MAS SELECTION ON OLEIC TYPE SUNFLOWER BREEDING

Goksel EVCI [1], Behiye Banu BILGEN [2], Veli PEKCAN [1], Ibrahim Mehmet YILMAZ [1], Sheida DANESHVAR [3], Çağlar ÇOLAK [4], Sami BULUT[5], Yalcin KAYA [4]

[1] Trakya Agricultural Research Institute, Turkey
[2] Namik Kemal University, Turkey, Agricultural Biotechnology Department, Turkey
[4] Trakya University, Genetics and Bioengineering Department, Turkey
[5] Trakya University, Department of Food Engineering, Turkey

yalcinkaya@trakya.edu.tr

Oleic type sunflower is new trend in sunflower production in the world. Its market is increasing year by year recently. On the other hand, new oleic type hybrids are developing and releasing into the market. High Oleic (HO) trait is controlling a gene calling *Ol* utilized and obtained from mostly to a high oleic mutation of variety Pervenets by Soldatov 1976. Although, there are some other sources for high oleic content up to 90% from Bulgaria and Italy, etc. Pervenets mutations are using worldwide as the donor to develop high oleic content inbred lines and hybrids in sunflower breeding programs. However, as a seed trait, oleic type plants could determine after harvest so it needs to wait until seed tests to select oleic types until seed trashing. However, when applied MAS analysis high oleic plants could be determined as much as early stages so it helps extremely to breeders both reducing costs and time wasting and also accurate selection. Different RAPD, SSR (microsatellite) markers were determined until today in different studies. These studies enabled to detect the genetic behavior of high oleic of QTL and linked markers efficiently then leaded to use of molecular tools practically in sunflower breeding programs. On the other hand, PCR analysis with HO specific fragments enabled to amplify either the Pervenets mutation itself or the polymorphism of the SSR locus (TTA repeat variability) located on the Δ12-desaturase gene intron. These markers lead to discriminate genotypes carrying Pervenets mutation and genotypes without mutation. Consequently, the HO PCR specific fragments or SSR markers may be used in selection programs to identify genotypes carrying the Pervenets mutation. However, these markers need further validations in different genetic sources to classify sunflower genotypes accurately based on their oleic acid contents. For example, the length of the SSR depend on the lines that have been used to convert the LO in HO. Therefore, amplified SSR locus should be sequenced from different progenies, because the SSR size estimation may vary depending of the plants and of the PCR reaction. Furthermore, HO PCR specific fragments could not able to distinguish homozygous HO genotypes from Heterozygous HO genotypes so this type primers may be used first selecting HO genotypes (both homozygous and heterozygous) and then extra selection with SSR markers should be done further. As results, further studies need on MAS selection in oleic acid content in sunflower and not dependable to genetic background, practical and widely used molecular markers determining HO in the breeding programs broadly were not released yet for public interest and uses.

Key Words : Sunflower, MAS, Oleic type, breeding