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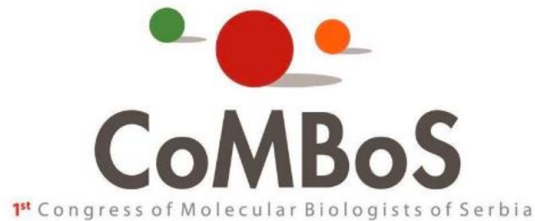


Dear colleagues,

It is our pleasure to invite you to attend the **First Congress of Molecular Biologists of Serbia** with international participation. CoMBoS will be held on **20 – 22 September 2017** at the beautiful **Ilija M. Kolarac** Endowment Building placed in the heart of Belgrade, Serbia (Student's Square 5).

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CoMBoS

1st Congress of Molecular Biologists of Serbia

KNJIGA SAŽETAKA BOOK OF ABSTRACTS



Beograd 2017 / Belgrade 2017



GENETIC DIVERSITY ANALYSIS USING MICROSATELLITE MARKERS FOR SELECTION OF POLLINATORS IN HYBRID SUGAR BEET BREEDING

Ksenija Taški-Ajduković, Živko Ćurčić, Nevena Nagl, Milada Isakov, Aranka Jevtić

Institute of Field and Vegetable Crops, Novi Sad, Serbia.

Introduction: Heterosis is an important method of increasing yield and improving quality in crops. Identifying combination of inbred lines with strong heterosis is the most important step in developing hybrids. The genetic diversity of parental lines has been proposed as a predictor of hybrid performance and heterosis.

Methods: The genetic diversity of 12 diploid sugar beet pollinators and 2 cytoplasmic male sterile lines were analyzed using 40 SSR loci. Depending on the presence of self-fertility gene pollinators classified as self-sterile (S^s) or self-fertile (S^f).

Results: In total, 129 SSR alleles were identified, with an overall 3.1 for S^s pollinators and 3.0 for S^f pollinators. The number and percentage of polymorphic loci were the highest in NS1 pollinator and CMS1. Among tested genotypes pollinators CR10 ($N_a=2.0$; $N_e=1.6$; $H_e=0.3$) and FC220 ($N_a=1.9$; $N_e=1.6$; $H_e=0.3$) exhibited the lowest level of variation, whereas pollinators EL0204 ($N_a=2.6$; $N_e=2.1$; $H_e=0.5$) and NS3 ($N_a=2.6$; $N_e=2.0$; $H_e=0.5$) had the highest. The genetic distance between the pollinators and the CMS lines was higher in the S^f than in the S^s crosses, but it was generally low indicating that the genetic base of the investigated germplasm was narrow. Cluster and correspondence analysis grouped sugar beet pollinators according to their origin.

Conclusion: Genetic diversity analysis of sugar beet pollinators is useful for breeding programs, as it helps in selecting the appropriate genetic material for the classification of parental lines, heterotic groups and predicting hybrid performances.

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