RINGKASAN

Padi merupakan tanaman penting yang berperan sebagai sumber pangan bagi masyarakat Indonesia. Konsumsi padi di Indonesia mengalami peningkatan dalam beberapa tahun berakhir. Namun, produksi padi di Indonesia cenderung menurun disertai volume impor yang lebih besar dibandingkan volume ekspor. Pemanfaatan padi varietas unggul nasional sebagai sumber genetik pemuliaan dapat dilakukan untuk meningkatkan kualitas dan kuantitas hasil. Oleh karena itu, kajian keragaman dan kekerabatan antar varietas menggunakan karakter gabah dan marka *Sequence-Tagged Site* (STS) perlu dilakukan untuk menghindari pengaruh silang dalam (*inbreeding effect*) pada proses pemuliaan. Penelitian ini bertujuan untuk: 1) mengevaluasi varians dan korelasi karakter gabah padi varietas unggul nasional; 2) mengevaluasi dan menganalisis keragaman genetik padi varietas unggul nasional berdasarkan karakter gabah; dan 3) mempelajari dan menganalisis keragaman genetik padi varietas unggul nasional berdasarkan marka STS. Informasi keragaman dan kekerabatan berdasarkan karakter gabah dan marka STS dapat digunakan sebagai bahan seleksi tetua, evaluasi pemuliaan, dan pertimbangan persilangan.

Penelitian ini dilaksanakan di Laboratorium Biologi Molekuler, Balai Besar Pengujian Standar Instrumen Bioteknologi dan Sumberdaya Genetik Pertanian, Badan Standarisasi Instrumen Pertanian Republik Indonesia, Bogor pada Januari hingga Juni 2024. Sebanyak 82 genotipe padi varietas unggul digunakan sebagai sampel studi. Empat karakter gabah yang terdiri atas panjang gabah, lebar gabah, ketebalan gabah, dan rasio panjang-lebar gabah serta sepuluh marka STS yang terdistribusi pada empat kromosom padi digunakan untuk mengukur keragaman genetik dan kekerabatan antar genotipe. Karakter gabah dievaluasi menggunakan *Analysis of Variance* (ANOVA) (α=5%), *Duncan's Multiple Range Test* (α=5%), korelasi *Pearson Product Moment*, dan *Principal Component Analysis*. Sementara itu, pengujian yang dilakukan pada data molekuler terdiri atas evaluasi profil marka STS dan evaluasi pohon filogenetik UPGMA.

Empat karakter gabah yang dievaluasi menunjukkan perbedaan signifikan antar varietas berdasarkan *Analysis of Variance* (ANOVA) (α=5%) dan *Duncan's Multiple Range Test* (α=5%). Setiap karakter gabah menunjukkan keterkaitan yang kuat antara satu karakter dengan karakter lain. Berdasarkan *Principal Component Analysis*, karakter gabah dapat menjadi diskriminator yang berkontribusi tinggi terhadap keragaman padi varietas unggul nasional dan dapat menghasilkan tiga kelompok utama. Analisis profil genetik dan kekerabatan berdasarkan marka STS menunjukkan bahwa padi varietas unggul memiliki tingkat keragaman yang rendah serta pola pengelompokan filogenetik yang tidak terlalu tegas. Sebagian besar genotipe yang diuji cenderung memiliki struktur subspesies *indica,* baik berdasarkan evaluasi karakter gabah maupun marka STS.

SUMMARY

Rice is an important crop being a staple food for most of the population in Indonesia. The consumption level of rice in Indonesia has increased in recent years. On the other hand, the decrease in production level with a higher volume of rice import over the export has been reported. The utilization of improved varieties as a genetic resource in rice breeding programs would be beneficial for enhancing both yield quality and quantity. Therefore, study of the genetic diversity and relatedness among improved rice varieties using grain traits and Sequence-Tagged Site (STS) markers should be taken into consideration to avoid inbreeding effects in the process of breeding programs. This research aimed: 1) to evaluate the variance and the correlation of grain traits among Indonesian improved rice varieties; 2) to evaluate and analyze the genetic diversity of Indonesian improved rice varieties based on grain traits; and 3) to study and analyze the genetic diversity of Indonesian improved rice varieties based on STS markers. The information of genetic diversity and relatedness based on grain traits and STS markers can be beneficial in considering parental selection, evaluating breeding programs, and considering crossing activity.

The research was conducted at The Laboratory of Molecular Biology, The Center for Standard Testing of Agricultural Biotechnology and Genetic Resources Instruments, Agricultural Instrument Standardization Agency of the Republic of Indonesia, Bogor in January until June 2024. A total of 82 accessions of Indonesian improved rice varieties were used to be evaluated. Four grain traits, consisting of grain length, grain width, grain thickness, and grain length-width ratio, along with ten STS markers which distributed over four rice chromosomes were used to estimate the genetic diversity and kinship among genotypes. Grain traits were analyzed using the Analysis of Variance (ANOVA) (α=5%), the Duncan's Multiple Range Test (α=5%), the correlation analysis of Pearson Product Moment, and the Principal Component Analysis. The assessment of molecular data was performed using a calculation of STS marker profiles and the evaluation of a phylogenetic tree based on UPGMA construction.

A total of four grains related traits being evaluated showed significant differences according to the Analysis of Variance (ANOVA) (α=5%) and the Duncan's Multiple Range Test (α=5%). Each trait also possessed a strong correlation between each other. Regarding to the Principal Component Analysis, grain traits could be a discriminator trait highly contributing to the diversity of Indonesian improved rice varieties and the grouping evaluation could result in three major groups. The analysis of the genetic profiles and relatedness based on STS markers exhibited that Indonesian improved rice varieties had a low genetic diversity with grouping pattern that was not clear enough. Most of the evaluated genotypes were inclined to have indica structure, according to both the grain traits evaluation and the STS markers evaluation.