REVIEW

of the official reviewer **Andrii Olexandrovych Butenko**, PhD of Agricultural Sciences, Associate Professor, Associate Professor of the Department of Agricultural Technology and Soil Science of Sumy National Agrarian University for the PhD thesis **Qiaoyan Chen** "Breeding and genetic bases of winter wheat ear traits",
submitted for Doctor of Philosophy scientific degree
Field of knowledge: 20 – Agricultural Sciences and Food
Specialty 201 – Agronomy

1 **Relevance of the dissertation topic**. Winter wheat is one of the world's three major grain crops, and China ranks first in the world in terms of both area planted and total wheat production. According to the prediction, by 2050, the world population will increase from the current 7 billion to9 billion, and the food production will have to be increased by more than 30% in order to meet the increasing consumption demand of human beings. Therefore, the cultivation of new varieties of the three major food crops, namely, high yielding and stable yielding wheat, rice and maize, is an effective way to satisfy the future demand of human beings for food. Yield is a quantitative trait controlled by multiple genes, with a complex genetic basis, and is easily influenced by the environment. Utilizing traditional breeding methods is time-and resource-consuming. However, with the development of molecular biology and biostatistics, QTL mapping of quantitative trait loci based on genetic mapping of molecular markers provides an effective technical means to study the genetics of quantitative traits.

Yield is composed of the spike number per unit area, grain number per spike and thousand grain weight. When the spike number per unit area and thousand grain weight are constrained, increasing the number of grains is the key to improving yield. Therefore, in crop improvement, molecular marker assisted selection does not require many years of breeding experience, not depending on the environment and the years of breeding experience, not depending on the environment and the developmental stage of the crop, and the monitoring of good alleles developmental stage of the crop, and the monitoring of good alleles effectively reduces or avoids the introduction of unfavorable genes.effectively reduces or avoids the introduction of unfavorable genes.

2. Connection of the research with scientific topics. Research on the topic of the dissertation took place within the framework of the scientific topic of Department of Selection and Seeds named after M.D. Honcharov "Develop bioadaptive and ecologically oriented technologies for growing grain crops, taking into account agrotechnical measures and agrobiological control of plant growth and development in the conditions of the North-Eastern Forest Steppe of Ukraine."

3. Scientific novelty and theoretical significance of the dissertation.
The genetic mechanism of grain number per spike of wheat was studied by using the extreme difference in grain number per spike of two parents (Mexico Large Spike and Bainong 419), and on the basis of eliminating the influence of acre spike number and 1000-grain weight on grain number per spike of parents and the targeted population, the research results would be more scientific and reliable.

4. Practical significance of the results of the dissertation. The author obtained results that can be used in the breeding practice of soft winter wheat. Thus, genetic control of the trait number of grains in the ear in the multi-grain variety "Megaclus Mexicani" will allow on this basis, to study the main molecular regulatory pathways genes determining the number of grains in an ear, which will contribute to the future study of relevant mechanisms and regulatory networks, as well as provide theoretical guidance for the future innovation of multigrain wheat germplasm. After cloning the target gene and verifying its function, combined with the vernalization chamber, artificial climate chamber, daylight intelligent greenhouse and large refrigeration greenhouse and other supporting facilities, it can ensure that at least three generations of wheat can be bred every year (12 months), which provides a guarantee for the addition of relevant experimental materials and the rapid construction of near isogenic lines.

5. The main results obtained personally by the author.

A map of the genetic linkage of wheat was created, which contains 143 molecular marker loci spanning 19 wheat chromosomes, with a total genome length of 3128.17 cM, the average distance between the markers is 25.23 cm and the minimum genetic distance of 3.57 cM.

The results of genetic linkage analysis showed that a total of nine additive loci associated with spike number were scanned in chromosomes 1 B, 2B, 2D, 3B, and 6 B, and their contribution to the genetic variability of phenotypic traits ranged from 4.922% to 21 ,1044%; among them, QGNS~1B and QGNS~1B and QGNS~3B2 were major loci with large genetic effects, explaining 21 .1044% and 15.8886% of the phenotypic variation.

