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UDC: 633.63-527.8:575.113

Riry Prihatini, Tri Budiyanti, and Noflindawati (Indonesian Tropical Fruit Research Institute)

Genetic Variability of Indonesian Papaya Accessions as Revealed by Random Amplified Polymorphic DNA and Morphological Characterization (Orig. Eng.)

IJAS, June 2019, vol. 20 no. 1, p. 1-8, 4 tab., 4 ill., 29 ref.

Diverse papaya (*Carica* sp.) accessions are found in many regions in Indonesia, but their genetic diversity have not yet been studied. Random Amplified Polymorphic DNA (RAPD) is a simple yet accurate method that can be used to examine the genetic diversity of papaya. The study aimed to examine the genetic diversity of Indonesian papaya accessions using RAPD markers and morphological characters. The RAPD was applied on 23 papaya accessions using 30 primers. The appearing bands were further analyzed with the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) and Principal Component Analysis (PCA). The molecular results were then compared to the fruit morphological data, including fruit shape, size, flesh color, texture, and flavor. The RAPD analysis revealed that the 23 papaya accessions clustered into six main clades with Dice-Sorensen coefficient similarity ranged from 0.71 to 0.98. The first group consisted of 11 accessions, including both the hybrids and local accessions. The second group consisted of eight accessions especially six Indonesian hybrids, a Mexican Hybrid and a Hawaiian hybrid. The other four groups had a single member namely Sicincin Panjang, Lokal Sumani, Cariso, and Carica. The molecular grouping, however, did not align with the fruit character grouping. Overall, it was implied that the Indonesian papaya accessions were genetically narrow, of which some accessions were closely related to Hawaiian and Mexican accessions. These results can be used as a reference on papaya crossbreeding program in Indonesia.

(Author)

Keyword: *Carica* sp., genetic diversity, morphological characters, PCA, RAPD]

UDC: 631.455.1-51:543.27-43

Eni Maftu'ah and Nur Wakhid (Indonesian Swampland Agriculture Research Institute)

Replacing Slash and Burn Practices with Slash and Composting to Reduce Carbon Dioxide Emissions from Degraded Peatland (Orig. Eng.)

IJAS, June 2019, vol. 20 no. 1, p. 9-18, 1 tab., 8 ill., 40 ref.

Slash and burn are commonly practiced in opening new field in tropical peatland. This method, if uncontrolled, may cause peat fires and increase CO_2 emissions. Therefore, alternative method of peatland preparation for agriculture is needed. The study aimed to obtain peatland preparation technologies to prevent peat fires and reduce CO_2 emissions. The study was conducted at degraded peatland in Kalampangan, Central Kalimantan from June to October 2017. Split plot design with three replications was used. The main plot was the type of land arrangement, i.e. without and with raised beds. The subplot was the type of land preparation, i.e. slash and burn, slash followed by composting the weeds, slash and make the weeds as mulches, and slash followed by composting the weeds and accompanied by plastic mulch. Soil characteristics, fires vulnerability, and CO_2 emissions were measured before and after land preparation. Results showed that slash and composting reduced CO_2 emission from cultivated peatland. Slash and burn resulted 4.98 t CO_2 ha^{-1} emissions per season, which is four times higher than slash followed by composting that produced 1.20 t CO_2 ha^{-1} per season. Groundwater level, redox potential (Eh), soil pH, and soil water content affected CO_2 emissions. Groundwater level and water content negatively correlated with CO_2 emissions. The shallow water level and the high water content, the lower is CO_2 emissions. The Eh and soil pH positively correlated with CO_2 emissions. The high positive value of Eh indicates that the soil was in high oxidative conditions, resulting in high CO_2 emissions.

(Author)

Keywords: CO_2 emissions, groundwater table, peat cultivation, peat soil

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UDC: 635.263-152.4

Lina Herlina[a], Reflinur[a], Sobirb, Awang Maharijaya[b], Suryo Wiyono[c], and Bonjok Istiaji[c] ([a]Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, [b]Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural University, [c]Department of Plant Protection, Faculty of Agriculture, Bogor Agricultural University)

Genetic Diversity of Indonesian Shallots Based on Bulb-Tunic Patterns and Morphological Characters (Orig. Eng.)

IJAS, June 2019, vol. 20 no. 1, p. 19-28, 5 tab., 4 ill., 25 ref.

