20th EUCARPIA General Congress

Abstracts

29 Aug – 1 Sep 2016
ETH Zurich, Switzerland

Editors:
Roland Kölliker and Beat Boller
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Plant Breeding: the Art of Bringing Science to Life

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Assessment of genetic diversity among oilseed rape (*Brassica napus* L.) cultivars using single locus microsatellite markers

Katarzyna Mikolajczyk[a], Joanna Nowakowska[a], Jan Bocianowski[b], Alina Liersch[a], Wieslawa Poplawska[a], Stanislaw Spasibionek[a], Teresa Cegielska-Taras[a] and Iwona Bartkowiak-Broda[a]

[a] *Plant Breeding and Acclimatization Institute-NRI, Research Division in Poznan, Poland*
[b] *Department of Mathematical and Statistical Methods, University of Life Sciences in Poznan, Poland*

kamik@nico.ihar.poznan.pl

The aim of this work is to analyze the molecular characteristics of a population including oilseed rape cultivars and breeding lines collected at the Plant Breeding and Acclimatization Institute-NRI in Poznan, Poland, and comprising double-low and traditional cultivars, F_1 *ogura* CMS hybrids and parental components, breeding lines with changed fatty acid composition - high oleic and low linolenic forms in addition to new *B. napus* genotypes obtained by resynthesis. A set of single locus microsatellites (STR, Short Tandem Repeats) was chosen for analysis, as, first of all, they are specific either for the *B. napus* A or C genomes, thus enabling the preliminary study of recombinant genomes rearrangements. Moreover, STR loci are universal, species-specific, evenly distributed throughout the genome and also the STR assay is easy to perform, repeatable and relatively cheap. CTAB extracted total DNA will be PCR amplified using STR loci specific primer pairs, labeled fluorescently by 'M13 tailing' method. Then, the amplified loci resolved by capillary electrophoresis will be analyzed and Nei and Li genetic similarity coefficients will be estimated followed by constructing of the UPGMA dendrogram to show genetic relationships among the surveyed collection with respect to previously obtained dendrogram using AFLP technique. The obtained results will be applied for further genetic analyses and association studies.

Acknowledgments: This work is supported by the Polish Ministry of Agriculture and Rural Development, Task No: 48.

Assesment of genetic diversity among oilseed rape (*Brassica napus* L.) cultivars using single locus microsatellite markers

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A set of 30 single locus microsatellites specific either for the *B. napus* A or C genomes was used (Fig. 1.)

Total DNA extracted using the modified CTAB was PCR amplified with primer pairs specific for 30 STR loci, fluorescently labeled by 'M13 tailing' method followed and analyzed by capillary electrophoresis

The presence of the *ogura* male-sterile cytoplasm (CMS) and the *Rfo* restorer gene was monitored with the multiplex PCR assay using specific SCAR markers and including also SNaPshot assay for allelic forms of the *FAD3* desaturase genes (Mikolajczyk et al., 2010; 2011) (Fig. 2.) while allelic forms of the *FAD2* desaturase genes were identified by specific CAPS markers (Falentin et al., 2007) (Fig. 3.)

Field trials were conducted in the 2015-2016 growing season in two environments, in completely randomized block design and in four repetitions (Fig. 4.)

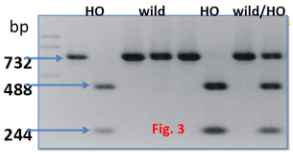


Fig. 3

Fig. 4

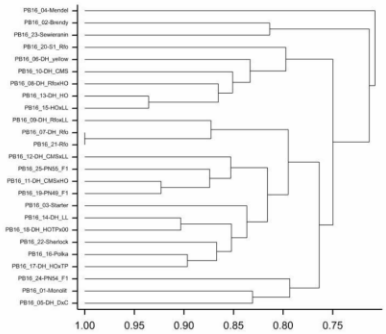


Fig. 5.


Fig. 1.

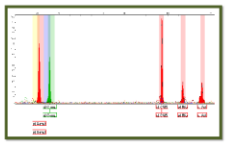
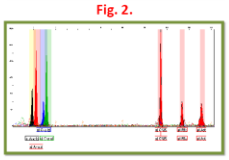


Fig. 2.



Nei and Li genetic similarity coefficients were estimated and the UPGMA dendrogram was constructed showing genetic relationships among the surveyed collection (Fig. 5.)

The Rfo restorer gene was detected in 7 genotypes and the ogura male-sterile cytoplasm in 11 genotypes

Homozygous mutated alleles of FAD2 desaurase were present in 3 genotypes and heterozygous in 2

Homozygous mutated alleles of FAD3 desaturase – in two

The evaluation of agronomical traits before winter dormancy revealed statistically significant differences among the genotypes

The obtained results will be applied for further genetic analyses and association studies

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