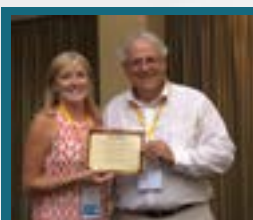


26th European Biotechnology Congress

September 26, 2022

WEBINAR



Scientific Tracks & Abstracts

The use of DArTseq technology to identify new SNP and SilicoDArT markers related to fusarium resistance and the yield-related traits components in maize

Aleksandra Sobiech

Poznan University of Life Sciences, Poland

Molecular analysis in maize focused on identifying new markers and QTL regions associated with loci that determine yield structure traits and Fusarium resistance. DNA analysis in the selection of parental components for heterotic crosses is an important tool for breeders, while fungi of the genus *Fusarium*, cause deterioration in nutritional value and forage quality due to the presence of harmful mycotoxins. The aim of this study was to identify and select new markers for maize (SNPs and SilicoDArT) linked to genes affecting yield components in maize, and markers that could be used for mass selection of fusarium-resistant varieties. The plant material consisted of 186 maize inbred lines. These lines came from two Polish experimental plots: Smolice Plant Breeding Ltd and Malopolska Plant Breeding Koberzyce Ltd. Of the 81,602 identified SilicoDArT and SNP markers, 15,409 (1559 SilicoDArT and 13,850 SNP) significantly associated with the yield components analyzed were selected by association mapping. The largest number of molecular markers were associated with cob length (1203), cob diameter (1759), core length (1201) and core diameter (2326). Of the 15,409 markers significantly associated with the yield component traits analyzed, 18 DArT markers were selected that were significant for the same four traits in both localities. These markers were used for physical mapping. As a result of the analyses, 6 of the 18 identified markers were found to be within genes. Also, 2962 (321 SilicoDArT and 2641 SNPs) significantly associated with plant resistance to fusarium were selected, of which 7 markers were significant at the 0.001 level. They were used for physical mapping. The analysis found that two of the seven selected markers (15.097-SilicoDArT and 58.771-SNP) are located within genes on chromosomes 2 and 3, respectively. Marker 15.097 is anchored to the gene encoding putrescine N-hydroxycinnamoyltransferase, while marker 58.771 is anchored to the gene encoding peroxidase precursor 72. Both of these genes may be associated with plant resistance to fusarium.

Biography

Aleksandra Sobiech is a PHD student in Poznan University of Life Sciences. She graduated master study of biotechnology in 2020. On her PHD she investigated Multidimensional exploration of molecular mechanisms involved in maize (*Zea mays*) fusarium resistance.

Received: August 19, 2022; **Accepted:** August 22, 2022; **Published:** September 26, 2022

Mitochondrial structure and activity can change

Maryam Sadat Moosavi
Ashrafi Isfahani University, Iran

Mitochondria are involved in the control of apoptosis, signals and chromatin structure change and affect the expression level. Mitochondria are dynamic organelles that have a specific shape and structure in each type of cell that helps cell differentiation; they are elongated, hollow, and small in normal cells, spherical and rod-like in melanoma cells. They accumulate in stem cells, but they do not have phosphorylationoxidative activity, and the energy of the cell is provided only through glycolysis. The important point is the difference in temperature and the difference in the energy level of this intracellular organelle, which It is usually ignored and only the amount of ATP production is considered in energy transfer. In the cell the temperature of the active mitochondria is about 50 degrees .According to the statement that the forces between the two strands of DNA is through the force of water, not hydrogen bonds, as well as the statement that water and heat easily leave mitochondria and Einstein's theory of mass and energy which says that Objects receive heat and go to a higher energy level. Above energy and movement, coldness is a sign of lack of energy. This shutting down of DNA, enzymes, cofactors and histones in stem cells is due to the reduction of mitochondrial activity and for this reason, by changing the structure and activity of cells from glycolysis to oxidativephosphorylation, this heat and energy for movement, unfolding, expression, proliferation, reproduction and differentiation are provided. The mainpoint is that the transfer of intelligent energy and the movement of mitochondria and the transfer of hot water due to the difference in density never mix with cold water to reach the desired point in the DNA and the same part is expressed and this difference in the location of gene expression is the same differentiation.

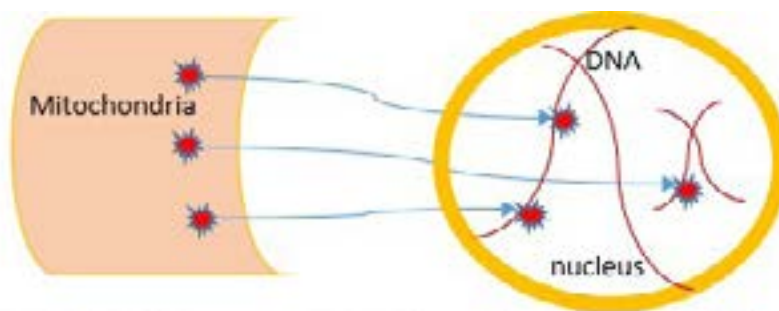


Figure 1: Mitochondria are connected to the nucleus. They transfer their energy and heat to the core through water. The exit of water and heat from mitochondria is very easy. This heat through the properties of water, which due to the difference in the density of the two environments of hot and cold water, never combine until this heat reaches the desired point in the DNA.

26th European Biotechnology Congress

September 26, 2022

WEBINAR

Biography

Maryam Mousavi received her bachelor's degree in genetics from the University of Isfahan. During this time, she learned some laboratory work. she completed her master's degree at Ashrafi University of Isfahani with the same professors of Isfahan University. She wrote several articles on different topics and learned laboratory work in a more specialized way. By reading many articles, she try to find answers to her questions and present them in the form of articles for further follow-up by people with more information and capabilities.

Received: September 02, 2022; **Accepted:** September 05, 2022; **Published:** September 26, 2022

Determination of molecular markers associated with the agronomic Traits in watermelon (*Citrullus lanatus*)

Omer Faruk Coskun

Hatay Mustafa Kemal University, Turkey

Yield, quality and other agronomic characteristics of horticultural crops are very important in terms of breeding selection criteria. By set a linkage between phenotype and genotype with the associating mapping technique, phenotype-related DNA markers can be detected. Association mapping involves searching for genotype-phenotype correlations in unrelated genotypes and often is more rapid and cost-effective than traditional linkage mapping. In this study, DNA markers related to some agronomic traits of watermelon populations were identified with the aid of association mapping technique. Inter-primer binding site (iPBS), inter simple sequence repeat (ISSR) and simple sequence repeat (SSR) markers were used to assess the genetic diversity of 96 watermelon genotypes. According to similarity coefficient, the lowest (0.29) and highest (0.99) similarities were detected between watermelon genotypes. The association maps revealed that general linear model (GLM) model yielded the best outcomes for 5 parameters and mixed linear model (MLM) models yielded the best outcomes for the other parameters. For all parameters, 8-69 related marker were identified, and regression models were able to explain related characters by between 11.3 - 84.7%. Two-marker model was able to explain yield values by 68.6%, three-marker model was able to explain glucose value by 62.8%. It was concluded that iPBS technique, which was used for the first time in watermelon, could reliably be used for association mapping. It was observed that watermelon genotypes exhibited a large diversity in morphological characteristics and a narrow diversity in genetic parameters. Present findings revealed that association mapping method for existing watermelon genotypes was an efficient method for identification of marker-trait relationships without generation a mapping population.

Biography

Omer Faruk COSKUN has completed his PhD from Erciyes University, Turkey.

Received: September 27, 2021; **Accepted:** September 30, 2021; **Published:** September 26, 2022