterization is more reliable by using DNA markers. Effective characterization of samples in collections and identification of duplicates is important from the economic aspect, ie. space saving and maintenance costs. The garlic collection of the Institute of Field and Vegetable Crops in Novi Sad (IFVCNS) includes 63 samples of autumn and 67 samples of spring garlic. These genotypes represent a valuable genetic pool for the selection of clones with appropriate characteristics, highly adapted for the production in the agro-climatic conditions of Serbia. Molecular characterization will provide more complete insight into diversity of samples, identification of potential duplicates and enable breeders more efficient selection and development of new cultivars.

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OBJECTIVES:

The objectives of this study were to assess diversity of autumn garlic collection based on SSR data and to identify potential duplicates in the collection.

METHOD / DESIGN:

From the IFVCNS autumn garlic collection 52 samples originating from 11 countries, were selected for analysis. DNA extraction from young leaves was performed according to the Somma (2004) protocol[55]. For molecular evaluation 30 SSRs markers were selected, while 10 SSRs were determined to be polymorphic. Separation of amplified PCR products was performed on metaphor agorase gel (3% and 3,5%) by horizontal electrophoresis. The visualization of the product was done under UV light on a Wilber Bio-Print device. All data analyzes were performed within the R software environment, version 4.0.5 (R Core Team, 2020).

RESULTS:

A total of 36 alleles were revealed by 10 polymorphic SSR loci. The number of alleles per locus ranged from 2 to 7, with an average number of 3.6. PIC values were 0.073-0.610 and the most informative markers were As 5944 and As 11065. The genetic distance between the analyzed genotypes ranged from 0 to 0.80 with an average value of 0.30. Out of a total of 52 samples in our study, 23.1% of the samples had an identical genotype for 10 examined SSR loci, with at least 1 genotype, while 76.9% were at a certain genetic distance with all analyzed samples. Molecular analysis provided distinguishing of most of the analyzed genotypes by PCoA and classification into 4 groups. No regularity in the grouping of genotypes according to origin was observed.

CONCLUSIONS:

The obtained results enabled more complete insight into diversity of collection and easier identification of potential genotypes for selection. Since this is the first research using DNA markers of the IFVCNS garlic collection, and considering the size and complexity of its genome, the obtained molecular results can be considered preliminary. Although the presence of duplicates in the collection was revealed based on 10 SSR loci these results represent guidelines for further research using more DNA markers.

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55 Somma, M. (2004): Extraction and purification of DNA. In M. Querci, M. Jermini, G. Van den Eede (ed.), The analysis of food samples for the presence of genetically modified organisms (Special Publication No. I.03.114) (Session 4, 13–17). European Commission DG-JRC.

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