

Summary and keywords

The answer to the needs of the agricultural sector in the 21st century is the implementation of biological progress in agricultural production, which allows for the improvement of food production and quality while improving the degree of utilization of inputs on chemical and technical means of production. Biological progress in the corn breeding and seed industry is unique in terms of the social and ecological aspects of innovation. It influences agricultural productivity and adapts cultivated corn varieties to market requirements and changing climatic conditions, but does not do so at the expense of the environment. Modern corn breeding around the world is based on a wide range of research techniques in the field of molecular genetics. Thanks to these technologies, we can identify regions of the genome associated with various phenotypic traits, including yield, which is fundamental to understanding and manipulating these regions. Therefore, the aim of the doctoral dissertation was to identify new molecular markers coupled with candidate genes that determine grain yield, kernel germination and early vigor of corn, thanks to the use of next-generation sequencing, association and physical mapping.

As a result of the analyses, 20 molecular markers were identified that were related to the germination capacity of grains and the vigor of seedlings. Of these, 6 markers were located inside genes. In 4 cases, according to literature reports, these genes may affect grain germination and vigor in maize. In the next stage of research, a total of 36 molecular markers related to crop structure features and yield were identified. Of these markers, 11 are located inside genes. In 5 cases, according to the latest literature reports, these genes are responsible for height of the yield. All identified, statistically significant molecular markers can be used in the maize breeding process to select parental components for crossbreeding. This will shorten the breeding cycle and at the same time save material resources.

Keywords: corn, yield, next-generation sequencing (NGS), association mapping, physical mapping, molecular markers.

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