Variation within bulb tunics has been used to determine the genetic diversity in Allium species, including shallots. However, no such study has been reported for shallots of Indonesia. The study aimed to analyze the genetic diversity of the Indonesian shallots based on the bulb-tunic patterns. Thirty-five shallot genotypes from main production centers in Indonesia were used. The ultrasculptures of the bulb tunics were examined by light microscopy, including the inner surface and cell shape patterns of the bulb tunics. The phenotypic data, i.e. quantitative and qualitative traits were subjected to the descriptive statistics, principal component, correlation, regression, and clustering analyses. The results showed that the bulb-tunic cell patterns were varied, which shared almost identical with 13 Allium species. Total bulb weight per genotype showed the greatest variation (cv = 89.10%) and significant correlation with bulb weight per plant (r = 0.773). The principle component analyses showed the cumulative proportion of 78% of the total morphological variation in all shallot genotypes. Based on clustering analysis, the genetic variation of Indonesian shallots

are grouped into twelve clusters with 50% genetic similarity. The study indicates that Indonesian shallots are genetically varied and could be useful for further utilization in their genetic improvement program.

(Author)

Keywords: bulb tunic, shallots, clustering, genetic diversity

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UDC: 637.52:575.113-224.2

Jessica G. Manalaysay[a], Nathaniel D. Antonio[b], Ralph Lorenz R. Apilado[b], Joseph F. Bambico[b] and Claro N. Mingalaa[c] ([a]Philippine Carabao Center National Headquarters and Gene Pool, Philippines, [b]College of Science, University of the Philippines, [c]Department of Animal Science, College of Agriculture, Central Luzon State University, Philippines)

Screening of the Acid Meat Condition in the Rendement Napole Gene using Polymerase Chain Reaction - Restriction Fragment Length Polymorphism (Orig. Eng.)

IJAS, June 2019, vol. 20 no. 1, p.29-34, 2 tab., 3 ill., 15 ref.

A mutation in the rendement napole (RN) gene causes the acid meat condition which results to poor meat quality due to its reduced water holding capacity, low pH, pale color, reduced processing and cooking yield due to increased drip, and strong metallic taste. This study was conducted to detect the mutation in the RN gene in 535 commercial breeder pigs from the Philippines. Blood collection was done then subjected to DNA extraction and genotyping using polymerase chain reaction - restriction fragment length polymorphism (PCRRFLP) using the enzyme BsrBI, then validated by DNA sequencing. Results revealed that 97.01% of the breeder pigs did not have the mutation in their RN gene, while 2.69% had at least one copy of the defective allele in their gene. The acid meat condition has only been previously detected in the Hampshire breed whereas this study found the mutations predominantly in Pietrain and Landrace breed they were classified as normal (rn/rn), heterozygous mutants (RN/rn), and homozygous mutants (RN/RN) which allowed breeding systems to be developed ensuring that all offspring are free of the defect. This genetic screening will help in detecting the presence of the defect in a given swine population and reduce the unwanted effects on meat quality thus increasing its market value.

(Author)

Keywords: Acid meat, gene screening, PCR-RFLP, RN gene

UDC: 635.64-142.72

Eny Ida Riyanti[*], Dwi Ningsih Susilowati, Karden Mulya and Edy Listanto ([*]Indonesian Center for Agriculture Biotechnology and Genetic Resources Research and Development)

Growth Improvement of Tomato with the Application of Bacterial Isolates Producing Indole Acetic Acid and Phosphate Solubilizer (Orig. Eng.)

IJAS, June 2019, vol. 20 no. 1, p.25-42, 4 tab., 0 ill., 33 ref.

Soil bacteria have important roles in biogeochemical cycle for soil fertility and have been manipulated for ecologically-friendly crop production. The search for beneficial association between microbes and plants for promoting growth and health should be studied for tomato growth improvement. The study aimed to evaluate 19 microbial isolates which produced indole acetic acid (IAA) affecting growth and development of tomato (Palupi variety), and molecularly identify the most effective isolates in improving tomato growth based on 16s rDNA sequences. The experiment was conducted in pots using a complete randomized design with three replications. The parameters observed included plant height, plant dry weight, root length, root dry weight, and fresh fruit weight. The isolates that significantly improved tomato growth were molecularly identified using 16s rRNA sequence. The phenotypic properties such as IAA content and phosphate solubilizing index (PI) of the superior isolates were determined. Results showed that the application of bacterial isolates on tomato significantly increased plant dry weight and fruit yield. From 19 isolates tested, Aj 3.7.1.14 significantly increased plant dry weight, root length, and fruit yield. This isolate produced IAA of about 14.77 ppm and PI of 1.86. Molecular analysis on Aj 3.7.1.14 demonstrated that the isolate had 89% similarity to Pseudomonas fragi. The identified P. fragi was found to be the most effective isolate for improving tomato growth and fruit yield. Another isolate, Bacillus amyloliquefaciens was found to promote root length, root dry weight, and fruit yield. These isolates are potential to be further investigated for field trials.

