INFORMATION AND NEW CONCLUSIONS FROM THE DISSERTATION

Dissertation title: Using of molecular markers to study of the improvement of the

chalkiness ratio in high-yielding rice varieties (Oryza sativa L.)

Specialty: Biotechnology; Code: 9420201

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Main contents of the dissertation:

- The parents were selected for the breeding program of rice varieties with the low chalkiness ratio in the sets of high-yielding rice varieties at Mekong Delta. (i) The phenotype assessment: The sets of high-yielding rice varieties were collected and used as the hybrid materials, including some of rice lines/varieties with less chalkiness level and some of rice lines/varieties with the potential high-yielding but high chalkiness level; The sets of high-yielding rice varieties were assessed about the chalkiness level; The set of rice varieties-hybrid materials were clustered on the phenotypic genetic diversity. (ii) The genotype assessment: The rice grains of source materials were assessed about the genotypes of un-chalkiness characteristic by SSR and Indel molecular markers. (iii) The parents were selected for the breeding with low chalkiness level: The rice varieties of parents were selected based on the combination between the phenotype and genotype assessment.

- The backcrossing hybrid populations were bred involved in the less chalkiness characteristic using molecular markers: These populations were BC_1F_1 BC_nF_1 .
- The backcrossing hybrid populations were screened *via* the mapping of GGT: The genotype of hybrid populations on chromosome 7 were checked based on the molecular markers with the polymorphism between the paternal and maternal plants; The GGT map was created to assess the genetic of the hybrid populations, and the desired target gene-carried individuals were screened, then.
- The promising rice lines were analyzed the interaction between genotype and environment: The promising rice lines were tested and selected on the large scale at the various locations of the Mekong Delta in Winter-Spring season 2016-2017 and Summer-Autumn season 2017.

New conclusions from the dissertation:

- The set of rice varieties-hybrid materials were analyzed on the genotypes and were found the eleven rice varieties, which carried genes with less chalkiness level,

these rice varieties were KDML105, OM10037, OM10258, OM10383, OM70L, TLR416, TLR417, TLR420, TLR426, TLR434, and RVT.

- The set of rice varieties-hybrid materials were analyzed both the genotype and phenotype and bred two rice varieties with very low chalkiness ratio RVT and TLR434, which were used as the target gene donor material, and the rice varieties with high chalkiness ratios but high-yielding, wide stability and adaptability OM3673 were used as the target gene recipient material.
- The promising hybrid combinations were generated under the current investigation.
- The hybrid screening method of the innovative backcrossing populations using the molecular markers on chromosome 7 were bred the eleven promising rice lines with low chalkiness level and will be used in the future.
- The promising two rice lines were bred with the best characteristics like highyielding, rice grain ratio with high chalkiness level were reduced very much, the ability of high stability and diverse adaptability with the different cultivation environment conditions.

New contributions of the dissertation:

- The study was assessed the parent materials to explore the un-chalkiness characteristic to help to provide the genetic information on the initial material in the breeding program of less chalkiness rice varieties.
- Besides, the breeding goals of the un-chalkiness-carried genes rice varieties, the study also mentioned in the high-yielding and the suitable growing time. These are decisive requirement to the rice varieties products can be widely used and developed when the study completion.
- The hybrid screening method of the innovative backcrossing populations via the molecular markers provided high efficiency and shortens the breeding time.
- The suggestions of the current study are the combination between the traditional breeding, molecular biology, and Bioinformatics in the study.

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