CENTRAL LUZON STATE UNIVERSITY

ESTABLISHMENT OF SIMPLE SEQUENCE REPEAT (SSR) MARKER SYSTEM FOR PURITY TESTING OF SELECTED THREE-LINE HYBRIDS

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JENNA MAE CANDELARIA BIENDIMA

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ABSTRACT

BIENDIMA, JENNA MAE CANDELARIA, Bachelor of Science in Biology, Department of Biological Sciences, College of Arts and Sciences, Central Luzon State University, Science City of Munoz, Nueva Ecija, Philppines, June 2017. **ESTABLISHMENT OF SIMPLE SEQUENCE REPEAT (SSR) MARKER SYSTEM FOR PURITY TESTING OF SELECTED THREE-LINE HYBRIDS.**

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Genetic purity assessment is very crucial for varietal identification. To improve these process molecular markers can provide an advance tool for accurate and precise identification. Establishing DNA fingerprinting is essential for testing the genetic purity in order to produce good quality seeds for plant breeders and before it was hand to farmers. This study was conducted to establish unique SSR markers for three-line hybrids, Mestiso 29, Mestiso 48, Mestiso 55, and PR47216H, and to detect the impurities by grow-out test DNA fingerprinting.

A rice panel was assembled which includes the four hybrids, their corresponding A line, B line, and R line, and three inbred varieties, PSB Rc18, PSB Rc82, and NSIC Rc222. DNA was extracted from the panel and the obtained DNA from the samples were used for downstream analyses. Polymorphism survey was conducted and four out of 200 SSR markers evaluated were found to show heterozygous banding patterns for the F_1

which were distinct from their corresponding parent lines and inbred varieties. F_1 seeds for each hybrid were used for standard grow-out test. Pre-determined off-types from the corresponding A line, R line, and inbred varieties from each hybrid were incorporated and replaced selected F_1 plants from the field. Using morphological characters, the pre-determined off-types were distinguished from the F_1 plants. However, additional off-types were not detected. Using the established SSR markers from the polymorphism survey, the samples from the grow-out test were subjected to molecular genotyping. Pre-determined off-types were distinguished based on their banding patterns and additional off-types were detected. Using RM6100, 5.19% were additionally detected to be off-types for Mestizo 29. For Mestiso 48, additional 10.51% were detected using RM574. For Mestiso 55, 9.86% were detected as additional contaminants using RM216. Lastly, for PR47216H, genotyping using RM440 detected 4.50% additional contaminants. The result showed that the established SSR markers were useful in detecting off-types. Utilization of these markers for genetic purity assessment of hybrids at the production level will help in the production of pure seeds and also for the farmers that depend on hybrid seeds.

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