One additional QTL locus was detected on QTGW~3B, which could explain 11.4727% of the phenotypic variation. Detection and analysis of epistatic QTL loci for spikelet number and 1000-grain weight showed that nine epistatic QTL loci were associated with spikelet number and 1000-grain weight. Among them, there were six epistatic QTL loci associated with the number of grains per ear, which were located on chromosomes 2 B, 2D, 3B, and 6 B, respectively, and the effect values of the QGNS~2B, QGNS~2D, and QGNS~3B1 loci were different. is less than zero. The genetic effect values of all loci were greater than zero. This

suggests that there are random loci on chromosomes that do not directly affect the phenotype, but these loci can affect phenotypic traits through interactions with each other.

The genetic contribution of these loci to the phenotypic variations of the mass of 1000 grains also shows a strong effect of epistasis.

It was 105 common and 79 new microRNAs, including 46, were identified known and 32 novel miRNAs from the 7 DAP library and 87 known and 78 novel miRNAs from the 14 DAP library, respectively. MicroRNA expression analysis. showed that 39 of these identified miRNAs, including 19 known and 20 new microRNAs, differentiated expressed between 7 DAP and 14 DAP. A total of 266 were provided targets for 40 known wheat miRNAs, 152 targets for 13 others known miRNAs of plants and 258 targets for 25 new miRNAs in small RNA and degradome analyses. It was foreseen twenty-three targets for 7 miRNAs with differential expression, including 3 known and 4 novel miRNAs. Most of these miRNAs potentially regulate multiple targets, while others act only on one target Functional analysis predicts that miRNAs and their targets are widely involved in the regulation of early grain development wheat and metabolism. Expression patterns of randomly selected miRNAs and targets were confirmed using quant of polymerase chain reaction in real time with sequential and reliable results.

An analysis of the plagiarism check report for the presence of textual borrowings (Strike plagiarism program) was carried out. The reviewers came to the conclusion that the dissertation work (Qiaoyan Chen) on the topic "Breeding and genetic bases of winterwheatear traits" is the result of independent research of the acquirer and does not contain elements of plagiarism and borrowing in accordance with the resolution of the CMU dated 12.01.2022 No. 44, paragraph 9. Ideas used, results and texts of other authors have a link to the corresponding source.

6. Number of scientific publications.

The main items of the thesis are presented in 12 scientific works: 3 articles in professional publications of Ukraine; 2 in the international scientometric citation databases Scopus and WoS; 7 abstracts of reports at international scientific and practical conferences and symposia.

7. Remarks and wishes regarding the content.

1. It is necessary to provide a description of the field experiment (soil and climatic conditions, tools and equipment, etc.)

2. When moving tables, you need to specify the name of the table on the new page.

3. The names of subdivisions should not be left separately at the end of the page; it is better to start them on a new page.

4. It is necessary to indicate the scheme of hybridization of wheat samples and describe the method of obtaining hybrids.

8. Correspondence of the thesis to the specialty and profile of the board:

Dissertation work of Qiaoyan Chen "Breeding and genetic bases of winter wheat ear traits", submitted for defense to the specialized academic council for obtaining the degree of Doctor of Philosophy in the field of knowledge 20 – Agricultural sciences and food in the specialty 201 – Agronomy according to its relevance, scientific and theoretical level, main results of validity, main provisions and the results published in professional publications, the novelty of the proposal and its practical significance meet the requirements of the Ministry of Education and Culture of Ukraine Order No. 40 of January 12, 2017 "On approval of requirements for the preparation of a dissertation" and Resolution of the Cabinet of Ministers of Ukraine of January 12, 2022 No. 44 "On approval of the Award Procedure degree of Doctor of Philosophy and annulment of the decision of the one-time specialized academic council of the institution of higher education, scientific institution on awarding the degree of Doctor of Philosophy" with changes introduced in accordance with Resolution of the Cabinet of Ministers No. 341 dated 03.21.2022. The content of the dissertation corresponds to the passport of the specialty.

Official Reviewer:
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