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STUDY OF MAIZE GENOTYPES RICH IN ANTHOCYANINS FOR HUMAN AND ANIMAL NUTRITION

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Flavonoids, a group of secondary metabolites belonging to the class of phenylpropanoids, play essential functions in plants. Besides, epidemiological studies suggested that regular consumption of flavonoid-rich foods or beverages is associated with a decreased risk of cardiovascular mortality. Among the flavonoids, it seems that anthocyanins might function as potent in vivo antioxidants: their long-term dietary potential health benefits can be proved by the use of plants that accumulate specific anthocyanins.

Maize could be an example of these functional foods: purple and blue corn are pigmented varieties rich in anthocyanins originally cultivated in South America. In maize, anthocyanins are synthesized by a complex pathway made up of more than 20 genes and regulated by two classes of transcription factors, *R1/B1* bHLH genes and *C1/Pl1/P1* MYB gene families. The presence of dominant alleles of these regulatory genes is necessary to accumulate the pigments.

The introgression of these alleles in european inbred lines and populations has been made for years in our experimental field. In this project NILs (Nearly Isogenic Lines), derived from six cicles of self-pollination after a cross between an inbred line and a line carrying the regulatory genes for anthocyanin accumulation in the pericarp (*B* and *Pl*), were studied. An unexpected variability in the anthocyanin content was discovered among the flours obtained from seeds of each ear of the NIL; this variability was due neither to differences in the pericarp thickness nor in the mean seed weights.

An epigenetic phenomenon was hypotesized to explain this variability. It is known in fact that the regulatory genes of the anthocyanin biosynthetic pathway are susceptible to silencing processes, thus the variation could be due to a partial switch off of the anthocyanin pathway genes. Preliminary results of regulatory and structural genes expression analysis seemed to support this hypothesis, however further experiments, such as azacitidine treatments and methylation –sensitive enzymes tests, are planned.

These results could allow a better understanding of the regulatory mechanisms of the anthocyanin pathway, with the aim to improve the genetic selection to obtain corn lines with the highest amount of these pigments.