(Author)

Keywords: bacterial isolate, indole acetic acids, phosphate solubilizer, tomato plant, 16s rDNA

UDC: 633.189.38-152.7

Nafisah[a*], Celvia Roza[a], Nani Yunani[a], Aris Hairmansis[a], Tita Rostiati[a], and Ali Jamil[b] ([a]Indonesian Center for Rice Research, [b]Directorate General of Food Crops, Ministry of Agriculture, Republic of Indonesia)

Genetic Variabilities of Agronomic Traits and Bacterial Leaf Blight Resistance of High Yielding Rice Varieties (Orig. Eng.)

IJAS, December 2019, vol. 20 no. 2, p.43-54, 5 tab., 2 ill., 67 ref.

Hundred of high yielding and bacterial leaf blight (Xanthomonas oryzae pv. oryzae, Xoo) resistant rice varieties released since the 1960s are important sources of genetic materials for exploring superior genotypes. The study aimed to evaluate the genetic resistance of 177 rice varieties to Xoo and their agronomic traits. The evaluations were conducted at the Indonesian Center for Rice Research Experimental Station during the wet season (December 2015-March 2016). The bacterial leaf blight resistance was evaluated for Xoo pathotypes III, IV, and VIII using the clipping method. The genetic variation among genotypes was categorized as low (0–10%), medium (10–20%), and high (>20%), whereas the heritability was categorized as low (0-30%), medium (3060%), and high (>60%). The variability of resistance to Xoo pathotypes, grain yield, and spikelet fertility was low, while the variability of plant height, productive tiller number, filled grain, and total spikelet was medium, and the variability of unfilled grain number was high. The 29 varieties were categorized as superior based on their agronomic traits or resistance to Xoo pathotypes. In conclusion, Batutegi and Fatmawati were superior in the total spikelet number, while Rojolele and Inpari 2 were supreme in the thousand-grain weight. Dodokan had a very short maturity, and Inpari 24, Conde, Kalimas, Angke, Inpari 17, and Inpara 8 had the highest resistance to Xoo pathotypes. The study implies that the identified rice superior genotypes could be used as genetic materials to design cross combinations for higher yield potential and BLB resistance varietal improvement.

(Author)

Keywords: Inbred rice, plant resistance, Xanthomonas oryzae pv. oryzae

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UDC: 634.773-142.72

Yaşar Akbaş[a], Lütfi Pirlak[a*], and Mesude Figen Dönmez[b] ([a]Department of Horticulture, Faculty of Agriculture, Selçuk University, Konya-Turkey, [b]Department of Plant Protection, Faculty of Agriculture, Iğdır University, Iğdır-Turkey)

Bacillus atrophaeus MFDV2 Rhizobacteria Isolate Increases Vegetative Growth, Yield, and Fruit Size of Banana Plant (Orig. Eng.)

IJAS, December 2019, vol. 20 no. 2, p.55-60, 4 tab., 0 ill., 26 ref.

Plant growth-promoting rhizobacteria have important roles in soil fertility and have been manipulated for ecologically friendly crop production. The study aimed to determine the effects of a biological agent (Bacillus atrophaeus MFDV2) on the growth, yield, and quality of the banana plant. The study was conducted in 2017–2018 using the banana Dwarf Cavendish clone. Bacterial isolate was cultured on nutrient agar and stored at 30 °C for 24 hours. The culture was then suspended in 0.1 M phosphate buffer to 109 CFU ml-1. The bacterial suspension was applied as foliar, soil and foliar + soil once every two months starting from February. One liter of suspension was applied on the soil and over the leaves per plant. The results showed that the effect of bacterial treatment did not increase stem circumference and leaf length, but it was a significant increase in plant height, leaf number, and leaf width. The effects of bacterial application on banana bunch weight and fruit growth were statistically significant. All applications significantly increased the weight, with the highest increase occurring in foliar finger + soil application. While the effects on the finger diameter were statistically similar. Application on leaf + root has been the biggest increase in finger length. The effects of bacterial applications increased N, P, and K contents in the leaves. The study concluded that the application of Bacillus atrophaeus MFDV2 increased the vegetative growth and fruit quality of the banana plant, so it is advisable to be used in organic banana farming.

(Author)

Keywords: Plant growth-promoting rhizobacteria, banana, organic farming

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UDC: 633.18-152.78

Angelita Puji Lestari[a], Suwarno[b], Trikoesoemaningtyas[b], Didy Sopandie[c], and Hajrial Aswidinnoor[c] ([a]Student at Graduate School of Department of Agronomy, Faculty of Agriculture, IPB University, [b]Muara Experimental Farm, Indonesian Center For Rice Research, [c]Department Of Agronomy, Faculty Of Agriculture, IPB University)

The Tolerance and Yield Components of Rice Breeding Lines Selected under Low and Optimum Nitrogen Conditions (Orig. Eng.)

IJAS, December 2019, vol. 20 no. 2, p.61-68, 4 tab., 1 ill., 47 ref.

One of the important issues on rice breeding is to develop new rice lines suitable for nitrogen efficiency in the suboptimum environment. The study aimed to evaluate the tolerance and yield components of rice breeding lines selected under low and high nitrogen conditions. The F6 generation from two cross-combinations of Gampai/IR77674 and Progol/Asahan, were evaluated in the dry season of 2014 under N suboptimum and N optimum conditions. A total of 172 lines plus six check varieties derived from the low and high N environment selection were evaluated under low N rate (34.5 kg N ha^{-1}) and high N rate (138 kg N ha^{-1}), arranged in an augmented design. Six check varieties were relocated three times in each block. Plot size was 5.5 m2 and plant spacing 20 cm x 20 cm. Data were collected for grain yield and major yield components. Results showed that the different status of nitrogen fertilizer affected the number of productive fillers, number of filled grains, 100-grain weight, and grain yield. Different cross combinations exhibited different results in the progeny performance. Ten lines have a higher yield also tolerant to low N condition, i.e. B14250F-6-9, B14250F-1-4, B14250F-9-9, B14250F-6-4, B14250F-5-2, B14262F-15-6, B14250F-2-6, B14262F-12-4, B14250F-5-1, and B14250F-11-4. Thus, to obtain the N tolerant lines, selection at a low N environment was more effective compared with the optimum selection environment.

(Author)

Keywords: Low nitrogen, optimum nitrogen, rice breeding, yield

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UDC: 633.74-152.8

Nur Ajijah[a] and Rr Sri Hartati[b] ([a]Indonesian Industry and Freshener Crops Research Institute, [b]Indonesian Center for Estate Crops Research and Development)

Primary and Secondary Somatic Embryogenesis of Cacao: The Effect of Explant Types and Plant Growth Regulators (Orig. Eng.)

IJAS, December 2019, vol. 20 no. 2, p.69-76, 2 tab., 4 ill., 25 ref.

The success of cacao somatic embryogenesis is affected by many factors, including the basal salt medium, the genotype, the explant type, and the concentration and composition of plant growth regulators (PGRs). The study aimed to evaluate the effects of PGRs composition on the primary somatic embryo (PSE) response and the effect of explant type and PGRs composition used in inducing PSE on the secondary somatic embryogenesis (SSE) response. PSEs were induced from basal petal and staminoid explants of MCC 01 and MCC 02 clones on DKW medium containing 2,4-D 2 mg l^{-1} + kinetin 0.5 mg l^{-1} or 2,4-D 2 mg l^{-1} + kinetin 0.125 – 0.250 mg l^{-1} + thidiazuron (TDZ) 2.5 – 5 µg l^{-1} or 2,4-D 2 mg l^{-1} + TDZ 10 µg l^{-1}. Genotype, explant type, and PGR composition dependently affected PSE response. The best PSE response was obtained from staminoid explant of MCC 02 clone on medium containing 2,4-D 2 mg l^{-1} + kinetin 0.5 mg l^{-1} (20%, 9 embryos). The explant type and PGR composition used in inducing PSEs affect the SSE response. The highest SSE response of MCC 01 clone was obtained from petal explant with medium containing 2,4-D 2 mg l^{-1} + kinetin 0.5 mg l^{-1}. The formation of SSEs could increase the multiplication rate of MCC 01 clone by 7 times.

(Author)

Keywords: explants, PGRs, primary somatic embryogenesis, secondary somatic embryogenesis, *Theobroma cacao* L.